

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# 융복합육종기술과 종자산업의 세계화

Fusion Technologies in Plant Breeding and  
Globalization of Seed Industry

- 일 시 | 2015년 7월 1일(수) ~ 3일(금)
- 장 소 | 부산 벅스코(Bexco) 컨벤션홀



주 최 | 사단법인 한국육종학회

공동주관 | 차세대BG21사업단 (식물분자육종사업단, 농생물게놈활용연구사업단, GM작물개발사업단)  
GSP사업단 (식량종자사업단, 원예종자사업단, 채소종자사업단)

동아대학교 농업생명과학연구소, 부산대학교 식물생명과학과, 충북대학교 농업과학기술연구소

서울대학교 식물유전체육종연구소, 서울대학교 채소육종연구센터, 제주대학교 아열대원예산업연구소

후 원 | 농촌진흥청, 국립식량과학원, 국립산림과학원, 한국농식품생명과학협회, 한국과학기술단체총연합회

# 사단법인 한국육종학회

## The Korean Society of Breeding Science

441-707 경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 학술협력실  
 Tel. 031-296-6898 Fax. 031-292-0804 E-mail. koreabreed@hotmail.com http://www.breeding.or.kr

### 2015년 학술발표회 준비위원회

위원장	조용구 충북대학교	박범석 농생물계농활용사업단	박수철 GM작물개발사업단
	고희중 식물분자유종사업단	노일섭 원예종자사업단	임용표 채소종자사업단
	최임수 식량종자사업단	강시용 한국원자력연구원	박용진 공주대학교
총무위원	박철수 전북대학교	박기훈 국립식량과학원	우선희 충북대학교
기획위원	정영수 동아대학교	임기병 경북대학교	김세현 국립산림과학원
	이금주 충남대학교	김용호 순천향대학교	정남진 전북대학교
	조용섭 농업기술실용화재단	장철성 강원대학교	김윤희 국립식량과학원
	최인수 부산대학교		
	윤무경 국립원예특작원		
편집위원	강병철 서울대학교	강권규 한경대학교	박순기 경북대학교
	이주경 강원대학교	이정동 경북대학교	권순욱 부산대학교
학술위원	조영찬 국립식량과학원	이주현 건국대학교	김성길 전남대학교
	강규석 서울대학교	이상직 농우바이오	소윤섭 충북대학교
	이병무 동국대학교	정종일 경상대학교	서학수 서울대학교
	문중경 국립식량과학원	박영훈 부산대학교	이재현 동아대학교
	김태호 국립농업과학원	김기택 농업기술실용화재단	박응준 국립산림과학원
재무위원	한지학 농우바이오	최규환 그린국제특허	최순호 농우바이오
	서정팔 농협종묘	김은현 동부팜한농	송준호 아시아종묘
	박희영 신젠타코리아	정운화 코레온	윤재복 (주)고추와 육종
	김완규 우리종묘		
설외위원	김보경 국립식량과학원	김용철 부산대학교	양태진 서울대학교
	최근진 국립종자원	이철호 국립식량과학원	김욱 고려대학교
	최홍규 동아대학교	박한용 세종대학교	이석영 농업유전자원센터
	이강섭 국립농업과학원	김동섭 한국원자력연구원	신학기 국립원예특작과학원
	하보근 전남대학교		
지원위원	임상종 국립식량과학원	김용권 신경대학교	김홍식 충북대학교
	안상낙 충남대학교	오대근 한국농수산대학	곽태순 상지대학교
	황영현 경북대학교	김태수 국립산림과학원	

### 2015년 한국육종학회 임원

회장	서용원 고려대학교		
차기회장	조용구 충북대학교		
부회장	김보경 국립식량과학원	정영수 동아대학교	박범석 국립농업과학원
	강시용 한국원자력연구원	임용표 충남대학교	한지학 (주)농우바이오
	김태수 국립산림과학원	김용철 부산대학교	
편집위원장	조용구 충북대학교	강병철 서울대학교	
편집이사	강권규 한경대학교	박순기 경북대학교	이주경 강원대학교
	이정동 경북대학교		
사무총장	박철수 전북대학교		
감사	조영찬 국립식량과학원	김동섭 한국원자력연구원	

본 학회사무와 학회지에 관련되는 모든 문서는 아래로 등기우송바랍니다.  
 학술발표회 관련 논문은 [www.breeding.or.kr](http://www.breeding.or.kr) 에서 논문검색 및 파일다운로드를 할 수 있습니다.  
 본 학회지에 등재된 논문의 판권은 한국육종학회에 있습니다.

총무사항 **박철수** 사무총장  
 441-707 경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 학술협력실  
 TEL. 031-296-6898 FAX. 031-292-0804 E-mail. koreabreed@hotmail.com

편집사항 **박순기** 편집이사  
 702-701 대구 북구 산격3동 경북대학교 농업생명과학대학 응용생명과학부  
 TEL. 053-950-7751 E-mail. breedit@hotmail.com

“이 발표논문집은 2015년도 정부재원(과학기술진흥기금 및 복권기금)으로 한국과학기술단체총연합회의 지원을 받아 발간되었음.”

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# 융복합육종기술과 종자산업의 세계화

Fusion Technologies in Plant Breeding and  
Globalization of Seed Industry

- 일 시 | 2015년 7월 1일(수) ~ 3일(금)
- 장 소 | 부산 벅스코(Bexco) 컨벤션홀

주 최 | 사단법인 한국육종학회

공동주관 | 차세대BG21사업단 (식물분자육종사업단, 농생물게놈활용연구사업단, GM작물개발사업단)  
GSP사업단 (식량종자사업단, 원예종자사업단, 채소종자사업단)

동아대학교 농업생명과학연구소, 부산대학교 식물생명과학과, 충북대학교 농업과학기술연구소

서울대학교 식물유전체육종연구소, 서울대학교 채소육종연구센터, 제주대학교 아열대원예산업연구소

후 원 | 농촌진흥청, 국립식량과학원, 국립산림과학원, 한국농식품생명과학협회, 한국과학기술단체총연합회



# Program

## 2015 한국육종학회- 차세대BG21사업단- GSP사업단 공동심포지엄

2015년 7월 1일(수) ~ 3일(금), 부산 Bexco 컨벤션홀

### 1일째 [2015. 7. 1. 수]

17:00~19:00	한국육종학회 확대이사회 및 조직위원회의
-------------	-----------------------

### 2일째 [2015. 7. 2. 목]

09:00~09:50	공동심포지엄 학술발표회 등록 및 포스터 부착
09:50~10:00	개회식 사회: 박철수 교수 (전북대학교, 육종학회 사무총장)
	개회사 조용구 교수 (충북대학교, 학술발표회 조직위원장)
	환영사 서용원 교수 (고려대학교, 한국육종학회 회장)
〈 1부. Plenary Session 〉	
	좌장 : 고희중 교수 (서울대학교)
10:00~10:40	· Changing Paradigms in Plant Breeding by New Breeding Technologies Dr. Ju-Kyung Yu, Syngenta, USA
10:40~11:20	· 종자산업의 현황과 작물육종 전략 한지학 R&D본부장, (주)농우바이오, Korea
11:20~12:00	· 종자산업의 세계화를 위한 글로벌 마케팅 전략 류경오 사장, (주)아시아종묘, Korea
12:00~13:20	점심시간
	좌장 : 박범석 박사 (국립농업과학원)
13:20~14:00	· Linking Genotypes and Yield Stability Phenotypes in Tomato Prof. Dani Zamir, Hebrew University of Jerusalem, Israel
14:00~14:40	· Understanding Oryza Genomes to maximize Genetic Variations for Crop Improvement 유익수 박사, (주)파이젠, Korea
14:40~15:20	· Small RNAs and the Regulation of Disease-Resistant Genes in Pepper 신찬석 교수, 서울대학교, Korea
15:20~15:40	휴 식

**2일째 [2015. 7. 2. 목]**

**< 2부. 한국육종학회 분과발표 & 포스터 발표 >**

15:40~17:40	<b>한국육종학회 분과발표 OA (수량 및 저항성육종)</b> 좌장 : 박기훈 박사 (국립식량과학원), 김용철 교수 (부산대학교)
	<b>한국육종학회 분과발표 OB (품질육종 및 유전변이)</b> 좌장 : 강병철 교수 (서울대학교), 강규석 교수 (서울대학교)
	<b>한국육종학회 분과발표 OC (분자육종 및 유전공학)</b> 좌장 : 정영수 교수 (동아대학교), 강시용 박사 (원자력연구원)
17:40~18:00	<b>한국육종학회 정기총회</b>
18:00~18:20	<b>포스터 발표</b>
18:20~18:50	특별공연 (국악 공연: 부산가야금연주단, 현악 공연: 부산대학교 예술대학)
18:50~	농우육종학회상 시상식 및 간담회

**3일째 [2015. 7. 3. 금]**

**< 3부. Plenary Session >**

	좌장 : 박수철 박사 (국립농업과학원)
08:30~09:10	· Genome Editing in Plants and Animals 김진수 교수, 서울대학교, Korea
09:10~09:50	· High-throughput Phenotype Analysis of Transgenic Plants for Product Development Dr. Dan Sung, Monsanto, USA
09:50~10:30	· Spectral Imaging Technologies for Assessment of Plant Characterization Dr. Moon-Sung Kim, USDA/ARS Beltsville, USA
10:30~10:40	휴 식

**< 4부. Concurrent Session >**

10:40~12:30	<b>국내 주요작물의 게놈전체연관분석(GWAS) 기술 현황과 전망 (농생명게놈활용연구사업단)</b> 좌장 : 박범석 박사 (국립농업과학원)
	· 벼의 핵심집단 GWAS 연구성과 및 금후발전방향 박용진 교수 (공주대학교)
	· 180k SNP array와 유전분석 집단 개발과 활용을 통한 유전체육종의 가능성 문중경 박사 (국립식량과학원)
	· Genetic Diversity and Construction of Core Collection in Capsicum 권진경 박사 (서울대학교)
	· 참외류 박과작물의 게놈전체연관분석(GWAS)을 위한 다중 염색체 (multiple reference) 해독 권석윤 박사 (한국생명공학연구원)
	· 과수 분야 핵심집단 및 게놈전체연관분석을 통한 유전체 육종 기반구축 김대일 교수 (충북대학교)

3일째 [2015. 7. 3. 금]

〈 4부. Concurrent Session 〉

10:40~12:30	<b>GM작물개발을 위한 신기술 활용 (GM작물개발사업단)</b>
	좌장 : 박수철 박사 (국립농업과학원), 이강섭 박사 (국립농업과학원)
	· 작물표현체 최근 연구 방향 권택륜 박사 (국립농업과학원)
	· 식물표현체를 이용한 작물육종효율 증진 김도순 박사 (서울대학교)
	· 외부 시그널 처리를 통한 작물의 주요 농업형질 개선 정미정 박사 (국립농업과학원)
	· 국립농업과학원 GMO 포장 소개 이강섭 박사 (국립농업과학원)
	<b>NGS 및 유전자 편집기술의 식물육종적 활용 (식물분자육종사업단)</b>
	좌장 : 양태진 교수 (서울대학교)
	· 유전체기반 육종을 위한 생물정보 분석 파이프라인 유익수 박사 (파이젠)
	· DNA-free Genome Editing in Plants 권순일 박사 ((재)차세대융합기술연구원)
	<b>식량종자의 효율적 개발을 위한 품목별 육종전략 (식량종자사업단)</b>
	좌장 : 최임수 박사 (국립식량과학원)
	· 옥수수 해외시장 진출을 위한 육종 방향 이명훈 교수 (동국대학교)
	· 비기주 저항성을 이용한 감자역병 품종육성 최도일 교수 (서울대학교)
<b>채소 및 원예종자사업단의 분자마커 개발현황과 실용화 전략 (원예종자사업단, 채소종자사업단)</b>	
좌장 : 노일섭 교수 (순천대학교), 임용표 교수 (충남대학교)	
· Gene-specific marker development of cabbage for an efficient molecular breeding 허윤강 교수 (충남대학교)	
· Molecular breeding strategies for pyramiding viral resistances in tomatoes and peppers 염인화 교수 (안동대학교)	
· High-density genetic map construction and QTL analysis for seed size of fruits and powdery mildew resistance in watermelon 이금표 교수 (중앙대학교)	
· Genomics approach to develop molecular markers for targeted breeding of radish 이지영 교수 (서울대학교)	
12:30~13:00	시상식 및 폐회

# ∴ Symposium Program

**Fusion Technologies in Plant Breeding and Globalization of Seed Industry**  
**Date and Place (2015. 7. 1~3) & BEXCO, BUSAN**

## July 1 (Wednesday)

17:00~19:00	The Extended Council Meeting and The Organizing Committee Meeting
-------------	---

## July 2 (Thursday)

09:00~09:50	Registration and Poster Mounting
-------------	----------------------------------

Opening Ceremony

Prof. Chulsoo Park, Chonbuk National University, Korea

09:50~10:00	Opening Address
-------------	-----------------

Prof. Yong-Gu Cho, Chair of Organizing Committee, Chungbuk University, Korea

Welcome Address

Prof. Yong-Weon Seo, President of KSBS, Korea University, Korea

### < Plenary Session 1 >

Chair : Prof. Hee-Jong Koh, Seoul National University

10:00~10:40	• Changing Paradigms in Plant Breeding by New Breeding Technologies
-------------	---

Dr. Ju-Kyung Yu, Syngenta, USA

10:40~11:20	• Current Status of Seed Industry and Crop Breeding Strategies
-------------	--

Dr. Chee-Hark Harn, Nongwoo Bio Co., Korea

11:20~12:00	• Global Marketing Strategies for Globalization of Seed Industry
-------------	--

CEO, Kyoung-Ou Ryu, Asia Seed Co. Ltd, Korea

12:00~13:20	Lunch
-------------	-------

Chair: Dr. Beom-Seok Park, National Academy of Agricultural Science

13:20~14:00	• Linking Genotypes and Yield Stability Phenotypes in Tomato
-------------	--

Prof. Dani Zamir, Hebrew University of Jerusalem, Israel

14:00~14:40	• Understanding Oryza Genomes to maximize Genetic Variations for Crop Improvement
-------------	---

Dr. Yeisoo Yu, Phyzen Genomics Institute, Phyzen Inc., Korea

14:40~15:20	• Small RNAs and the Regulation of Disease-Resistant Genes in Pepper
-------------	--

Prof. Chanseok Shin, Seoul National University, Korea

15:20~15:40	Coffee Break
-------------	--------------

**July 2 (Thursday)**

**〈 Oral Presentation & Poster Session 〉**

15:40~17:40	<b>OA. Breeding for yield increase and resistant variety</b> Chair: Ki-Hun Park (NACS), Yong-Chul Kim (BSU)
	<b>OB. Breeding for quality improvement, Genetic variation</b> Chair: Byoung-Cheorl Kang (SNU), Kyu-Seok Kang (SNU)
	<b>OC. Molecular breeding and biotechnology</b> Chair: Young-Soo Chung (DAU), Si-Yong Kang (KAEI)
17:40~18:00	<b>General Meeting</b>
18:00~18:20	<b>Poster Presentation</b>
18:20~18:50	Musical Performance (Korean Folk Music & String Ensemble, Busan University)
18:50~	Nongwoo Breeding Science Awards Ceremony & Dinner

**July 3 (Friday)**

**〈 Plenary Session 2 〉**

	Chair: Dr. Soo-Chul Park, National Academy of Agricultural Science
08:30~09:10	· <b>Genome Editing in Plants and Animals</b> Prof. Jin-Su Kim, Seoul National University, Korea
09:10~09:50	· <b>High-throughput Phenotype Analysis of Transgenic Plants for Product Development</b> Dr. Dan Sung, Monsanto, USA
09:50~10:30	· <b>Spectral Imaging Technologies for Assessment of Plant Characterization</b> Dr. Moon-Sung Kim, USDA/ARS Beltsville, USA
10:30~10:40	Coffee Break

**〈 Concurrent Session 〉**

10:40~12:30	<b>Current Status and Prospects of GWAS in Major Crops in Korea</b> Chair: Dr. Beom-Seok Park (NAAS)
10:40~12:30	<b>New Technologies for GM Crop Development</b> Chair: Dr. Soo-Chul Park, Dr. Kang-Seob Lee (NAAS)
10:40~12:30	<b>NGS and Gene Editing for Plant Breeding</b> Chair: Prof. Tae-Jin Yang (SNU)
10:40~12:30	<b>Breeding Strategies of Crop Species for Efficient Variety Development</b> Chair: Dr. Im-Soo Choi (NICS)
10:40~12:30	<b>Current Status of Molecular Marker Development and Strategies for Practical Use</b> Chair: Prof. Ill-Sup Nou (SCNU), Prof. Yong-Pyo Lim (CNU)
12:30~13:00	Awards Ceremony & Closing Remark

# Contents

## 연사 발표

SYMP-01	Changing paradigms in plant breeding by new plant breeding technologies ..... 3 <i>Ju-Kyung Yu</i>
SYMP-02	Current Status of Seed Industry and Crop Breeding Strategies ..... 4 <i>Chee-Hark Harn</i>
SYMP-03	Global Marketing Strategies for Globalization of Seed Industry ..... 5 <i>Kyoung-Ou Ryu</i>
SYMP-04	Geno-Pheno in plant breeding ..... 6 <i>Dani Zamir</i>
SYMP-05	Understanding <i>Oryza</i> Genomes to maximize Genetic Variations for Crop Improvement ..... 7 <i>Yeisoo Yu</i>
SYMP-06	Small RNA studies reveal a role for miRNAs and their targets in the regulation of NB-LRR disease resistance genes in pepper ..... 8 <i>June Hyun Park, Igojo Kang, Chanseok Shin</i>
SYMP-07	RNA-guided Genome Editing in Animals and Plants ..... 9 <i>Jin-Soo Kim</i>
SYMP-08	High-throughput phenotype analysis of transgenic plants for product development ..... 10 <i>Dan Sung</i>
SYMP-09	Spectral Imaging Technologies for Assessment of Plant Characteristics ..... 11 <i>Moon S. Kim</i>

## 구두 발표

### 수량 및 저항성육종 (Breeding for yield increase and resistant variety)

OA-01	QTL mapping of Fusarium wilt resistance in radish ( <i>Raphanus sativus</i> L.) ..... 15 <i>Xiaona Yu, Su Ryun Choi, Yong Pyo Lim</i>
OA-02	Existence of qualitative resistance against blackleg disease in <i>Brassica oleracea</i> L. and detection of gene-specific single nucleotide polymorphism ..... 16 <i>Arif Hasan Khan Robin, Jong-In Park, Nasar Uddin Ahmed, Rawnak Laila, Ill-Sup Nou</i>

OA-03	<b>Expression profiling of two contrasting bulb onion lines (<i>Allium cepa</i> L.) under Photoperiod and Drought Conditions</b> .....	17
	<i>Ranjith Kumar Manoharan, Jeong Suk Hyeon Han, Senthil Kumar Thamilarasan, Jong-In Park, Ill-Sup Nou</i>	
OA-04	<b>TIFY family genes in Chinese cabbage (<i>Brassica rapa</i> ssp. <i>pekinensis</i>): A Genome-wide analysis reveals their stress and hormone responsive patterns</b> .....	18
	<i>Gopal Saha, Jong-In Park, Nasar Uddin Ahmed, Md. Abdul Kayum, Ill-Sup Nou</i>	
OA-05	<b><i>De novo</i> assembly and transcriptome analysis of bulb onion (<i>Allium cepa</i>) during cold acclimation using contrasting genotypes</b> .....	19
	<i>Senthil Kumar Thamilarasan, Jeong Suk Hyeon Han, Jong-In Park, Ill-sup Nou</i>	
OA-06	<b>Characterization of regulatory genes for anthocyanin biosynthesis pathway and cold/freezing tolerance in <i>Brassica rapa</i></b> .....	20
	<i>Nasar Uddin Ahmed, Jong-In Park, Ill-Sup Nou</i>	

---

**품질 육종 및 유전변이(Breeding for quality improvement, Genetic variation)**

---

OB-01	<b>Fine mapping the UV-B resistance gene in soybean using 180K Axiom SoyaSNP assay</b> ·	21
	<i>Sungmin Kim, Ju Seok Lee, Sumin Park, Kyungryun Kim, Mijung Cho, Eunsil Kim, Bo-Keun Ha, Sungtaeg Kang</i>	
OB-02	<b>Nucleotide polymorphisms in genes controlling panicle development are associated with the number of spikelets per panicle in rice</b> .....	22
	<i>Su Jang, Gileung Lee, Chang Soo Yoo, Hee-Jong Koh</i>	
OB-03	<b>Genetic mapping of quantitative trait loci controlling seed weight in an interspecific soybean recombinant inbred line population</b> .....	23
	<i>Krishnanand P Kulkarni, Minsu Kim, Jeong Hwa Kim, Sovetgul Asekova, Jong Tae Song, Jeong-Dong Lee</i>	
OB-04	<b>Rice PCR1 affects grain weight and zinc accumulation</b> .....	24
	<i>Hyun-Sook Lee, Won-Yong Song, Sang-Nag Ahn</i>	
OB-05	<b>저온 및 식물생장조정제 처리가 더덕속 종자의 발아에 미치는 영향</b> .....	25
	<i>이상권, 류수노, 최은영</i>	
OB-06	<b>등숙기 적산온도가 기능성 쌀품종 ‘슈퍼자미’의 수량과 C3G 함량에 미치는 영향</b> .....	26
	<i>유정, 함태호, 김혜자, 박미영, 권순욱, 류수노</i>	
OB-07	<b>Identification and characterization of differentially expressed genes in response to ionizing radiations in rice</b> .....	27
	<i>Hong-Il Choi, Soon-Jae Kwon, Jung Eun Hwang, Injung Jung, Sung Min Han, Sun-Goo Hwang, Cheol Seong Jang, Si-Yong Kang, Dong Sub Kim</i>	

**분자유종 및 유전공학(Molecular breeding and biotechnology)**

OC-01	<p><b>Construction of high resolution genetic map and QTL mapping for clubroot resistance using genotyping-by-sequencing analysis in cabbage</b> ..... 28</p> <p><i>Jonghoon Lee, Nur Kholilatul Izzah, Beom-Soon Choi, Ho Jun Joh, Sang-Choon Lee, Sampath Perumal, Joodeok Seo, Kyounggu Ahn, Eun Ju Jo, Gyung Ja Choi, Ill-Sup Nou, Yeisoo Yu, Tae-Jin Yang</i></p>
OC-02	<p><b>Fine mapping the soybean foxglove aphid resistance gene <i>Raso2</i> in soybean using 180K Axiom® SoyaSNP genotyping assay</b> ..... 29</p> <p><i>Ju Seok Lee, Sungmin Kim, Sumin Park, Kyungryun Kim, Mijung Cho, Eunsil Kim, Jin Kyo Jung, Jeong-Dong Lee, Jung-Kyung Moon, Namshin Kim, Soon-chun Jeong, Sungtaeg Kang</i></p>
OC-03	<p><b>Characterization and genetic mapping of a abaxially rolled leaf mutant in rice.</b> ..... 30</p> <p><i>Hyerim Lee, Yoye Yu, Hee-Jong Koh</i></p>
OC-04	<p><b>Sound waves delay tomato fruit ripening by negatively regulating ethylene biosynthesis and signaling genes</b> ..... 31</p> <p><i>Mi-Jeong Jeong, Joo-Yeol Kim, Jin Su Lee, Soo In Lee, Jin-A Kim</i></p>
OC-05	<p><b>형질전환 events에서 elite event를 신속히 선발하는 방법 및 선발 event의 분석</b> ..... 32</p> <p><i>정순천, 백인순, 김보민, 김지홍, 김유진, 옥은수, 김창기, 한지학</i></p>
OC-06	<p><b>Expression analysis of two rice pollen-specific promoters using homologous and heterologous systems</b> ..... 33</p> <p><i>Tien Dung Nguyen, Moe Moe Oo, Sunok Moon, Hyun-Kyung Bae, Sung Aeong Oh, Moon-Soo Soh, Jong Tae Song, Jeong Hoe Kim, Ki Hong Jung, Soon Ki Park</i></p>
OC-07	<p><b>Genome wide resequencing for KRICE_CORE reveals their potentials for the future breeding, functional and evolutionary studies in the post-genomic era</b> ..... 34</p> <p><i>Tae-Sung Kim, Kyu-Won Kim, Qiang He, Min-Young Yoon, Won-Hee Ra, Feng Peng Li, Wei Tong, Jie Yu, Win Htet Oo, Buung Choi, Eun-Beom Heo, Yoo-Hyun Cho, Byoung-Kook Yun, Chang-Yong Lee, Donghwan Shim, Beom-Seok Park, Yong-Jin Park</i></p>

**포스터 발표**

**수량 및 저항성육종 (Breeding for yield increase and resistant variety)**

PA-01	<p><b>양질 다수성 장류용 콩 “대찬”</b> ..... 37</p> <p><i>강범규, 김현태, 이영훈, 이병원, 최만수, 한원영, 김현영, 전명기, 이석기, 고종민, 윤홍태, 백인열, 이영희</i></p>
PA-02	<p><b>소립 다수성 나물용 콩 “해원”</b> ..... 38</p> <p><i>강범규, 김현태, 이영훈, 조상균, 이병원, 최만수, 전명기, 심하식, 하태정, 고종민, 윤홍태, 백인열, 이영희</i></p>

PA-03	<b>QTL analysis for drought tolerance using introgression lines from a cross between Milyang 23 and <i>O. glaberrima</i></b> ..... 39 <i>Ju-Won Kang, Dong-Min Kim, Hyun-Sook Lee, Yeo-Tae Yoon, Sang-Nag Ahn</i>
PA-04	<b>국산밀 품종의 파성 및 숙기관련 특성 분석</b> ..... 40 <i>강천식, 고윤희, 손재한, 김경훈, 박종철, 오영진, 김양길, 김경호, 정영근, 김보경</i>
PA-05	<b>Comparison of seed priming methods for germination in sorghum (<i>Sorghum bicolor</i> (L.) Moench)</b> ..... 40 <i>Du Hyun Kim, Hyeonjun Hong, Ki-Yeul Jung</i>
PA-06	<b>A New Wheat Variety, “Jojoong” with Pre-harvest Sprouting Resistance, Early Maturity, High Yield and Good Noodle Quality</b> ..... 41 <i>Chon-Sik Kang, Kyeong-Hoon Kim, Young-Keun Cheong, Jae-Han Son, Jong-Chul Park, Kyong-Ho Kim, Kwang-Geun Park, Ouk-Kyu Han, Gi-Heung Hong, Jin-Kyeong Choi, Seong-Tae Lee, Jeong-Suk Bae, Bo-Kyeong Kim, Chulsoo Park</i>
PA-07	<b>조숙, 내병성 및 논재배 적응성이 강한 유채 1대잡종 ‘조안’</b> ..... 42 <i>김광수, 이영화, 장영석, 최규환, 강달순, 김성택, 이경보</i>
PA-08	<b>Comparison of seed priming methods for germination in sorghum (<i>Sorghum bicolor</i> (L.) Moench)</b> ..... 43 <i>Du Hyun Kim, Hyeonjun Hong, Ki-Yeul Jung</i>
PA-09	<b>Effects of priming treatments on germination of <i>Setaria viridis</i> L. seeds</b> ..... 43 <i>Du Hyun Kim, Hyeonjun Hong, Ki-Yeul Jung</i>
PA-10	<b>중국 운남성 고지대에서의 우리 벼 품종의 작물학적 특성</b> ..... 44 <i>김명기<sup>1</sup>* 양창인, 이상복, 현웅조, 백남현, 이점호</i>
PA-11	<b>벼 조생종 수발아, 잎도열병 및 흰잎마름병 저항성 중간모본 ‘중모1031’</b> ..... 44 <i>김명기, 서정필, 원용재, 안억근, 정국현, 백만기, 최임수, 조영찬, 윤광섭, 김연규, 홍하철, 윤영환, 이정희</i>
PA-12	<b>Distinct reactions of two Tunisian durum wheat to salinity stress</b> ..... 45 <i>Sang Heon Kim, Inès Yacoubi, Yong Weon Seo</i>
PA-13	<b>벼흰잎마름병 발병상습지에서 벼 품종 ‘해품’의 저항성 발현</b> ..... 45 <i>김우재, 박종호, 김현순, 박현수, 하기용, 고재권, 김보경</i>
PA-14	<b>벼멸구 저항성 유전자 다양화를 위한 DNA 마커 탐색</b> ..... 46 <i>김우재, 김현순, 하기용, 강경호, 정지웅, 전재범, 조성우, 김보경</i>
PA-15	<b>우리나라에서 벼 꽃가루배양의 실용화와 금후전망</b> ..... 46 <i>김현순, 강경호, 남정권, 김우재, 정지웅, 백소현, 신운철, 강현중, 고재권, 김기영, 김보경, 이승엽</i>
PA-16	<b>내도복 증만생 벼 담수직파 검용 “중모1041”</b> ..... 47 <i>김정주, 백만기, 남정권, 김보경, 하기용, 김기영, 고종철, 고재권, 김우재, 백소현, 신운철, 박현수, 조영찬, 이점호, 김현순, 임청택, 박기훈</i>

PA-17	대립 내탈립 무비린내 콩 “미소” ..... 48 김현태, 고종민, 한원영, 강범규, 이영훈, 이병원, 최만수, 김현영, 전명기, 문중경, 윤홍태, 백인열, 이영희
PA-18	도복과 탈립에 강한 다수성 콩 “대풍2호” ..... 49 김현태, 이영훈, 이병원, 최만수, 강범규, 한원영, 김현영, 전명기, 이석기, 고종민, 윤홍태, 백인열, 이영희
PA-19	다변량 분석에 의한 콩 품종 분류 ..... 49 이가영, 광병삼, 광상철, 김용현, 장은규, 김홍식
PA-20	미나리 실생묘를 이용한 수경재배와 관행재배의 생산성 및 품질 비교 ..... 50 김효중, 이유석, 김희곤, 손동모, 나혜영
PA-21	품질이 우수한 내병·다수성 조생찰벼 ‘운일찰’ ..... 50 남정권, 신운철, 김기영, 박현수, 백만기, 김정주, 조영찬, 하기용, 김우재, 김보경
PA-22	열대형 옥수수 반수체 유기체(Inducer)인 Tails의 국내적응성 평가 ..... 51 류시환, 최재근, 박종열, 서영호, 박기진, 용우식, 노상득, 이장용, 김정희
PA-23	반수체 밀 집단을 이용한 국수 면대 색깔 QTL 분석 ..... 51 강혜정, 강천식, 김학신, 박철수
PA-24	벼 중만생 고품질 내병 내도복 다수성 벼 ‘신보’ 육성 ..... 52 박노봉, 여운상, 이지윤, 권오덕, 박동수, 이종희, 조준현, 송유천, 김상열, 오성환, 손영보, 장재기, 남민희, 권영업, 이영희
PA-25	Influence of haplotype combinations of genes involved in regulation of rice grain size and development of a regression equation model ..... 53 Jonghwa Park, Chan-mi Lee, Backki Kim, Hee-Jong Koh
PA-26	국내 밀 계통 및 재래종의 <i>Rht-1</i> , <i>Vrn-1</i> , <i>Ppd-1</i> 의 유전적 조성이 주요 농업 형질에 미치는 영향 ..... 54 조은진, 강천식, 정지웅, 윤영미, 박철수
PA-27	국내 밀 품종들의 <i>Vrn-1</i> 과 <i>Ppd-1</i> 대립유전자 변이와 농업형질과의 관계 ..... 54 조은진, 강천식, 윤영미, 박철수
PA-28	반해성 유전자 <i>Rht</i> 가 국내 밀 품종의 농업형질에 미치는 영향 ..... 55 조은진, 강천식, 윤영미, 박철수
PA-29	평야지 적응성 향상을 위한 벼흰잎마름병 및 줄무늬잎마름병 저항성 유전자 집적 조생 계통 개발 ..... 55 박현수, 남정권, 김기영, 김우재, 정지웅, 백만기, 김정주, 조영찬, 이점호, 김보경
PA-30	벼흰잎마름병 저항성 고품질 중만생 벼 신품종 ‘만백’ ..... 56 박현수, 백만기, 김보경, 김기영, 하기용, 신운철, 고재권, 남정권, 김우재, 조영찬, 이점호, 김현순, 고종철, 김정주, 박종호
PA-31	벼 중만생 고품질 복합내병성 ‘안백’ ..... 56 백만기, 박현수, 정종민, 김기영, 남정권, 김정주, 조영찬, 김보경
PA-32	소득후작 적응 복합내병성 준조생 벼 “중모1039호” ..... 57 신운철, 김우재, 박현수, 남정권, 이점호, 김보경, 강위금

PA-33	<b>Tomato germplasm with resistance to multiple species of <i>Xanthomonas</i> causing bacterial spot</b> ..... 57 <i>Sung-Chur Sim, David M. Francis</i>
PA-34	<b>총체사료용 벼 신품종 ‘녹우’</b> ..... 58 <i>안역근, 정응기, 이상복, 최용환, 양창인, 원용재, 전용희, 이규성, 홍하철, 정오영, 최임수, 모영준, 김정주, 조영찬, 장재기, 하운구, 김명기, 서정필, 이정희, 정국현, 정종민, 정지웅, 박향미, 이점호</i>
PA-35	<b>중산간지 지역에 따른 미세온도변화와 벼 생육양상의 차이</b> ..... 58 <i>양창인, 김명기, 백남현, 강위금, 신운철, 김미향, 조현숙</i>
PA-36	<b>A New Forage Barley Cultivar with Semi-Smooth Awn and High Yielding ‘Miho’</b> ..... 59 <i>Young-Jin Oh, Tae-Il Park, Hyoung-Ho Park, Ouk-Kyu Han, Jong-Chul Park, Tae-Hwa Song, Yang-Kil Kim, Hyeon-Jung Kang, Jae-Seong Choi, Yun-Woo Jang, Kwang-Geun Park, Jong-Ho Park, Chon-Sik Kang, Young-Keun Cheong, Kyong-Ho Kim, Bo-Kyeong Kim, Geon-Sig Yun, Gi-Heung Hong, Jeong-Suk Bae, Seong-Tae Lee</i>
PA-37	<b>열대아시아지역 적응성 벼 신품종 ‘아세미1호’ 개발</b> ..... 60 <i>원용재, 하운구, 정응기, 강경호, 최임수, 홍하철, 조영찬, 정오영, 장재기, 양운호, 정국현, 이규성, 여운상, 양창인, 김명기, 서대하, 성낙식, 윤광섭, 성열규, 이점호, 김보경</i>
PA-38	<b>An RNA-Seq transcriptome analysis of rice genes in response to water deficiency in soil</b> ..... 60 <i>Yo-Han Yoo, Anil Kumar N.C, Ki-Hong Jung</i>
PA-39	<b>Identification of QTL for grain quality traits using introgression lines derived from an interspecific cross in rice</b> ..... 61 <i>Yeo-Tae Yun, Chong-Tae Chung, Yeong-Ju Lee, Han-Jung Na, Jae-Chul Lee, Kwang-Won Lee, Young-Hwan Yoon, Ju-Won Kang, Hyun-Sook Lee, Sang-Nag Ahn</i>
PA-40	<b>The development of physiological phenotyping parameter to characterize early stress responses in rice plants</b> ..... 61 <i>Hye-Jin Yoon, Kyung Hwan Kim, Yeon-Hee Lee, Eun-Jung Suh, Taek-Ryun Kwon</i>
PA-41	<b>분지 각도가 좁은 신초형 종실용 들깨 신품종 ‘소담’</b> ..... 62 <i>이명희, 배석복, 김성엽, 오은영, 김명식, 오기원, 정찬식, 오인석</i>
PA-42	<b>Development of female (F) locus specific co-dominant molecular marker in cucumber (<i>Cucumis sativus</i> L.)</b> ..... 62 <i>Khin Thanda Win, Chunying Zhang, Kihwan Song, Sanghyeob Lee</i>
PA-43	<b>펠릿 재료가 카멜리나 종자의 발아에 미치는 영향</b> ..... 63 <i>박민우, 최충원, 이상협</i>
PA-44	<b>중부지역 적응 중생 복합내병성 고품질 벼 품종 ‘선품’ 개발</b> ..... 63 <i>이정희, 정응기, 원용재, 양창인, 조영찬, 김명기, 서정필, 최임수, 이상복, 정오영, 안역근, 오세관, 정종민, 홍하철, 현웅조, 모영준, 양운호, 이점식, 이점호, 김보경</i>
PA-45	<b>QTL Mapping for shoot fresh weight in a RIL population developed from a cross of wild and cultivated soybean</b> ..... 64 <i>Sovetgul Asekova, Krishnanand P Kulkarni, JeongHwa Kim, Minsu Kim, Jiho Park, Hyun-Jee Kim, J. Grover Shannon, Jeong-Dong Lee</i>

PA-46	옥수수 유망 자식계통들에 대한 잡종강세 및 수량관련 형질의 유전분석 ..... 64 <i>박종열, 박기진, 사구진, 이주경</i>
PA-47	Detection of novel QTLs for foxglove aphid resistance in soybean ..... 65 <i>Sumin Park, Ju Seok Lee, Sungmin Kim, Kyungryun Kim, Mijung Cho, Eunsil Kim, Jin Kyo Jung, Jeong-Dong Lee, Sungtaeg Kang</i>
PA-48	Identification of quantitative trait loci related to grain filling under low temperature condition ..... 65 <i>Jong-Min Jeong, Ung-Jo Hyun, Ji-Ung Jeung, Kyung-Ho Kang, Young-Chan Cho, Bo-Kyeong Kim</i>
PA-49	경기지역 콩 다수확 선도단지 조성을 위한 품종선발 및 작부체계 연구 ..... 66 <i>장은규, 이진구, 한정아, 송정순, 김진영, 강창성, 윤홍태</i>
PA-50	강원지역에서 파종량이 호밀 “곡우”의 생육특성에 미치는 영향 ..... 66 <i>조영일, 이동우, 김영호, 안경구, 박덕심, 김인혜, 조용섭, 한옥규, 이종경</i>
PA-51	Development of QTL-NIL to Blast Resistance Originated from Korean Weedy Rice ..... 67 <i>Young-Chan Cho, Man-Ki Baek, Jung-Pil Suh, Yong-Jae Won, Jong-Min Jeong, Hyun-Su Park, Jeong-Ju Kim, Jeong-Kwon Nam, Ki-Young Kim</i>
PA-52	Overexpression of CIPK 15 improved tolerance to pre-harvest sprouting in rice ..... 68 <i>Dal-A Yu, Hye-Jung Lee, Joonki Kim, Me-Sun Kim, Marjohn Nino, Sothea Ouk, Seong-Dong Kim, Ill-sup Nou, Yong-Gu Cho</i>
PA-53	중만생 내병 다수성 찰벼 품종 ‘중모1044호’ ..... 68 <i>하기용, 박현수, 남정권, 백만기, 김기영, 김우재, 김현순, 김보경, 김정주, 조영찬, 고재권</i>
PA-54	개화기가 빠르고, 내병성 다수성인 구기자 신품종 「청홍」 ..... 69 <i>주정일, 박영춘, 윤덕상, 이보희, 최택용, 김현호</i>
PA-55	Screening for Resistance of Tomato Genetic Resources to Bacterial wilt caused by <i>Ralstonia solanacearum</i> ..... 69 <i>On-Sook Hur, Sang Gyu Kim, Ho-Cheol Ko, Su Ran Ahn, Jung-Sook Sung, Na-Young Ro, Sukyeung Lee, Yu-mi Choi, Do yoon Hyun, Kyoung-Yul Ryu, Hyung-Jin Baek</i>
PA-56	Overexpression of <i>Brassica rapa</i> cysteine protease improves rice resistance to bacterial blight ..... 70 <i>Marjohn Nino, Sailila E. Abdula, Hye-Jung Lee, Dal-A Yu, Seon-Kyeong Song, Eun-Ju Jeong, Kwon-Kyoo Kang, Ill-sup Nou, Yong-Gu Cho</i>
PA-57	온도구배하우스를 이용한 기후변화 대응 밀 생육반응 비교 ..... 71 <i>하건수, 조수현, 임수정, 변학수, 오혜진, 신은영, 임혜리</i>
PA-58	중북부 고랭지 적응 내냉성 조생 벼 진부61호 ..... 71 <i>현용조, 정종민, 강경호, 정지용, 이상복, 이정희, 성열규, 이점호</i>
PA-59	고구마뿌리혹선충 저항성 식용 고구마 신품종 ‘풍원미’ ..... 72 <i>이형운, 이준설, 정미남, 한선경, 김재명, 안승현, 양정욱, 남상식, 송연상, 최규환, 문진영, 최인후, 황엄지, 이경보</i>

PA-60	Association of haplotype variations in <i>GmCHX1</i> with salt tolerance in wild and cultivated soybeans, ..... 73 <i>Jeong Hwa Kim, Jong-Tae Song, Jeong-Dong Lee</i>
-------	---

---

**품질 육종 및 유전변이(Breeding for quality improvement, Genetic variation)**

---

PB-01	야생벼 이용 총체사료 적성 계통육성 ..... 74 <i>강경호, 안억근, 정지웅, 김석만, 정종민, 전재범, 현웅조</i>
PB-02	감마선 처리에 의한 정원장미 돌연변이 유기 ..... 75 <i>고갑천, 한태호, 기광연</i>
PB-03	호밀 왜성 유전자가 외관 형태에 미치는 효과 ..... 76 <i>구자환, 황종진, 한옥규, 김대욱, 권순중, 박광근, 이점호</i>
PB-04	면 가공용 시종밀가루의 품질 분석 ..... 76 <i>김경훈, 김경민, 박형호, 현종내, 권영업</i>
PB-05	감마선 조사에 의한 포인세티아 품종 육성 ..... 77 <i>O Hyeon Kwon, Bong Sik Yoo, Su Young Lee, Hye Jin Lee</i>
PB-06	Genome-wide structural variation by different types of ionizing irradiation sources ..... 78 <i>Soon-Jae Kwon, Hong-II Choi, Jung Eun Hwang, Injung Jung, Sung Min Han, Jin-Baek Kim, Joon-Woo Ahn, Sang Hoon Kim, Yeong Deuk Jo, Si-Yong Kang, Dong-Sub Kim</i>
PB-07	하얀꽃이 피는 경관용 유채 ‘중모7003’ ..... 79 <i>김광수, 이영화, 장영석, 최규환, 강달순, 김성택, 이경보</i>
PB-08	Genetic Diversity of Rice Landraces Collected in Cordillera Region, Philippines ..... 80 <i>Backki Kim, Sheryl N. Sierra, Hong-Yeol Kim, Hee-Jong Koh</i>
PB-09	Differentially expressed proteins between two Korean inbred lines under drought stress at vegetative stage ..... 81 <i>Sang Gon Kim, Seonghyu Shin, Hwan Hee Bae, Jin-Seok Lee, Jung-Tae Kim, Min Jung Seo, Beom-Young Son, Jeom Ho Lee, Seong-Bum Baek</i>
PB-10	주성분 분석 및 군집 분석을 이용한 자생국화의 휘발성 향기성분 분류 ..... 81 <i>김수정, 하태정, 김중윤, 유동림, 서종택, 김윤희, 홍수영, 남정환, 손황배, 장동철, 김기선</i>
PB-11	흑색 활성 고품질 다수성 겉보리 신품종 ‘흑수정찰’ ..... 82 <i>김양길, 이미자, 박종철, 강천식, 김경호, 김상민, 최인배, 한옥규, 윤건식, 배정숙, 조수현, 최재성, 박광근, 오영진, 정영근, 박기훈</i>
PB-12	Selection of mutant related to salt and drought tolerance in rice with expression microarray ..... 82 <i>Joung Sug Kim, Kyong-Mi Jun, Hyejin Yoon, Songhwa Chae, Yoon Mok Pahk, Yeon-Ki Kim, Baek-hie Nahm</i>

PB-13	<b>Development of the <i>Tos17</i>-insertional mutants and functional analysis of transcription factors involved in seed development</b> ..... 83 <i>Joung Sug Kim, Songhwa Chae, Kyong-Mi Jun, Yoon Mok Pahk, Yeon-Ki Kim, Baek-hie Nahm</i>
PB-14	<b>Phenotypic screening and breeding with colored wheat by mutation breeding technique</b> ... 83 <i>Jin-Baek Kim, Min Jeong Hong, Young Ha Yoon, Dong Sub Kim, Soon-Jae Kwon, Hong Il Choi, Si-Yong Kang, Yong Weon Seo</i>
PB-15	<b>전정에 의한 다래 과실의 등급별 생산특성</b> ..... 84 <i>김철우, 박영기, 김만조, 김세현, 김재희</i>
PB-16	<b>콩 유전자원의 isoflavone 함량변이</b> ..... 84 <i>김현명, 이지석, 이재원, 김보경, 황세구, 김홍식</i>
PB-17	<b>Chemical Components in the Leaves of Selected Mutant Cultivars of kenaf (<i>Hibiscus cannabinus</i> L.)</b> ..... 85 <i>Jaihyunk Ryu, Sang-Wook Jeong, Seung Bin Im, Joon-Woo Ahn, Soon-Jae Kwon, Dong Sub Kim, Jin-Baek Kim, Sang Hoon Kim, Si-Yong Kang</i>
PB-18	<b>Negative roles of MAPK signaling cascades for itrogen-fixing nodule formation in <i>Medicago truncatula</i></b> ..... 85 <i>Wonsil Bae, Jinsoo Lee, Hojin Ryu</i>
PB-19	<b>표피가 매끈하고 육질이 단단하며 근장이 짧은 무 ‘원교10045호’ 육성</b> ..... 86 <i>박수형, 윤무경, 박민영, 장하영, 채원병, 서명훈</i>
PB-20	<b>Breeding of new walnut cultivar, “Golden-ball”</b> ..... 86 <i>Youngki Park, Chul-Woo Kim, Sea-Hyun Kim, Mahn-Jo Kim, Jae-Hee Kim</i>
PB-21	<b>Identification of genus <i>Vigna</i> using ITS2 and <i>matK</i> as a two-locus DNA barcode</b> ..... 87 <i>Jae-Wan Park, Sebastin Raveendar, Jung-Ro Lee, Gi-An Lee, Young-Ah Jeon, Eun Seong Park, Yang-Hee Cho, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung</i>
PB-22	<b>A New Peanut Variety “Daan” with High Yield and Disease Resistance</b> ..... 87 <i>Suk-Bok Pae, Myung-Hee Lee, Sung-Up Kim, Chung-Dong Hwang, Ki-Won Oh, Chan-Sik Jung, Deuk-Young Song, In-Youl Baek, Young-Hee Lee</i>
PB-23	<b>A New Dark Purple Peanut Variety “Heuksaeng”</b> ..... 88 <i>Suk-Bok Pae, Chan-Sik Jung, Ki-Won Oh, Sung-Up Kim, Myung-Hee Lee, Chung-Dong Hwang, Deuk-Young Song, In-Youl Baek, Young-Hee Lee</i>
PB-24	<b>무 모식물체의 광 환경 조절을 통한 소포자 유래 배 발생효율 증진</b> ..... 88 <i>배은지, 나해영</i>
PB-25	<b>미나리 종자의 저온 증적처리 및 세척방법</b> ..... 89 <i>배은지, 황순임, 나해영</i>
PB-26	<b>Glycoalkaloids content in tuber peel and cortex of 24 potato cultivars of Korea</b> ..... 89 <i>Hwang-Bae Sohn, Su-Jeong Kim, Yu-Young Lee, Hyang-Mi Park, Manjulatha Mekapogu, Su-Young Hong, Jeong-Hwan Nam, Jin-Cheol Jeong, Kibum Kweon, Yul-Ho Kim</i>

PB-27	<b>단간 내도복 중생 메조 ‘단아메’ 육성</b> ..... 90 <i>고지연, 이재생, 송석보, 최명은, 우관식, 고종철, 김기영, 정태욱, 오인석</i>
PB-28	<b>흰앙금 제조특성이 우수한 팔 신품종 ‘흰나래’ 육성</b> ..... 90 <i>송석보, 이재생, 고지연, 우관식, 최명은, 정태욱, 문중경, 고종철, 오인석, 최유미</i>
PB-29	<b>안면도 소나무 채종원 종자생산 진단을 위한 구과분석</b> ..... 91 <i>송현진, 배태웅, 문병호, 이성기, 이병실</i>
PB-30	<b>홍화 집단교배 및 유전자지도 작성을 위한 수집자원의 선발</b> ..... 92 <i>이정훈, 안찬훈, 이윤지, 허목, 안태진, 김영국, 차선우</i>
PB-31	<b>A Genetic Linkage Map based on AFLP markers in China type Tea Plant</b> ..... 92 <i>Yali Chang, Eun-Ui Oh, Min-Seuk Lee, Kwan-Jeong Song</i>
PB-32	<b>Radiation impacts on morphological and qualitative properties in common buckwheat (<i>Fagopyrum esculentum</i>) and tatar buckwheat (<i>Fagopyrum tataricum</i>) seeds</b> ..... 93 <i>Je-Hyeok Yu, Min-Heon Yun, Seon-Mo Yang, Dong-Seop Kim, Young-Ho Yun, Kyung-Ho Ma, Eun-Ho Son, Sok-Young Lee, Hong-Sig Kim, Sun-Hee Woo</i>
PB-33	<b>Heterogeneity of CMA Banding Patterns in Jeju Citrus Landraces</b> ..... 94 <i>Kyunguk Yi, Chi-Won Chae, Young-Chul Park, Ho-Bang Kim, Kwan-Jeong Song</i>
PB-34	<b>Antioxidant activity and total phenolic and flavonoid contents of 10 <i>Vicia</i> species</b> ..... 94 <i>Kyung Jun Lee, Gi-An Lee, Young-Ah Jeon, Jung-Ro Lee, Sok-Young Lee, Kyung-Ho Ma, Jong-Wook Chung</i>
PB-35	<b>Genetic diversity base on agrinomical traits and SSR markers in Korean rice landraces</b> ..... 95 <i>Kyung Jun Lee, Jong-Ro Lee, Gi-An Lee, Sebastin Raveendar, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung</i>
PB-36	<b>Variation of pre-harvest sprouting and ABA content in rice germplasm</b> ..... 95 <i>Gi-An Lee, Young-Ah Jeon, Ho-Sun Lee, Jong-Wook Chung, Do-Yoon Hyun, Jung-Ro Lee, Myung-Chul Lee, Kyung-Ho Ma, Sok-Young Lee</i>
PB-37	<b><i>Brachypodium distachyon</i> mutants induced by gamma radiation contain reduced lignin content</b> ..... 96 <i>Man Bo Lee, Yong Weon Seo</i>
PB-38	<b>Development and characterization of endophyte free tall fescue variety Greenmaster3ho</b> ..... 97 <i>Sang-Hoon Lee, Ki-Won Lee, Ki-Yong Kim, Hee Jung Ji, Tae Young Hwang, Hyung Soo Park, Hyun Seok Chae</i>
PB-39	<b>딸기 동양계와 미국 품종간 여교잡 횟수에 따른 분리집단의 변화</b> ..... 97 <i>이선이, 김승유, 김대영, 노일래</i>
PB-40	<b>Evaluation of genetic diversity of Asian landrace wheat based on HMW glutenin subunit and maturity</b> ..... 98 <i>Sukyeung Lee, Yu-mi Choi, Do yoon Hyun, Myung-chul Lee, Sejong Oh, On sook Hur, Hocheol Ko, Na-Young Ro</i>

PB-41	<b>Analysis of genetic diversity and cytoplasm male-sterility types in radish germplasm</b> ... 98 <i>O New Lee, Hyo Joung Kwon, Mi Kyung Han, Han Yong Park</i>
PB-42	<b>녹색자엽 검정콩 유전자원의 농업형질 및 품질관련 성분 평가</b> ..... 99 <i>이은자, 최홍집, 배정숙, 한윤열, 김세중, 이정동</i>
PB-43	<b>벼의 수형과 도정특성간의 관계</b> ..... 99 <i>이정희, 원용재, 안억근, 정국현, 이상복, 전용희, 장재기, 하운구, 정응기, 이점호</i>
PB-44	<b>Genetic diversity of super-sweet corn inbred lines using SSR and SSAP markers.</b> ..... 100 <i>Woo Ri Ko, Hong-Jib Choi, Kyu Jin Sa, Ju Kyong Lee</i>
PB-45	<b>Genetic diversity and relationships among rice accessions (<i>Oryza Sativa</i> L.) of cultivated and weedy types using CACTA-TD and AFLP markers</b> ..... 100 <i>Rahul Vasudeo Ramekar, Muhammad Qudrat Ullah Farooqi, Kyu Jin Sa, Kyong-Cheul Park, Ju Kyong Lee</i>
PB-46	<b>Genetic diversity, population structure, and association mapping of biomass traits in maize with simple sequence repeat markers</b> ..... 101 <i>Jong Yeol Park, Rahul Vasudeo Ramekar, Kyu Jin Sa, Ju Kyong Lee</i>
PB-47	<b>고품질 복합내병성 벼 신품종 “새신”</b> ..... 101 <i>이지운, 이종희, 조준현, 오성환, 손영보, 황운하, 박수권, 신동진, 송유천, 박동수, 김상열, 박인희, 여운상, 최대식, 남민희, 이영희</i>
PB-48	<b>카로티노이드를 함유한 노랑찰옥수수 ‘황미찰’ 육성</b> ..... 102 <i>이진석, 손범영, 신성후, 김정태, 배환희, 서민정, 김상곤, 백성범, 박장환, 이점호, 김성국, 정태욱, 권영업</i>
PB-49	<b>Mutation induced with gamma-ray irradiation in Rose cultivar (<i>Rosa Hybrida</i> Hort.)</b> ..... 102 <i>Hyo-Jeong Lee, Sang Hoon Kim, Ye-Sol Kim, Yeong Deuk Jo, Dong Sub Kim, Si-Yong Kang</i>
PB-50	<b>Study of anthocyanin accumulation in lettuce cultivars by different environments with digital phenotyping and next generation sequencing (NGS) technologies</b> ..... 103 <i>Sungyul Chang, Eun-Hee Soh, Chee Hark Harn, Hyoung Seok Kim</i>
PB-51	<b>Identification of Hybrids using SSR markers from Polyembryonic Citrus Breeding Lines.</b> · 103 <i>Sun-Yung Yoon, Hyo-Min Ahn, Hyun-Jeong Oh, Kyung-Hwan Boo, Ho-Bang Kim, Gyoeng-Lyong Jeon</i>
PB-52	<b>Assessment of Growth Characteristics and Cell Wall Components in Mutant Cultivars of Kenaf (<i>Hibiscus cannabinus</i>)</b> ..... 104 <i>Sang Wook Jeong, Jaihyunk Ryu, Seung Bin Im, Soon-Jae Kwon, Joon-Woo Ahn, Jin-Baek Kim, Sang Hoon Kim, Hee-Bong Lee, Si-Yong Kang</i>
PB-53	<b>Complete chloroplast genome sequence of <i>Capsicum baccatum</i> var. <i>baccatum</i></b> ..... 104 <i>Tae-Sung Kim, Jung-Ro Lee, Sebastin Raveendar, Gi-An Lee, Young-Ah Jeon, Ho-Sun Lee, Eun Seong Park, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung</i>
PB-54	<b>황색 반겹꽃 대륜화 절화용 거베라 ‘레몬비치’ 육성</b> ..... 105 <i>정용모, 황주천, 진영돈, 이병정, 이상대, 이영병, 권오창</i>

PB-55	<b>The Complete Chloroplast Genome Sequence of Korean Landrace “Subicho” (<i>Capsicum annuum</i> var. <i>annuum</i>)</b> ..... 106 <i>Sebastin Raveendar, Young-Ah Jeon, Jung-Ro Lee, Gi-An Lee, Kyung Jun Lee, Yang-Hee Cho, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung</i>
PB-56	<b>The complete chloroplast genome of <i>Capsicum annuum</i> var. <i>glabriusculum</i> using Illumina sequencing</b> ..... 106 <i>Sebastin Raveendar, Jung-Ro Lee, Donghwan Shim, Kyung Jun Lee, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung</i>
PB-57	<b>The Complete Chloroplast Genome of <i>Capsicum frutescens</i> L.</b> ..... 107 <i>Jung-Ro Lee, Donghwan Shim, Gi-An Lee, Sebastin Raveendar, Na-Young Ro, Young-Ah Jeon, Yang-Hee Cho, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Jeong</i>
PB-58	<b>Content of <i>Trans</i>-Resveratrol in Soybean Mature Seed</b> ..... 107 <i>Sang-Woo Choi, Sung-Jin Han, Jong-Il Chung</i>
PB-59	<b>토마토 잎 추출물의 항염증 활성 검정 및 steroid glycoalkaloids 분석</b> ..... 108 <i>김효정, 이경준, 이기안, 전영아, 이호선, 마경호, 이석영, 이동진, 정종욱</i>
PB-60	<b>토마토 잎 추출물의 항산화 활성 검정 및 flavone aglycones 분석</b> ..... 109 <i>김효정, 이경준, 이기안, 전영아, 이정로, 박은성, 이호선, 조양희, 마경호, 이석영, 이동진, 정종욱</i>
PB-61	<b>Seed traits of <i>y9ti</i> genotype in soybean</b> ..... 109 <i>Sang-Woo Choi, Sung-Jin Han, Jong-Il Chung</i>
PB-62	<b>대추나무 품종식별을 위한 Microsatellite DNA표지 개발</b> ..... 110 <i>조아르나, 신유승, 김영미, 김종환, 정지희</i>
PB-63	<b>Classification of Korean rice varieties based on growth characteristics</b> ..... 110 <i>Me-Sun Kim, Hye-Jung Lee, Dal-A Yu, Joonki Kim, Franz Nogoy, Eun-Ju Jeong, Jang-Hwan You, Yong-Gu Cho</i>
PB-64	<b>High tryptophan rice with an improved eating quality</b> ..... 111 <i>Franz Marielle Nogoy, Hye-Jung Lee, Marjohn Nino, Me-Sun Kim, Sothea Ouk, Yu-Jin Jung, Kwon-Kyoo Kang, Ill-sup Nou, Yong-Gu Cho</i>
PB-65	<b>Protein expression pattern of soybean sprouts at different germination temperatures</b> ..... 111 <i>Man-Soo Choi, Sung-Cheol Koo, Hyun-Tae Kim, Beom-Kyu Kang, In-Seok Oh, Hong-Tai Yun</i>
PB-66	<b>Modification of starch composition using RNAi targeting of <i>SSS1</i> gene in rice</b> ..... 112 <i>Hye-Jung Lee, Moo-Geun Jee, Dal-A Yu, Me-Sun Kim, Joonki Kim, Seon-Kyeong Song, Kwon-Kyoo Kang, Yong-Gu Cho</i>
PB-67	<b>Growth and Yield characteristics of Orchardgrass ‘Onnuri 2 ho’ Variety</b> ..... 113 <i>Hee Chung, Ji, Ki Yong, Kim, Tae Young Hwang, Hyun Seok Chae, Seong Tae Lee</i>
PB-68	<b>Agricultural Characteristics and SSR Profiling of Soybean from Korea, China, Japan and Southeast Asia</b> ..... 114 <i>Yu-Mi Choi, Sukyeung Lee, Do yoon Hyun, Sejong Oh, Myung-Chul Lee, Hocheol Ko, On-Sook Hur, Na-Young Ro, Yeon-Ju Jeong</i>

PB-69	<b>A Red Single Freesia ‘Cutie Red’ for Pot Plant</b> ..... 114 <i>Youn Jung Choi, Hyang Young Jeoung, Dae Hoe Goo, Yun Im Kang, Hae Ryong Cho</i>
PB-70	<b>수량많고 껍질 벗김성이 뛰어난 잎자루 채소용 고구마 우수계통 선발</b> ..... 115 <i>한선경, 안승현, 김재명, 송연상, 이형운, 양정욱, 이준설, 남상식, 이정보</i>
PB-71	<b>절화 알스트로메리아 ‘씨엔알스호프’의 육성과 특성</b> ..... 116 <i>한수범, 박성화, 김정석, 박형빈, 안주희, 한태호</i>
PB-72	<b>정원용 장미 대목으로 사용되는 찔레 경지삽 발근 효율 증진 연구</b> ..... 117 <i>김정석, 강성환, 한수범, 박성화, 안주희, 한태호</i>
PB-73	<b>황기의 유효성분 대량생산을 위한 기내배양 조건정립</b> ..... 118 <i>허목, 엄유리, 안태진, 이정훈, 김영국, 차선우</i>
PB-74	<b>발아자극물질 Strigolactone 혼합물의 발아자극활성</b> ..... 119 <i>김현일, 샤 시오난, 키스기 타카야, 요네야마 카오리, 요네야마 코이치</i>
PB-75	<b>국내 블루베리 품종 구분을 위한 형태적 특성 비교</b> ..... 120 <i>김수진, 고상욱, 남종철, 정성민, 허윤영</i>
PB-76	<b>Gibberellin Application at Pre-bloom in Grapevines Alters GABA-shunt Resulting in Accumulation of GABA (<math>\gamma</math>-aminobutyric acid) at Full Bloom</b> ..... 121 <i>Chan Jin Jung, Youn Young Hur, Sung-Min Jung, Sang-Uk Koh, Jong-Chul Nam</i>
PB-77	<b>국내 블루베리 품종 구분을 위한 형태적 특성 비교</b> ..... 122 <i>김수진, 고상욱, 남종철, 정성민, 허윤영</i>
PB-78	<b>발아자극물질 Strigolactone 혼합물의 발아자극활성</b> ..... 123 <i>김현일, 샤 시오난, 키스기 타카야, 요네야마 카오리, 요네야마 코이치</i>
PB-79	<b>Analysis of transcriptional regulation of Arabidopsis <i>PIF</i> family genes in response to abiotic stresses</b> ..... 124 <i>Jin-Seok Moon, Satoshi Kidokoro, Daisuke Todaka, Sayuri Igusa, Junya Mizoi, Kazuo Shinozaki, Kazuko Yamaguchi-Shinozaki</i>
PB-80	<b>Characterization of the Koji (<i>Aspergillus oryzae</i>) in four wheat varieties</b> ..... 124 <i>Jong-Nae Hyun, Hyung-ho Park, Kyung-Hun Kim, Kyung-Min Kim, Jee-Yeon Ko, Young-Up Kweon, Chon-Sik Kang, Sang-Jong Lim, Jae-Hyun Kim</i>
PB-81	<b>A high tocopherol content rice cultivar ‘Tocomi-1’</b> ..... 125 <i>Jung Eun Hwang, In Jung Jung, Sung Min Han, Jin-Baek Kim, Si-Yong Kang, Dong Sub Kim</i>
PB-82	<b>고생장성의 복색 흙꽃 절화용 스프레이국화 ‘매직발라드’ 육성</b> ..... 126 <i>황주천, 진영돈, 정용모, 안동춘, 이병정, 이상대, 정병룡</i>

**분자육종 및 유전공학(Molecular breeding and biotechnology)**

PC-01	<b>Genetic Analysis and Fine Mapping of Panicle Tip Mutant pnt in rice (<i>Oryza sativa</i> L.)</b> 127 <i>Abebe Megersa Diriba, Dongryung Lee, Jeonghwan Seo, Backki Kim, Zhuo Jin, Hee-Jong Koh</i>
PC-02	<b>Phylo rice transcription factor database: a resource for phylogenomics based systematic analysis of rice transcription factor for functional studies</b> ..... 127 <i>Anil Kumar N.C, Yo-Han Yoo, Ki-Hong Jung</i>
PC-03	<b>Map-based cloning to identify gene involving in male gametophyte development in Arabidopsis</b> ..... 128 <i>Thi Hoai Thuong Nguyen, Hyo-Jin Park, Tien Dung Nguyen, Sung Aeong Oh, Soon Ki Park</i>
PC-04	<b>Molecular characterization and functional analysis of the UDP-glucose 4-epimerase (<i>BrUGE</i>) gene family in response to biotic and abiotic stress in Chinese cabbage (<i>Brassica rapa</i>)</b> ..... 128 <i>Yu Jin Jung, Boo Min Yun, Hyun Ji Kim, Yong Gu Cho, Ill Sup Noh, Kwon Kyoo Kang</i>
PC-05	<b>A Map-based Cloning Approach for the Identification of a Low Temperature Sensitive Gene <i>sy-2</i> in Chilli pepper (<i>Capsicum chinense</i>)</b> ..... 129 <i>Li Liu, Min-Young Kang, Jin-Ho Kang, Yeong Deuk Jo, Sota Koeda, Munetaka Hosokawa, Doil Choi, Byoung-Cheorl Kang</i>
PC-06	<b>Characterization and interaction analysis of two QTLs, <i>QTL5-1</i> and <i>QTL5-2</i>, controlling <i>Phytophthora capsici</i> resistance in <i>Capsicum annuum</i> using near-isogenic lines</b> ..... 130 <i>Hyeon-Seok Jeong, Muhammad Irfan Siddique, Jeong-Tak An, Ki-Taek Kim, Gyung Ja Choi, Darush Struss, Byoung-Cheorl Kang</i>
PC-07	<b>한국 들잔디에서의 <math>\beta</math>-,3-glucanase 유전자의 cloning</b> ..... 131 <i>강소미, 강지남, 강홍규, 선현진, 권용익, 고석민, 이효연</i>
PC-08	<b>환경스트레스 내성 들잔디 (<i>Zoysia japonica</i> Steud.)의 형질전환체 개발</b> ..... 132 <i>박미영, 선현진, 이동희, 류기중, 이효연</i>
PC-09	<b>제초제저항성 GM들잔디 유래 초형개선 신품종 잔디(JG21-MJ) 계통의 분자생물학적 특성 평가</b> ... 132 <i>정하나, 좌지방, 선현진, 권용익, 강홍규, 이효연</i>
PC-10	<b>Cloning of <i>WRKY</i> genes, induced by stresses in <i>Zoysia japonica</i> Steud.</b> ..... 133 <i>Woo-Nam Kim, Yong-Ik Kwon, In-Ja Song, Bo-Hwa Hwang, Dong-Sun Lee, Hyo Yeon Lee</i>
PC-11	<b>Antifungal activities of zoysiagrass (<i>Zoysia japonica</i> Steud.) chitinases against <i>Rhizoctonia solani</i> and analysis of fungus responsive cis-elements in chitinase genes promoter</b> ... 134 <i>Ji-Nam Kang, So-Mi Kang, Hong-Gyu Kang, Hyeon-Jin Sun, Yong-Ik Kwon, Suk-Min Ko, Hyo-Yeon Lee</i>
PC-12	<b>The Karyotype Analysis of <i>Lilium</i> Species Native to China</b> ..... 134 <i>Ge Guo, Ki-Byung Lim</i>

PC-13	<b>Bio assay of DNP , 9 Response in Rice Screening with Whitebacked planthopper</b> ..... 135 <i>Sopheap Yun, Vicheka Than, Kyung-A kim, Hyun-Suk Lee, Gi-Hwan Yi, Byung-Wook Yun, Kyung-Min Kim</i>
PC-14	<b>Timing screening effects and QTLs analysis of Whiteback planhopper Resistance Cheongcheong/Nagdong Double haploid Rice</b> ..... 136 <i>Sopheap Yun, Hyun-Suk Lee, Than Vicheka, Gi-Hwan Yi, Kyung-Min Kim</i>
PC-15	<b>QTLs for detecting DNA markers related to alkali digestion value in rice grain using doubled haploid population</b> ..... 137 <i>Hyun-Suk Lee, Gyu-Ho Lee, A-Ra Cho, Gihwan Yi, Kyung-Min Kim</i>
PC-16	<b>Practical use of standard set of microsatellites based classification of primary pears and Korean native pears (<i>Pyrus</i> spp.)</b> ..... 138 <i>Keumsun Kim, Hyunsuk Shin, Youngjae Oh, Sewon Oh, Jungyeon Won, Hyeondae Han, Yoon-Kyeong Kim, Seolah Kim, Sung-II Oh, Mingi Lee, Daeil Kim</i>
PC-17	<b>Distinct roles of <i>E3</i>-parologue genes promote early flowering in late flowering soybean cultivars</b> ..... 139 <i>Kil Hyun Kim, Min-Jung Seo, Jin-Seok Lee, Hwan Hee Bae, Jung-Tae Kim, Beom-Young Son, Seong-Bum Baek, Jeom-Ho Lee, Jung-Kyung Moon, Chang-Hwan Park</i>
PC-18	<b>Evidence of whole genome duplication in <i>Panax ginseng</i> draft sequence</b> ..... 140 <i>Nam-Hoon Kim, Woojong Jang, Murukarthick Jayakodi, Sang-Choon Lee, Yun Sun Lee, Junki Lee, Beom-Soon Choi, Tae-Jin Yang</i>
PC-19	<b>Identification and characterization of novel phosphate starvation signaling mutant in <i>Arabidopsis</i></b> ..... 141 <i>Hyun Jin Chun, Mi Suk Park, Byung-Jun Jin, Min Chul Kim</i>
PC-20	<b>Metabolic analysis of high salt-adapted <i>Arabidopsis</i> suspension cultured cells</b> ..... 142 <i>Hyun Jin Chun, Wook-Hun Jung, Mi Suk Park, Hyun Min Cho, Dae-Jin Yun, Young-Shick Hong, Min Chul Kim</i>
PC-21	<b>Integrating Omics Analysis of Salt Stress-Responsive Genes in Rice</b> ..... 143 <i>Seo-Woo Kim, Hee-Jeong Jeong, Ki-Hong Jung</i>
PC-22	<b>Development of a simple PCR marker linked to the gene conferring resistance to downy mildew (<i>Peronospora destructor</i>) in onion (<i>Allium cepa</i> L.)</b> ..... 143 <i>Seongjun Kim, Sunggil Kim</i>
PC-23	<b>nSSR 표지를 이용한 안면도지역 곰솔 채종원과 자연집단의 교배양식 유전모수 연간 변이</b> ..... 144 <i>김영미, 홍경낙, 박유진, 홍용표, 박재인</i>
PC-24	<b>백합나무 (<i>Liriodendron tulipifera</i>) 체세포배 유래 순화묘의 활착율 향상을 위한 몇가지 황산화제 처리 효과</b> ..... 144 <i>김용욱, 김지아, 문홍규, 정수진, 이나မ်</i>
PC-25	<b>QTL-seq analysis of flowering time in radish</b> ..... 145 <i>Youn-Sung Kim, Chan-Sup Ko, Eun-Ju Lee, Jeong-Pal Suh, Jae-Yong Lee, Hye-Sun Cho</i>

PC-26	다양한 농도의 사과, 감자 및 바나나 추출물 처리가 형질전환 팔레놉시스 원기체유사체 생장 및 증식에 미치는 영향 ..... 145 <i>노희선, 박선경, 김종보</i>
PC-27	A highly sensitive real-time PCR systems for detecting rice grain-derived food ingredients in commercial mixed-flour Products ..... 146 <i>Ju-Hee Kim, Sun-Goo Hwang, Cheol Seong Jang</i>
PC-28	Profiling of differentially expressed genes with space environments exposed Brachypodium seeds ..... 146 <i>Jin-Baek Kim, Min Jeong Hong, Young Ha Yoon, Dong Sub Kim, Sang Hoon Kim, Joon-Woo Ahn, Yeong Deuk Jo, Si-Yong Kang</i>
PC-29	Complete chloroplast genome of <i>Codonopsis lanceolata</i> and <i>Platycodon grandiflorus</i> : insight into evolution of the Asterales and development of molecular marker. .... 147 <i>Jin-hyuk Kim, Sun-Goo Hwang, Cheol-Seong Jang</i>
PC-30	MAB SNP marker development to accelerate the breeding of Chinese cabbage ..... 147 <i>Jinhee Kim, Do-Sun Kim, Hye-Eun Lee, Yul-Kyun Ahn, Jeong Ho Kim</i>
PC-31	CSGM Designer: a convenient platform for designing cross-species intron-spanning genic markers ..... 148 <i>Jin-Hyun Kim, Chaeyoung Lee, Joo-Seok Park, Douglas R. Cook, Hong-Kyu Choi</i>
PC-32	Molecular mapping of QTLs related to cold tolerance at seedling stage in rice ..... 149 <i>Tae Heon Kim, Yeon-Jae Hur, Saisbeul Lee, Ji-Yoon Lee, Youngbo Son, Sung Hwan Oh, Sang-Ik Han, Jun-Hyun Cho, You-Chun Song, Jong-Hee Lee, Min-Hee Nam, Dong-Soo Park, Yeong-Up Kwon, Dongjin Shin</i>
PC-33	Up-dating of new dCAPS markers for mapping yield-related traits using MGRIL ..... 150 <i>Ye-Ji Lee, Hyun-Ju Lee, In-Seon Jeong, Seon-Hwa Bae, Hyeon-So Ji, Gang-Seob Lee, Ung-Han Yoon, Jang-Ho Hahn, Tae-Ho Kim</i>
PC-34	Development of simple sequence repeat (SSR) markers from ramie ( <i>Boehmeria nivea</i> L.) and application to the genetic resources ..... 151 <i>Yoon Kyung Uhm, Hye-young Lee, Jinkyu Woo, JiHyeon Kim, Young-Mi Kim, Yong-Su Jung, Hyun Sam Lee, Sanghyun Lee, Ho Bang Kim</i>
PC-35	Functional analysis of a stress-related gene <i>BrTSR53</i> conferred salt tolerance in Yeast ..... 152 <i>A-Ram Kim, Hyemin Lim, Hyun-Ju Hwang, Sung Han Park, Chang-Kug Kim, Hyeonso Ji, Jung-Il Cho, Soo-Chul Park, Gang-Seob Lee</i>
PC-36	A conserved oligomeric Golgi complex component-related protein is essential for pollen development in <i>Arabidopsis</i> ..... 153 <i>Tien Dung Nguyen, Binbin Li, Sung Aeong Oh, Soon Ki Park</i>
PC-37	Identification of microspore-active promoters using transgenic rice and <i>Arabidopsis</i> .... 154 <i>Tien Dung Nguyen, Moe Moe Oo, Sung Aeong Oh, Thi Hoai Thuong Nguyen, Hyo-Jin Park, Jong Tae Song, Moon-Soo Soh, Ki-Hong Jung, Soon Ki Park</i>

PC-38	<b>Development of Multiplex PCR for Species-Specific Identification of the Poaceae family Based on chloroplast <i>rpoC2</i> genes</b> ..... 155 <i>Jun-Cheol Moon, Ju-Hee Kim, Cheol Seong Jang</i>
PC-39	<b>Development of marker-free transgenic rice expressing wheat storage protein, <i>TaGlu-Ax1</i>, for increasing quality processing of bread and noodle</b> ..... 156 <i>Soo-Kwon Park, So-Hyeon Baek, Dool-Yi Kim, Myoung-Ryoul Park, Na-Ra Lee, Kyoung Soon Shin, Su-Kyoung Jeon, Eun-Jae Kim, Sun-Lim Kim, Jung-Kyoung Moon</i>
PC-40	<b>Delimitation of Genomic Location for <i>Fr1</i> locus Conferring Resistance to Fusarium Crown Root Rot in Tomato</b> ..... 157 <i>Bichsaem Kim, Jihyun Hwang, Joon Young Kim, Byung Sup Kim, Sung Ran Min, Huijung Jung, Ill-Sup Nou, Younghoon Park</i>
PC-41	<b>A new approach for detecting natural selection signature among rice in-paralogs</b> ..... 157 <i>Kyu-Won Kim, Tae-Sung Kim, Yong-Jin Park</i>
PC-42	<b>Transcriptome changes in rice (<i>Oryza sativa</i> L.) for high zinc content at the early milky stage</b> ..... 158 <i>Eun-Beom Heo, Min-Young Yoon, Buung Choi, Donghwan Shim, Beom-Seok Park, Won-Il Kim, Yong-Jin Park</i>
PC-43	<b>Resequencing reveals different domestication rate for <i>BADH1</i> and <i>BADH2</i> in rice (<i>Oryza sativa</i>)</b> ..... 159 <i>Qiang He, Jie Yu, Tae-Sung Kim, Yoo-Hyun Cho, Young-Sang Lee, Yong-Jin Park</i>
PC-44	<b>Discovery of a novel fragrant allele and development of functional markers for fragrance in rice</b> ..... 160 <i>Qiang He, Yong-Jin Park</i>
PC-45	<b>Orthologous based study to detect the fast evolutionary genes related to rice pre-harvest sprouting</b> ..... 161 <i>Wei Tong, Tae-Sung Kim, Kyu-Won Kim, Yong-Jin Park</i>
PC-46	<b>A chloroplast variation map generated using whole genome re-sequencing of Korean landrace rice reveals phylogenetic relationships among <i>Oryza sativa</i> subspecies</b> ..... 162 <i>Wei Tong, Qiang He, Xiao-Qiang Wang, Min-Young Yoon, Won-Hee Ra, Feng Peng Li, Jie Yu, Win Htet Oo, Sun-Kyung Min, Buung Choi, Eun-Beom Heo, Byoung-Kook Yun, Kyu-Won Kim, Tae-Sung Kim, Chang-Yong Lee, Yong-Jin Park</i>
PC-47	<b>Evolutionary study for rice iron uptake from Korean authentic rice core set</b> ..... 163 <i>Buung Choi, Min-Young Yoon, Tae-Sung Kim, Kyu-Won Kim, Donghwan Shim, Beom-Seok Park, Won-Il Kim, Yong-Jin Park</i>
PC-48	<b>A computer program for combining SNP information and estimating SNP-related statistics</b> ..... 163 <i>Chang-Yong Lee, Yong-Jin Park</i>
PC-49	<b>Evolutionary study for rice flowering time genes in Korean authentic rice core set</b> ..... 164 <i>Min-Young Yoon, Tae-Sung Kim, Kyu-Won Kim, Yong-Jin Park</i>

PC-50	<b>Evolution related genes of salt tolerance in rice revealed by McDonald–Kreitman Test</b> .... 165 <i>Jie Yu, Tae-Sung Kim, Kyu-Won Kim, Yong-Jin Park</i>
PC-51	<b>Transcriptome changes of rice (<i>Oryza sativa</i> L.) in oil accumulation at the early milky stage</b> ..... 166 <i>Win Htet Oo, Tae-Sung Kim, Donghwan Shim, Beom-Seok Park, Yong-Jin Park</i>
PC-52	<b>A pipeline for genome assisted breeding to efficiently exploit useful alleles from rice germplasm</b> ..... 166 <i>Tae-Sung Kim, Kyu-Won Kim, Yong-Jin Park</i>
PC-53	<b>Generation and characterization of T-DNA insertion population for genetically-modified rice</b> ..... 167 <i>Hyemin Lim, A-Ram Kim, Hyun-Ju Hwang, Jung-Il Cho, Hyeonso Ji, Chang-Kug Kim, Soo-Chul Park, Gang-Seob Lee</i>
PC-54	<b>Molecular dissection of a rice RING finger protein induced by salt and drought treatments</b> ..... 168 <i>Yong Chan Park, Cheol Seong Jang</i>
PC-55	<b>Dissection of Korean landrace chamoë (<i>Cucumis melo</i> var. <i>makuwa</i>) genome</b> ..... 168 <i>Inkyu Park, Jae-Pil Choi, Jungeun Kim, Jeongyeo Lee, Soohwan Lim, Mi-Ye Lee, Hey-Ran Kim</i>
PC-56	<b>Profile of econdary metabolites and related gene expressions of <i>Panax ginseng</i> adventitious roots induced from 5 korean ginseng cultivars cultured in bioreactors</b> ..... 169 <i>Hyun-Seung Park, Dong-Kyu Lee, Yun Sun Lee, Sang-Choon Lee, Murukarthick Jayakodi, Sung Won Kwon, Tae-Jin Yang</i>
PC-57	<b>Gene identification of Arabidopsis gametophytic mutation showing aberrant pollen phenotype using map-based cloning approach</b> ..... 169 <i>Hyo Jin Park, Nguyen Thi Hoai Thuong, Tien Dung Nguyen, Sung Aeong Oh, Soon Ki Park</i>
PC-58	<b>Mapping QTLs of resistance to head splitting in cabbage (<i>Brassica oleracea</i> L. var. <i>capitata</i> L.)</b> ..... 170 <i>Wenxing Pang, Xiaonan Li, Seong Ho Lee, Dasom Kim, Sang Heon Oh, Su Ryun Choi, Yong Pyo Lim</i>
PC-59	<b>Characterization and analysis of <i>OsUPS</i>, a U-box containing E3 ligase that respond to phosphate starvation in rice.</b> ..... 171 <i>Ki-Deuk Bae, Doh-hoon Kim</i>
PC-60	<b>Cloning and identification of the partial major ampullate silk protein gene from the spider <i>Araneus ventricosus</i> in rice.</b> ..... 171 <i>Ki-Deuk Bae, Doh-Hoon Kim</i>
PC-61	<b>Identification and analysis of <i>osgasd</i> gene.</b> ..... 172 <i>Ki-Deuk Bae, Doh-Hoon Kim</i>
PC-62	<b>OsMYB4p, an R2R3-type MYB transcription factor, improves phosphate uptake in rice</b> .. 172 <i>Ki-Deuk Bae, Doh-Hoon Kim</i>

PC-63	<b>Characterizaataion and histological analysis of leaf development related gene in rice.</b> ... 173 <i>Ki-Deuk Bae, Doh-hoon Kim</i>
PC-64	<b>Study of transgenic rice plants in rich expressed sheep serotonin N-Acetyltransferase</b> · 173 <i>Yeong Byeon, Hyoung Yool Lee, Kyoungwhan Back</i>
PC-65	<b>Presence of melatonin 2-hydroxylase in rice (<i>Oryza sativa</i>) plants</b> ..... 174 <i>Yeong Byeon, Kyoungwhan Back</i>
PC-66	<b>Production of doubled haploids through micropore culture in F1 hybrids of yellow sarson and turnip rape of <i>Brassica rapa</i></b> ..... 174 <i>Mi-Suk Seo, Mi-Sun Moon, Kyung-gin Lee, So Youn Won, Sangho Kang, Seong-Han Sohn, Jung Sun Kim</i>
PC-67	<b>RNA-seq analysis on tetralocular ovary and high seed yields in yellow sarson of <i>Brassica rapa</i></b> ..... 175 <i>Mi-Suk Seo, So Youn Won, Sangho Kang, Seong-Han Sohn, Jung Sun Kim</i>
PC-68	<b>Genome-wide identification of pepper NB-LRR gene family and their evolutionary history in Solanaceae</b> ..... 175 <i>Eunyoung Seo, Seon-In Yeom, Seungill Kim, Joohyun Lee, Saet-Byul Kim, Eunbi Choi, Eun Hye Choi, Doil Choi</i>
PC-69	<b>Suitability of Fourier Transform Infrared Spectroscopy as a screening method for the production of useful mutant lines in <i>Panax ginseng</i></b> ..... 176 <i>Javzandulam Ulziisaikhan, Jun-Ying Zhang, Hong-Yu Li, Hyeon-Jin Sun, Somi Kim, Sung-Jun Song, Hyo-Yeon Lee</i>
PC-70	<b>Gene transferability between herbicide-resistant <i>B. napus</i> and Korean varieties of <i>B. rapa</i></b> ..... 177 <i>Soo-In Sohn, Young-Ju Oh, Si-Myung Lee, Sung-Dug Oh, Gang-Seob Lee, Doh-Won Yun, Hyun-Suk Cho</i>
PC-71	<b>Molecular marker evaluated for heat tolerance in wheat</b> ..... 177 <i>Jae-Han Son, Kyeung-Hoon Kim, Chon-Sik Kang, Young-Keun Cheong, Jong-Chul Park, Kyong-Ho Kim, Yang-Kil Kim, Young-Jin Oh, Jong-Ho Park, Tae-Hwa Song, Jae-Seong Choi, Bo-Kyeong Kim</i>
PC-72	<b>Meta-analysis of QTL involved in drought tolerance and grain yield of maize</b> ..... 178 <i>Kitae Song, Hyo-chul Kim, Seungho Shin, Kyung-Hee Kim, Jun-Cheol Moon, Jae Yoon Kim, Byung-Moo Lee</i>
PC-73	<b>Screening of rice drought tolerant germplasms and drought tolerant QTL mapping</b> ..... 179 <i>Dongjin Shin, Tae-Heon Kim, Sang-Ik Han, Ji-Yoon Lee, Youngbo Son, Sung Hwan Oh, Yeon-Jae Hur, Saisbeul Lee, Jun-Hyun Cho, Jong-Hee Lee, You-Chun Song, Min-Hee Nam, Dong-Soo Park, Yeong-Up Kwon</i>
PC-74	<b>DNA Profiling and Variety Identification using Insertion-Deletion (InDel) Polymorphisms in Cultivated Tomato</b> ..... 179 <i>Minkyung Kim, Sung-Chur Sim</i>

PC-75	<b>Proline accumulation and related gene expression in response to higher temperatures during deacclimation in peach shoot tissues</b> .....	180
	<i>Hyunsuk Shin, Sewon Oh, Keumsun Kim, Youngjae Oh, Jungyeon Won, Hyeondae Han, Daeil Kim</i>	
PC-76	<b>Fine Mapping of the Root-Knot Nematode (<i>Meloidogyne incognita</i>) Resistance Gene (<i>Me7</i>) using an F2 Population in Pepper</b> .....	181
	<i>Amornrat Changkwian, Ji-Woong Han, Jong-Ho Lee, Gyung-Ja Choi, Byoung-Cheorl Kang</i>	
PC-77	<b>알스트로메리아의 환경위해성 평가를 위한 생물학적 특성평가 방법</b> .....	182
	<i>안주희, 문초아, 한수범, 박성화, 김정석, 박태성, 한태호</i>	
PC-78	<b>Development of gene-based markers for pink fruit peel color in tomatoes</b> .....	182
	<i>Marina Lee, Jungsu Jung, Hyun Jung Kim, Je Min Lee, Inhwa Yeam</i>	
PC-79	<b>Biosafety assessment and molecular biological characteristics for <math>\beta</math>-carotene biofortified transgenic rice</b> .....	183
	<i>Sung-Dug Oh, Soo-Yun Park, Doh-Won Yun, Soo-In Sohn, Hyun Suk Cho, Si Myung Lee</i>	
PC-80	<b>Assessment of gene flow from disease resistant (OsCK1) genetically modified rice to its non-GM rice and weedy rice</b> .....	183
	<i>Sung-Dug Oh, Si Myung Lee, Soo-In Sohn, Hyun Suk Cho, Doh-Won Yun</i>	
PC-81	<b>Changes in proline content and related gene expression under artificial deacclimation and reaclimation during ecodormant state in <i>Prunus persica</i></b> .....	184
	<i>Sewon Oh, Hyunsuk Shin, Keumsun Kim, Youngjae Oh, Jungyeon Won, Hyeondae Han, Daeil Kim</i>	
PC-82	<b>Identification of single-nucleotide polymorphisms in <i>Sw-5b</i> resistance gene and development of a SNP marker to <i>Tomato spotted wilt virus</i> in tomato</b> .....	184
	<i>Hyung Jin Lee, Bo-Young Kim, Chang-Sik Oh</i>	
PC-83	<b>Development of the single-nucleotide polymorphism marker in <i>Cf-9</i> gene conferring resistance to a leaf mold pathogen <i>Cladosporium fulvum</i> in tomato</b> .....	185
	<i>Bo-Young Kim, Hyung Jin Lee, Chang-Sik Oh</i>	
PC-84	<b>Molecular characterization of transgenic plants using Next Generation Sequencing and Junction Sequence Analysis</b> .....	185
	<i>Ji Hye Ohn, Andre Silvanovich, Carl Garnaat, Colton Kessenich, Qing Tian</i>	
PC-85	<b>QTL analysis for Agronomic Traits of Rice Recombinant Inbred Lines under Different Environments</b> .....	186
	<i>Mi-Ok Woo, Xing Huang, Eunbyeol Koh, Hee-Jong Koh</i>	
PC-86	<b>Proteome alterations towards understanding molecular mechanism upon copper stress in Sorghum</b> .....	187
	<i>Swapan Kumar Roy, Soo Jeong Kwon, Won-Ju Lee, Jong-Ho Yang, Sang-Woo Kim, Tae-Wook Jung, Jung-In Kim, Tae-Seok Ko, Sun-Hee Woo</i>	
PC-87	<b>Proteome analysis unravelling cadmium toxicity and tolerance in Sorghum leaves</b> .....	188
	<i>Swapan Kumar Roy, Sang-Woo Kim, Jong-Ho Yang, Seong-Woo Cho, Tae-Wook Jung, Jung-In Kim, Tae-Seok Ko, Sun-Hee Woo</i>	

PC-88	<b>Protein profile changes induced by hormones in diploid and tetraploid roots of <i>Platycodon grandiflorum</i></b> ..... 189 <i>Soo-Jeong Kwon, Swapan Kumar Roy, Won-Ju Lee, Hae-Ryong Jeong, Hag-Hyun Kim, Yong-Gu Cho, Hee-Ock Boo, Sun-Hee Woo</i>
PC-89	<b>Proteome responses of diploid and tetraploid root: Towards understanding functional characterization in <i>Platycodon grandiflorum</i></b> ..... 190 <i>Soo-Jeong Kwon, Swapan Kumar Roy, Min-Heon Yun, Je-Hyeok Yu, Hag-Hyun Kim, Hee-Ock Boo, Moon-Soon Lee, Sun-Hee Woo</i>
PC-90	<b>Development of a PCR marker for monitoring of transgene introgression in resveratrol-enriched transgenic rice plant</b> ..... 191 <i>Yang Qin, So-Hyeon Baek, Soon-Jong Kweon, Taek-Ryoun Kwon, Myung-Ho Lim, Kong-Sik Shin, Hyun-Suk Cho, Hee-Jong Woo</i>
PC-91	<b>Selection of <math>\beta</math>-carotene enhanced transgenic soybean containing single-copy transgene and analysis of integration sites</b> ..... 191 <i>Yang Qin, Soon-Jong Kweon, Young-Soo Chung, Sun-Hwa Ha, Kong-Sik Shin, Myung-Ho Lim, Taek-Ryoun Kwon, Soon Ki Park, Hyun-Suk Cho, Hee-Jong Woo</i>
PC-92	<b>Comparative nutritional analysis for marker-free transgenic <i>Bt</i> rice and non-transgenic counterparts</b> ..... 192 <i>Hee-Jong Woo, Kong-Sik Shin, Myung-Ho Lim, Jin-Hyoung Lee, Yang Qin, Soon Ki Park, Hyun-Suk Cho</i>
PC-93	<b>Characterization of chrysanthemum genome by NGS</b> ..... 192 <i>So Youn Won, Seulki Lee, Jae-A Jung, Jung Sun Kim, Sangho Kang, Seong-Han Sohn</i>
PC-94	<b>미성숙화기를 이용한 ‘우람’ 역대 식물체 재분화</b> ..... 193 <i>유경단, 장윤희, 안종웅, 최인후, 문윤희, 차영록, 이지은, 안기홍, 이정보</i>
PC-95	<b>Rice FLAVIN-BINDING, KELCH REPEAT, F-BOX 1 (OsFKF1) promotes flowering independent of photoperiod.</b> ..... 194 <i>Su-Hyun Han, Soo-Cheul Yoo, Nam-Chon Paek</i>
PC-96	<b>Investigation of Saponin Biosynthesis Related Uridine Diphosphate Glycosyltransferase(UGT) Genes in <i>Platycodon grandiflorum</i> Using RNA-seq</b> ..... 194 <i>Jemin Yoo, Yurry Um, Yi Lee</i>
PC-97	<b>Analysis of Phylogenetic Relationship in <i>Platycodon grandiflorum</i> using RAPD Molecular Marker</b> ..... 195 <i>Jemin Yoo, So Hyeon Park, Yurry Um, Yi Lee</i>
PC-98	<b>Investigation of Cytochrome P450 Genes Related to Saponin Biosynthesis in <i>Platycodon grandiflorum</i> Using RNA-Seq Analysis</b> ..... 195 <i>Jemin Yoo, Yurry Um, Yi Lee</i>
PC-99	<b>Genome-wide identification of Receptor-like Protein in <i>Capsicum annuum</i></b> ..... 196 <i>DongKue Yun, BoSeu Park, JuneSung Lee, Won-Hee Kang, Seungill Kim, Myung-Shin Kim, Doil Choi, Seon-In Yeom</i>

PC-100	The <i>Citrus unshiu</i> carotenoid isomerase gene, <i>CuCRTISO</i> , has a activity of the carotenoid isomerase in the tomato <i>CRTISO</i> mutant <i>Tangerine</i> . <i>Chang-Ho Eun, In-Jung Kim</i>	196
PC-101	Phylogenomic analysis and a systematic view of MLO family in rice <i>Van Ngoc Tuyet Nguyen, Ki-Hong Jung</i>	197
PC-102	Functional characterization of soybean <i>FT</i> homologs in photoperiod-dependent flowering time control <i>Kyung-Hee Lee, Cheol Woo Choi, Wook-Hun Jung, Min-Chul Kim</i>	197
PC-103	Transgenic Forage Plants Overexpressing a alfalfa <i>Hsp23</i> Gene Exhibit Enhanced Tolerance to Abiotic Stresses <i>Ki-Won Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang, Sang-Hoon Lee</i>	198
PC-104	음나무( <i>Kalopanax septemlobus</i> ) 종자유래 식물체 재생과 재생 식물체의 ISSR에 기초한 유전적 다양성 분석 <i>이나념, 김지아, 김용욱, 최용의, 문흥규</i>	198
PC-105	식물성 오일의 혈중 지질 수치 감소 효과 <i>최정란, 김형욱, 장인건, 이상협</i>	199
PC-106	Characterization of Siberian wild rye grass <i>EsHsp16.9</i> Gene and Their Expression under Various Environmental Conditions <i>Sang-Hoon Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang, Ki-Won Lee</i>	200
PC-107	벼 줄무늬 잎마름병의 주요 유전자 <i>Stv-b</i> 관련 QTL 탐색 <i>이셋별, 허연재, 김태현, 신동진, 한상익, 조준현, 이지운, 손영보, 남민희, 송유천, 이종희, 김경민, 권영엽, 박동수</i>	201
PC-108	Characterization and Genetic Mapping of Narrow and Adaxially Rolled Leaf Mutant in Rice <i>Yoon Kyung Lee, Yunjoo Lee, Hee-Jong Koh</i>	201
PC-109	Production of soybean transgenic plants to improve agronomic traits <i>Yoon Jeong Lee, Jin Ho Yang, Jin Sol Park, Hye Jeong Kim, Hyun Suk Cho, Jae Seong Kim, Hyun Hee Im, Ki Jung Lee, Jeong Il Kim, Soon Chun Jeong, Dong Hee Lee, Yung Soo Chung</i>	202
PC-110	Proteomic Analysis of High and Low- Molecular Weight Subunits in Korean Common Wheat Cultivars <i>Jong-Yeol Lee, Hye-Rang Beom, Sun-Hyung Lim, Young-Mi Kim</i>	202
PC-111	Comprehensive Identification of Low-Molecular-Weight Glutein Subunit Genes and Their Protein Products in a Korean Common Wheat Variety "Keumkang" <i>Hye-Rang Beom, Sun-Hyung Lim, Young-Mi Kim, Jong-Yeol Lee</i>	203
PC-112	Activation of Anthocyanin Biosynthesis by Expression of the Radish R2R3 MYB Transcription Factor gene <i>RsMYB1</i> <i>Sun-Hyung Lim, Sun-Hwa Ha, MinJi Choi, Da-Hye Kim, Sang-Kyu Park, Jong-Yeol Lee, Young-Mi Kim</i>	204

PC-113	<b>Comparative Whole-Genome Analysis of Tall Transgenic Bt Line and wild-type Line</b> ···· 205 <i>Jin-Hyoung Lee, Kong-Sik Shin, Seok-Cheol Suh, Hee-Jong Woo, Myung-Ho Lim, Yang Qin, Taek-Ryoun Kwon, Soon-Ki Park, Hyun-Suk Cho</i>
PC-114	<b>Predicting consensus sequence of pre-mRNA splicing signals in legume family</b> ········ 205 <i>Chaeyoung Lee, Jin-Hyun Kim, Joo-Seok Park, Hong-kyu Choi</i>
PC-115	<b>Analysis of Genetic Diversity and Evaluation of Phenotypic Traits in Chrysanthemums</b> · 206 <i>Byung-Chun In, Sung-Chur Sim, Hyung-Won Choi, Sukyoung Jung, Yealim Yi, Bo-Kyung Choi, Yong-Seok Oh, Chang-Kyu Lee, Jin Hee Lim</i>
PC-116	<b>Development of SNP markers associated with citrus canker</b> ······························· 207 <i>Sanghyun Lim, Seunghee Ko, Young Chul Park, Yoon Kyung Uhm, Jae Joon Kim, Kwan Jeong Song, Ho Bang Kim</i>
PC-117	<b>TE-TRAP : New Marker System for Gamma Irradiated Sorghum (<i>Sorghum bicolor</i> L.)</b> ···· 208 <i>Seung Bin Im, Jaihyunk Ryu, Sang-Wook Jeong, Soon-Jae Kwon, Joon-Woo Ahn, Dong Sub Kim, Hee-bong Lee, Si-Yong Kang</i>
PC-118	<b>Functional Characterization of <i>PaLEAFY</i>, a <i>FLORICAULA/LEAFY</i> orthologue in <i>Phalaenopsis aphrodite</i></b> ······························· 208 <i>Seonghoe Jang</i>
PC-119	<b>Analysis of Candidate Genes for Grain Weight Traits Using NILs from An Interspecific Cross in Rice</b> ··· 209 <i>Yun-A Jeon, Dong-Min Kim, Hyun-Sook Lee, Ju-Won Kang, Yun-Joo Kang, Sang-Nag Ahn</i>
PC-120	<b>Delaying the tomato fruit ripening by sound wave treatment</b> ······························· 209 <i>Mi-Jeong Jeong, Joo-Yeol Kim, Jin Su Lee, Soo In Lee, Jin-A Kim</i>
PC-121	<b>Enhanced post-germinative growth of encapsulated somatic embryos of Siberian ginseng (<i>Eleutherococcus senticosus</i>) by carbohydrate addition to the encapsulation matrix.</b> ···· 210 <i>Su-Jin Jung, Ui-Soo Yoon, Yong-Eui Choi</i>
PC-122	<b>Characterization of roles of soybean <i>GIGANTEA</i> genes in day-length dependent flowering</b> ··· 210 <i>Wook-Hun Jung, Cheol Woo Choi, Kyung Hee Lee, Hyun Min Cho, Min Chul Kim</i>
PC-123	<b>Characterization of <i>OsJAC1</i> which is responding to different types of ionizing radiation</b> · 211 <i>In jung Jung, Jung Eun Hwang, Sung Min Han, Hong-Il Choi, Soon-Jae Kwon, Jin-Baek Kim, Si-Yong Kang, Dong Sub Kim</i>
PC-124	<b><i>De novo</i> transcriptome assembly of <i>Perilla citriodora</i> and expression profile study</b> ······· 211 <i>Junkyoung Choe, Woo Kyung Lee, Ji-Eun Kim, Myoung Hee Lee, Tae-ho Kim, Sung- Hwan Jo, Jeong-Hee Lee</i>
PC-125	<b>Investigation of morphological characteristics and pollen germination in <i>Senna tora</i></b> ···· 212 <i>Jin-Tae Jeong, Seon-Woo Cha, Bo-Keun Ha</i>

PC-126	<b>Molecular Breeding of Pepper Varieties (<i>Capsicum annuum</i>) Containing High Levels of Capsinoids</b> ..... 213 <i>Hyeon-Seok Jeong, Hee-Bum Yang, Siyoung Jang, Yeong Deuk Jo, Byoung-Cheorl Kang</i>
PC-127	<b>Genome Cloud 서버 연결 NCBI-SRA 데이터를 이용한 SNP 마커 발굴용 컨베이어 QUEUE 시스템 개발</b> ..... 214 <i>최준경, 이봉우, 김지은, 오재은, 이보미, 이정희, 조성환</i>
PC-128	<b>Developing Marker and Fine Mapping of the Powdery Mildew Resistance Gene in <i>Capsicum annuum</i></b> ..... 215 <i>Jinkwan Jo, Gyung Ja Choi, Jin-Kyung Kwon, Byoung-Cheorl Kang</i>
PC-129	<b>Transformation of soybean with AT-hook binding protein genes to delay senescence</b> ... 215 <i>Hyun Suk Cho, Jin Ho Yang, Jin Sol Park, Hye Jeong Kim, Yoon Jeong Lee, Jae Seong Kim, Hyun Hee Im, Ki Jung Lee, Dong Hee Lee, Yung Soo Chung</i>
PC-130	<b>Development of novel strategy for antifungal crop using trans-kingdom small RNA movement</b> ..... 216 <i>Byung-Jun Jin, Hyun Jin Chun, Min Chul Kim</i>
PC-131	<b>Caffeic acid O-methyltransferase (COMT) is involved in the melatonin synthesis in rice (<i>Oriza sativa</i>) plants</b> ..... 216 <i>Geun-hee Choi, Yeong Byeon, Hyoung Yool Lee, Kyoungwhan Back</i>
PC-132	<b>Development of <i>Oryza sativa</i> Alternative Spliced Transcripts Detecting Microarray</b> ..... 217 <i>Songhwa Chae, Kyong-Mi Jun, Joung Sug Kim, Baek-Hie Nahm, Yeon-Ki Kim</i>
PC-133	<b>Season-related variations of growth and metabolic profiles in <i>Pinus densiflora</i></b> ..... 218 <i>Mi Na Choi, Hyo-Ryeon Lee, Eung-Jun Park</i>
PC-134	<b>Systemic analyses of expression patterns and structural variation of soybean flowering genes in natural accessions</b> ..... 218 <i>Cheol-Woo Choi, Wook-Hun Jung, Kyung-Hee Lee, Min-Chul Kim</i>
PC-135	<b>Characterization of the aquaporin family genes and stress responsive expression profiling in <i>Brassica rapa</i></b> ..... 219 <i>Md. Abdul Kayum, Jong-In Park, Nasar Uddin Ahmed, Gopal Saha, Ill-Sup Nou</i>
PC-136	<b>Carotenoids Synthesis Gene Analysis in pepper</b> ..... 220 <i>Ayoung Jung, Hyeon-Seok Jeong, Dong Kyu Lim, Yeaseong Ha, Arti Rai, Jin-Kyung Kwon, Sung Won Kwon, Byoung-Cheorl Kang</i>
PC-137	<b>Isolation and Characterization of Pepper Genes Interacting with CMV-P1 Helicase Domain</b> ..... 220 <i>Yeaseong Ha, Joung-Ho Lee, Yoomi Choi, Min-Young Kang, JeeNa Hwang, Won-Hee Kang, Byoung-Cheorl Kang</i>
PC-138	<b>Genotyping-by-sequencing (GBS) for assessment of genetic diversity in pepper germplasm</b> ..... 221 <i>Koeun Han, Heayoung Lee, Jin-Kyung Kwon, Byoung-Cheorl Kang</i>

PC-139	<b>Effects of ionizing irradiation on mutation induction and nuclear DNA content in <i>Oryza Sativa</i> L.</b> ..... 221 <i>Sung Min Han, Jung Eun Hwang, In jung Jung, Hong-Il Choi, Soon-Jae Kwon, Jin-Baek Kim, Si-Young Kang, Dong Sub Kim</i>
PC-140	<b>Classification of Asian pears (<i>Pyrus</i> spp.) using the 12 standard set of microsatellite reference alleles</b> ..... 222 <i>Hyeondae Han, Youngjae Oh, Hyunsuk Shin, Sewon Oh, Jungyeon Won, Seolah Kim, Junhyeong Park, Yoon-kyeong Kim, Gidong Hwang, Daeil Kim</i>
PC-141	<b>Analysis of transcriptional regulation of Arabidopsis <i>PIF</i> family genes in response to abiotic stresses</b> ..... 223 <i>Jin-Seok Moon, Satoshi Kidokoro, Daisuke Todaka, Sayuri Igusa, Junya Mizoi, Kazuo Shinozaki, Kazuko Yamaguchi-Shinozaki</i>
PC-142	<b>Development of molecular markers for evaluation of low temperature germinability in rice germplasm</b> ..... 223 <i>Do Yoon Hyun, Sukyeung Lee, Yu-Mi Choi, Myung-Chul Lee, Se Jong Oh, Thomas H. Tai</i>
PC-143	<b>Expression of anthocyanin biosynthesis-related genes in wheat grain development</b> ..... 224 <i>Min Jeong Hong, Young Ha Yoon, Dong Sub Kim, Sang Hoon Kim, Joon-Woo Ahn, Si-Yong Kang, Yong Weon Seo, Jin-Beak Kim</i>
PC-144	<b>DNA 바코드 분석을 통한 국내 자생 난지형 잔디의 분류</b> ..... 224 <i>양대화, 홍민지, 정옥철, 진일두, 박미영, 김양지, 이효연</i>
PC-145	<b>국내 자생 난지형 잔디의 FTIR을 이용한 대사체 분석 및 구별</b> ..... 225 <i>홍민지, 양대화, 안명숙, 정옥철, 진일두, 김석원, 이효연</i>
PC-146	<b>들잔디(<i>Zoysia japonica</i> Steud.)의 상동재조합 효율 분석</b> ..... 226 <i>홍민지, 김재훈, 이효연, 권용익</i>
PC-147	<b>Development of Novel SSR Markers using NGS sequencing and Genetic Relationship Analysis in Blueberry (<i>Vaccinium</i> spp.)</b> ..... 227 <i>Jee-Hwa Hong, Eun-Jo Shim, Moo-Kyoung Yoon, Eun-Hee Soh</i>
PC-148	<b>C<sub>0</sub>t Analysis of <i>Chrysanthemum boreale</i>: the Realization of its Genome Characteristics</b> · 228 <i>Abigail Rubiato Cuyacot, So Youn Won, Sang Kun Park, Seong-Han Sohn, Ki-Byung Lim, Hyun Hee Kim, Franklin Hinosa Mancía, Yoon-Jung Hwang</i>
PC-149	<b>Overexpression of the RNA binding gene from <i>Medicago truncatula</i> regulates flowering time</b> ..... 229 <i>Hyun-Ju Hwang, Hyemin Lim, A-Ram Kim, Dae-Woo Lee, Jong-Seong Jeon, Jong Won Han, Gang-Seob Lee</i>
PC-150	<b>Seed color effect on germination rate and antioxidant activity under salt stress in wheat</b> ..... 230 <i>Paulina Calderón Flores, Dae Yeon Kim, Yong Weon Seo</i>

PC-151	<b>Intronic long noncoding RNA and sumoylation of histone methyltransferase contribute to control of flowering time in rice</b> .....	230
	<i>Ye Jin Kwon, Do Youn Kim, Sung-il kim, Jun Soo Kwak, Jong Tae Song, Hak Soo Seo</i>	
PC-152	<b>Flowering time is repressed by sumoylation of FLC</b> .....	231
	<i>Jun Soo Kwak, Sung-Il Kim, Do Youn Kim, Ye Jin Gyeon, Hak Soo Seo</i>	
PC-153	<b>Analysis of Phylogenetic Relationship of <i>Codonopsis lanceolata</i> Cultivated in Korea using RAPD Makers</b> .....	231
	<i>Jinsu Gil, Serim Kiml, Yurry Um, Seon-Woo Cha, Yi Lee</i>	
PC-154	<b>RNA seq Transcriptional Analysis of Pre-harvest Sprouting Korean Wheat</b> .....	232
	<i>Dae Yeon Kim, Jae Yoon Kim, Yong Weon Seo</i>	
PC-155	<b>Genome-wide transcription profiling of inflorescence development in wheat</b> .....	233
	<i>Dae Yeon Kim, Min Jeong Hong, Yong Weon Seo</i>	
PC-156	<b>Genome wide DNA methylation analysis of chromo methylase CMT3 and E3 sumo ligase AtSIZ1 mutants.</b> ....	234
	<i>Do Youn Kim, Ye-Jin Kwon, Sung-il Kim, Jun Soo Kwak, Min Kim, Jong Tae Song, Hak Soo Seo</i>	
PC-157	<b>Analysis of genetic diversity of <i>Codonopsis lanceolata</i> cultivated in Korea using SSR makers</b> .....	235
	<i>Serim Kim, Ji Hee Jeong, Jinsu Gil, Tae Dong Kim, Yurry Um, Ok Tae Kim, Ho Bang Kim, Hee Chung, Yi Lee</i>	
PC-158	<b>The Effects of ehanolic superjami bran extract on glucose and lipid metabolism in ovariectomized rats</b> .....	236
	<i>Su-Jin Nam, Mi-Young Kang</i>	
PC-159	<b>Repression of <i>DFR1</i> expression by <i>w3</i> mutation in Soybean</b> .....	236
	<i>Gyu Tae Park, Jagadeesh Sundaramoorthy, Jeong-Dong Lee, Hak Soo Seo, Jong Tae Song</i>	
PC-160	<b>Phylogenetic Relationship Analysis of <i>Adenophora triphylla</i> var. <i>japonica</i> HARA Local Collections using RAPD Markers</b> .....	237
	<i>Ki-Chan Park, Jinsu Gil, Serim Kim, Young-Guk Kim, Seon-Woo Cha, Yi Lee</i>	
PC-161	<b>The Arabidopsis abscisic acid receptors RCAR4 and RCAR5 promote disease resistance through regulation of stomatal aperture</b> .....	237
	<i>Woonhee Baek, Chanmi Park, Hyunhee Joo, Sung Chul Lee</i>	
PC-162	<b>Identification of Expansin Genes in <i>Platycodon grandiflorum</i> A. Using RNA-seq Analysis</b> .....	238
	<i>Sang Ik Park, Jemin Yoo, Yurry Um, Yi Lee</i>	
PC-163	<b>Functional roles of the pepper lipoxigenase, <i>CaLOX1</i>, in osmotic, drought, and high salinity tolerance</b> .....	239
	<i>Woonhee Baek, Chanmi Park, Hyunhee Joo, Sung Chul Lee</i>	
PC-164	<b>Agronomic traits evaluation of wheat germplasms</b> .....	240
	<i>Jin Seok Yoon, Yong Weon Seo</i>	

PC-165	<i>Capsicum baccatum</i> 종내 교잡에서 SNP 분자표지를 이용한 유전자 지도 작성 ..... 241 이예린, 정구미, 김해인, 은민호, 이준대
PC-166	Classification of Celiac disease epitopes of $\omega$ -gliadin through data mining and compared with Chinese spring genome sequence ..... 242 Cheol Won Lee, Yong Weon Seo
PC-167	The E3 Ubiquitin Ligase COP1 Regulates Thermosensory Flowering by Triggering GI Degradation in Arabidopsis ..... 243 Kiyoung Jang, Su-Jin Jung, Hong Gil Lee, Nam-Chon Paek, Pil Joon Seo
PC-168	The pepper RING finger protein CaRING1 plays a role in abscisic acid signaling and drought tolerance ..... 244 Hyunhee Joo, Woonhee Baek, Chanmi Park, Sung Chul Lee
PC-169	The CabZIP2 pepper pathogen-induced bzip transcription factor positive regulator of disease resistance by promoting PR protein induction ..... 244 Hyunhee Joo, Woonhee Baek, Chanmi Park, Sung Chul Lee
PC-170	갈색 기능성쌀 신품종 슈퍼홍미의 작물학적 특성과 성분 특성 ..... 245 함태호, 권순욱, 류수노
PC-171	조생 기능성쌀 빠른슈퍼자미와 만생 기능성쌀 늦은슈퍼자미 품종의 작물학적 특성 ..... 245 함태호, 권순욱, 류수노
PC-172	천연색소 C3G 고함유 만생, 대립 “슈퍼자미2호” 벼 품종 ..... 246 함태호, 권순욱, 류수노
PC-173	대립, 천연색소 C3G 고함유 “대립자미” 기능성 신품종 쌀의 이화학적 특성 ..... 247 함태호, 류수노, 강미영
PC-174	눈이 크고 C3G색소 고함유 품종 “큰눈자미” 기능성 쌀의 이화학적 특성 ..... 248 함태호, 류수노, 권순욱

## 차세대BG21사업단

### 농생물게놈활용연구사업단

OD-01	Achievements and Perspectives of GWAS Case Study in Rice Core Set ..... 253 Yong-Jin Park, Tae-Sung Kim, Kyu-won Kim, Chang-Yong Lee, Ju-Hyun Lee, Yong-Soo Choi, Il-Pyung Ahn, Won-Il Kim, Boem Seok Park
OD-02	고밀도 콩 SNP array 이용 유전분석 집단 및 유전체 육종 토대 구축 ..... 254 문중경, 강성택, 정순진, 김남신, 전태환
OD-03	Genome-wide association study (GWAS) in pepper using a core collection ..... 254 Hea-Young Lee, Ho-Cheol Go, On-Suk Heo, Jin-Kyung Kwon, Byoung-Cheorl Kang

OD-04	<b>Multiple reference genome of Cucurbits (melon and Korean melon) for Genome Wide Association Study (GWAS)</b> ..... 255 <i>Ah-Young Shin, HyeRan Kim, Jongmoon Ahn, Seokhyeon Nahm, Jeong Mee Park, Suk-Yoon Kwon</i>
-------	--

OD-05	<b>과수 분야 핵심집단 및 게놈전체연관분석을 통한 유전체 육종 기반구축</b> ..... 256 <i>김대일, 허운영, 최철, 김정희, 김윤경, 오상근, 박범석</i>
-------	---

---

**GM작물개발사업단**

---

OE-01	<b>피노믹스 연구개발 동향 : 혁신 플랫폼</b> ..... 259 <i>권택윤, 김경환, 윤혜진, 이성근</i>
-------	---

OE-02	<b>식물표현체 기술을 이용한 작물육종효율 증진</b> ..... 260 <i>김도순, 이태영, 김진원</i>
-------	--

OE-03	<b>Sound waves delay tomato fruit ripening by negatively regulating ethylene biosynthesis and signaling genes</b> ..... 261 <i>Mi-Jeong Jeong, Joo-Yeol Kim, Jin Su Lee, Soo In Lee, Jin-A Kim</i>
-------	---

OE-04	<b>국립농업과학원 농업생명자원부 GM격리포장 소개 및 운영계획</b> ..... 262 <i>이강섭</i>
-------	---

---

**식물분자유종사업단**

---

OF-01	<b>유전체기반 분자유종을 위한 생물정보분석 파이프라인</b> ..... 265 <i>유익수</i>
-------	--

OF-02	<b>DNA-free Genome Editing in Plants</b> ..... 265 <i>Soon-Il Kwon, Je Wook Woo, Jungeun Kim, Jin-Soo Kim, Sunghwa Choe</i>
-------	--

---

**식물분자유종사업단**

---

PD-01	<b>Soybean germplasm, a rich genetic resource to be explored for the identification of salt tolerance genes and their mechanism of action</b> ..... 266 <i>Sajeesh Kappachery, Jagadeesh Sundaramoorthy, Gyu Tae Park, Jeong-Dong Lee, Hak Soo Seo, Jong Tae Song</i>
-------	--

PD-02	<b>Isolation of rice T-DNA tagged mutants being resistant to brassinosteroid (BR) biosynthetic inhibitor Propiconazole (Pcz)</b> ..... 267 <i>Claudia Corvalán, Soon Il Kwon, Haerim Kim, Doyeon Kim, Jewook Woo, Sunghwa Choe</i>
-------	---

PD-03	<b>Identification and characterization of the novel gene encoding a protein responsible for biosynthesis of DDMP saponin in soybean</b> ..... 268 <i>Jagadeesh Sundaramoorthy, Gyu Tae Park, Sajeesh Kappachery, Jeong-Dong Lee, Hak Soo Seo, Jong Tae Song</i>
-------	--

PD-04	<b>Small RNA and degradome profiling reveals a role for miRNAs and their targets in the regulation of NB-LRR disease resistance genes</b> ..... 269 <i>June Hyun Park, Igojo Kang, Chanseok Shin</i>
PD-05	<b>Molecular breeding and commercialization of high yielding rice through the modification of plant type and introduction of new alleles.</b> ..... 270 <i>Hee-Jong Koh</i>
PD-06	<b>Detection of a new genetic locus for the high amylose content in rice mutant.</b> ..... 270 <i>Heng Wang, SeongGyu Jang, DaEun Lim, Ji-Ung Jeung, Soon-Wook Kwon</i>
PD-07	<b>염생식물 나문재의 종자구조 및 염농도에 따른 유묘생장 특성</b> ..... 271 <i>권혁규, 전효진, 백정선, 신소희, 정재혁, 이승재, 정남진</i>
PD-08	<b>Analysis of Phylogenetic Relationship from <i>Angelica gigas</i> collected in Korea using RAPD Markers</b> ..... 272 <i>Jinsu Gil, Serim Kiml, Yurry Um, Ok Tae Kim, Hee Chung, Seon-Woo Cha, Yi Lee</i>
PD-09	<b>Protein phosphatase 2C induced by abscisic acid positively regulates <i>Rsv3</i>-mediated extreme resistance</b> ..... 272 <i>Jang-Kyun Seo, Sun-Jung Kwon, Won Kyong Cho, Hong-Soo Choi, Kook-Hyung Kim</i>
PD-10	<b>Evaluation of sprouting rate of mature and developing seeds in red grain wheat (<i>Triticum aestivum</i> L.)</b> ..... 273 <i>Dae Yeon Kim, Oonha Shin, Yong Weon Seo</i>
PD-11	<b>Potential hybrids of <i>Miscanthus sinensis</i> x <i>M. sacchariflorus</i> revealed by morphological traits analysis</b> ..... 273 <i>Soo-Hyun Lim, Hae-Rim Park, Dong-Gil Kim, DoKyoung Lee, Gyoungju Nah, Do-Soon Kim</i>
PD-12	<b>Complete chloroplast genomes of two <i>Miscanthus</i> species</b> ..... 274 <i>Gyoungju Nah, Ji-Hoon Im, Soo-Hyun Lim, Kyunghee Kim, Do-Soon Kim</i>
PD-13	<b>Quantitative shotgun proteomic analysis of rice anther under the cold stress</b> ..... 274 <i>Joohyun Lee, Mijeong Kim, Yoonjung Lee</i>
PD-14	<b>무(radish)에서 자가불화합(self-incompatibility)을 결정하는 <i>S</i> locus core region에 위치한 <i>SLL2</i> 유전자 변이를 이용한 <i>S</i> haplotyping 시스템 구축</b> ..... 275 <i>김대현, 김성길</i>
PD-15	<b>E3 SUMO ligase AtSIZ1 regulates the amounts of nutrient reservoir cruciferins in <i>Arabidopsis thaliana</i> seed.</b> ..... 276 <i>Sung-Il Kim, Joo Yong Kim, Do youn Kim, Ye Jin Gyeon, Jun Soo Kwak, Hak Soo Seo</i>
PD-16	<b>Genetic diversity analysis of wild <i>Codonopsis lanceolata</i> in Korea using SSR makers</b> ... 276 <i>Serim Kim, Ji Hee Jeong, Jinsu Gil, Tae Dong Kim, Yurry Um, Ok Tae Kim, Ho Bang Kim, Yi Lee</i>
PD-17	<b>Soybean molecular breeding platform based on variation blocks</b> ..... 277 <i>Yul-Ho Kim, Hyang-Mi Park, Sunghoon Lee, Yu-Young Lee, Su Jeong Kim, Whang-Bae Sohn, Su-Young Hong, Jeong-Hwan Nam, Kibum Kweon, Jin-Cheol Jeong</i>

PD-18	<b>Overexpression of the <i>Arabidopsis</i> vacuolar H<sup>+</sup>-pyrophosphatase <i>AVP1</i> gene in rice plants improves grain yield under paddy field conditions</b> ..... 278 <i>Il-Sup Kim, Young-Saeng Kim, Yul-Ho Kim, Hyang-Mi Park, Ho-Sung Yoon</i>
PD-19	<b>SNP 마커를 이용한 고추의 적색소 함량 연관 QTL mapping</b> ..... 278 <i>김정호, 안율균, 이해은, 김진희, 김도선, 조명철, Sandeep Karna</i>
PD-20	<b>Identification of modulatory elements in xylem development for biomass production</b> ..... 279 <i>Jinu Kim, Hwi Seong Jeon, Hong Joo Cho, Soon Il Kwon, Young Hoon Jung, Jae-Soon Lee, Eun Woon Noh, Kyoung Heon Kim, Ohkmaek, Park</i>
PD-21	<b>The Effects of Superjami bran on in vitro and in vivo antioxidative and bone mineral density activities in ovariectomized rats</b> ..... 279 <i>Su-Jin Nam, Mi-Young Kang</i>
PD-22	<b>Cloning and functional characterization of an acyl-ACP thioesterase (CvFatB) from <i>Cuphea viscosissima</i> in <i>Arabidopsis</i></b> ..... 280 <i>Kyung Hee Roh, Han-chul Kang, Jong-Bum Kim, Hyun Uk Kim, Kyeong-Ryeol Lee</i>
PD-23	<b>The influence of silver thiosulfate and thidiazuron on shoot regeneration from cotyledon explants of <i>Brassica napus</i></b> ..... 280 <i>Kyung Hee Roh, Han-chul Kang, Jong-Bum Kim, Hyun Uk Kim, Kyeong-Ryeol Lee</i>
PD-24	<b>A review on change in plant proteome following biotic stress.</b> ..... 281 <i>R. Krishna, Ravi Gupta, Chul Woo Min, So Wun Kim, Sun Tae Kim</i>
PD-25	<b>천연색소 C3G 고함유 “슈퍼자미” 기능성 신품종 쌀의 이화학적 특성</b> ..... 281 <i>류수노, 함태호, 강미영</i>
PD-26	<b>Searching For Transcription Factors Involved In Ammonium Assimilation and Root Growth in Rice Plants</b> ..... 282 <i>Ryza A. Priatama, Vikranth Kumar, Jin-hee Jeong, Chang-deok Han</i>
PD-27	<b>MSP1 triggers cell death and defense response in rice</b> ..... 282 <i>Qingfeng Meng, Yiming Wang, Kyu Young Kang, Ravi Gupta, Sun Tae Kim</i>
PD-28	<b>Overexpression of a novel E3 ubiquitin ligase causes coiled branches phenotype in <i>Arabidopsis</i></b> ..... 283 <i>Gyu Tae Park, Jagadeesh Sundaramoorthy, Jeong-Dong Lee, Hak Soo Seo, Jong Tae Song</i>
PD-29	<b>Self-directed control of the diurnal CONSTANS dynamics in <i>Arabidopsis</i> photoperiodic flowering</b> ..... 284 <i>Mi-Jeong Park, Young-Ju Kwon, Kyung-Eun Gil, Pil Joon Seo, Jae-Hoon Jung, Chung-Mo Park</i>
PD-30	<b>CaLEA1 is a late embryogenesis abundant protein in pepper that positively regulates abscisic acid signaling, drought and salt stress response</b> ..... 284 <i>Chanmi Park, Hyunhee Joo, Woonhee Baek, Sung Chul Lee</i>
PD-31	<b>The putative E3 ubiquitin ligase CaAIR1 in pepper regulates abscisic acid signaling and drought stress response</b> ..... 285 <i>Chanmi Park, Hyunhee Joo, Woonhee Baek, Sung Chul Lee</i>

PD-32	<b>Comparative transcriptome analysis of tolerant rice mutant and its wild type in response to arsenate stress</b> .....	285
	<i>Hyeon Mi Park, Sun-Goo Hwang, Cheol Seong Jang</i>	
PD-33	<b>Mutation of <i>SPOTTED LEAF3 (SPL3)</i> impairs abscisic acid-responsive signaling and delays leaf senescence in rice</b> .....	286
	<i>Seung-Hyun Wang, Jung-Hyun Lim, Yasuhito Sakuraba, Nam-Chon Paek</i>	
PD-34	<b>Study on Phenotypes and Agronomical utility of a Rice <i>GT1 (grassy tillers 1, OsGT1)</i> Homologue</b> .....	286
	<i>Vikranth Kumar, Yuan Hu Xuan, Byoung Il Je, Soon Ju Park, Jin Huang, Jing Miao Liu, Ryza A. Priatama, Vimal Raj K, Sung Hoon Kim, Jin-hee Jeong, Chang-deok Han</i>	
PD-35	<b>Genome-specific transcripts analysis in a 2BS.2RL wheat-rye translocation using custom array</b> .....	287
	<i>Yong-Jin Lee, Tong-Geon Lee, Yong-Weon Seo</i>	
PD-36	<b>Global investigation of small RNA expression on nutrient stress responses provides information on nutrient-responsive microRNAs involved in crop productivity</b> .....	288
	<i>Sang-Yoon Shin, Dooyoung Lee, Ju-Kon Kim, Chanseok Shin</i>	
PD-37	<b><i>OsVIL</i> genes, which encode PRC2 chromatin remodeling factors, may be used for improving grain yield by increasing biomass in rice.</b> .....	289
	<i>Jung-Il Yang, Hee Joong Jeong, Lae-Hyeon Cho, Jinmi Yoon, Gynheung An</i>	
PD-38	<b>Structural and Functional Insights into Enzymes in Nitrogen Remobilization Pathway</b> .....	290
	<i>Inchul Shin, Kitae Han, Sangkee Rhee</i>	
PD-39	<b>고추 탄저병 및 CMV 저항성 마커 개발과 복합내병성 품종 육성과제 진도 보고</b> .....	290
	<i>박석진, 도재왕, 한정현, 윤재복</i>	
PD-40	<b>유전체기반 분자유종시스템 구축</b> .....	291
	<i>유의수, 최범순, 이승욱, 김정희, 진행운, 이현오, 신지연, 박미소, 강정대</i>	
PD-41	<b>The <i>Arabidopsis</i> MYB96 Transcription Factor Is a Positive Regulator of <i>ABI4</i> in the Control of Seed Germination</b> .....	292
	<i>Kyounghee Lee, Hong Gil Lee, Seongmun Yoon, Hyun Uk Kim, Pil Joon Seo</i>	
PD-42	<b>페튜니아 원형질체 배양을 통한 CRISPR/Cas9 기반 타겟형질 교정</b> .....	293
	<i>이종숙, 최서희, 박누리, 하혜정, 배상수, 이궁주</i>	
PD-43	<b>InsP6-Sensitive Variants of the <i>Gle1</i> mRNA Export Factor Rescue Growth and Fertility Defects of the <i>ipk1</i> Low-Phytic-Acid Mutation</b> .....	293
	<i>Ho-Seok Lee, Du-Hwa Lee, Hyun-Sook Pai</i>	
PD-44	<b>Development of EMS mutant populations in <i>Capsicum annuum</i> and identification of non-pungent mutants</b> .....	294
	<i>Muhammad Irfan Siddique, Koeun Han, Doyeon Hwang, Hee-Jin Jeong, Arti Rai, Byoung-Cheorl Kang</i>	

PD-45	Development of a New Wheat Mutant of Low-Molecular-Weight Glutenin Subunit at <i>Glu-B3</i> Locus ..... 294 <i>Jong-Yeol Lee, Hye-Rang Beom, Sun-Hyung Lim, Young-Mi Kim, Chul-Soo Park</i>
PD-46	Integrated analysis of the transcriptomes and primary metabolite profiles of adventitious roots of <i>P. ginseng</i> cultivars ..... 295 <i>Yun Sun Lee, Hyun-Seung Park, Dong-Kyu Lee, Murukarthick Jayakodi, Nam-Hoon Kim, Sang-Choon Lee, Jinkyung Kim, Hana Lee, Dong-Yup Lee, Sung Won Kwon, Tae-Jin Yang</i>
PD-47	고추 유용 형질 연관 분자표지의 Fluidigm용 SNP 분자표지로의 전환 ..... 296 <i>김해인, 이예린, 정규미, 은민호, 이준대</i>
PD-48	야생벼 유전자원의 수량안정성 유전자 탐색 이용 ..... 297 <i>이현숙, 강주원, 상세티, 전윤아, 레이잉핀, 노심, 코코명, 강윤주, 윤여태, 안상낙</i>
PD-49	Development of molecular markers tightly linked to bacterial wilt resistance genes in pepper ( <i>Capsicum annuum</i> L.) ..... 298 <i>Daewoong Lee, Yul-Kyun Ahn, Younghoon Park, Tae-Hwan Jun</i>
PD-50	화피를 제거한 통통마디 종자의 발아특성과 염농도에 따른 초기생육 특성 ..... 299 <i>전효진, 권혁규, 백정선, 신소희, 정재혁, 이승재, 정남진</i>
PD-51	Drought stress-responsive transcript analysis of wheat-rye translocation line using cDNA-AFLP ..... 300 <i>Woo Joo Jung, Yong Weon Seo</i>
PD-52	Targeted mutagenesis of SSS4A gene related starch biosynthesis using gene editing technology in Dongjin rice ..... 301 <i>Yu Jin Jung, Maral Tsevelkhoroloo, Hyun Ju Lee, Yeo Jin Jung, Hyo Ju Lee, Yong Gu Cho, Kwon Kyoo Kang</i>
PD-53	Toward mapping of genes conferring broad spectrum resistance to rice brown planthopper ..... 302 <i>Hyeonso Ji, Eokkeun Ahn, Seung-Bum Lee, Seok-Chul Suh</i>
PD-54	Identification of quantitative trait loci for fusarium wilt resistance in radish ( <i>Raphanus sativus</i> ) ..... 302 <i>Juyeon Jung, Jaehwang Ryu, Yeonok Choi, Young-Pyo Lee</i>
PD-55	Overexpression of the 3' half of the <i>PHYB</i> phytochrome partially suppresses dwarfism in the brassinosteroid-insensitive <i>brit-5</i> mutant ..... 303 <i>Yu Jeong Jeong, Soon Il Kwon, Silki Park, Su Jeoung Suh, Richard Cha, Yoong Eun Kim, Sunghwa Choe</i>
PD-56	Quantitative trait locus mapping and candidate gene analysis for heading date in an early maturing rice mutant induced by gamma irradiation ..... 304 <i>Sun-Goo Hwang, Cheol-Seong Jang</i>
PD-57	초형개량 초다수성 콩 분자육종 Molecular breeding for high-yielding soybean with improved plant type ..... 304 <i>이석하, 정지원</i>

PD-58	간척지 재배 가능한 내염성 사료용 콩 선발 ..... 305 <i>이정동, 김정화, 김민수, 박철우, 정재은, 아세코바소베틀, 한두호, 송종태</i>
-------	--

**GSP 사업단**

**GSP 식량종자사업단**

OG-01	옥수수의 해외시장 진출을 위한 육종연구에 대한 제안 ..... 311 <i>이명훈</i>
OG-02	Multiple Recognition of RXLR Effectors is Associated with Nonhost Resistance of Pepper Against <i>Phytophthora infestans</i> ..... 312 <i>Doil Choi</i>

**GSP 원예종자사업단 & GSP 채소종자사업단**

OH-01	Gene-specific marker development of cabbage for an efficient molecular breeding ..... 315 <i>Yoonkang Hur, Yong-Pyo Lim, Ill-Sup Nou</i>
OH-02	Molecular breeding strategies for pyramiding viral resistances in tomatoes ..... 316 <i>Inhwa Yeam</i>
OH-03	High-density genetic map construction and QTL analysis for seed size of fruits and powdery mildew resistance in watermelon ..... 317 <i>Gung Pyo Lee</i>
OH-04	Genomics approach to develop molecular markers for targeted breeding of radish ..... 318 <i>Ji-Young Lee, Kook Hui Ryu, Jung-Hun Lee, Khushboo Rastogi, Goh Choi</i>

<b>2015년 한국육종학회상</b>	..... 321
----------------------	-----------

<b>색인</b>	..... 325
-----------	-----------

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# 연사발표





---

**SYMP-01****Changing paradigms in plant breeding by new plant breeding technologies**

Ju-Kyung Yu

Syngenta Seeds, USA

Plant breeding is based on understanding genetics and mechanical systems to improve crop production. During the last century, conventional plant breeding, mostly based in the evaluation at the phenotypic level, had been successful in increasing crop yields. Within the last two decades there has been significant crop improvement due to the application of molecular genetics and genomics to improve efficiency and accuracy in plant breeding.

One of the key global challenges of the 21st century is the production of enough food for an ever increasing world population. Agricultural productivity needs to be increased while addressing the issues of scarcity of arable land and water, impact of changing climate and preservation of natural resources. Improvement of crop yields on limited agricultural resources requires concerted efforts using scientific and technological advances in multiple disciplines. Multidisciplinary approaches are being conducted to enhance crop improvement and meet resource needs. This session will address new plant breeding paradigms through the integration of multiple perspectives. The paradigm shift has occurred through the integration of five key components for crop improvement: 1) continued improvement of genomic tools, 2) information technology including open source data, 3) advanced analytical methods such as mathematical modeling and simulation, 4) adaption of non-crop information, and 5) increased importance of breeding operation enhancement.



## **Current Status of Seed Industry and Crop Breeding Strategies**

Chee-Hark Harn

Nongwoo Bio Co., Korea

Crop produce comes from seeds. It is important to have elite seeds for cultivation and harvesting. There are two major types of seeds in the seed market: F1 hybrid seeds and open-pollinated seeds (OP, traditionally pollinated). Farmers in developed countries plant F1 hybrid in most cases, while farmers in developing countries plant mainly OP. In fact, 60-70% of seeds planted in India and China are OP because OP is significantly cheaper. There are several reasons why the seed industry is important. First is for global food security. Based on the fact that the global population continues to increase steadily, additional productivity of 70% will be required to feed the global population by the year 2050. Second, seeds were traditionally used as food, both fresh and feed, but have now become materials for future industries of medicine, pharmaceuticals, functional foods, energy, and may other applications. Third, new breeding programs based on biotechnology have changed the seed market dramatically. These programs are highly competitive and indeed play a major role, not only in the reduction of breeding time, the development of various genetic sources, the enhancement of purity and cost-saving, but also for the selection of value-added varieties.

In Korea, F1 breeding began 65 years ago and the breeding programs for several vegetables and rice are in the top class worldwide. In addition, for the first time in 1999, a private seed company in Korea employed biotechnology for the purpose of crop breeding to develop platform technologies that could be utilized in the breeding practice. The major achievement so far is the development of DNA markers associated with resistance to disease, tolerance to the environment, and functional aspects. The application of genotyping has made many services possible, such as the purity control of F1 and inbred lines, variety verification, MAS (marker assisted selection), and MAB (marker assisted backcrossing). In addition, cell fusion and DH technologies have helped breeders to solve breeding limitations. There have been many cases of successful crop transformations, however, no GM varieties have been successfully commercialized in Korea. I bet this is inevitable, though. And it should be, because Korea imports lots of GM products, equivalent to \$3 billion every year.

More seed production and higher crop quality require new R&D strategies for breeding practices in the seed industry. Thanks to genomics information with big data and anti-GMO policies, new technologies are on the horizon, including genomic breeding, genome editing, in silico breeding and NBT (new plant breeding technology). I am going to talk more about the direction and strategy of R&D for crop breeding.

---

**SYMP-03**



## **Global Marketing Strategies for Globalization of Seed Industry**

Kyoung Ou Ryu

Asia Seed Co. Ltd., Korea

The size of the global seed market and the volume of seed trading have rapidly increased in the 21st century where the total market size by 2012 was approximately 45 billion USD, of which 79% were field crops, 17% were vegetables and 4% were forage and turf. While the volume of the trade and the market as a whole expanded, the share of the market also changed as the top 9 largest seed companies controlled 62% of the market in 2012 as opposed to just 17% in 1996. As for the regional status of the market size, North America and Asia-Pacific regions had 69% of the total market worth in 2014. The changes in the seed market led to various adjustments in the seed trading regulations where the protective behaviors of major players affected the entire market.

Asia Seed Co., Ltd. is a vegetable seed company founded in 1992 and is thriving each year in exporting new hybrid vegetable seeds to clients around the world. As a second mover to the saturated market that is dominated by a few companies with large shares, the company has set up four major strategies to compete in the global market. First and the most important strategy is to increase investment in R&D portion and strengthen it. In most types of businesses, investing in R&D is the key to success. Especially in the vegetable seed industry, the competitiveness of a company is decided by the variety of its seeds that result from the R&D department. The second strategy is the localization and incorporation of the company. Globally, vegetable crops vary while the domestic Korean varieties are not even known in other countries. To overcome this problem, it is important to open branches and subsidiaries to enter the market with local types of varieties that will appeal to customers and farmers. In relationship to R&D investment, Asia Seed Co., Ltd. has already set up a breeding system in India and keep expanding to other nations as well. The third strategy is to develop new materials for both the niche market and new possibilities. The last strategy is to have manpower training system that is required in all other industries. In order to assess the performance of our hybrid seeds, trained managers will need to travel and visit plots to acquire the results of trial and offer instructions when they are not satisfactory. Moreover, it is essential for collecting genetic materials from around the globe in order to develop better hybrids for the future of the company.

Seed exporting, while difficult, can be a charming and lucrative business. With enthusiasm in dealing with challenges and opportunities, I will contribute more ideas and know-hows on how the company deals with those choices and possibilities.

**\*Corresponding Author:** E-mail: [ceo@asiaseed.co.kr](mailto:ceo@asiaseed.co.kr)

---

**SYMP-04**



## **Geno-Pheno in plant breeding**

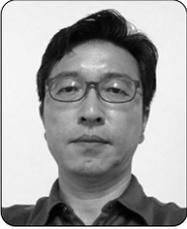
Dani Zamir

The Hebrew University of Jerusalem, Faculty of Agriculture, Israel

In crop genetics and breeding research, phenotypic data are collected for each plant genotype, often in multiple locations and field conditions, in search of the genomic regions that confer improved traits. Currently, virtually none of the data generated from the hundreds of phenotypic studies conducted each year are being made publically available as raw data; thus there is little we can learn from past experience when making decisions about how to breed better crops for the future. This ongoing loss of phenotypic information, particularly about crop productivity, must be stopped if we are to meet the considerable challenge of increasing food production sufficiently to meet the needs of a growing world population. I will present a number of plant-breeding case studies that demonstrate the value of introgressions from wild tomato species and of sharing information on crop plant genotypes and phenotypes.

**\*Corresponding Author:** Tel. +972 8 948 9092, E-mail: [dani.zamir@mail.huji.ac.il](mailto:dani.zamir@mail.huji.ac.il)

---

**SYMP-05****Understanding *Oryza* Genomes to maximize Genetic Variations for Crop Improvement**

Yeisoo Yu

Phyzen Genomics Institute, Phyzen Inc., Korea

Next generation sequencing (NGS) technologies provide a fast and easy way to understand the plant genomes, transcriptomes, regulatory elements and their interactions. About a decade ago, rice was the only crop that whole genome sequence information was publicly available but today many agricultural crops including maize, soybean, tomato, potato, cotton have been sequenced and many more will be available. Moreover newly developed method such as Genotyping-By-Sequencing (GBS) allows efficiently collecting sequence information from hundreds of individuals in population to identify genetic variations, detect quantitative trait loci (QTLs) and develop molecular markers. Coupled with high-throughput phenotyping, the accumulated genomic information will be effectively utilized in crop improvement by genomics-assisted breeding, genome-wide association mapping (GWAS) and genomic selection (GS).

Rice is one of the important staple crops providing daily nutrition to more than a half of the world population. The genus *Oryza* consists of 23 species including two domesticated rice and it has been classified into 10 distinct genome types, represented by six diploids (A, B, C, E, F, and G) and four allotetraploids (BBCC, CCDD, HHJJ, and HHKK). It shows wide ranges of phenotypic variations to biotic and abiotic stress thus is considered a genetic reservoir of unique allelic variation for rice improvement. International collaborative efforts have been focused on generating the *Oryza* genomics resources including reference genome, transcriptome, smallRNAs, methylome and resequencing of many accessions to collect genetic variations and better understand the 15 MY evolution of *Oryza*. The *Oryza* genomic resources will be a backbone to layer various omics data to catalogue more genetic variations within and between *Oryza* species and the untapped genetic diversities existing in wild *Oryza* species will be finally translated to crop improvement.



## Small RNA studies reveal a role for miRNAs and their targets in the regulation of NB-LRR disease resistance genes in pepper

June Hyun Park<sup>1</sup>, Igojo Kang<sup>1</sup>, Chanseok Shin<sup>1,2,3\*</sup>

<sup>1</sup>Department of Agricultural Biotechnology, Seoul National University, Seoul, 151–921, Republic of Korea,

<sup>2</sup>Research Institute of Agriculture and Life Sciences,

<sup>3</sup>Plant Genomics and Breeding Institute, Seoul National University, Seoul, 151–921, Republic of Korea

MicroRNAs (miRNAs) are a class of non-coding RNAs approximately 21-nt in length which play important roles in regulating gene expression in plants. Although many miRNA studies have focused on a few model plants, miRNAs and their target genes remain largely unknown in hot pepper (*Capsicum annuum*), one of the most important crops cultivated worldwide. We here employed high-throughput sequencing to comprehensively identify small RNAs and their targets in pepper. From these, we identified several novel targets of miRNAs, including the major *de novo* methylation enzyme involved in RNA-directed DNA methylation in plants. Furthermore, we identified several highly abundant 22-nt miRNA families that target conserved domains in NB-LRRs. We showed that transient co-expression of the miRNA with NB-LRRs, resulted in the attenuation of the hypersensitive responses in *Nicotiana benthamiana*, suggesting that interaction between miRNA family and disease resistance proteins is likely to serve as a conserved trigger for defense mechanism in Solanaceae. This work provides the first reliable draft of the small RNA transcriptome in pepper that offers an expanded picture of miRNAs in relation to NB-LRR regulation, providing a basis for understanding the functional roles of miRNAs in disease resistance.

---

**SYMP-07**



## **RNA-guided Genome Editing in Animals and Plants**

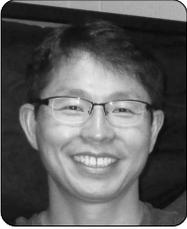
Jin-Soo Kim

Center for Genome Engineering, Institute for Basic Science, Seoul, South Korea  
Department of Chemistry, Seoul National University, Seoul, South Korea

Genome editing that allows targeted mutagenesis in higher eukaryotic cells and organisms is broadly useful in biology, biotechnology, and medicine. We have developed zinc finger nucleases (ZFNs), transcription activator-like effector nucleases (TALENs), and Cas9 RNA-guided engineered nucleases (RGENs), derived from the type II CRISPR/Cas prokaryotic adaptive immune system, to cleave chromosomal DNA in a targeted manner, producing DNA double-strand breaks in cells, the repair of which via endogenous systems gives rise to targeted genome modifications. The Cas9 protein, when complexed with small guide RNAs (sgRNAs), recognizes and cleaves target DNA sequences complementary to the guide RNAs *in vivo*, inducing targeted genome modifications at high frequencies in cultured cells and whole organisms. Despite broad interest in RNA-guided genome editing, RGENs are limited by off-target mutations. Here, we show that off-target effects of RGENs can be reduced below the detection limits of deep sequencing by choosing unique target sequences in the genome and modifying both guide RNA and Cas9. Furthermore, we deliver purified recombinant Cas9 protein complexed with sgRNAs (RGEN ribonucleoproteins (RNPs)) to animal embryos and cultured human cells including hard-to-transfect pluripotent stem cells to achieve highly efficient RNA-guided genome editing in cells and whole organisms. RGEN RNPs cleave chromosomal DNA almost immediately after delivery and are degraded rapidly in cells, reducing off-target effects and mosaicism.

---

**SYMP-08**



## **High-throughput phenotype analysis of transgenic plants for product development**

Dan Sung

Yield trait program, Monsanto, 110 TW Alexander Dr, RTP NC 27709

The world population is projected to reach to 9.6 billion people by 2050. With increasing population and improving living standards, the demand for food is accelerating. In order to meet increasing demand for food while the arable land and other resources are decreasing, agriculture needs all the tools available to sustainably increase crop yields. Development of effective GM traits to protect crops from abiotic and biotic stressors is a critical aspect of sustainable yield improvement. Efficient identification of traits and rapid integration of the traits into commercial elite germplasm requires robust and rapid traits testing. Monsanto have developed numerous high-throughput phenotyping platforms to support rapid trait identification and integration. Selected phenotyping platforms will be reviewed to gain understanding on how they are utilized for trait phenotyping.

---

**SYMP-09**



## **Spectral Imaging Technologies for Assessment of Plant Characteristics**

Moon S. Kim

Environmental Microbial and Food Safety Laboratory  
Agricultural Research Service, USDA,  
10300 Baltimore Ave.  
Beltsville MD 20705 USA  
Moon.Kim@ARS.USDA.GOV

Many spectral imaging technologies are available to nondestructive means to assess plant status including abiotic and biotic stress conditions. In recent years, ARS has developed various sensing and instrumentation technologies for agricultural applications. These include hyperspectral imaging for visible/near-infrared (NIR) reflectance and fluorescence imaging, and multispectral laser-induced fluorescence imaging. Hyperspectral imagery is a fusion of imaging and traditional spectroscopy. We recently expanded the hyperspectral capabilities to include rapid macro-scale Raman chemical imaging. The current state of the art of imaging technologies and their potential applications for characterization of the plant status are presented.



## 구두발표

- OA. 수량 및 저항성육종 (Breeding for yield increase and resistant variety)
- OB. 품질 육종 및 유전변이(Breeding for quality improvement, Genetic variation)
- OC. 분자육종 및 유전공학(Molecular breeding and biotechnology)





**QTL mapping of Fusarium wilt resistance in radish (*Raphanus sativus* L.)**

Xiaona Yu, Su Ryun Choi, Yong Pyo Lim\*

Molecular Genetics and Genomics Laboratory, Department of Horticulture, Chungnam National University, Daejeon 305-764, Korea

Fusarium wilt (FW), caused by the soil-borne fungal pathogen *Fusarium oxysporum* is a serious disease in cruciferous plants, including the radish (*Raphanus sativus*). To identify quantitative trait loci (QTL) or gene(s) conferring resistance to FW, we constructed a genetic map of *R. sativus* using an F<sub>2</sub> mapping population derived by crossing the inbred lines '835' (susceptible) and 'B2' (resistant). A total of 220 markers distributed in 9 linkage groups (LGs) were mapped in the *Raphanus* genome, covering a distance of 1041.5 cM with an average distance between adjacent markers of 4.7 cM. Comparative analysis of the *R. sativus* genome with that of *Arabidopsis thaliana* and *Brassica rapa* revealed 21 and 22 conserved syntenic regions, respectively. QTL mapping detected a total of 8 loci conferring FW resistance that were distributed on 4 LGs, namely, 2, 3, 6, and 7 of the *Raphanus* genome. Of the detected QTL, 3 QTLs (2 on LG 3 and 1 on LG 7) were constitutively detected throughout the 2-years experiment. QTL analysis of LG 3, flanked by ACMP0609 and *cnu\_mBRPGM0085*, showed a comparatively higher logarithm of the odds (LOD) value and percentage of phenotypic variation. Synteny analysis using the linked markers to this QTL showed homology to *A. thaliana* chromosome 3, which contains disease-resistance gene clusters, suggesting conservation of resistance genes between them.

Keywords: *Raphanus sativus*, Comparative mapping, Fusarium wilt resistant, QTL\*Corresponding Author: E-mail: [yplim@cnu.ac.kr](mailto:yplim@cnu.ac.kr)

## **Existence of qualitative resistance against blackleg disease in *Brassica oleracea* L. and detection of gene-specific single nucleotide polymorphism**

Arif Hasan Khan Robin, Jong-In Park, Nasar Uddin Ahmed, Rawnak Laila, Ill-Sup Nou\*

Department of Horticulture, Suncheon National University

Blackleg disease caused by *Leptosphaeria maculans*, is the most devastating disease of Brassica germplasm worldwide that causes million tonnes of crop losses per year throughout the world. To date, a total of 12 race-specific resistance genes of *Brassica napus* to *L. maculans* have been reported but linkage mapping analysis reveals that all of those loci are located in A genome i.e., in *B. rapa* chromosomes. *B. oleracea* has high ancestral synteny with *B. rapa* through their evolution. We believe that presence of qualitative resistance is possible in *B. oleracea* germplasm. The present study was therefore planned to find out any race-specific qualitative resistance gene present in C genome of *B. oleracea*. A total of 16 microsatellite markers were used which are linked to seven different *Rlm* and *Lep* genes of *B. napus* to screen 32 inbred lines of cabbage. Primers were designed based on homology assessment in corresponding nucleotide sequence available in Bolbase (a *B. oleracea* genome database, <http://www.ocri-genomics.org/bolbase/index.html>), located in *B. oleracea* scaffolds/chromosomes. Out of 16 SSR markers, 13 were found polymorphic which indicates possible existence of resistant genes in cabbage lines. The inbred lines are then assessed against two *L. maculans* stains with known avirulent genes. Some inbred lines were hypersensitive against gene-specific virulent strains of *L. maculans* that confirmed existence of *Rlm1*, *Rlm2*, *Rlm4*, *LepR3* and *LepR4* in the cabbage lines. In this way we were able to select out resistant and susceptible lines against each resistant gene. The gene-specific polymorphic SSR marker regions were cloned and sequenced and candidate SNPs were identified for confirmation of their functionality.

\*Corresponding Author: E-mail: nis@suncheon.ac.kr

## **Expression profiling of two contrasting bulb onion lines (*Allium cepa* L.) under Photoperiod and Drought Conditions**

Ranjith Kumar Manoharan, Jeong Suk Hyeon Han, Senthil Kumar Thamilarasan, Jong-In Park, Ill-Sup Nou\*

Department of Horticulture, Suncheon National University, Suncheon, Jeonnam 540–950, Republic of Korea

Onion and other *Allium* vegetables have been valued since antiquity for their pungent flavor and aroma. Modern science has confirmed traditional benefits that the organosulfur compounds that impart flavor also confer significant human health benefits such as reduced blood clotting and antimicrobial properties. Glucose, fructose and sucrose comprises majority of onion bulb dry matter content. The sugars, pyruvic acid accumulation and transcript level of some transcription factors involved in the biosynthesis of high sugars and pyruvic acid. These profiles were compared with two different lines 36101 (early) and 36122(Late) of bulb onion (*Allium cepa* L.) growing under drought and photoperiod condition using High Performance Liquid Chromatography (HPLC) and Quantitative real time PCR using FT genes. We identified the gene AcFT4 was responsible for early and late bulb initiation in the onion lines. The cultivar lines 36101 and 36122 were used to identify potential genes controlling pungency and sugar. The comparative analysis of two lines showed significant positive phenotypic and genetic correlations. Sugar and pungency profile showed significant difference between two lines. FT gene expression and pungency level was high in onion lines during drought stress. In this study, we proposed the biochemical characterization of two line and genes involved in the bulb formation were also studied. There is a correlation between sugars and pungency level during the drought stress. These results could be presumably used as useful information to obtain onion varieties rich in sugars and pungency.

Keywords: *Allium cepa* L., Pungency, Sugars, Bulb formation

\*Corresponding Author: Tel. +82-61-750-3249, E-mail: nis@suncheon.ac.kr

## TIFY family genes in Chinese cabbage (*Brassica rapa ssp. pekinensis*): A Genome-wide analysis reveals their stress and hormone responsive patterns

Gopal Saha, Jong-In Park, Nasar Uddin Ahmed, Md. Abdul Kayum, Ill-Sup Nou\*

Department of Horticulture, Sunchon National University, Suncheon 540–950, Korea

The TIFY family is composed of a plant-specific group of genes with diversity of functions. This family represents four subfamily of proteins viz. ZML, TIFY, PPD and JASMONATE ZIM-domain (JAZ) proteins. TIFY proteins especially, JAZ proteins have been reported to perform different biological processes, such as developmental and stresses and hormone responses in *Arabidopsis* and rice. However, there is no information about this family genes in Brassicaceae. This study identifies 36 TIFY genes in *Brassica rapa*, an economically important crop species from this family. An extensive *in silico* analysis through phylogenetic grouping, protein motif organization and intron-exon distribution also confirmed 4 subfamilies of BrTIFY proteins. Out of 35 *BrTIFY* genes, we identified 21 under JAZ subfamily besides 7 TIFY, 6 ZML and 2 PPD. An extensive expression profiling of 21 *BrTIFY JAZs* both in tissues and organs of *B. rapa* revealed differential expression patterns. Almost all the *BrTIFY JAZs* predominantly expressed in leaves and flower buds. Besides, in a flower stage specific expression analysis we observed 14 *BrTIFY JAZs* with constitutive expression patterns. This indicates BrTIFY proteins have a strong involvement in the development of *B. rapa* flowers. Our protein interaction study also reveals the strong association of these proteins with the fertility and defense processes of *B. rapa*. To elucidate the stress responsiveness of *BrTIFY* genes, we analyzed the low temperature-treated whole-genome microarray data set and found almost all the *BrTIFY JAZs* were having variable transcript abundance in two contrasting inbred lines of *B. rapa*. Subsequently, all 21 *BrTIFY JAZs* were validated in response to cold stress in the same two lines via qPCR, where 9 genes were found to show up- regulation. And, a high and differential qPCR expression pattern of all the *BrTIFY JAZs* was also recorded against JA. Additionally, *BrTIFY JAZs* were tested against salt, drought, Fusarium, ABA and SA treatments and a considerable number of genes were found to be induced. The extensive annotation and transcriptome profiling reported in this study will be useful for understanding the involvement of TIFY genes in stress resistance and different developmental functions, which ultimately provides the basis for functional characterization and exploitation of the candidate genes for genetic engineering of *B. rapa*.

\*Corresponding Author: Tel. +82-61-750-3249, E-mail: nis@sunchon.ac.kr

## ***De novo* assembly and transcriptome analysis of bulb onion (*Allium cepa*) during cold acclimation using contrasting genotypes**

Senthil Kumar Thamilarasan, Jeong Suk Hyeon Han, Jong-In Park, Ill-sup Nou\*

Department of Horticulture, Suncheon National University, 413 Jungangno, Suncheon, Jeonnam 540–950, Republic of Korea

Bulb onion (*Allium cepa*) is one of the second most widely cultivated and consumed vegetable crops in the world. During winter where the temperature can be as low, plant could get cold injury and limit the production of bulb onion. However, the genomic resources available for bulb onion are still very limited. To date, no studies about heritably durable cold and freezing tolerance were carried out in bulb onion genotypes using high-throughput sequencing technology was applied. We sequenced cold (2°C) freezing (-5 and -15°C) treated and control (25°C) samples of contrasting genotypes of *A. cepa* lines and obtained 4,52,194,370 total high quality reads. After *de novo* assembly reads were assembled into 54,047 genes finally generated with an average length of 1,331 bp. Based on the similarity search aligning all genes with known public non-redundant (NR) database, including Swiss-prot, KEGG and COG. Differentially expressed genes (DEGs) were investigated using FPKM method. Overall, 92,862 genes were differentially regulated in all libraries were identified. Additionally, increase our understanding of the DEGs, we performed GO and KEGG pathway enrichment analyses. Based on FDR≤0.01 value in cold freezing tolerant line candidate genes were selected and discussed. Finally 25 candidate genes were examined using qRT-PCR were differentially regulated and known to be associated with cold and freezing stresses. Moreover, *in silico* prediction of putative molecular marker 4,437 SSRs and 6,076 SNPs. Our study is the first to provide the transcriptome sequence resource of *Allium* spp., for cold and freezing stress. We identified large set of genes to determine its DEGs profile under cold and freezing condition using two different genotypes. These data provides a valuable resource of genetic and genomic studies of *Allium* spp.

Keywords: Bulb onion, cold, freezing stresses, Transcriptome, *de novo*, DEGs

\*Corresponding Author: Tel. +82-61-750-3249, E-mail: nis@sunchon.ac.kr

## **Characterization of regulatory genes for anthocyanin biosynthesis pathway and cold/freezing tolerance in *Brassica rapa***

Nasar Uddin Ahmed, Jong-In Park, Ill-Sup Nou\*

Department of Horticulture, Suncheon National University, 255 Jungang-ro, Suncheon, Jeonnam 540-950, Republic of Korea

Anthocyanins are responsible for vivid colors of flowers, fruits and vegetative tissues and biosynthesis of it is primarily controlled by several structural and regulatory genes. The regulatory mechanism of this pathway is still unknown. This study identified 19 transcription factors of *Brassica rapa* and investigated their regulatory function in anthocyanin biosynthesis pathway genes and cold and/or freezing tolerance in *B. rapa*. Expression analysis of these genes in the pigmented and non-pigmented portion of leaves of different lines of *B. rapa* revealed that BrMYB2-2 and BrTT8 showed responses contrasting with anthocyanin accumulation and cold stress. Sequences of these genes were analyzed and compared with similar gene sequences from other species and a high degree of homology with their respective functions was found. Co-regulated *cis* -elements were found in promoters of *BrPAL1*, *BrCHS*, *BrF3H1*, *BrF3'H1*, *BrFLS*, *BrBAN*, *BrDFR8*, *BrANS1*, and BrMYB2-2 and BrTT8 had binding sites of the promoters of those structural genes. Thus, the above results suggest the association of BrMYB2-2 and BrTT8 with regulation of anthocyanin biosynthesis pathway genes and cold and freezing stress tolerance and might be useful resources for development of cold resistant *Brassica* crops with desirable colors as well.

\***Corresponding Author:** Tel. +82-61-750-3249, E-mail: nis@sunchon.ac.kr

## **Fine mapping the UV-B resistance gene in soybean using 180K Axiom SoyaSNP assay**

Sungmin Kim<sup>1</sup>, Ju Seok Lee<sup>1</sup>, Sumin Park<sup>1</sup>, Kyungryun Kim<sup>1</sup>, Mijung Cho<sup>1</sup>, Eunsil Kim<sup>1</sup>, Bo-Keun Ha<sup>2</sup>,  
Sungtaeg Kang<sup>1\*</sup>

<sup>1</sup>Department of Crop Science & Biotechnology, Dankook University, Cheonan, 330–714, Korea

<sup>2</sup>Department of Plant Biotechnology, Chonnam National University, Gwangju, 500–757, Korea

The depletion of stratospheric ozone has resulted in increased amount of ultraviolet-B radiation (UV-B: 280-320 nm) reaching the Earth's surface and could cause significant biological effect in plants. In this study, putative quantitative trait loci (QTL), which is responsible to UV-B resistance in soybean, was identified using recently developed high-density 180K Axiom SoyaSNP genotyping array. A population of 115 recombinant inbred lines (RILs) derived from a cross between susceptible Keunolkong and resistant Iksan 10 was analyzed. A total 8,970 polymorphic SNP markers were used to construct linkage map. The both parents and RILs were grown with supplemental UV-B radiation in a greenhouse condition. Three categories of UV-B induced morphological damage, degree of leaf chlorosis, leaf shape change, and total plant damage were evaluated. Using composite interval mapping analysis, one major QTL associated with all of the phenotypic traits was detected on 7.7cM of soybean chromosome 7 with 22 of LOD score accounting for about 60% of phenotypic variance. Also, the allele from Iksan 10 were responsible for the UV-B resistance. Thus, the UV-B resistance QTL on chromosome 7 from Iksan 10 was designated to *qUVBRI*, corresponding to 30kb on the Williams 82 genome assembly (Glyma2.0) including 7 candidate genes. This result could be useful in breeding for new foxglove aphid resistant soybean cultivars. In addition, these results provided useful information not only for marker-assisted selection for UV-B resistance soybean, but also for the future identification of putative candidate genes, responsible for UV-B resistance in soybean.

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

## **Nucleotide polymorphisms in genes controlling panicle development are associated with the number of spikelets per panicle in rice**

Su Jang, Gileung Lee, Chang Soo Yoo, Hee-Jong Koh\*

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

The number of spikelets per panicle in rice is determined by characters of the panicle such as the number of primary branches (PB) and secondary branches (SB) and panicle length (PL). It is a quantitative traits controlled by several genes. In this study, the nucleotide polymorphism and haplotype diversity of coding region of genes related to number of spikelets per panicle (SPP), including *APO1*, *APO2*, *FONI*, *DEP1*, *GN1a*, *GHD8*, *HDI*, and *SPI*, were analyzed using 45 varieties which showed significant phenotypic variations for PL, PB, SB and SPP. Significant correlations were observed among all the panicle traits. A total of 151 polymorphisms, including 114 SNPs and 26 indels were detected in coding region of 8 genes which constructed 52 haplotypes. Neutrality tests revealed that population subdivision event or balancing selection occurred in locus of *APO2*, *FONI*, and *HDI* whereas no significant deviation from neutrality was detected in the other genes, suggesting a neutral evolution. Based on the results of GLM association analysis, 34 polymorphic sites in 6 genes were significantly related with the 4 panicle related-traits. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

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

## **Genetic mapping of quantitative trait loci controlling seed weight in an interspecific soybean recombinant inbred line population**

Krishnanand P Kulkarni, Minsu Kim, Jeong Hwa Kim, Sovetgul Asekova, Jong Tae Song, Jeong-Dong Lee\*

School of Applied Biosciences, Kyungpook National University, Daegu 702–701, Republic of Korea

Seed weight (SW), often expressed as 100-seed weight (HSW), is an important yield component in soybean and has been found to show positive correlation with seed yield. It is shown to behave as a quantitative trait controlled by many loci that are largely unclear. In this study, we represent the identification of chromosomal regions controlling the seed weight in soybean. We used a Recombinant Inbred Line (RIL) population, consisting of 188 lines derived from a cross of a wild soybean PI483463 (HSW: 0.85g) and a cultivated soybean cultivar Hutcheson (HSW: 14.05g) to identify the chromosomal regions controlling the SW trait. The population, along with parental samples and check, William82 (HSW: 21.2g) was grown for four years and phenotype data was recorded postharvest. A total of 535 SNP and 16 SSR markers, polymorphic between the parents were employed to genotype the RILs using Golden gate assay to develop the linkage map. Whole genome QTL scanning identified a total of 17 QTLs, spanning 10 chromosomes for the 100-seed weight. All these QTLs explained phenotypic variation (PV) in the range of 3.77 to 12.33%. Of the 17 QTLs, 2 QTLs *qSWA1-1* and *qSWD2-1*, found to be the consistent QTLs, expressing in all the four environments. The QTL *qSWD2-1* explained highest contribution to the total PV with 10.04 -12.23 %. The remaining 15 QTLs were identified in at least one environment with PV ranging up to 10.39%. The findings from this study will provide useful information to understand the genetic and molecular basis of SW and facilitate further genomic research leading to the yield improvements in soybean.

## Rice PCR1 affects grain weight and zinc accumulation

Hyun-Sook Lee<sup>1</sup>, Won-Yong Song<sup>2</sup>, Sang-Nag Ahn<sup>1</sup>

<sup>1</sup>College of Agriculture and Life Sciences, Chungnam National University, Daejeon, Korea

<sup>2</sup>POSTECH-UZH Cooperative Laboratory, Department of Integrative Bioscience and Biotechnology, Pohang University of Science and Technology, Pohang, Korea

Plants strictly regulate the uptake and distribution of Zinc (Zn), which is essential for growth and development. *Arabidopsis thaliana* plant cadmium resistance 2 (AtPCR2), a protein containing a placenta-specific 8 domain (PLAC8), is specifically expressed in the vascular tissue and epidermis of roots and is thought to act as a Zn efflux transporter (Song et al. 2010). Proteins containing PLAC8 domain function as major organ size regulators in *Solanum lycopersicum* and *Zea mays*, and putative metal ion transporters in *Arabidopsis thaliana*, *Oryza sativa* and *Brassica juncea*. But, there are no reports which showed that the protein containing PLAC8 have the function both of seed size regulation and metal homeostasis.

In our study, we found that plant cadmium resistance 1 (PCR1) influences on both Zn accumulation and grain weight in rice. The expression of *OsPCR1* is elevated in developing seeds of introgression line for *GW2*, which encodes a protein known to regulate grain weight. Grain weight of *OsPCR1* knockout and knockdown lines decreased than the wild type, while *OsPCR1* overexpression lines produced heavier grains. Furthermore, the grains of *OsPCR1* knockdown lines exhibited substantially higher Zn and lower Cd concentrations than the control. We identified some variation in the *OsPCR1* amino acid sequence between the japonica and indica rice types using 15 different rice varieties. Japonica-type PCR1 had a shorter N-terminus than did PCR1 in the other rice types. Furthermore, japonica-type grains accumulated less Zn than did indica-type grains. Our study suggests that rice PCR1 maintains metal ion homeostasis and grain weight and might have been selected for during domestication.

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

## 저온 및 식물생장조정제 처리가 더덕속 종자의 발아에 미치는 영향

이상권\*, 류수노, 최은영

서울시 종로구 대학로 86 한국방송통신대학교 농학과

초롱꽃과 더덕속 식물인 더덕과 만삼의 종자 발아 특성 조사로 종자입모을 향상을 위한 재배기술 개발의 기초 자료로 활용하고자 온도별 종자발아실험, 식물생장조정제 처리 효과구명, 종자 보관에 따른 발아율 등을 조사하였다. 실험에 사용한 재료중 더덕 종자는 강원도 농업기술원 산채연구소에서 2013년 가을에 채종한 종자를 분양 받아 사용하였고, 만삼 종자는 강원도 정선 재배농가에서 2013년 가을에 채종한 종자를 분양 받아 풍선법으로 정선한 후 종자봉투에 봉입 후 실험실(20℃)에 두어 실험할 때마다 꺼내어 사용하였다.

저온처리 온도는 5℃의 냉장고를 사용하여 1주, 2주, 4주간 저온처리 후 각각 20, 25, 30℃의 항온조건으로 옮겨 매일 발아 상태를 조사하였다.

발아 촉진 목적으로 사용된 식물생장조정제는 3종으로 GA<sub>3</sub>는 정량 후 증류수에 넣어 교반하여 사용하였고, BAP와 키네티는 용액 상태로 구입하여 시험 농도로 희석하여 사용하였다.

온도별 발아시험 결과 더덕은 20℃에서, 만삼은 15℃에서 각각 89%의 높은 발아율을 보였으며 30℃에서 더덕은 27%, 만삼은 2%의 낮은 발아율을 보였다.

5℃의 조건에서 더덕은 2주간, 만삼은 4주간 처리 후에 20, 25, 30℃에서 평균 발아율이 향상되었다. 더덕은 저온처리 기간에 배의 발달이 있었고 저온처리기간과 배의 발달과는 고도로 유의한 정의 상관관계가 있었다. 더덕과 만삼은 고온일수록 발아율이 저하되는 경향이 있었다. 만삼에서 GA<sub>3</sub> 처리농도와 발아율은 고도로 유의한 정의 상관관계를 보였다. 2주간 저온 처리 후 500ppm 복합처리에서 95%의 높은 발아율을 나타내었다. 그러나 더덕은 GA<sub>3</sub> 처리 후 발아율이 증가되지 않았다. 더덕, 만삼 종자에 사이토키닌 처리에서 처리농도와 발아율과는 고도로 유의한 부의 상관관계를 보였고 발아가 전혀 되지 않는 경우도 있었다. 더덕과 만삼 종자는 상온에서 1년간 보관 후 발아율이 크게 하락하였으나 저온냉장고에서 1년간 보관 후 더덕과 만삼의 발아율은 각각 75%, 79%로 높았다.

\*주저자: Tel. 010-4914-2396, E-mail: elcapitan@hanmail.net

## 등숙기 적산온도가 기능성 쌀품종 ‘슈퍼자미’의 수량과 C3G 함량에 미치는 영향

유정<sup>1</sup>, 함태호<sup>1</sup>, 김혜자<sup>1</sup>, 박미영<sup>1</sup>, 권순욱<sup>2</sup>, 류수노<sup>1</sup>

<sup>1</sup>서울 종로구 대학로 86 한국방송통신대학교 농학과

<sup>2</sup>경상남도 밀양시 삼랑진읍 부산대학교 식물생명과학과

국민경제와 삶의 질 향상에 따른 국민들의 건강에 대한 관심에 부응하여 유색미 품종들에 대하여 본격적으로 연구가 진행되고 있는 중이다. 그러나 이들 유색미에 함유된 생리활성물질들은 재배환경에 따라 변이가 크기 때문에 재배기술의 개선이 요구된다. 한국방송통신대학교 농학과에서 개발한 유색미 벼품종 슈퍼자미를 실험품종으로 2013년과 2014년도에 등숙기 별로 시료를 채취하여 출수 후 등숙기 적산온도에 따른 수량성과 C3G함량 등을 검토하였다.

2013년의 적산온도와 일조시간의 합은 3,511°C와 1,304시간, 2014년은 3,362°C와 1,241시간으로, 두 실험년도 간에는 적산온도와 일조시간의 합에서 차이가 컸다. 평균기온, 최고기온, 최저기온은 2013년이 2014년에 비하여 생육기간 전반에 걸쳐 높았다. 일조시간은 2014년이 2013년보다 약 104시간이 적었다. 또한 강수량은 2013년과 2014년의 우기가 집중된 7~9월의 강수량은 599.3mm와 601.7mm를 기록하여 비슷하였으며, 8~9월의 강수량은 2014년이 많았다. 벼의 생육단계별 기상특징을 보면 2013년의 평균기온은 감수분열기와 개화기 사이가 2014년에 비해 높은 온도로 경과한 특징을 보였으며, 일조시간은 감수분열기와 개화기에는 2013년이 2014년에 비하여 길었고, 등숙기에는 2013년이 2014년에 비하여 짧아 생육단계별로 차이가 컸다.

2014년이 2013년보다 천연색소 C3G함량이 높게 나타났다. 2014년의 등숙기는 2013년보다 일평균기온이 1.4~1.6°C 저온에 경과하였고, 일조시간의 경우 2013년의 283시간, 2014년이 335시간으로 2014년이 52시간 길었으며, 일교차는 2013년이 10.4°C, 2014년이 11.3°C로 2014년의 일교차가 크게 나타난 결과로 판단되었다.

종합적으로, 2013년의 적정 수확시기는 현미수량과 C3G함량, 등숙률 등을 감안할 시 출수 후 35~40일이 경과한 등숙기 적산온도가 803.7~893.1°C인 때가 적당한 것으로 판단되며, 2014년의 적정 수확시기는 출수 후 39~44일이 경과한 등숙기 적산온도가 835.3~919.32°C인 때가 적당한 것으로 판단되었다. 기능성 쌀 슈퍼자미는 출수 후 35일에서 44일경이 생리적 성숙시기로 평가되었다.

\*주저자: Tel. 010-3720-1008, E-mail: yboomb@hanmail.net

## **Identification and characterization of differentially expressed genes in response to ionizing radiations in rice**

Hong-Il Choi<sup>1</sup>, Soon-Jae Kwon<sup>1</sup>, Jung Eun Hwang<sup>1</sup>, Injung Jung<sup>1</sup>, Sung Min Han<sup>1</sup>, Sun-Goo Hwang<sup>2</sup>, Cheol Seong Jang<sup>2</sup>, Si-Yong Kang<sup>1</sup>, Dong Sub Kim<sup>1\*</sup>

<sup>1</sup>Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongseup 580–185, Republic of Korea.

<sup>2</sup>Plant Genomics Lab, Department of Applied Plant Sciences, Kangwon National University, Chuncheon, 200–713, Republic of Korea.

Exposure to ionizing radiation is regarded as a kind of abiotic stresses that can change the expression of genes in living organisms. This study aimed on investigating the variations in gene expressions induced by two different types of irradiations with different doses, which were low linear energy transfer (LET) gamma rays (100, 200, and 400 Gy) and high LET ion-beams (20, 40, and 80 Gy) on rice. RNA sequencing was carried out using the Illumina HiSeq-2500 platform. The average amount of reads were 4.8 Gb per individual, and 5 to 8% of the reads were removed after quality control. More than 90% of the RNA-seq reads were mapped to the rice reference genome sequence (IRGSP-1.0). A total of 247 differentially expressed genes (DEGs) were identified by comparison of the gene expression levels between the wildtype and the irradiated individuals. The 247 DEGs were divided into five modules and 27 intra-modular hub genes were found using the weighted correlation network analysis (WGCNA) method. The MEturquoise module had the most number of genes with 75 related to carbohydrate and small molecule metabolic processes. The co-expression network reconstructed using ARACNE (algorithm for reconstruction of accurate cellular networks) showed specific up- or down-regulation of the genes in each module according to the types and doses of radiation. This study will contribute to understanding the gene expression responses to ionizing irradiation.

**\*Corresponding Author:** Tel. 063-570-3311, E-mail: [bioplant@kaeri.re.kr](mailto:bioplant@kaeri.re.kr)

## Construction of high resolution genetic map and QTL mapping for clubroot resistance using genotyping-by-sequencing analysis in cabbage

Jonghoon Lee<sup>1</sup>, Nur Kholilatul Izzah<sup>1,2</sup>, Beom-Soon Choi<sup>3</sup>, Ho Jun Joh<sup>1</sup>, Sang-Choon Lee<sup>1</sup>, Sampath Perumal<sup>1</sup>, Joodeok Seo<sup>4</sup>, Kyounggu Ahn<sup>4</sup>, Eun Ju Jo<sup>5</sup>, Gyung Ja Choi<sup>5</sup>, Ill-Sup Nou<sup>6</sup>, Yeisoo Yu<sup>3</sup>, Tae-Jin Yang<sup>1,7\*</sup>

<sup>1</sup>Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Republic of Korea

<sup>2</sup>Indonesian Research Institute for Industrial and Beverage Crops (IRIIBC), Pakuwon, Sukabumi, Indonesia.

<sup>3</sup>Phyzen Genomics Institute, 501-1, Gwanak Century Tower, Gwanak-gu, Seoul, 151-836, Republic of Korea

<sup>4</sup>Joeun Seed, #174, Munbang-Ri, Cheonhan-Myun, Goesan-Gun, Chungcheongbuk-Do, 367-833, Korea

<sup>5</sup>Research Center for Biobased Chemistry, Korea Research Institute of Chemical Technology, Yusong-Gu, Daejeon, 305-600, Republic of Korea

<sup>6</sup>Department of Horticulture, Suncheon National University, Suncheon, 540-950, Republic of Korea

<sup>7</sup>Crop Biotechnology Institute/GreenBio Science and Technology, Seoul National University, Pyeongchang 232-916, Korea

Clubroot is a devastating disease caused by *Plasmodiophora brassicae* and results in severe losses of yield and quality in *Brassica* crops including *Brassica oleracea*. Therefore, it is important to identify resistance gene for CR disease and apply it to breeding of *Brassica* crops. In this study, we applied genotyping-by-sequencing (GBS) technique to construct high resolution genetic map and mapping of clubroot resistance (CR) genes. A total of 18,187 GBS markers were identified between two parent lines resistant and susceptible to the disease, of which 4,103 markers were genotyped in all 78 F<sub>2</sub> plants generated from crossing of both parent lines. The markers were clustered into nine linkage groups spanning 879.9 cM, generating high resolution genetic map enough to refine reported reference genome of cabbage. In addition, through QTL analysis using 78 F<sub>2:3</sub> progenies and mapping based on the genetic map, two and single major QTLs were identified for resistance of race 2 and race 9 of *P. brassicae*, respectively. These QTLs did not show collinearity with CR loci found in Chinese cabbage (*Brassica rapa*) but roughly overlapped with CR loci identified in cabbage for resistance to race 4. Taken together, genetic map and QTLs obtained in this study will provide valuable information to improve reference genome and clubroot resistance in cabbage.

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

## **Fine mapping the soybean foxglove aphid resistance gene *Raso2* in soybean using 180K Axiom® SoyaSNP genotyping assay**

Ju Seok Lee<sup>1</sup>, Sungmin Kim<sup>1</sup>, Sumin Park<sup>1</sup>, Kyungryun Kim<sup>1</sup>, Mijung Cho<sup>1</sup>, Eunsil Kim<sup>1</sup>, Jin Kyo Jung<sup>2</sup>, Jeong-Dong Lee<sup>3</sup>, Jung-Kyung Moon<sup>4</sup>, Namshin Kim<sup>5</sup>, Soon-chun Jeong<sup>6</sup>, Sungtaeg Kang<sup>1\*</sup>

<sup>1</sup>Department of Crop Science & Biotechnology, Dankook University, Cheonan, 330–714, Korea

<sup>2</sup>National Institute of Crop Science, RDA, 151 Seodun-dong, Suwon 441–857, Korea.

<sup>3</sup>Division of Plant Bioscience, Kyungpook National Univ., Daegu 702–701, Korea

<sup>4</sup>National Institute of Crop Science, Rural Development Administration, Suwon 441–857, Korea

<sup>5</sup>Korean Bioinformation Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon 305–806, Korea

<sup>6</sup>Bio-Evaluation Center, Korea Research Institute of Bioscience and Biotechnology, Cheongju 363–883, Korea

Foxglove aphid, *Aulacorthum solani* (Kaltenbach), is a Hemipteran insect that infected a wide variety of plants worldwide and caused serious yield losses in crops. The foxglove aphid resistance gene, *Raso2* was previously mapped from PI 366121 (*Glycine soja* Sieb. and Zucc.) to a 26cM marker interval on soybean chromosome 7. The development of additional genetic markers, which are mapped closer to *Raso2* were required to accurately position the gene to improve the effectiveness of marker assisted selection. The objective of this study was to narrow down the putative QTL region, which is responsible to foxglove aphid resistance in PI366121 using recently developed high-density 180K Axiom SoyaSNP genotyping array. One hundred and forty one F<sub>8</sub>-derived F<sub>12</sub> recombinant inbred lines developed from a cross of susceptible Williams 82 and resistant PI 366121, were used to generate a fine map of *Raso2* interval. The phenotyping of antibiosis and antixenosis was done through choice and no-choice assays with total plant damage (TPD) and primary infestation leaf damage (PLD). The composite interval mapping analysis showed that the physical interval between two flanking makers, which was corresponding to *Raso2*, was narrowed down to 500kb on the Williams 82 genome assembly (Glyma2.0), instead of 4Mb in the previous report using Goldengate assay. In the *Raso2* interval, there are about 60 candidate genes, including 4 of NBS-containing putative R genes. This result could be useful in breeding for new foxglove aphid resistant soybean cultivars.

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

## **Characterization and genetic mapping of a abaxially rolled leaf mutant in rice.**

Hyerim Lee, Yoye Yu, Hee-Jong Koh\*

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

Leaves are the organ for photosynthesis, respiration and transpiration, and have a major effect on crop yield. Therefore, leaf shape and structure are important agronomic traits in breeding for ideal type plant. We obtained a new abaxially rolled leaf mutant from Ilpum (*Oryza sativa ssp. japonica*) by the treatment of ethyl methane sulfonate (EMS). The abaxially rolled leaf mutant showed reduced plant height and panicle length, increased tiller number and panicle number than Ilpum. LRI (Leaf rolling index) analysis showed that the mutant have high value compared to the wild-type. In cross section analysis, the mutant was observed to have increased of bulliform cell number and size, and led to the outcurved leaf rolling. The phenotypes of the F1 plants derived from the cross between the mutant and Ilpum were normal. In F2 population, segregation ratio between the wild type and the mutant was 3:1. This genetic analysis indicated that leaf rolling is controlled by single recessive gene. Bulk segregant analysis (BSA) and genetic mapping were conducted using F2 population derived from the cross between mutant and Milyang23 (*Oryza sativa ssp. indica*). According to the results, the gene was located on the long arm of chromosome 2. Fine mapping is in progress.

This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

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

## **Sound waves delay tomato fruit ripening by negatively regulating ethylene biosynthesis and signaling genes**

Mi-Jeong Jeong<sup>1\*</sup>, Joo-Yeol Kim<sup>1</sup>, Jin Su Lee<sup>2</sup>, Soo In Lee<sup>1</sup>, Jin-A Kim<sup>1</sup>

<sup>1</sup>Department of Agricultural Biotechnology, National Academy of Agricultural Science (NAAS), 370 Nongsaengmyeong-ro, Wansan-gu, Jeonju, Jeollabuk-do, 560-500, Korea

<sup>2</sup>Postharvest Research Team, National Institute of Horticultural and Herbal Science (NIHHS), 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, 565-852, Korea

Regulation of fruit ripening may help extend fruit shelf life and prevent losses due to spoilage. Here, we investigated whether sound treatment could delay tomato fruit ripening. We treated harvested tomato fruits with low-frequency sound waves (1 kHz) for 6 h, and then monitored various characteristics of the fruits over 14-day period at 23±1°C. Seven days after the treatment, 85% of the treated fruits were green, versus fewer than 50% of the non-treated fruits. Most of the tomato fruits had switched to the red ripening stage by 14 days after treatment. Ethylene production and respiration rate were lower in the treated than non-treated tomatoes. Furthermore, changes in surface color and flesh firmness were delayed in the treated fruits. To investigate how sound wave treatment affects fruit ripening, we analyzed the expression of ethylene-related genes by quantitative real-time RT-PCR analysis. We found that the expression level of several ethylene biosynthetic and ethylene signaling pathway-related genes was influenced by sound wave treatment. These results demonstrate that sound wave treatment delays tomato fruit ripening by altering the expression of important genes in the ethylene biosynthesis and ethylene signaling pathways.

**\*Corresponding Author:** Tel. 063-238-4617, E-mail: center1097@korea.kr

## 형질전환 events에서 elite event를 신속히 선발하는 방법 및 선발 event의 분석

정순천<sup>1\*</sup>, 백인순<sup>1</sup>, 김보민<sup>2</sup>, 김지홍<sup>1</sup>, 김유진<sup>1</sup>, 육은수<sup>1</sup>, 김창기<sup>1</sup>, 한지학<sup>2</sup>

<sup>1</sup>충북 청주시 청원구 오창읍 한국생명공학연구원 바이오평가센터

<sup>2</sup>경기도 여주시 농우바이오 생명공학연구소

잠재적 안전성에 대한 논란으로 인하여 신규 개발되는 유전자변형작물은 고전적인 신품종과는 달리 환경 및 식품으로서의 안전성이 검증되어야 한다. 유전자변형작물의 안전성 평가는 개발되는 형질전환집단에서 선발된 하나의 elite event에 대해 이루어지는데, 본 평가 대상 elite event는 유전자의 삽입으로 인한 비의도적인 형질 변화가 최소화된 event이어야 한다. 분자유전학적으로 비의도적인 유전자 삽입 효과가 최소화되기 위해서는 단일 복제수의 도입유전자가 식물 유전체의 intergenic region에 삽입될 것을 요구한다. 본 연구의 목적은 배추줄나방 내성을 부여하는 CryIAc1 유전자가 형질 전환된 49 event의 양배추 형질전환집단에서 elite event를 선발하는 것이다. 먼저 도입 유전자 cassette이 tandem repeat로 빈번히 삽입되는 현상에 착안하여 도입유전자 cassette의 양 말단에서 제작한 primer의 방향에 따른 모든 조합을 사용하여 PCR을 수행하였다. 본 삽입구조 분석을 통하여 49개 event 중 36개 event는 tandem repeat의 구조로 도입유전자가 2개 복제 수 이상 삽입되었음을 알 수 있었다. 선발된 13개 event에 대하여 Southern blot 분석을 실시한 결과 7개 event가 단일 복제수의 도입유전자를 가짐을 알 수 있었다. 마지막으로 7개 event에 대한 삽입위치를 inverse PCR 기법을 사용하여 해명한 결과는 3개 event에서 단일 복제수의 도입유전자가 양배추 genome의 intergenic region에 삽입되었음을 알 수 있었다. 결론적으로, 본 연구 결과는 형질전환시의 도입유전자가 다중 복제수로 삽입될 시에 tandem repeat로 빈번히 삽입되는 현상에 기초하여 대량의 형질전환집단에서 elite event를 신속히 선발하는 방법을 제시하였다. 선발된 event의 분자유전학적 분석이 현재 진행되고 있다.

\*주저자: E-mail: scjeong@kribb.re.kr

## Expression analysis of two rice pollen-specific promoters using homologous and heterologous systems

Tien Dung Nguyen<sup>1</sup>, Moe Moe Oo<sup>1</sup>, Sunok Moon<sup>3</sup>, Hyun-Kyung Bae<sup>1</sup>, Sung Aeong Oh<sup>1</sup>, Moon-Soo Soh<sup>2</sup>, Jong Tae Song<sup>1</sup>, Jeong Hoe Kim<sup>4</sup>, Ki Hong Jung<sup>3</sup>, Soon Ki Park<sup>1\*</sup>

<sup>1</sup>School of Applied Biosciences, Kyungpook National University, Korea.

<sup>2</sup>Department of Molecular Biology, Sejong University, Korea.

<sup>3</sup>Graduate School of Biotechnology & Crop Biotech Institute, Kyung Hee University, Korea.

<sup>4</sup>Department of Biology, Kyungpook National University, Korea.

Tissue-specific promoters are a very useful tool for manipulating gene expression in a target tissue or organ; however, their range of applications in other plant species has not been determined, to date. In this study, we identified two late pollen-specific rice promoters (*ProOsLPS10* and *ProOsLPS11*) via meta-anatomical expression analysis. We then investigated the expression of both promoters in transgenic rice (a homologous system) and *Arabidopsis* (a heterologous system) using *ProOsLPS10* or *ProOsLPS11::GFP-GUS* constructs. As predicted by microarray data, both promoters triggered strong GUS expression during the late stages of pollen development in rice, with no GUS signals detected in the examined microspores and sporophytic tissues. Interestingly, these promoters exhibited different GUS expression patterns in *Arabidopsis*. While in *Arabidopsis*, the *OsLPS10* promoter conferred GUS expression at the uni- and bi-cellular microspore stages, as well as at the shoot apical region during the seedling stage, the *OsLPS11* promoter was not active in the pollen at any stage, or in the examined sporophytic tissues. Furthermore, by performing a complementation analysis using a *sidecar pollen (scp)* mutant that displays developmental defects at the microspore stage, we found evidence that *OsLPS10*, which can be an applied promoter expressed in *Arabidopsis*, is useful for directing gene expression in the early stages of pollen development. Our results indicate that the *OsLPS10* and *OsLPS11* promoters can drive the expression of target genes during the late stages of pollen development in rice, but not in *Arabidopsis*. Our results also emphasize the necessity of confirming the applicability of an established promoter to heterologous systems.

\*Corresponding Author: Tel. 053-950-7751, E-mail: [psk@knu.ac.kr](mailto:psk@knu.ac.kr)

## **Genome wide resequencing for KRICE\_CORE reveals their potentials for the future breeding, functional and evolutionary studies in the post-genomic era**

Tae-Sung Kim<sup>1,5</sup>, Kyu-Won Kim<sup>1,5</sup>, Qiang He<sup>1</sup>, Min-Young Yoon<sup>1</sup>, Won-Hee Ra<sup>1</sup>, Feng Peng Li<sup>1</sup>, Wei Tong<sup>1</sup>, Jie Yu<sup>1</sup>, Win Htet Oo<sup>1</sup>, Buung Choi<sup>1</sup>, Eun-Beom Heo<sup>1</sup>, Yoo-Hyun Cho<sup>2</sup>, Byoung-Kook Yun<sup>3</sup>, Chang-Yong Lee<sup>3</sup>, Donghwan Shim<sup>4</sup>, Beom-Seok Park<sup>4</sup>, Yong-Jin Park<sup>1,5\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Seedpia, 85, Maesil-ro, Kwonsun-ku, Suwon, 441–882 Republic of Korea

<sup>3</sup>Department of Industrial & Systems Engineering, Kongju National University, Cheonan 330–717, Republic of Korea

<sup>4</sup>The Agricultural Genome Center, National Academy of Agricultural Science, Rural Development Administration, Jeonju, Republic of Korea

<sup>5</sup>Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

Rice germplasm collections continue to grow in number and size around the world. Since maintaining and screening such massive resources remain as a great challenge, it is important to establish piratical ways to manage them. A core collection, by definition, refers to a subset of entire population but preserves most of the possible genetic diversity, enhancing the efficiency for germplasm utilizations. Here we reports the whole genome resequencing of the 137 Korean rice core set (KRICE\_CORE) that represents 25,604 rice germplasms deposited in Korean genebank of Rural Development Administration (RDA). We implemented the Illumina HiSeq 2000 and 2500 platform to produce short reads and then assembled those with 9.8x depth using Nipponbare as a reference. Comparisons of the sequences with the reference genome yield more than 15 million(M) single nucleotide polymorphisms (SNPs) and 1.3M insertion/deletion (INDELs). Phylogenetic and population analyses using 2,046,529 high quality SNPs successfully assigned each rice accessions to the relevant subgroups, suggesting those SNPs comprehensively capture evolutionary signatures accumulated in rice subpopulations. Furthermore, genome-wide association studies (GWAS) for 4 exemplary agronomic traits from the KRICE\_CORE manifest the utility of KRICE\_CORE, identifying previously defined gene or novel genetic polymorphisms that potentially regulate the important phenotypes. This study provides strong evidences that the size of KRICE\_CORE is small but contains such a high genetic and functional diversity across the genome. Thus those resequencing results will be useful for future breeding, functional and evolutionary studies in the post-genomic era.

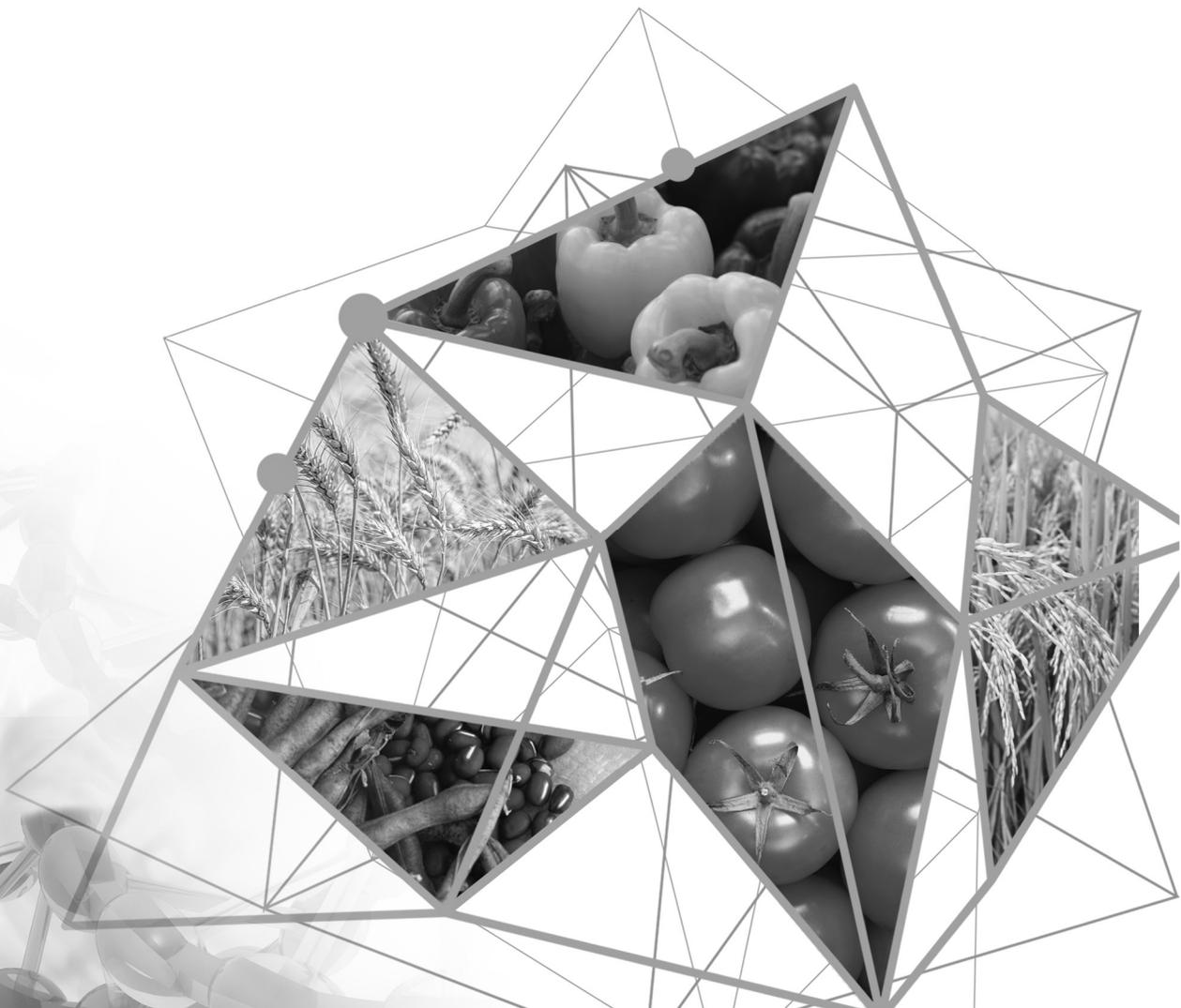
**\*Corresponding Author:** Tel. 041-330-1201, E-mail: [yjpark@kongju.ac.kr](mailto:yjpark@kongju.ac.kr)

## 포스터발표

PA. 수량 및 저항성육종 (Breeding for yield increase and resistant variety)

PB. 품질 육종 및 유전변이(Breeding for quality improvement, Genetic variation)

PC. 분자육종 및 유전공학(Molecular breeding and biotechnology)





## 양질 다수성 장류용 콩 “대찬”

강범규<sup>1\*</sup>, 김현태<sup>1</sup>, 이영훈<sup>3</sup>, 이병원<sup>4</sup>, 최만수<sup>1</sup>, 한원영<sup>3</sup>, 김현영<sup>1</sup>, 전명기<sup>2</sup>, 이석기<sup>5</sup>, 고종민<sup>3</sup>, 윤홍태<sup>1</sup>, 백인열<sup>6</sup>, 이영희<sup>7</sup>

<sup>1</sup>경남 밀양시 점필재로20 국립식량과학원 발작물개발과

<sup>2</sup>경남 창원시 의창구 창이대로 71 창원농업기술센터

<sup>3</sup>경남 밀양시 점필재로20 국립식량과학원 생산기술개발과

<sup>4</sup>경기도 수원시 권선구 서호로 54 국립식량과학원 수확후이용과

<sup>5</sup>전북 전주시 완산구 농생명로 300 농촌진흥청 국외농업기술과

<sup>6</sup>전북 완주군 이서면 혁신로181 국립식량과학원 기획조정과

<sup>7</sup>경남 밀양시 점필재로20 국립식량과학원 남부작물부

장류용 콩의 표준품종인 ‘대원콩’은 탈립에 매우 강하고 종실의 모양과 색택이 매우 우수하여 널리 재배되고 있다. 하지만 착협고가 높지 않고 재배시 도복에 약한 단점이 있어 기계화 적응성을 높이고 재배특성을 향상시키기 위해 이를 개량할 필요가 있다. 국립식량과학원에서는 2003년 단경 내도복 콩 품종육성을 목표로 모본을 ‘수원224호’, 부본을 ‘YS1325(동산121/Sprite87)’로 인공교배하여 2004~2005년 F<sub>1</sub>, F<sub>2</sub>를 집단 전개하고 2006~2007년 SSD로 세대축진하여 F<sub>6</sub> 이후 계통전개 하였다. 종실이 구형이며 제색이 없으며 도복에 강한 계통을 선발하여 2010년부터 2년간의 생산성검정과 3년간의 지역적응성검정을 거쳐 ‘대찬(밀양244호)’을 육성하고 2014년 품종보호출원 및 국가품종목록으로 등재하였다. ‘대찬’은 화색이 백색이고, 모용색이 회색, 종자는 구형이며 종피색과 제색이 황색으로 ‘대원콩’과 유사하다. 개화기는 8월 2일, 성숙기는 10월 13일로 ‘대원콩’보다 생육기간이 다소 짧으며 경장은 68cm로 ‘대원콩’보다 작고 주경절수는 15개, 분지수는 3개, 착협고는 15cm로 ‘대원콩’보다 크다. 종실의 장폭비는 0.97로 ‘대원콩’과 유사하고 100립중은 24.5g으로 ‘대원콩’보다 0.9g 작았다. 병 저항성 검정 결과 불마름병 저항성이 검정포장과 유묘검정에서 ‘대원콩’보다 강했다. 전국 11개 지역에서 수행한 지역적응시험에서 ‘대찬’의 수량은 전국평균 321kg/10a, 적응지역 평균 330kg/10a로 ‘대원콩’보다 각각 17%, 16% 증수하였다.

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

## 소립 다수성 나물용 콩 “해원”

강범규<sup>1\*</sup>, 김현태<sup>1</sup>, 이영훈<sup>2</sup>, 조상균<sup>4</sup>, 이병원<sup>5</sup>, 최만수<sup>1</sup>, 전명기<sup>3</sup>, 심하식<sup>6</sup>, 하태정<sup>7</sup>, 고종민<sup>2</sup>, 윤홍태<sup>1</sup>, 백인열<sup>8</sup>, 이영희<sup>9</sup>

<sup>1</sup>경남 밀양시 점필재로20 국립식량과학원 발작물개발과

<sup>2</sup>경남 밀양시 점필재로20 국립식량과학원 생산기술개발과

<sup>3</sup>경남 창원시 의창구 창이대로 71 창원농업기술센터

<sup>4</sup>강원도 철원군 동송읍 태봉로 2346 국립식량과학원 철원출장소

<sup>5</sup>경기도 수원시 권선구 서호로 54 국립식량과학원 수확후이용과

<sup>6</sup>전북 전주시 완산구 국립농업과학원

<sup>7</sup>전북 전주시 완산구 농생명로 300 농촌진흥청 연구성과관리과

<sup>8</sup>전북 완주군 이서면 혁신로181 국립식량과학원 기획조정과

<sup>9</sup>경남 밀양시 점필재로20 국립식량과학원 남부작물부

콩나물의 연간 소비량은 약 36만톤이며 시장규모는 약 5,000억 원으로 추정하고 있다. 장류는 약 9,800억 원, 두부의 시장규모는 약 5,400억 원으로 이와 비교했을 때 콩 가공식품 중 콩나물이 차지하는 비중은 세 번째로 많다. 나물용 콩 종실의 수요량은 약 6만 톤이며 생산량은 약 1만 톤에 불과한데 단위 면적 당 수량을 10kg 향상시키면 자급률을 1.14% 올릴 수 있어 수량성이 높은 나물용 콩을 개발할 필요가 있다. 이에 국립식량과학원에서는 2003년 ‘보석’을 모본으로 ‘소명콩’을 부분으로 인공교배하여 ‘04~’09년 F<sub>1</sub>~F<sub>6</sub> 계통 전개 및 선발과 ‘10~’14년 생산성검정시험과 지역적응시험을 수행하여 양질 소립 내병 다수성 특성의 ‘해원(밀양253호)’를 육성하여 2014년 품종보호 출원 및 국가품종목록으로 등재하였다. ‘해원’의 엽형은 피침형이며 화색은 자색, 모용색은 회색, 협색은 황색, 종피는 구형이며 황색 종피에 제색은 담갈색이다. 2012~2014년 4개 지역에서 수행된 지역적응시험에서 조사된 가변특성은 경장이 평균 55cm로 나물용 콩 표준품종인 ‘풍산나물콩’과 비슷하고 개화기와 성숙기는 7월 29일 및 10월 6일로 약간 빠르다. 주경의 마디수는 16개, 분지수는 4개로 ‘풍산나물콩’보다 많았으며, 도복에 강하다. 병해 김정포장에서 자연이병과 8ra 균주의 인공접종 결과 불마름병에 강한 저항성을 나타내었으며, 모자이크 바이러스 유묘접종에서 모자이크 증상을 보였으나 포장에서의 이병정도는 ‘풍산나물콩’보다 적었다. 종실 100립중은 8.1g으로 ‘풍산나물콩’보다 3.1g 작은 소립이며 콩나물 수율이 513%로 ‘풍산나물콩’과 비슷하였으나, 지역적응시험에서 적응지역의 수량성적은 16% 증수하여 337kg/10a로 개발된 나물용 콩 품종 중 가장 높았다.

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

## QTL analysis for drought tolerance using introgression lines from a cross between Milyang 23 and *O. glaberrima*

Ju-Won Kang<sup>1</sup>, Dong-Min Kim<sup>2</sup>, Hyun-Sook Lee<sup>1</sup>, Yeo-Tae Yoon<sup>3</sup>, Sang-Nag Ahn<sup>1\*</sup>

<sup>1</sup>Department of Agronomy, Chungnam National University, Daejeon 305–333, Korea

<sup>2</sup>Department of Variety Testing, Korea Seed & Variety Service, Gimcheon 740–220, Korea

<sup>3</sup>Chungnam Agricultural Research and Extension Services, Yesan 340–861, Korea

Drought stress is one of the major stresses affecting growth and productivity in rice. Drought tolerance is a complex trait governed by quantitative trait loci(QTLs) making it difficult to understand mechanisms underlying it. We generated a set of 55 introgression lines via backcrosses using Milyang23, the Korean Tongil-type rice variety as the recurrent parent and *Oryza glaberrima* (IRGC Acc. No. 103544) as a donor parent. 139 SSR markers were used to genotype 55 introgression lines. The 55 introgression lines with Milyang23 were evaluated for physiological traits such as fresh shoot weight (FSW), fresh root weight (FRW) and dry shoot weight (DSW) under the control and 30% PEG-treated condition. Three lines (IL9, IL12, and IL55) showing significant difference with Milyang23 were selected for further analysis. Genotyping revealed that three lines had four, four and two *O. glaberrima* homozygous segments, respectively. IL9 performed better than Milyang23 in all traits measured in the 30% PEG-treated condition. IL9 possessed four *O. glaberrima* introgressions on chromosomes 1, 2, 6 and 7. IL12 performed better than Milyang23 in FSW and FRW and contains four *O. glaberrima* introgressions on chromosomes 3 and 6. IL55 contains two *O. glaberrima* introgressions on chromosomes 2 and 6. Three lines shared the *O. glaberrima* segment delimited by markers RM133-RM225 at chromosomes 6. This region corresponds to the QTL region for drought tolerance reported by other previous studies. Although IL9 and IL12 showed improved drought tolerance at the seedling and vegetative stage, they performed poor under the drought stress at the reproductive stage implying that the level of drought tolerance differs according to the growth stage in rice. IL55 was not significantly different from Milyang 23 in SPP and FER and had significantly higher no. of the total grain than Milyang 23. This result seems to indicate that IL55 will be a good resource for drought tolerance breeding. The population would be useful not only in developing drought tolerant lines in the breeding program but also in fine-mapping the genes/QTLs for drought tolerance.

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

---

**PA-04****국산밀 품종의 파성 및 숙기관련 특성 분석**

강천식<sup>1</sup>, 고윤희<sup>1\*</sup>, 손재한<sup>1</sup>, 김정훈<sup>2</sup>, 박종철<sup>1</sup>, 오영진<sup>1</sup>, 김양길<sup>1</sup>, 김경호<sup>1</sup>, 정영근<sup>1</sup>, 김보경<sup>1</sup>

<sup>1</sup>전북 완주군 이서면 국립식량과학원 작물육종과

<sup>2</sup>경남 밀양시 점필재로 국립식량과학원 논이용작물과

밀은 세계 3대 식량작물 중 하나이며 국내에서도 1인당 연간 34kg을 소비하여 쌀 다음으로 소모량이 많은 작물이다. 국내 밀 육성은 농가소득 향상을 위한 수량성 증진뿐만 아니라 이모작 재배가 가능하도록 숙기 단축을 위하여 주력하고 있다. 이에 조숙 밀 품종개발을 위한 숙기 관련 특성을 분석하여 육종프로그램에 정보를 제공하기 위하여 본 연구를 수행하였다. 숙기관련 특성분석은 국내에서 개발된 올밀 등 38품종을 이용하였으며, 파성조사를 위한 춘화처리는 4°C에서 3주간 저온처리를 실시하여 온실에 이식한 후 24시간 일장을 처리하여 엽수, 지엽전개기, 출수기 등을 조사하였다. 파성 판정 결과 국내 대부분의 품종은 II(춘파형)~III(양절형)의 분포를 보였다. 즉, 올밀 등 25품종의 파성은 II로 춘파형이었고, 그루밀 등 13 품종은 III으로 춘파와 추파가 가능한 양절형이었다. 저온 무처리구의 지엽전개기는 평균 2월 11일(최저 3월 3일, 조중밀~최대 3월 30일, 그루밀)로 평균 67일(최소 47일, 조중밀~최대 94일, 그루밀)이 소요되었다. 엽수는 평균 9매(최소 7매~최대 11매), 출수기는 평균 3월 11일(최소 2월 21일~최대 4월 9일)로 품종간 차이를 나타냈다. 출수기가 빠를수록 엽수가 적으며 지엽전개기가 빠르고, 파성은 낮은 결과를 나타냈다. 이러한 결과는 파성이 낮으면서 엽수가 적고 지엽전개기가 짧은 특성이 조숙밀 품종을 개발하기 위해서는 지표로 활용할 수 있다는 것을 나타낸다.

\*주저자: Tel. 063-238-5043, E-mail: kyh2417@korea.kr

**PA-05****Comparison of seed priming methods for germination in sorghum (*Sorghum bicolor* (L.) Moench)**

Du Hyun Kim<sup>1\*</sup>, Hyeonjun Hong<sup>1</sup>, Ki-Yeul Jung<sup>2</sup>

<sup>1</sup>Department of Genetic Engineering, Dong-A University, Pusan 604-714, Republic of Korea

<sup>2</sup>Cereal Crop Research Division, NICS, RDA, Milyang, 627-830, Republic of Korea

This study was conducted to affirm the potential of seed priming techniques for optimizing mechanized growing technologies to maintain production of sustainable small cereal crops. Seed priming conditions were preliminary tested in laboratory. Sorghum seeds were hydroprimed and osmoprimed comprising a total of 33 treatments of different priming combination along with control. Seed primed in aerated solution of distilled water, PEG<sub>8000</sub> (-0.15 MPa and -0.3 MPa), KCl(1% and 2%), KH<sub>2</sub>PO<sub>4</sub> (0.5% and 1.0%), KNO<sub>3</sub> (1.0% and 3.0%), CaCl<sub>2</sub> (1.0% and 3.0%) solutions for 6, 12, 24 hours at 15°C. Maximum seed germination percentage, germination rate and reduced mean germination times (MGT) were observed when the seeds primed by CaCl<sub>2</sub> 1.0% for 24 h, whereas the lowest germination percentage observed in seeds which treated with KNO<sub>3</sub> 3% solution. Priming improved the MGT, germination index, and germination rate of all primed seeds statistically comparing to control. The MGT reduced by increase of treatment time. Further studies for field performance of primed seeds are needed.

\*Corresponding Author: Tel. 051-200-7531, E-mail: dhkimhort@dau.ac.kr

## A New Wheat Variety, “Jojoong” with Pre-harvest Sprouting Resistance, Early Maturity, High Yield and Good Noodle Quality

Chon-Sik Kang<sup>1\*</sup>, Kyeong-Hoon Kim<sup>2</sup>, Young-Keun Cheong<sup>1</sup>, Jae-Han Son<sup>1</sup>, Jong-Chul Park<sup>1</sup>, Kyong-Ho Kim<sup>1</sup>, Kwang-Geun Park<sup>3</sup>, Ouk-Kyu Han<sup>3</sup>, Gi-Heung Hong<sup>4</sup>, Jin-Kyeong Choi<sup>5</sup>, Seong-Tae Lee<sup>6</sup>, Jeong-Suk Bae<sup>7</sup>, Bo-Kyeong Kim<sup>1</sup>, Chulsoo Park<sup>8</sup>

<sup>1</sup>National Institute of Crop Science, RDA, Wanju 565–851, Korea

<sup>2</sup>Department of Southern Area, National Institute of Crop Science, RDA, Miryang 627–803, Korea

<sup>3</sup>Department of Central Area, National Institute of Crop Science, RDA, Suwon 441–100, Korea

<sup>4</sup>Chungnam Agricultural Research & Extension Service, Yesan 340–861, Korea

<sup>5</sup>Jeonnam Agricultural Research & Extension Service, Naju 520–715, Korea

<sup>6</sup>Gyeongnam Agricultural Research & Extension Service, Jinju 660–985, Korea

<sup>7</sup>Gyeongbuk Agricultural Research & Extension Service, Daegu 702–320, Korea

<sup>8</sup>Department of Crop Science and Biotechnology, Chonbuk National University, Jeonju 561–756, Korea

“Jojoong”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “Suwon272/Olgeuru/Keumkang/Suwon252” during 2002. “Jojoong” was evaluated as “Iksan360” in advance yield trial test in 2011. It was tested in the regional yield trial test between 2012 and 2014. “Jojoong” is an awned, semi-dwarf and hard winter wheat, similar to “Keumkang” (check cultivar). The heading and maturing date of “Jojoong” were earlier to “Keumkang”. “Jojoong” had lower test weight (799 g/L) and 1,000-grain weigh (35.6g) than “Keumkang” (816 g/L and 45.5g, respectively). “Jojoong” showed resistance to winter hardiness and pre-harvest sprouting, which lower withering rate on the high ridge (10.5%) and rate of pre-harvest sprouting (10.5%) than “Keumkang” (31.7 and 21.4%, respectively). “Jojoong” showed similar protein content (12.5%), SDS-sedimentation volume (43.5ml) and gluten content (8.6%) to “Keumkang” (12.9%, 58.5ml and 8.5%, respectively). It showed higher lightness (93.17) in flour color than “Keumkang” (91.95, respectively). “Jojoong” showed higher lightness (81.50) of noodle dough sheet than “Keumkang” (80.95). “Jojoong” exhibited similar hardness (3.84N) and higher springiness and cohesiveness of cooked noodles (0.94 and 0.66) compared to “Keumkang” (3.88N, 0.90, and 0.62, respectively). Average yield of “Jojoong” in the regional adaptation yield trial test was 5.09 MT/ha in upland and 5.35 MT/ha in paddy field, which was 9% and 8% higher than those of “Keumkang” (4.67 MT/ha and 4.92 MT/ha, respectively).

\*Corresponding Author: Tel. 063-238-5227, E-mail: kcs1209@koera.kr

## 조숙, 내병성 및 논재배 적응성이 강한 유채 1대잡종 ‘조안’

김광수<sup>1\*</sup>, 이영화<sup>1</sup>, 장영석<sup>1</sup>, 최규환<sup>2</sup>, 강달순<sup>3</sup>, 김성택<sup>4</sup>, 이경보<sup>1</sup>

<sup>1</sup>농촌진흥청 국립식량과학원 바이오에너지작물센터

<sup>2</sup>전라북도농업기술원

<sup>3</sup>경상남도농업기술원

<sup>4</sup>제주특별자치도농업기술원

최근 화석연료 사용에 따른 이산화탄소의 농도 증가와 지구온난화로 인해 친환경에너지의 중요성이 대두됨에 따라 식물성 기름을 활용하여 생산한 바이오디젤의 수송용 에너지로의 사용이 급격히 증가하고 있다. 유채(*Brassica napus* L.)는 예로부터 식용유를 생산하기 위해 주로 동계 기름작물로 재배되어 왔으나, 우리나라도 바이오디젤 원료로서 유채기름에 대한 관심의 증가로 재배면적이 꾸준히 증가하고 있다. 유채의 재배면적 확대를 위해서는 논재배가 필수적으로 벼와 이모작이 가능한 조숙성이며 균핵병 등의 병해에도 강한 유채 품종육성이 절실하다. 이에 따라 국립식량과학원 바이오에너지작물연구소에서 균핵병에 강하며 논재배에 적합한 품종의 육성을 목표로 2009년도에 ‘목포-CGMS’(웅성불임, 종자친)와 ‘8630-B-6-5-3-6’(임성회복 화분친)을 교배하여 우수한 특성을 나타내는 1대잡종 ‘단교71호’를 선발하여, 2010~2011년에 걸쳐 1대잡종 품종인 ‘선망’을 대비품종으로 하여 생산력검정시험을 실시하였으며, 2012~2014년에 전남, 전북, 경남 및 제주 등 4개 지역에서 지역적응시험을 실시하였다. 생산력검정시험과 지역적응시험을 통하여 농업적인 특성, 지방함유량, 지방산의 조성 및 글루코시놀레이트의 함량 등을 분석한 결과, ‘단교71호’는 대비품종인 ‘선망’에 비해 조숙이며, 논재배에 대한 적응성이 강하며 내병성 및 내도복성이 강하여 조안(Joan)으로 명명하였다. 1대잡종 ‘조안’은 조숙종으로 개화기(4월 10일)와 성숙기(6월 4일)가 ‘선망’에 비해 3~4일 빠르다. 수량은 279kg/10a로 ‘선망’에 비해 6%가 증수되었고, 균핵병과 도복저항성에 강하다. 기름함량은 44.5%로 ‘선망’보다 높고, 올레인산 함량이 69.5%로 ‘선망’의 67.2%에 비해 2.3% 높았으며, 에루신산은 전혀 없고 글루코시놀레이트 함량은 1.85mg/g으로 국제허용기준치인 3.0mg/g 이하이다. ‘조안’의 기름성분 중 불포화지방산인 올레인산의 함유량이 높아 식용과 바이오디젤 원료용으로 적합하다.

\*주저자: Tel. 061-450-0133, E-mail: ajuga@korea.kr

---

**PA-08**

## **Comparison of seed priming methods for germination in sorghum (*Sorghum bicolor* (L.) Moench)**

Du Hyun Kim<sup>1\*</sup>, Hyeonjun Hong<sup>1</sup>, Ki-Yeul Jung<sup>2</sup>

<sup>1</sup>Department of Genetic Engineering, Dong-A University, Pusan 604-714, Republic of Korea

<sup>2</sup>Cereal Crop Research Division, NICS, RDA, Milyang, 627-830, Republic of Korea

This study was conducted to affirm the potential of seed priming techniques for optimizing mechanized growing technologies to maintain production of sustainable small cereal crops. Seed priming conditions were preliminary tested in laboratory. Sorghum seeds were hydroprimed and osmoprimed comprising a total of 33 treatments of different priming combination along with control. Seed primed in aerated solution of distilled water, PEG<sub>8000</sub> (-0.15 MPa and -0.3 MPa), KCl(1% and 2%), KH<sub>2</sub>PO<sub>4</sub>(0.5% and 1.0%), KNO<sub>3</sub>(1.0% and 3.0%), CaCl<sub>2</sub>(1.0% and 3.0%) solutions for 6, 12, 24 hours at 15 °C. Maximum seed germination percentage, germination rate and reduced mean germination times (MGT) were observed when the seeds primed by CaCl<sub>2</sub> 1.0% for 24 h, whereas the lowest germination percentage observed in seeds which treated with KNO<sub>3</sub> 3% solution. Priming improved the MGT, germination index, and germination rate of all primed seeds statistically comparing to control. The MGT reduced by increase of treatment time. Further studies for field performance of primed seeds are needed.

\*Corresponding Author: Tel. 051-200-7531, E-mail: dhkimhort@dau.ac.kr

**PA-09**

## **Effects of priming treatments on germination of *Setaria viridis* L. seeds**

Du Hyun Kim<sup>1\*</sup>, Hyeonjun Hong<sup>1</sup>, Ki-Yeul Jung<sup>2</sup>

<sup>1</sup>Department of Genetic Engineering, Dong-A University, Pusan 604-714, Republic of Korea

<sup>2</sup>Cereal Crop Research Division, NICS, RDA, Milyang, 627-830, Republic of Korea

Poor germination and labor intensive thinning of seedling after sowing are major deterrents in *Setaria viridis* production. Seed priming has the potential to improve the seedling emergence and economic feasibility by combined with seed coating for optimizing mechanized growing technologies to small cereal crops. The objective of this study was to determine the effective seed priming conditions on the improved germination in the laboratory. Seeds were hydro primed with distilled water for 6, 12, 24 hours and osmoprimed with PEG<sub>8000</sub> (-0.15 MPa and -0.3 MPa), KCl (1% and 2%), KH<sub>2</sub>PO<sub>4</sub>(0.5% and 1.0%), KNO<sub>3</sub>(1.0% and 3.0%), CaCl<sub>2</sub> (1.0% and 3.0%) solutions for 6, 12, 24 hours at 15 °C. Our results demonstrate that treating *S. viridis* seeds with PEG -0.3 MPa solution for 12h increased to maximum germination percentage to 97%, whereas the lowest germination percentage observed in seeds which treated with by CaCl<sub>2</sub> 1.0% for 24h and KCl 1% for 6h. Priming reduced the mean germination times (MGT) of all priming treated seeds statistically comparing to control. There was significant interaction between treatment and time. Further studies for field performance of primed seeds are needed.

\*Corresponding Author: Tel. 051-200-7531, E-mail: dhkimhort@dau.ac.kr

## PA-10

### 중국 운남성 고지대에서의 우리 벼 품종의 작물학적 특성

김명기<sup>1\*</sup>, 양창인<sup>1</sup>, 이상복<sup>2</sup>, 현용조<sup>3</sup>, 백남현<sup>1</sup>, 이점호<sup>2</sup>

<sup>1</sup>강원도 철원군 동송읍 국립식량과학원 철원출장소

<sup>2</sup>강기도 수원시 권선구 서둔동 국립식량과학원 중부작물과

<sup>3</sup>강원도 춘천시 우두동 국립식량과학원 춘천출장소

지구 온난화 등 기후변화 과정에서 저온 내습으로 냉해 피해에 대비 우리 품종의 내냉성을 증진시키고자 우리 품종을 2013년과 2014년 2년간 중국 운남성 마룽(해발 2,124m) 지역에서 작물학적 특성 및 내냉성 등을 조사하였고, 마룽시험지의 벼 재배기간의 기상 분석을 실시하였다.

벼 재배기간의 최고기온은 20.4~26.9℃로 우리나라 철원의 21.1~30.2℃보다는 낮았다. 그리고 평균기온은 19.4℃ 범위에서 기온변화가 적었다. 또 최저기온은 출수기와 등숙기인 7월과 8월에는 평균 16.9℃로 철원의 20.8℃보다 약 4℃로 낮았다.

작물학적 특성에서 출수기는 오대벼 7월27일, 진부벼 7월22일로 철원에서보다는 2~3일이 출수가 지연되었다. 간장은 2품종 평균 60cm로 철원보다 15cm가 작았다. 주당수수는 2품종 모두 8개로 철원의 13개보다 5개 적었다. 반면 수당입수는 오대벼가 93개, 진부벼가 74개로 철원에서보다 오대벼는 25개, 진부벼는 6개가 많았다. 내냉성과 관련된 임실율은 오대벼가 72.5%, 진부벼가 75.0%였으며, 등숙율은 2품종 평균 61.7%로 철원의 88.2%에 비하여 매우 낮았다. 그러나 진부벼는 69.1%로 중국 품종 운갱20호의 56.0%보다 다소 높아 진부벼는 내냉성이 다소 강한 것으로 판단된다. 현미 천립중은 오대벼가 27.3g, 진부벼가 26.9g으로 철원에서의 천립중보다 약간 무거운 편이었다. 쌀 수량은 평균 333kg/10a로 중국 품종에 비하여는 매우 낮았다. 중국 운남성 고지대에서 우리 품종을 시험한 결과 진부벼는 내냉성이 다소 강한 것으로 판단되어 우리 품종의 내냉성 증진을 위한 육종재료로 활용 가치가 있을 것으로 생각된다.

\*주저자: Tel. 033-455-2031, E-mail: kimmk6690@korea.kr

## PA-11

### 벼 조생종 수발아, 잎도열병 및 흰잎마름병 저항성 중간모본 '중모1031'

김명기<sup>1</sup>, 서정필<sup>2</sup>, 원용재<sup>1</sup>, 안역근<sup>1</sup>, 정국현<sup>1</sup>, 백만기<sup>1</sup>, 최임수<sup>1</sup>, 조영찬<sup>1</sup>, 윤광섭<sup>1</sup>, 김연규<sup>1</sup>, 홍하철<sup>1</sup>, 윤영환<sup>3</sup>, 이정희<sup>1</sup>

<sup>1</sup>전라북도 완주군 이서면 국립식량과학원

<sup>2</sup>전라북도 전주시 완산구 농촌진흥청

<sup>3</sup>충청남도 예산군 신임면 충청남도농업기술원

벼 품종 '중모1031'은 기상이변으로 조생종 벼 재배지대의 재해 및 병해 발생 증가에 대비 벼 조생종 품종의 내재해성 및 내병성을 증진할 목적으로 2002년 하계에 인공교배하여 계통육종법으로 육성하여 2011~2013년 3년간 지역적 응시험을 실시한 결과 수발아, 잎도열병 그리고 흰잎마름병이 강함이 인정되어 2013년 12월 농촌진흥청 농작물직무 육성신품종선정위원회에서 중간모본으로 선정되었다.

'중모1031'는 출수기가 보통기 보비재배에서 7월25일로 오대벼와 같은 조생종이다. 간장은 60cm로 작고, 도복시험에서 쓰러짐에 강하였다. 주당수수는 13개로 오대벼와 비슷하나 수당입수는 80개로 오대벼보다 13개가 많았다. 현미 천립중은 오대벼의 26.3g보다 작은 22.0g의 단원립이다. 잎도열병과 흰잎마름병(K1~K3)에는 저항성이지만 기타 바이러스 및 충해에는 약하였다. 수발아율도 4.5%로 강하였다. 쌀 수량은 5.47톤/ha로 오대벼보다 5%정도 다소 증수되었으며, 쌀 외관인 심복백이 없어 오대벼에 비하여 맑다. 그래서 중모1031은 조생종으로서 잎도열병과 흰잎마름병에 강한 복합내병성이며, 도복 및 수발아에도 강한 조생종 품종의 특성을 가지고 있어 특히 조생종 품종에 흰잎마름병 및 수발아에 강한 품종을 육성하는데 중간모본으로서의 활용 가치가 높을 것으로 판단된다.

\*주저자: Tel. 033-455-2031, E-mail: kimmk6690@korea.kr

## Distinct reactions of two Tunisian durum wheat to salinity stress

Sang Heon Kim<sup>1</sup>, Inès Yacoubi<sup>2</sup>, Yong Weon Seo<sup>1\*</sup>

<sup>1</sup>Department of Biosystems and Biotechnology, Korea University, Seoul 136-713, Republic of Korea

<sup>2</sup>Centre de biotechnologie de Sfax (CBS), Sfax, Tunisia

Durum wheat (*Triticum turgidum* L. ssp. *durum*) is a global staple food crops. However, saline soil reduces the production of durum wheat in a lot of countries including Tunisia. This problem would be more severe as soil salinization ascribed by the global climate changes and worldwide water deficiencies. To overcome this circumstance, we performed two experiments related to salinity stress tolerance of durum wheat. Two Tunisian durum wheat cultivars ('Om Rabia', 'Mahmoudi') were applied to examine the reaction to salt stress. At the third leaf stage, salt stress was treated by submerging the pots into 500 mM NaCl for 5 mins everyday instead of irrigation in greenhouse. The treatment was applied for 1 week and their tolerances to salt stress were determined by comparing their growth parameters to the control plants. Total RNA was extracted and Quantitative reverse transcript PCR (qRT-PCR) using the genes linked with the salt tolerance was performed. The plant height and leaf chlorophyll content were reduced during salt stress treatment in both cultivars. The growth parameters of 'Om Rabia' was reduced less than that of 'Mahmoudi'. The transcription level of the genes linked with the salt tolerance was greater in 'Om Rabia' than in 'Mahmoudi'. These results will be fruitful to future breeding program for salt tolerant tetraploid durum wheat.

Acknowledgement: This work was supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MEST) (No. 2012K1A3A1A09028123).

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

## 벼흰잎마름병 발병상습지에서 벼 품종 '해품'의 저항성 발현

김우재\*, 박종호, 김현순, 박현수, 하기용, 고재권, 김보경

전북 완주군 이서면 국립식량과학원 작물육종과

벼흰잎마름병은 벼에 큰 피해를 주는 병으로 매년 많은 발생량을 보인다. 이에 새로운 저항성 품종 '해품'을 전남 장흥의 발병상습지에 재식하여 저항성 발현 정도를 조사하였다. 벼흰잎마름병 균계별 저항성 반응 실험에서 공시재료의 벼흰잎마름병 저항성 특성은 '해품'은 *Xa3*와 *xa5* 저항성 유전자를 가지고 있어 K1, K2, K3, K3a 균계에 강한 반응을 보인 반면, *Xa1*을 가진 '호평'과 '일미'는 K1에만 저항성을 보였다. 전남 장흥 발병상습지에서 시기별 생육 및 발병은 2014년 9월 중순 집중호우 이후 이병성 품종인 '호평'에 발병을 시작으로 10월 중순엔 병반면적율은 '해품'이 4.7%였고 '호평'과 '일미'는 50%이상이었다. 등숙률은 '해품' 94%, '호평' 77.5%, '일미' 70%였다. 수량성은 '해품'보다 '호평'은 18%, '일미'는 22% 감소되었다. '호평'과 '일미'는 심복백과 청미 발생이 '해품'보다 심하였는데 이는 발병에 따른 지엽고사로 광합성이 부족하여 발생한 것으로 생각된다. 최근 벼흰잎마름병균의 레이스변화에 따른 기존 저항성 품종의 이병화는 수량감소와 품질저하를 가져오고 있다. 새로운 균계에 대응하는 저항성 품종의 개발은 이러한 단점을 근본적으로 해결할 수 있는 방법이 될 것이다.

\*주저자: Tel. 063-238-5235, E-mail: suwonman@korea.kr

---

## PA-14

### 벼멸구 저항성 유전자 다양화를 위한 DNA 마커 탐색

김우재\*, 김현순, 하기용, 강경호, 정지웅, 전재범, 조성우, 김보경

전북 완주군 이서면 국립식량과학원 작물육종과

기상조건의 변화로 우리나라에 벼멸구의 발생이 점차 증가하며 피해가 커지고 있다. 이에 다양한 벼멸구 저항성 유전자를 가진 벼 품종의 육성이 필요하다. 국내 육성 자포니카 벼 품종 중 벼멸구 저항성 품종은 *Bph18* 유전자를 가진 ‘안미’를 제외하고 모두 *bph2*(‘화청’, ‘하남’, ‘다청’, ‘친농’, ‘친들’) 유전자를 가지고 있다. 유묘검정 결과 *bph2* 유전자를 가진 품종은 벼멸구 흡즙에 중도저항성을 보인 후 4주 이상 지나며 고사되는 반면, ‘안미(*Bph18*)’는 계속해서 강한 저항성 반응을 나타낸다. 인공교배를 통해 *Bph18* 유전자를 가진 계통을 육성하였다. 빠른 DNA 마커 검정을 위해 12번 염색체의 *Bph18* 유전자와 연관된 마커를 검색하여 PCR 후 전기영동을 수행한 결과 RM3331이 저항성 유전자별 밴드의 위치가 다른 증폭 반응을 보였다. 각 계통에 대한 밴드분석 결과 벼멸구 저항성 유전자가 없는 ‘TN1’과 ‘호평’은 위치가 다른 밴드를 보였는데 이는 인디카와 자포니카의 유전적 백그라운드의 차이로 프라이머의 증폭 부위가 달라 발생한 것으로 추측된다. *Bph18* 유전자를 가진 ‘익산562호’와 *Bph1* 유전자를 가진 ‘청청벼’, ‘Mudgo’, ‘IR09N379’의 밴드 위치가 같은 것은 두 유전자가 중복되어 위치해 있기 때문인 것으로 보인다. 따라서 RM3331로 생성된 PCR 산물의 크기는 제한효소 처리없이 2% agarose gel로 분석이 가능한 간편성을 가지고 있지만, 저항성 유전자가 중복되어 있는 *Bph18*과 *Bph1* 유전자를 구분하기는 어려우며 벼멸구 저항성 유전자를 가지고 있지 않은 계통과의 구분에 선택적으로 사용하는 것이 적합할 것으로 보인다.

\*주저자: Tel. 063-238-5235, E-mail: suwonman@korea.kr

## PA-15

### 우리나라에서 벼 꽃가루배양의 실용화와 금후전망

김현순<sup>1\*</sup>, 강경호<sup>1</sup>, 남정권<sup>1</sup>, 김우재<sup>1</sup>, 정지웅<sup>1</sup>, 백소현<sup>1</sup>, 신운철<sup>1</sup>, 강현중<sup>1</sup>, 고재권<sup>1</sup>, 김기영<sup>1</sup>, 김보경<sup>1</sup>, 이승엽<sup>2</sup>

<sup>1</sup>전북 완주군 이서면 농촌진흥청 국립식량과학원

<sup>2</sup>전북 익산시 원광대학교 생명자원과학대학

벼 꽃가루(약) 배양은 유용유전자의 조기고정으로 육종년한 단축을 위한 육종법으로 실용화되고 있다. 국내에서는 이 배양법에 의해 1985년 처음으로 농촌진흥청에서 화신벼를 육성한 이래 현재까지 20여 품종이 육성되었고, 국외에서는 IRRI에서 1995년 첫 약배양 유래 품종이 육성되었다.

국내에서 이 육종법은 전통교배육종에 비해 품종육성 기간을 2년정도 단축시켰다. 도입초기의 주요 목적형질은 양질, 내병충성이 강화된 품종이 육성되었으며 최근 2000년대 들어서는 기능성 등을 포함하고 있다. 그간 국내 약배양 유래 품종육성 수는 1985년 이래 전통교배 품종수의 약 8%정도였으며, 농가재배 면적은 지난 30여년 동안 2,200천 ha정도 재배되어 왔다. 주요 육성품종으로는 화성, 화선찰, 화영, 화봉, 호평으로 꾸준히 재배되고 있는 실정이다. 우리나라에서 벼 약배양 기술은 어느 작물보다 일찍 시작하여 생명공학의 기초를 이루어 성공적으로 실용화를 이루어 냈고, 앞으로도 기후변화 등에 좀 더 다양한 유용형질이 요구되는 즈음, 이 약배양법은 유용변이체 및 형질전환체 등을 조기 고정하는데 중요기술로 이용하게 될 것이다.

\*주저자: Tel. 063-238-5231, E-mail: kimhs123@korea.kr

## 내도복 중만생 벼 답수직파 겸용 “중모1041”

김정주<sup>1\*</sup>, 백만기<sup>1</sup>, 남정권<sup>1</sup>, 김보경<sup>1</sup>, 하기용<sup>1</sup>, 김기영<sup>1</sup>, 고종철<sup>2</sup>, 고재권<sup>1</sup>, 김우재<sup>1</sup>, 백소현<sup>3</sup>, 신운철<sup>4</sup>, 박현수<sup>1</sup>, 조영찬<sup>1</sup>, 이점호<sup>5</sup>, 김현순<sup>1</sup>, 임청택<sup>1</sup>, 박기훈<sup>5</sup>

<sup>1</sup>전라북도 완주군 이서면 혁신로 국립식량과학원 작물육종과

<sup>2</sup>경상북도 밀양시 점필재로 국립식량과학원 남부작물부 발작물개발과

<sup>3</sup>전라북도 완주군 이서면 혁신로 국립식량과학원 작물기초기반과

<sup>4</sup>경상북도 상주시 하서면 중화로 국립식량과학원 상주출장소

<sup>5</sup>경기도 수원시 권선구 수인로 국립식량과학원 중부작물부 중부작물과

벼 중만생 답수직파 겸용 “중모1041”은 생산비 절감을 위한 직파적응성 고품질 품종개발을 목적으로 국립식량과학원 벼육종재배과에서 2006/2007년 동계에 중만생 내도복성 계통인 익산496호 (IT235289)와 다수성 계통인 밀양172호 (IT212472)를 인공교배하여 교잡육종법으로 육성되었다. 인공교배 후 분리세대인 F<sub>2</sub> 및 F<sub>3</sub>는 집단으로 전개하여 초형 및 이삭특성을 고려하여 포장선발하고 F<sub>4</sub>이후부터는 계통으로 전개하여 주요 병해충 및 미질 특성을 고려하여 선발하였으며 그 중 중만생종이면서 내도복성 계통인 HR26974-B-2-1을 선발하였다. 2011~2012년에 걸쳐 생산력검정시험을 실시하여 초형이 우수하고 단간 내도복성이면서 수량성이 우수하여 “익산555호”로 계통명을 부여하였다. 2012~2014년 3년간 지역적응시험을 수행한 결과 직파적응성이 좋고 밥맛이 양호한 계통으로 농촌진흥청의 농작물 직무육성신품종 선정심의회를 거쳐 “중모1041”로 명명되었다. 주요특성으로 보통기 보비재배시 출수기는 8월 14일로 중만생종이고 간장이 74 cm로 단간이고 수장은 21 cm이며 m<sup>2</sup>당 수수는 310개이다. 직파재배의 경우 도복에 의한 수량성 및 품질 저하가 우려되는데 “중모1041”은 동안벼보다 3절간장은 다소 길지만 도복지수가 낮아 내도복성을 갖추고 있다. 5월 상순에 답수직파를 할 경우 야간 저온에 의한 발아율 저하로 입모 확보가 어려운데 13°C에서 15일간 저온발아특성을 조사한 결과 “중모1041”은 저온발아율이 83%로 남평벼 42%보다 2배 정도 높아 13°C 저온에서 우수한 발아특성을 갖추고 있다. 또한, 도열병에 중도저항성이고 흰잎마름병균 K1, K2 및 K3에 저항성이며 줄무늬잎마름병에도 강한 특성을 갖추고 있다. 그러나, 애멸구, 벼멸구 등 해충에 대한 저항성은 없다. “중모1041”의 현미 천립중은 24.8g으로 남평벼보다 무거우며 쌀수량은 보통기 보비재배시 5.89 Mt/ha로 남평벼 대비 4% 높고 답수직파재배시 5.4 Mt/ha으로 동안벼 대비 4% 높은 수량성을 나타낸다. 중만생 내도복 답수직파재배 겸용 벼 “중모1041”의 적응지역은 충남 이남 내륙평야지 (충남, 전남북)이다.

\*주저자: Tel. 063-238-5215, E-mail: jjkim74@korea.kr

## 대립 내탈립 무비린내 콩 “미소”

김현태<sup>1\*</sup>, 고종민<sup>2</sup>, 한원영<sup>2</sup>, 강범규<sup>1</sup>, 이영훈<sup>2</sup>, 이병원<sup>3</sup>, 최만수<sup>1</sup>, 김현영<sup>1</sup>, 전명기<sup>4</sup>, 문중경<sup>5</sup>, 윤홍태<sup>1</sup>, 백인열<sup>6</sup>, 이영희<sup>7</sup>

<sup>1</sup>경남 밀양시 점필재로20 국립식량과학원 발작물개발과

<sup>2</sup>경남 밀양시 점필재로20 국립식량과학원 생산기술개발과

<sup>3</sup>경기도 수원시 권선구 서호로 54 국립식량과학원 수확후이용과

<sup>4</sup>경남 창원시 의창구 창이대로 71 창원농업기술센터

<sup>6</sup>전북 완주군 이서면 혁신로181 국립식량과학원 작물기초기반과

<sup>6</sup>전북 완주군 이서면 혁신로181 국립식량과학원 기획조정과

<sup>7</sup>경남 밀양시 점필재로20 국립식량과학원 남부작물부

콩의 종실에서 존재하는 lipoxxygenase는 콩의 비린내를 유발하는 원인이 되고 있으며 콩의 가공을 위해 열을 가하여야 하는 원인중의 하나가 되고 있다. 콩의 가공 특히 두유제조에서의 효과적인 가공을 위해 종실의 lipoxxygenase가 없는 ‘진품콩2호’가 개발되었으나 수량성이 낮고 병에 다소 약하며 탈립이 심하였다. 이러한 문제를 해결하기 위해 대립 다수성인 ‘대망2호’를 모본으로 하고 ‘진품콩2호’를 교배하여 대립이면서 탈립에 강하고 수량성이 높은 ‘미소(밀양249호)’를 개발하였다.

‘미소’는 종실에서 콩의 비린내에 관여하는 세가지 lipoxxygenase 효소가 모두 활성을 나타내지 않는 무비린내 품종이다. 꽃색은 백색으로 ‘진품콩2호’와 차가 있으나 엽형, 모용색, 협색 등의 질적특성은 ‘진품콩2호’와 유사하다. 개화기는 8월 6일, 성숙기는 10월 17일로 ‘진품콩2호’보다 각각 7일, 8일 늦은 만숙종이다. 주경장이 77cm로 ‘진품콩2호’보다 5cm 정도 더 크지만 지역적응시험 시험포장과 밀식재배를 통한 검정포장에서 ‘진품콩2호’보다 도복에 강하였다. 종실의 크기는 100립중이 28.2g으로 21.9g인 ‘진품콩2호’보다 6.3g 더 무거운 대립으로 종실이 굵으면서도 성숙후 종자의 탈립이 거의 없으며, 건조기를 이용한 성숙꼬투리의 협개열성을 조사한 결과에서도 ‘진품콩2호’보다 내탈립성이 강하였다. 불마름병 저항성은 8ra접종시엔 ‘진품콩2호’와 비슷한 정도로 발병하였으나 시험포장과 검정포장에서는 이병되지 않았다. 지역적응성 검정시험에서 평균수량이 10a당 314kg으로, ‘진품콩2호’보다 18% 증수하였다. 두부와 비지수율은 ‘진품콩2호’와 비슷하며 두유의 고형분 비율은 ‘진품콩2호’보다 다소 낮았으나 ‘대원콩’과는 비슷하였다.

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

## PA-18

### 도복과 탈립에 강한 다수성 콩 “대풍2호”

김현태<sup>1\*</sup>, 이영훈<sup>2</sup>, 이병원<sup>3</sup>, 최만수<sup>1</sup>, 강범규<sup>1</sup>, 한원영<sup>2</sup>, 김현영<sup>1</sup>, 전명기<sup>4</sup>, 이석기<sup>5</sup>, 고종민<sup>3</sup>, 윤홍태<sup>1</sup>, 백인열<sup>6</sup>, 이영희<sup>7</sup>

<sup>1</sup>경남 밀양시 점필재로20 국립식량과학원 발작물개발과

<sup>2</sup>경남 밀양시 점필재로20 국립식량과학원 생산기술개발과

<sup>3</sup>경기도 수원시 권선구 서호로 54 국립식량과학원 수확후이용과

<sup>4</sup>경남 창원시 의창구 창이대로 71 창원농업기술센터

<sup>5</sup>전북 전주시 완산구 농생명로 300 농촌진흥청 국외농업기술과

<sup>6</sup>전북 완주군 이서면 혁신로181 국립식량과학원 기획조정과

<sup>7</sup>경남 밀양시 점필재로20 국립식량과학원 남부작물부

콩 품종 ‘대풍’은 국내 육성품종 최초로 10a당 300kg을 초과하는 높은 수량성과 재배안정성을 갖추었음에도 종자 외관의 결함으로 상품성이 낮아 보급이 확대되지 못하고 있다. 콩의 수량성 향상과 상품성 향상을 위해, ‘대풍’을 활용하여 수량성과 안정성을 갖추면서 종자품위를 개선한 품종을 만들고자 연구하였다. ‘대풍2호’는 ‘대풍’을 모본으로 하고, ‘수원190호’와 ‘대원콩’을 교배한 대립계통을 부분으로 하여 2003년도에 교배하여 계통육성법에 따라 육성한 ‘밀양242호’이다. 대풍콩의 단점인 배꼽색을 없애고, 종자모양이 ‘대풍’보다 구형에 더 가까우며 종피의 색택이 좋아 종자품위가 우수하다. ‘대풍2호’의 엽형은 ‘대풍’이 난형인데 반해 피침형으로 수광태세가 좋으며, 꽃색은 백색, 모용색과 협색은 갈색으로 ‘대풍’과 같다. 성숙기는 10월 14일로 ‘대풍’보다 3일 늦으며 ‘대원콩’과 비슷하다. 불마름병과 도복에 강하며, 성숙후 꼬투리의 탈립에 강하다. 종실 100립중은 20.9g으로 ‘대풍’과 비슷하며 ‘대원콩’보다는 4.4g 작은 중립 품종이다. 지역적응성 검정시험에서 제주지역을 제외한 적응지역 평균수량이 10a당 345kg으로, ‘대원콩’보다 21% 더 높으며, ‘대풍’의 99%로서 대등한 수준이다. 두부와 메주, 청국장 제조시 수율이 높으며 청국장의 점성성분인  $\gamma$ -PGA함량이 45.5mg/g으로 대원콩의 35.3mg/g보다 높다.

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

## PA-19

### 다변량 분석에 의한 콩 품종 분류

이가영<sup>1</sup>, 광병삼<sup>1</sup>, 광상철<sup>1</sup>, 김용현<sup>1</sup>, 장은규<sup>2</sup>, 김홍식<sup>1\*</sup>

<sup>1</sup>충청북도 청주시 서원구 충대로1 충북대학교 농업생명환경대학 식물자원학과

<sup>2</sup>경기도 연천군 신서면 도신로 3번길 42 경기도 농업기술원

국내에서 육성된 172품종의 양적 형질을 다변량으로 분석하여 유연관계를 해석하고, 품종을 분류하여 신품종 육성의 기초 자료로 이용코자 하였다. 국내에서 육성된 콩 172품종의 군집분석 결과 7군으로 분류되었다. 제 I 군에는 장단백목 외 13품종이 속하였으며, 100립중이 가장 무거운 품종들이 포함되었다. 제 II 군에는 충북백 외 111품종이 속하였으며, 생육일수가 짧으며, 1주종실중이 작은 품종들이 포함되었다. 제 III 군에는 호서콩 외 5품종이 속하였으며, 생육일수가 긴 만생종들이 포함되었다. 제 IV 군에는 팔달콩 외 3품종이 속하였으며, 뚜렷한 특징을 보이지 않은 품종들이 포함되었다. 제 V 군에는 광교콩 외 26품종이 속하였으며, 생육일수가 가장 짧은 조생종이었고, 경장이 짧은 품종들이 포함되었다. 제 VI 군에는 소명콩 외 5품종이 속하였고, 분지수가 많은 품종들이 분류되었다. 제 VII 군에는 아가4호 외 3품종이 속하였고, 경장, 협수 및 1주립수가 가장 많은 품종들과 100립중이 가장 작은 품종들이 포함되었다.

\*주저자: Tel. 043-261-2531, E-mail: hongsigk@chungbuk.ac.kr

## 미나리 실생묘를 이용한 수경재배와 관행재배의 생산성 및 품질 비교

김효중<sup>1\*</sup>, 이유석<sup>1</sup>, 김희곤<sup>1</sup>, 손동모<sup>1</sup>, 나해영<sup>2</sup>

<sup>1</sup>전남 나주시 산포면 산제리 전라남도농업기술원 원예연구소

<sup>2</sup>전남 무안군 청계면 청계리 국립목포대학교 원예과학과

본 시험은 최근 미나리 가격상승과 관련하여 관행 물논재배의 약성노동, 수확, 선별, 포장 등 과다노동력 투입과, 인건비 상승으로 지속적인 경영비 상승을 보이고 있는 미나리의 작업편이성, 생산성 향상을 도모하고자 미나리 종자를 이용한 밭 재배 및 수경재배의 관행재배 대비 경제성을 분석하고자 실시하였다. 시험은 4~5월까지 실시하였으며, 초장은 관행재배 41.1cm, 밭 재배가 13.0cm, 수경재배가 31.3cm로 관행재배가 가장 길었으며, 종자를 이용한 밭 재배 및 수경재배의 주당 줄기 수는 밭 재배가 3.3줄기, 수경재배가 6.1줄기로 밭 재배보다는 수경재배에서 줄기발생율이 높게 조사되었다. 줄기당 엽수는 줄기무게는 관행재배가 4.4g, 토양재배가 0.6g, 수경재배가 6.5g으로 수경재배가 가장 무겁게 측정되었다. 각 재배방법의 단위면적 수량은 관행재배가 3.8kg/m<sup>2</sup>, 밭 재배 0.2kg/m<sup>2</sup>, 수경재배 1.3kg/m<sup>2</sup>로 나타났다.

\*주저자: Tel. 061-330-2544, E-mail: plantmaniac@korea.kr

## 품질이 우수한 내병·다수성 조생찰벼 ‘운일찰’

남정권<sup>1\*</sup>, 신운철<sup>2</sup>, 김기영<sup>1</sup>, 박현수<sup>1</sup>, 백만기<sup>1</sup>, 김정주<sup>1</sup>, 조영찬<sup>1</sup>, 하기용<sup>1</sup>, 김우재<sup>1</sup>, 김보경<sup>1</sup>

<sup>1</sup>전북 완주군 혁신로 181, 국립식량과학원 작물육종과

<sup>2</sup>경북 상주시 화서면 중화로 2161, 국립식량과학원 상주출장소

국내 찰쌀 가격은 년차간 가격차이가 크고 특히 8월말 이후 재배면적에 따라 가격 변동이 심하므로 조기 출하할 수 있는 조생종 찰벼 품종의 개발이 필요하다. 이에 국립식량과학원은 2005년 하계에 조생종이면서 다수성인 운광을 모본으로 하고 찰성이 우수한 상주찰벼를 부분으로 하여 인공교배를 하고, 그로부터 육성된 F<sub>3</sub> 이후 계통은 계통육종법에 따라 우량계통을 선발하였다. 선발된 우량계통은 ‘운봉52호’의 계통명을 부여하여 2012~2014년까지 3년간 지역적응시험을 실시한 결과 그 우수성이 인정되어 ‘운일찰’로 품종명을 부여하였다. ‘운일찰’의 출수기는 7월 28일로 ‘오대’보다 1일 늦은 조생종이며, 간장은 64cm로 단간이며 내도복성이다. ‘운일찰’은 벼흰잎마름병(K<sub>1</sub>~K<sub>3</sub>)과 도열병에 강하나 기타 병해충에는 약한 품종이다.

‘운일찰’의 쌀 수량은 2012~2014년 실시한 지역적응시험 보통기 보비재배에서 5.33MT/ha로 오대에 비해 1% 높고, 소득후작 재배에서 수량은 4.96MT/ha으로 ‘금오’보다 6% 높았다. ‘운일찰’의 적응지역은 중북부평야, 중산간지 및 남부고랭지이다. 이 품종은 추석전 조기 출하용으로 확대보급 할 가치가 있는 조생찰벼이다.

\*주저자: Tel. 063-238-5213, Email: namjk725@korea.kr

## PA-22

### 열대형 옥수수 반수체 유기체(Inducer)인 Tails의 국내적응성 평가

류시환\*, 최재근, 박종열, 서영호, 박기진, 용우식, 노상득, 이장용, 김정희

강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

전통적인 방법에 의한 옥수수 계통육종은 99% 이상의 순도를 고정하기 위해 7회 이상의 인공교배(selfing)를 수행하여야 한다. 이러한 단점을 보완하고자 최근에 선진국을 중심으로 배가반수체(Doubled Haploid) 방법에 의한 계통육종 방법이 실용화되고 있으며, 배가반수체 방법에 의하면 2~3년 만에 순도 100%의 계통을 육성할 수 있다. 배가반수체 기술 도입을 위해서는 반수체 유기체(Inducer)의 확보가 필수이며, 강원도농업기술원 옥수수연구소에서는 국외 선진기술인 배가반수체 기술을 도입하여 국내의 옥수수 계통육종에 활용하고자 국제옥수수·밀연구소(CIMMYT)로부터 반수체 유기체의 사용 권리를 확보하였다. CIMMYT의 유기체인 Tails는 열대형 유기체이므로 국내에서의 생육특성 및 적응성 평가를 우선적으로 검토하였다. 2014년 홍천지역에서의 Tails의 생육특성은 4월 23일 포트 파종하여 5월 14일 비닐피복 포장에 정식하였을 때 출사기가 7월 4일로 출사일수는 72일이었으며 화분비산기는 7월 1일에서 11일까지 유지되었다. Tails의 간장은 196cm 착수고는 83cm로 착수고율은 42%이었다. Tails의 줄기 절간의 안토시아닌 색소는 강하며, 엽초의 안토시아닌 색소도 중간정도이므로 일반적인 옥수수와 구분이 용이한 특성을 보인다. 자체보유 찰옥수수 및 일반옥수수 집단과 교배한 결과 41%의 반수체 유기율을 보였다. 열대자원의 경우 온대지방에서 영양생장만 지속하고 생식생장으로 전환이 안 되는 경우가 많은데, Tails의 경우는 국내에서의 생육 및 화분생산이 정상적으로 이루어지고 적응성도 우수한 것으로 평가되었다. 이 결과에 따라 국내에서 반수체 유기체를 위한 Tails의 활용은 그 가치가 높을 것으로 판단된다.

\*주저자: Tel. 033-248-6913, E-mail: shr8921@korea.kr

## PA-23

### 반수체 밀 집단을 이용한 국수 면대 색깔 QTL 분석

강혜정<sup>1,2</sup>, 강천식<sup>2</sup>, 김학신<sup>2</sup>, 박철수<sup>1\*</sup>

<sup>1</sup>전라북도 전주시 덕진구 전북대학교 농업생명과학대학 작물생명과학과

<sup>2</sup>전라북도 완주군 이서면 국립식량과학원

본 연구는 국내 밀 소비 증진을 위해 소비자가 선호하는 국수 면대 선발에 적용이 가능한 SSR 마커를 선별하기 위하여 금강밀과 올그루밀을 이용하여 제작된 반수체 114 계통을 이용하였다. 2011년과 2012년에 국립식량과학원에서 재배 및 수확된 종자를 이용하여 제분을 하여 밀가루 색깔을 측정하였고, 가수량 34%로 국수면대를 제작하여 국수면대의 색깔을 측정하였다. 밀가루 및 면대의 색깔은 CIE-LAB를 이용하여 L(밝기), a(적색도), b(황색도)를 측정하였다. 교배본에서 다형성을 보인 140개 SSR 프라이머를 검정하여 밀가루 및 면대 색깔에 관련된 SSR 마커를 찾았다. 5D 염색체에 위치한 *Xgwm190*은 밀가루 색에 대한 표현형 변이를(2011년, 2012년 반복 재배한 밀의 평균값) 13.3~22.8% 설명할 수 있었고, 국수 면대의 L, a값의 표현형 변이를 각각 11.8%과 24.1%를 설명할 수 있었다. *Xbarc81*과 *Xgwm133* 마커는 밀가루(2012년 생산)의 b값에 대한 표현형 변이를 7.9%, 2011년 생산된 밀가루로 만든 국수면대의 표현형은 9.8% 설명하였다. 국내 24개 밀 품종들의 밀가루와 국수면대 색깔에 대한 *Xgwm190*의 적용 가능성을 평가한 결과, *Xgwm190*의 유전적 표현형이 금강밀과 같은 a 유전자형에 속한 14개의 국내 품종의 밀가루와 국수면대의 L값은(91.6과 83.5) 올그루와 같은 b 유전자형 품종보다(93.6과 85.1) 더 낮은 값으로 나타났다. 이러한 결과를 보았을 때, *Xgwm190*는 국내 밀 품종의 선택 개선을 위한 표지인자로 활용이 가능할 것이다.

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

## 벼 중만생 고품질 내병 내도복 다수성 벼 ‘신보’ 육성

박노봉<sup>1\*</sup>, 여운상<sup>2</sup>, 이지윤<sup>2</sup>, 권오덕<sup>1</sup>, 박동수<sup>2</sup>, 이종희<sup>4</sup>, 조준현<sup>2</sup>, 송유찬<sup>2</sup>, 김상열<sup>1</sup>, 오성환<sup>2</sup>, 손영보<sup>2</sup>, 장재기<sup>3</sup>, 남민희<sup>2</sup>, 권영업<sup>2</sup>, 이영희<sup>2</sup>

<sup>1</sup>경북 영덕군 병곡면 원황길 44 농촌진흥청 국립식량과학원 영덕출장소

<sup>2</sup>경남 밀양시 내이동 점필재로 20 국립식량과학원 남부작물부

<sup>3</sup>경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부

<sup>4</sup>전북 전주시 완산구 농생명로 300 농촌진흥청 연구정책국

국립식량과학원 영덕출장소에서 2002년 하계에 동해안 및 영남지역에서 출수기가 적당하면서 밥맛이 뛰어나고 재배 안정성이 높은 벼 품종을 육성할 목적으로 밥맛이 좋고 외관이 깨끗한 ‘영덕34호’를 모본으로하고 다수성이면서 밥맛이 우수하고 초형이 좋은 ‘새계화’를 부분으로 인공교배 후 계통육종법으로 전개하면서 예비선발시험, 2009년 생산력검정예비시험, 2010년 생산력검정본시험 결과 중만생이면서 다수성이고 쌀 외관이 우수하면서 재배 안정성인 YR24264-25-3-2을 선발하여 ‘영덕55호’로 명명하였다. 2011~2013년까지 3년간 지역적응시험을 실시한 결과 중만생종이면서 쌀 품위가 좋고 밥맛이 양호하며 내병성이 양호한 것으로 평가되어 2013년 12월 농작물직무육성신품종 선정위원회에서 ‘신보’로 명명하였다. 출수기는 보통기 평균 8월 12일로 중만생종 품종이며, 직립초형이고 탈립은 잘되지 않고 이삭추출은 양호 하고 까락이 거의 없으며, 수당립수는 ‘화성벼’ 보다 많으며 현미천립중도 21.9g으로 ‘화성벼’ 보다 더 가볍다. 도정특성은 ‘화성벼’와 비슷하고 쌀알 모양이 둥근 단원형이며 맑고 투명하며 밥맛은 “화성벼”와 보다 우수하다. 불시출수는 안되는 편이고, 위조현상에 강하고 성숙기 엽노화가 느린 편이며 내냉성은 ‘화성벼’와 보다 약한 중약이며, 잎도열병 에 중강의 저항성을 보였고, 오갈병과 흰잎마름병(K<sub>1</sub>, K<sub>2</sub>, K<sub>3</sub>)에 는 강하나 줄무늬잎마름병 및 검은줄오갈병에 약하고 벼멸구 등 충해에는 감수성이다. 쌀 수량성은 지역적응시험 보통기재배 9개소에서 5.67MT/ha로 ‘화성벼’ 보다 4% 증수되었으며, 이모작 및 만식적응성도 높아, 적응지역을 중부평야지, 남부중산간지, 동해안냉조풍지 및 영남평야지로 하여 보급하게 되었다.

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

## **Influence of haplotype combinations of genes involved in regulation of rice grain size and development of a regression equation model**

Jonghwa Park, Chan-mi Lee, Backki Kim, Hee-Jong Koh\*

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

The world population has been continuously increasing and has led to the growing demand for rice. It is therefore important to pay as much attention to the enhancement of grain yield as well as grain quality. Grain size is one of the major factors determining grain yield and quality. A large number of genes are known to be involved in regulation of grain size. However, the influence of their haplotype combination is still largely unknown. Of the previously characterized genes, we especially focused on the six genes (*GS3*, *GS5*, *GS6*, *GW2*, *qSW5/GW5*, and *GW8/OsSPL16*) to expand our understanding of regulation of grain size and to develop a regression equation model that can be used for molecular rice breeding. A total of 215 rice germplasms, which originated or developed from 28 rice-consuming countries, were used in this study. The genotyping analysis revealed that different alleles of the six genes were widely distributed in our germplasm collection and also showed significant associations with the differences in grain size. Interestingly, we found that the relatively small number of haplotype combinations preserved in diverse rice germplasms and showed significant associations with the differences in grain size. In addition, we also found that a single gene-specific allelic variation plays an important role in regulation of grain size in the presence of a certain type of haplotype combination. Based on these results, we developed a regression equation model for prediction of rice grain size. We expect that our model can be used for rice molecular breeding to develop new rice varieties having a grain size in a particular range. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

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

## 국내 밀 계통 및 재래종의 *Rht-1*, *Vrn-1*, *Ppd-1*의 유전적 조성이 주요 농업 형질에 미치는 영향

조은진<sup>1</sup>, 강천식<sup>2</sup>, 정지웅<sup>2</sup>, 윤영미<sup>1,2</sup>, 박철수<sup>1\*</sup>

<sup>1</sup>전라북도 전주시 덕진구 전북대학교 농업생명과학대학 작물생명과학과

<sup>2</sup>전라북도 완주군 이서면 국립식량과학원

본 연구는 국내 밀 품종의 숙기 단축을 위해서 국내 밀 계통 및 재래종 410 계통의 간장, 파성과 감광성에 관련이 있는 유전자로 알려진 *Rht-1*, *Vrn-1*, *Ppd-1* 유전자의 조성을 분석하였다. 분석에 이용된 국내 밀 재료는 국립 유전자원 센터에서 분양 받았으며, 국내 육성 밀 계통은 111개였으며, 238개 국내 재래종과 61개 북한 수집종을 포함하고 있으며, 간장, 수장과 출수기를 조사하였다. 410개 국내 밀은 모두 *vrn-1*과 *Ppd-A1b* 유전자를 지니는 것으로 나타났으며, *Rht-B1a*, *Rht-D1a*, *vrn-B1*, *Vrn-D1*, *Ppd-B1b*와 *Ppd-D1a* 유전자는 대립되는 유전자에 비해서 발생빈도가 높은 것으로 나타났다. 국내 재래종과 비교했을 때 육성계통은 *Rht-D1*, *Ppd-B1*과 *Ppd-D1* 유전자의 발생 빈도가 상이한 것으로 나타났으며, 북한 수집종은 국내 육성계통 및 재래종과 비교하였을 때 *Rht-B1b*와 *Vrn-D1* 유전자의 발현 빈도가 높은 것으로 나타났다. 국내 육성 계통은 국내 재래종과 북한 수집종에 비해 출수기는 중간 수준이었지만 간장과 수장은 짧은 것으로 나타났다. *Rht-B1a*, *vrn-D1*, *Ppd-B1b*과 *Ppd-D1b* 유전자를 지닌 밀은 상대 대립유전자보다 간장과 수장이 긴 것으로 나타났으며, *Vrn-B1b*와 *vrn-D1* 유전자를 지닌 밀은 *Vrn-B1*와 *Vrn-D1* 유전자를 지닌 밀에 비해서 출수기가 늦은 것으로 나타났으며, *Rht-B1b*와 *Rht-D1b* 유전자를 가지는 밀은 *Rht-B1*과 *Rht-D1*의 유전적 조성에서 출수기가 가장 늦고, 간장이 가장 짧은 것으로 나타났다. 반면에 *Ppd-B1b*와 *Ppd-D1b* 유전자를 지닌 밀은 *Ppd-B1*과 *Ppd-D1* 유전자 조합에서 간장과 수장이 가장 긴 것으로 나타났다.

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

## 국내 밀 품종들의 *Vrn-1*과 *Ppd-1* 대립유전자 변이와 농업형질과의 관계

조은진<sup>1</sup>, 강천식<sup>2</sup>, 윤영미<sup>1,2</sup>, 박철수<sup>1\*</sup>

<sup>1</sup>전라북도 전주시 덕진구 전북대학교 농업생명과학대학 작물생명과학과

<sup>2</sup>전라북도 완주군 이서면 국립식량과학원

본 연구는 파성과 감광성에 관련이 있는 유전자인 *Vrn-1*과 *Ppd-1*의 국내 밀 품종의 유전적인 변이가 농업 형질에 미치는 영향을 분석하였다. 국내 밀 품종은 *vrn-A1*, *vrn-B1*, *Ppd-A1*과 *Ppd-D1* 유전자좌에서는 변이가 없었으며, *Vrn-D1*과 *Ppd-B1*에서만 변이를 나타내었고, *vrn-D1*과 *Ppd-B1b*의 발생 빈도가 높게 나타났다. 국내 밀 품종의 춘화처리 여부와 지엽 발생시기 차이를 분석한 결과, 춘화처리와 상관없이 추파성으로 *vrn-D1*를 지닌 품종은 *Vrn-D1a*를 지닌 품종보다 지엽 출현이 늦었다. 춘화처리를 하지 않은 경우에 *vrn-D1*를 지닌 품종은 *Vrn-D1a*를 지닌 품종 보다 많은 최종 엽수를 나타내었지만, 춘화처리는 국내 밀 품종에 있어서 *Ppd-1* 유전자의 조성과는 상관이 없는 것으로 나타났다. 주요 농업형질과 관계를 조사한 결과 *Vrn-D1a*를 지닌 품종은 *vrn-D1* 보다 수량이 높았으며, 천립중은 낮았다. 수량에 있어서 *Vrn-D1a*와 *Ppd-B1b*를 지닌 품종이 554kg/10a으로 *vrn-D1a*와 *Ppd-B1*를 지닌 품종의 500kg/10a 보다 높았다.

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

## 반왜성 유전자 *Rht*가 국내 밀 품종의 농업형질에 미치는 영향

조은진<sup>1</sup>, 강천식<sup>2</sup>, 윤영미<sup>1,2</sup>, 박철수<sup>1\*</sup>

<sup>1</sup>전라북도 전주시 덕진구 전북대학교 농업생명과학대학 작물생명과학과

<sup>2</sup>전라북도 완주군 이서면 국립식량과학원

본 연구는 반왜성(Semi-dwarf) 유전자인 *Rht*(Reduced height)가 국내 밀 품종의 주요 농업 형질에 미치는 영향을 평가하기 위해서 2010년부터 2014년까지 5년 동안 27 품종에 대한 분석을 실시하였다. *Rht* 유전자의 조성은 *Rht-B1*, *Rht-D1*과 *Rht8*에 대해서 분석하였으며, 농업형질은 간장, 수장, 1수립수, 리터중과 천립중을 조사하였다. *Rht-B1a*(70.4%)와 *Rht-D1a*(51.9%)의 발생 빈도가 대립형질에 비하여 높게 나타났으며, 13개 품종은 *Rht-B1a*와 *Rht-D1b* 두 대립 유전자를 가지는 것으로 나타났으며, *Rht-B1b*와 *Rht-D1b* 유전자가 동시에 발현하는 품종은 없었다. *Rht8*의 유전적 변이에서는 올밀과 남해밀이 *Rht8*<sub>206bp</sub>을 나타냈고 나머지 품종은 *Rht8*<sub>196bp</sub>을 나타냈다. *Rht-D1a*와 *Rht8*<sub>196bp</sub> 유전자를 가지는 품종은 다른 품종에 비하여 천립중과 리터중이 높은 것으로 나타났으며, *Rht-B1a*와 *Rht-D1a*를 가지는 품종은 다른 품종에 비해서 1수립수가 낮은 것으로 나타났다. *Rht8*<sub>206bp</sub> 유전자를 지닌 올밀과 남해밀은 *Rht-B1*과 *Rht-D1* 유전자의 조성에 상관 없이 리터중이 낮은 것으로 나타났다. *Rht-B1a*, *Rht-D1a*와 *Rht8*<sub>196bp</sub> 유전자를 지닌 품종은 다른 유전적 조성을 지닌 품종에 비해 1수립수가 낮은 것으로 나타났지만, 반 왜성 유전자의 형질 변화는 국내 품종에 있어서 간장과 수장에는 영향이 없는 것으로 나타났다.

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

## 평야지 적응성 향상을 위한 벼흰잎마름병 및 줄무늬잎마름병 저항성 유전자 집적 조생 계통 개발

박현수<sup>1\*</sup>, 남정권<sup>1</sup>, 김기영<sup>1</sup>, 김우재<sup>1</sup>, 정지웅<sup>1</sup>, 백만기<sup>1</sup>, 김정주<sup>1</sup>, 조영찬<sup>1</sup>, 이점호<sup>2</sup>, 김보경<sup>2</sup>

<sup>1</sup>전라북도 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

<sup>2</sup>경기도 수원시 권선구 수인로 125 농촌진흥청 국립식량과학원 중부작물부

본 연구는 조생종 벼의 평야지 적응성을 향상시키고자 벼흰잎마름병 및 줄무늬잎마름병에 대한 저항성 유전자가 집적된 저항성 계통을 개발하고 이들의 저항성 성능검정과 수량성 등 농업형질을 분석하여 육종사업에 반영하고자 수행하였다. *Xa3*를 가지고 있는 운광과 *Xa4+xa5+Xa21+Stvb-i*를 가지고 있는 SR30075 조합 계통을 모본으로 하여 분자표지를 이용하여 저항성 유전자가 집적된 F<sub>3</sub>계통을 선발하였고 운광에 여교배하였다. 여교배 이후에 K3a균계에 대한 생물검정 및 수량성 등 농업형질에 대한 조사를 통해 RL1(BC<sub>1</sub>F<sub>7</sub>), RL2-5(BC<sub>2</sub>F<sub>6</sub>) 등 5개 조생종 저항성 계통을 육성하였다. 분자표지로 저항성 유전자를 확인한 결과 RL1은 *Xa3+xa5+Xa21+Stvb-i*를 가지고 있었고 RL2, RL3와 RL5는 *Xa3+Xa21+Stvb-i*, RL4는 *Xa21*를 보유하고 있었다. 줄무늬잎마름병은 저항성 유전자 *Stvb-i*의 유무에 의해서 저항성이 결정되었다. 벼흰잎마름병 유전자 조합 *Xa3+xa5+Xa21*과 *Xa3+Xa21*의 계통의 경우 K1, K2, K3, K3a 균계 및 16개 수집 균주에 대해서 저항성 반응을 나타냈으며, K3a균계 접종시에 현미수량, 등숙률 및 현미 완전미율이 대조구와 차이가 없어 저항성 증진을 위한 유망조합으로 판단되었다. RL1은 목표 저항성 유전자를 가지고 있고 저항성 성능도 우수하였으나 간장이 크고 도복에 불안정하였으며 수량이 운광의 80%로 낮고 미질이 좋지 않았다. RL5는 운광에 여교배가 2회 되어 선발된 계통으로 저항성 유전자 *Xa3+Xa21+Stvb-i*를 가지고 있어 벼흰잎마름병 및 줄무늬잎마름병에 대한 효과적인 저항성원으로 판단되었고, 운광보다 단간으로 도복에 안정적인 특성을 나타냈으며 다수성이고 미질이 양호하였다.

\*주저자: Tel. 063-238-5202, E-mail: mayoe@korea.kr

## 벼흰잎마름병 저항성 고품질 중만생 벼 신품종 ‘만백’

박현수<sup>1\*</sup>, 백만기<sup>1</sup>, 김보경<sup>1</sup>, 김기영<sup>1</sup>, 하기용<sup>1</sup>, 신운철<sup>2</sup>, 고재권<sup>1</sup>, 남정권<sup>1</sup>, 김우재<sup>1</sup>, 조영찬<sup>1</sup>, 이점호<sup>3</sup>, 김현순<sup>1</sup>, 고종철<sup>4</sup>, 김정주<sup>1</sup>, 박종호<sup>1</sup>

<sup>1</sup>전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

<sup>2</sup>경상북도 상주시 화서면 중화로 2161, 국립식량과학원 상주출장소

<sup>3</sup>경기도 수원시 권선구 수인로 125 국립식량과학원 중부작물과

<sup>4</sup>경상북도 밀양시 점필재로 520 국립식량과학원 발작물개발과

벼흰잎마름병 저항성 고품질 중만생 벼 ‘만백’은 남부지역을 중심으로 병원성이 강한 벼흰잎마름병균의 확대에 의한 피해가 증가함에 따라서 이에 대응할 목적으로 국립식량과학원에서 개발하였다. 2008/09년 동계에 최고품질 벼 품종으로 밥맛이 좋은 호품을 모본으로 하고 호품과 벼흰잎마름병 저항성유전자가 집적된 계통 SR30075-2-1-21-2-2-1을 교배한 F<sub>1</sub>을 부분으로 하여 여교배하였다. 2009년 하계에 우량 품종을 조기에 개발하고자 BC<sub>1</sub>F<sub>1</sub>세대에서 약배양을 수행하여 423계통을 육성하였다. 병원성이 강한 벼흰잎마름병 K3a균계에 대한 저항성 검정과 초형 및 미질 등 농업형질을 고려하여 선발된 계통들에 대해서 생산력검정을 수행하였다. 출수기가 남평벼보다 늦은 중만생종이며 엽색이 진하고 내도복 직립초형인 HR28423-AC52를 선발하여 ‘익산551호’로 계통명을 부여하고 2012~2014년 3년간 지역적응성 시험을 수행하였다. ‘익산551호’는 벼흰잎마름병 저항성유전자 *Xa3*와 *xa5*를 함께 가지고 있어 우리나라 벼흰잎마름병 대표균계인 K1, K2, K3, K3a에 저항성을 나타내며 16개 수집 균주에 대해서도 광범위한 저항성을 보였다. 또한 벼줄무늬잎마름병에 강하고 수발아에 내성을 나타냈다. 도정특성이 양호하고 쌀의 외관품위가 맑고 투명하며 밥맛 관능검정에서 우수한 특성이 인정되어 직무육성 신품종 선정위원회에서 벼 신품종 ‘만백’으로 명명되었다. 벼흰잎마름병이 상습적으로 발병하는 지역에는 ‘만백’의 재배를 추천하여 고품질이면서 친환경적인 쌀 생산을 기대한다.

\*주저자: Tel. 063-238-5202, E-mail: mayoe@korea.kr

## 벼 중만생 고품질 복합내병성 ‘안백’

백만기<sup>\*</sup>, 박현수, 정종민, 김기영, 남정권, 김정주, 조영찬, 김보경

전라북도 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

‘안백’은 쌀 외관품위가 우수하고 밥맛이 좋으며 내병성이 우수한 남부지역 적응 고품질 품종개발을 목적으로 2006년 하계에 국립식량과학원 벼맥류부에서 흰잎마름병에 강한 익산493호(진백)을 모본으로 청호와 영덕44호를 인공 교배 한 F<sub>1</sub>을 부분으로 삼원교배하여 F<sub>4</sub>이후부터는 계통육종법에 의하여 선발하면서 주요 병해충 및 미질검정을 실시하였다. 생산력검정시험 결과 단간이며 흰잎마름병 및 줄무늬잎마름병에 저항성이고 쌀 외관품위가 우수한 고품질의 HR6723-B-5-2-2 계통을 선발하여 ‘익산549호’로 계통명을 부여했다. ‘익산549호’는 2012~2014년 지역적응시험을 실시한 결과 중만생종으로 도열병에 중도 저항성이며 흰잎마름병((K<sub>1</sub>~K<sub>3</sub>, K<sub>3a</sub>) 및 줄무늬잎마름병에 강하고 오갈병에 중도저항성이다. 쌀의 외관은 투명하고 심복백이 없으며 밥맛이 좋으며 제현율과 현백율, 완전미도 정수율이 남평벼보다 높은 품종으로 우수성이 인정되어 2014년 12월 농촌진흥청의 농작물 직무육성신품종 선정심의회에서 품종명 ‘안백’이라 명명하였고 충남이남평야지 및 서남부해안지(충남, 전남북, 경남북)에 적응하는 품종이다. 재배상 유의점은 키다리병 예방을 위하여 철저한 종자소독을 하여야 하며 질소질 비료 과용시 미질저하, 등숙저하, 숙색불량 및 병해충 발생이 우려되므로 적정 균형시비 하여야 하고 검은 줄오갈병과 멸구류에 약하므로 적기 방제가 필요하며 냉해에 약하므로 냉수용출답이나 만식재배는 피해야 한다.

\*주저자: Tel. 063-238-5214, E-mail: baekmg@korea.kr

## 소득후작 적응 복합내병성 준조생 벼 “중모1039호”

신운철<sup>1\*</sup>, 김우재<sup>2</sup>, 박현수<sup>2</sup>, 남정권<sup>2</sup>, 이점호<sup>3</sup>, 김보경<sup>2</sup>, 강위금<sup>1</sup>

<sup>1</sup>경북 상주시 화서면 중화로 2161, 국립식량과학원 상주출장소

<sup>2</sup>전북 완주군 이서면 혁신로 181, 국립식량과학원 작물육종과

<sup>3</sup>경기 수원시 권선구 수인로 125, 국립식량과학원 중부작물과

“중모1039호”는 국립식량과학원 상주출장소에서 중산간지 적응 복합내병성 고품질 벼를 육성하고자 2007년 하계에 고품질인 무사시노7과 고시히카리와 벼멸구 저항성 계통인 익산495호를 교배한 계통을 인공교배한 F<sub>1</sub> 계통을 세대축진을 위하여 약배양을 실시하여 식물체를 양성한 후 계통육종법에 의하여 육성 선발하면서 주요 농업형질 조사 및 병해충-미질검정을 실시하였다. 2010~2011년 생산력검정을 실시한 결과 내도복이고 복합내병성이며 수량성이 우수한 HR27645AC166-4 계통을 선발하여 “상주48호”로 계통명을 부여하였다. 2012~2014년 지역적응성시험을 실시한 결과 대조품종에 비해 수량성이 높고 내도복성이며 도열병, 흰잎마름병 및 줄무늬잎마름병에 강하며 외관품질과 도정특성이 매우 우수하여 2014년 농작물 직무육성 신품종 선정심의회에서 신품종으로 선정하여 “중모1039호”라 명명하였다. “중모1039호”는 평균 출수기가 보통기 보비재배에서 8월 3일로 오대벼보다 8일 늦고 만기재배에서 8월 26일로 금오벼보다 1일 빠른 준조생 품종이다. 간장이 62cm로 단간이며, 주당수수가 오대벼보다 많으며 등숙비율이 85.6%로 오대벼보다 높고 현미천립중이 21.7g으로 중소립종이다. “중모1039호”는 도열병, 흰잎마름병, 줄무늬잎마름병에 모두 저항성인 복합내병성 품종이다. 쌀알은 심복백이 거의 없이 맑고 투명하며 도정률 및 완전미 도정수율이 각각 76.7, 72.4%로 오대벼보다 높다. 쌀수량은 지역적응시험 보통기 보비재배와 만기재배에서 각각 5.47, 5.04MT/ha로 오대벼와 금오벼보다 5% 증수하였다. “중모1039호”의 적응지역은 남부중산간지, 북부평야지 및 중산간지, 남부고냉지, 동북부해안지이다.

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

## Tomato germplasm with resistance to multiple species of *Xanthomonas* causing bacterial spot

Sung-Chur Sim<sup>1</sup>, David M. Francis<sup>2</sup>

<sup>1</sup>Sejong University, Dept. of Bioresources Engineering, Seoul, 143-747, Korea

<sup>2</sup>The Ohio State University, Ohio Agricultural Research and Development Center, Dept. of Horticulture and Crop Science, Wooster, OH 44691, USA

Bacterial spot of tomato is a disease complex caused by at least four species of *Xanthomonas* and leads to severe yield and quality losses in humid growing conditions in the world. Five physiological species (T1-T5) have been defined by their virulence on tomato varieties. These races are associated with three species: *X. euvesicatoria* (T1), *X. vesicatoria* (T2), and *X. perforans* (T3-T5). Recent epidemics of *X. gardneri* has occurred in the Midwest United States. In this study, we developed germplasm with resistance to multiple species of bacterial spot. Six advanced breeding lines with at least three different source of resistance were crossed and their F<sub>1</sub> hybrids were inter-mated to produce a complex breeding population consisting over 1,100 progeny. Three lines (OH7663, OH7667 and 2k7-6117-S2) were selected by field evaluations of the population against T1, T2, T3, and *X. gardneri*. Graphical genotypes demonstrated that these breeding lines contain a QTL and Rx-4/Xv3 in coupling phase on chromosome 11 as well as Rx-3 on chromosome 5. In order to test the combining ability of the lines, we developed hybrids from multiple crosses and conducted replicated field trials to evaluate bacterial spot resistance and yield. As a male parent, OH7663 showed acceptable combining ability for yield and for resistance against multiple species of *Xanthomonas*. Several hybrids produced yields that were not significantly different from yields of commercial varieties.

## 총체사료용 벼 신품종 ‘녹우’

안억근<sup>1\*</sup>, 정응기<sup>1</sup>, 이상복<sup>1</sup>, 최용환<sup>2</sup>, 양창인<sup>2</sup>, 원용재<sup>1</sup>, 전용희<sup>1</sup>, 이규성<sup>3</sup>, 홍하철<sup>2</sup>, 정오영<sup>4</sup>, 최임수<sup>1</sup>, 모영준<sup>2</sup>, 김정주<sup>2</sup>, 조영찬<sup>2</sup>, 장재기, 하운구<sup>1</sup>, 김명기<sup>2</sup>, 서정필<sup>4</sup>, 이정희<sup>1</sup>, 정국현<sup>1</sup>, 정종민<sup>2</sup>, 정지웅<sup>2</sup>, 박항미<sup>2</sup>, 이점호<sup>1</sup>

<sup>1</sup>농촌진흥청 국립식량과학원 중부작물부

<sup>2</sup>농촌진흥청 국립식량과학원

<sup>3</sup>농촌진흥청 국립농업과학원

<sup>4</sup>농촌진흥청

최근 쌀 재고량 증가 및 생산성 향상으로 증산된 잉여량의 인위적 조정에 의해 벼 재배면적이 줄어들고 있어 식량안보나 논외의 공익적 기능에 악영향을 미치고 있다. 또한 세계 곡물가격의 잦은 변동으로 축산농가의 경영부담이 지속적으로 증가하고 있는 실정이다. ‘녹우’는 출수기가 중부 및 호남평야지에서 각각 8월 22일과 8월 21일로 ‘녹양’보다 13일, 8일 늦고 영남평야지에서는 8월 23일로 ‘녹양’보다 9일 늦은 만생종이다. 보통기 다비재배로 4개소에서 실시한 지역적응시험 결과 평균 총체건물수량이 16.5 MT/ha으로 기존 품종인 ‘녹양’보다 14% 증수되었다. 또한 직파재배시 중요한 저온발아성이 좋고 파종 후 30일째 묘의 길이가 21.8 cm로 양호한 편이며 간장이 122cm로 길지만 좌절증이 높아 포장 도복에도 강한 편이다. 잎도열병 발못자리 검정결과 14지역 중 3지역을 제외한 모든 지역에서 중정도 이상의 저항성 반응을 보였고 목도열병은 포장검정에서 거의 발생하지 않았다. 흰잎마름병, 바이러스병 및 충에는 모두 약한 반응을 보였다. 현미 장폭비는 2.01로 ‘녹양’과 비슷하며 아밀로스 함량이 26.3%로 높은 편이다. 사료적성은 ‘녹양’에 비해 조회분 및 조지방의 함량은 높으나 조단백질은 5.3%로 낮고 가소화양분총량(TDN, total digestible nutrients)이 68.8%로 양호한 편이다. 열대자포니카 벼를 이용하여 육성된 ‘녹우’는 차후에 논 농업다양화 및 조사료 자급률 증대에 기여할 것으로 기대된다.

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

## 중산간지 지역에 따른 미세온도변화와 벼 생육양상의 차이

양창인\*, 김명기, 백남현, 강위금, 신운철, 김미향, 조현숙

전라북도 완주군 이서면 혁신로 181 국립식량과학원

오대벼의 재배안정성을 파악하기 위해 중산간지 2지역에서 벼 군락주위의 온도변화에 따른 생육양상을 조사하였다. 조생종 재배지역인 철원과 상주에서 벼를 재배하는 경우 재배환경과 생육양상이 비슷할 것으로 여겨졌으나 온도변화와 벼 생육에서 상이한 패턴을 보였다. 시험지의 위치를 보면 철원은 위도가 38°15′, 경도 127°15′, 표고 192m 이고 상주는 위도 36°26′, 경도 127°26′, 표고 285m에 소재하였다. 벼 식물체 주변의 온도변화를 살펴보기 위하여 생육시기를 이앙기-분얼초기, 분얼초기-분얼성기, 분얼성기-유수형성기, 유수형성기-출수기, 출수기-수확기로 나누어 조사하였고 온도변화는 대기와 군락내 온도, 수온, 지온 등으로 나누어 5월20일부터 9월27일까지 조사하였다. 주요온도의 변화를 비교해 보면 이앙기-분얼초기, 분얼초기-분얼성기는 철원에서 상주보다 높았으며 생육중·후반기에 이르러 분얼성기-유수형성기, 유수형성기-출수기, 출수기-수확기에는 상주지역에서 높았다. 특히 대기 평균 온도의 지역간 차이는 컸으나 지온의 평균온도는 그 차이가 적은 편이었다. 한편 철원과 상주의 생육양상의 차이를 비교해 보기 위해서 초장(cm)이나 경수/수수(개/m<sup>2</sup>) Biomass(g/m<sup>2</sup>)를 조사해본 결과 생육전반기에는 철원지역에서 생육이 월등히 왕성했고 분얼성기를 지나면서 생육후반기에는 상주지역에서 생육이 훨씬 양호했다. 위도는 높지만 표고가 낮은 편인 철원은 초기생육을 조장하고 표고는 높지만 위도가 낮은 남쪽에 위치한 상주지역에서는 후기생육에 유리한 온도조건이어서 초기에 왕성한 생육이 필요한 조생종인 오대벼는 철원에서 생육이 적당한 것으로 추정되지만 일장 일조량 강수량 등을 포함하여 정밀한 검토가 요구된다.

\*주저자: Tel. 033-455-2031, E-mail: yci212@korea.kr

## **A New Forage Barley Cultivar with Semi-Smooth Awn and High Yielding ‘Miho’**

Young-Jin Oh<sup>1\*</sup>, Tae-Il Park<sup>1</sup>, Hyoung-Ho Park<sup>3</sup>, Ouk-Kyu Han<sup>2</sup>, Jong-Chul Park<sup>1</sup>, Tae-Hwa Song<sup>1</sup>, Yang-Kil Kim<sup>1</sup>, Hyeon-Jung Kang<sup>1</sup>, Jae-Seong Choi<sup>1</sup>, Yun-Woo Jang<sup>3</sup>, Kwang-Geun Park<sup>2</sup>, Jong-Ho Park<sup>1</sup>, Chon-Sik Kang<sup>1</sup>, Young-Keun Cheong<sup>1</sup>, Kyong-Ho Kim<sup>1</sup>, Bo-Kyeong Kim<sup>1</sup>, Geon-Sig Yun<sup>4</sup>, Gi-Heung Hong<sup>5</sup>, Jeong-Suk Bae<sup>6</sup>, Seong-Tae Lee<sup>7</sup>

<sup>1</sup>National Institute of Crop Science, RDA, Wanju-gun, 565-851, Korea

<sup>2</sup>Dept. of Central Area, National Institute of Crop Science, RDA, Suwon, 441-100, Korea

<sup>3</sup>Dept. of Southern Area, National Institute of Crop Science, RDA, Miryang, 627-803, Korea

<sup>4</sup>Chungbuk Agricultural Research & Extension Service, Cheongwon 363-880, Korea

<sup>5</sup>Chungnam Agricultural Research & Extension Service, Yesan 340-861, Korea

<sup>6</sup>Gyeongbuk Agricultural Research & Extension Service, Daegu 702-320, Korea

<sup>7</sup>Gyeongnam Agricultural Research & Extension Service, Jinju 660-985, Korea.

The purpose of development new variety ‘Miho’ (*Hordeum vulgare* L.) is a favorite with livestock feed and develop varieties resistant to disease and lodging. ‘Miho’ was carrying the growth habit of group III, green and mid-wide leaf. Awn that are related to preference of livestock is a semi-smooth awn. This cultivar had 96cm of culm length, 650 of spikes per m<sup>2</sup>. Heading date of ‘Miho’ is April 27, and maturing dates on May 30, which were later than cultivar ‘Youngyang’. It also showed strong winter hardiness, and similar resistance to shattering and BaYMV compared with those of check one. The best thing among the traits of one is a new good quality with the plant green at the latter growing period. The average forage dry matter yield in the regional yield trial was about 13.1, 12.1 MT per ha in upland and paddy field, respectively, which were 9%, 2% higher than that of the check cultivar. It’s also showed 6.8% crude protein, 27.1% ADF (acid detergent fiber), and 67.5% TDN (Total Digestible Nutrients), including higher silage quality for whole crop barley. This cultivar would be suitable for the area whose daily minimum temperature was above -8°C in January in Korean peninsula.

**\*Corresponding Author:** Tel. 063-238-5224, E-mail: ohyj5894@korea.kr

---

**PA-37****열대아시아지역 적응성 벼 신품종 ‘아세미1호’ 개발**

원용재<sup>1\*</sup>, 하운구<sup>1</sup>, 정응기<sup>1</sup>, 강경호<sup>1</sup>, 최임수<sup>1</sup>, 홍하철<sup>1</sup>, 조영찬<sup>1</sup>, 정오영<sup>2</sup>, 장재기<sup>1</sup>, 양운호<sup>1</sup>, 정국현<sup>1</sup>, 이규성<sup>3</sup>, 여운상<sup>1</sup>, 양창인<sup>1</sup>, 김명기<sup>1</sup>, 서대하<sup>1</sup>, 성낙식<sup>1</sup>, 윤광섭<sup>1</sup>, 성열규<sup>1</sup>, 이점호<sup>1</sup>, 김보경<sup>1</sup>

<sup>1</sup>농촌진흥청 국립식량과학원

<sup>2</sup>농촌진흥청

<sup>3</sup>농촌진흥청 국립농업과학원

열대지역은 낮의 길이가 짧고(단일조건) 기온이 높아 온대벼를 재배하면 이앙 후 25일 경 이삭이 나오는 불시출수현상이 나타나 정상적인 생육을 기대할 수 없고, 수량은 약 1톤/ha로 정상치의 15% 정도 수준에 불과하다. ‘아세미1호’는 이러한 장벽을 타파하기 위해 육성한 품종으로 낮의 길이에 감응하지 않고 꽃이 피는 비감광성이고, 온대지역과 열대지역에서 잘 자라는 광지역적응성이다. ‘아세미1호’의 출수기는 중부평야지 보통기 재배에서 7월28일인 조생종으로 반직립성 초형이며, 이삭추출도 양호하고 탈립은 잘 된다. 저온발아성이 높고, 잎도열병에는 강하지만 다른 병해충에는 약하였다. 또한 쌀이 맑고 단백질함량은 7.4%로 다소 높으며, 도정특성은 ‘화성’보다 미흡하였다. 수량성은 중부평야지 4개소에서 582kg/10a로 ‘화성’ 대비 108%, 중산간지에서 605kg/10a로 ‘오대’ 대비 109%로 높았으며, 조기재배에서 549 kg/10a 로 ‘조평’ 대비 105%, 소득작물 후작에서도 521 kg/10a 로 ‘금오’ 대비 112%로 높았다. 필리핀 현지에서도 내도복, 다수성으로 평가되었다. 벼키는 89cm, 주당수수 13개, 현미천립중이 23g이었으며 도정률은 현지 품종 IR 72가 62%인데 ‘아세미1호’는 65%로 높았고 수확량도 5.2 t/ha으로 IR72보다 10%가까이 높았다. 특히, 열대아시아지역에서 우리 입맛에 맞는 쌀을 생산할 수 있는 기반을 마련하고, 기후온난화에 대응하여 고온 적응 품종 개발을 위한 중간모본으로 활용이 기대된다.

\*주저자: Tel. 031-695-4030, E-mail: yjwon@korea.kr

**PA-38****An RNA-Seq transcriptome analysis of rice genes in response to water deficiency in soil**

Yo-Han Yoo, Anil Kumar N.C, Ki-Hong Jung\*

Department of Plant Molecular Systems Biotechnology & Crop Biotech Institute, Kyung Hee University, Yongin 446-701, Republic of Korea

Water-deficiency is one of the most serious challenges which restrict crop production. Root is the primary tissues exposed to water limitation in soil. Although a number of transcriptome data under water limitation have been produced in rice, but most of them have analyzed the effect of leaf or shoot. Thus, understanding of relating molecular mechanism is still limited. To get global view of the effect on water deficiency in rice root, we carried out RNA-Seq experiment. To do this, we compared the RNA-Seq transcriptome data of 3 day samples under water deficiency with those of unstressed rice roots with unstressed control. As a result, we identified 1,098 genes upregulated in water stress condition for 3 days. Gene ontology (GO) enrichment analysis revealed that 18 GO terms are overrepresented. Of them, valyl-tRNA aminoacylation, transcription from RNA polymerase II promoter, glycine catabolic process, and L-phenylalanine catabolic process are more significant, indicating that transcription of new transcripts, control of translation fidelity, and reuse of primary and secondary metabolites can be activated during water stress.

\*Corresponding Author: E-mail: khjung2010@khu.ac.kr

## Identification of QTL for grain quality traits using introgression lines derived from an interspecific cross in rice

Yeo-Tae Yun<sup>1</sup>, Chong-Tae Chung<sup>1</sup>, Yeong-Ju Lee<sup>1</sup>, Han-Jung Na<sup>1</sup>, Jae-Chul Lee<sup>1</sup>, Kwang-Won Lee<sup>1</sup>, Young-Hwan Yoon<sup>1</sup>, Ju-Won Kang<sup>2</sup>, Hyun-Sook Lee<sup>2</sup>, Sang-Nag Ahn<sup>2\*</sup>

<sup>1</sup>Chungnam Agricultural Research and Extension Services, Yesan 340–861, Republic of Korea

<sup>2</sup>College of Agri. & Life Sci., Chungnam National University, Daejeon 305–764, Republic of Korea

96 BC<sub>3</sub>F<sub>5</sub> introgression lines derived from a cross between Hwaseong and *O. rufipogon* were genotyped with 131 simple sequence repeat (SSR) markers to identify and characterize quantitative traits loci (QTLs) associated with grain quality traits in rice. 96 BC<sub>3</sub>F<sub>5</sub> lines displayed a wide range of variation for days to heading and agronomic traits. Results indicated that one major QTL (*qDTH6*) on chromosome 6 was associated with significant variation for days to heading. 83 lines without the *O. rufipogon* segment at *qDTH6* were selected and analyzed for grain quality traits. QTL analysis was conducted for two groups, 96 and 83 introgression lines, and a total of 25 QTLs were detected for rice quality traits. 16 QTLs were detected in a group of 93 lines, 11 QTLs detected in a group of 83 lines, and 2 QTLs were commonly identified in both groups. Most of the QTLs detected in this study were located on the same or adjacent regions as those reported by the previous studies, and the wild alleles negatively affected quality traits. In contrast, the wild allele at *qGCR9* for the glossiness of cooked rice on chromosome 9 contributed to an increase in glossiness which is positively correlated with rice eating quality. Three ILs with the wild allele at *qGCR9* displayed better eating quality than the recurrent parent, Hwaseong. To confirm the effect of *qGCR9*, high density mapping of the *qGCR9* with a series of NILs will be conducted.

\*Corresponding Author: Tel. 042-821-5728, E-mail: ahnsn@cnu.ac.kr

## The development of physiological phenotyping parameter to characterize early stress responses in rice plants

Hye-Jin Yoon<sup>1\*</sup>, Kyung Hwan Kim<sup>1</sup>, Yeon-Hee Lee<sup>1</sup>, Eun-Jung Suh<sup>1</sup>, Taek-Ryun Kwon<sup>2</sup>

<sup>1</sup>Molecular Breeding Division, Department of Agricultural Biotechnology, National Academy of Agricultural Science, RDA, 560–500, KOREA

<sup>2</sup>Biosafety Division, Department of Agricultural Biotechnology, National Academy of Agricultural Science, RDA, 560–500, KOREA

Research on salinity stress has strongly increased over the last decade, as salinity stress is a main key factor limiting the global crop production in many regions of the world. In recent years, it is possible to obtain a large amount of genotypic data in a short time due to a reduction in genotyping costs. This wave of genomic information has effected the development of new strategies for the integration of molecular information in breeding programs. However, phenotyping is still a manual activity, and different from each species, environment, and trait. It often generates high labor costs, and can be sensitive to environmental changes, and sometimes includes the individual biased assessments from different people.

There is a strong demand for phenotypic data of high quality. The current objective of phenomics is phenotyping a large number of individuals for many traits in a nondestructive manner and with good accuracy.

Here we described the image-based technology as applied to alleviate the bottleneck for the development of high-throughput phenotyping platforms. Several trials to measure stress responses of rice plantlets based on image data under the salinity condition are underway to develop automation for the next-level of phenotyping.

\*Corresponding Author: Tel: 063-238-4659, E-mail: hyejinyoon@korea.kr

---

**PA-41****분지 각도가 좁은 신초형 종실용 들깨 신품종 ‘소담’**

이명희\*, 배석복, 김성업, 오은영, 김명식, 오기원, 정찬식, 오인석

경상남도 밀양시 점필재로 20 국립식량과학원 발작물개발과

들깨는 꿀풀과 1년생 식물로 우리나라 주요 유지작물 중 하나이다. 들깨의 국내 재배면적은 2013년 30.1천 ha에서 2014년 37.5천 ha로 약 20% 이상 늘어나고, 2014년 들기름 일본 수출이 늘어나면서 수요가 증대되고 있다. 그 이유로 들기름의 지방산 조성 중 60% 이상을 차지하고 있는 알파-리놀렌산이 심장질환 예방, 학습능력 향상, 알레르기 치료 등에 효과가 있는 것으로 알려져 있기 때문이다. 들깨는 주로 조미용이나 착유용으로 많이 이용되므로, 종피가 부드럽고 기름함량이 많은 품종을 선호하고 있다. 2014년에 개발된 ‘소담’은 2004년에 K015926을 모본으로 하고 IT274257(밀양27호)를 부분으로 하여 육성된 품종으로 계통육종법에 따라 육성하였으며, 수량 및 종실특성이 우수하여 2012년 ‘밀양61호’로 계통명을 부여하였다. ‘소담’은 특히 분지수가 11개로 적으며 분지각도가 좁은 신초형이다. 종피는 회백색이며, 부드럽고 기름함량이 46.4%로 높다. ‘소담’은 성숙기 10월 2일로 기존 품종보다 4일 빠르며, 6월 중하순경 파종하였을 경우, 경장이 116 cm이고, 화방군수가 83개로 많았다. 종실의 수량성은 3년간 지역적응시험 결과 표준품종인 새엽실들깨보다 95% 수준이며, ha당 수량은 0.97MT이다.

\*주저자: Tel. 055-350-1212, E-mail: emhee@korea.kr

**PA-42****Development of female (*F*) locus specific co-dominant molecular marker in cucumber (*Cucumis sativus* L.)**

Khin Thanda Win<sup>1</sup>, Chunying Zhang<sup>1</sup>, Kihwan Song<sup>1</sup>, Sanghyeob Lee<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Engineering, Senjong University, Seoul 143-747, Republic of Korea

<sup>2</sup>Planr Engineerinf Research Institute, Senjong University, Seoul 143-747, Republic of Korea

Cucumber is a typical monoecious plant with individual male and female flowers, and sex expression in cucumber is mainly determined by three major genes: *F/f*, *M/m* and *A/a*. Gynoecy plays an important role in cucumber hybrid breeding and use of gynoecious lines as maternal parent ensures high productivity. The purpose of this study is to identify a co-dominant molecular marker linked to *F* locus to distinguish homozygous and heterozygous gynoecious plants for cucumber breeding programme. Firstly, we analyzed the sequence polymorphism of 5 gynoecious and 5 monoecious inbred lines to detect polymorphism to develop the marker linked to *F* locus. A pair of specific primer based on insertion/deletion polymorphism on branched-chain amino acid transaminase (*BCAT*) gene was designed and examined the polymorphism in the parents, *F*<sub>1</sub> and *F*<sub>2</sub> segregating population derived from gynoecious (WJEF11) and monoecious (WNEF8) inbred lines. The result showed that the specific fragment amplified with *Cs-Female-F/Cs-Female-R*, was identified as a co-dominant marker and co-segregated with sex phenotype in *F*<sub>2</sub> population. Furthermore, we present a new linkage map for *F* locus using Indel markers. This is the first report for the development of *F* locus specific co-dominant marker which can distinguish homozygous and heterozygous gynoecious and it could be used in marker-assisted selection in cucumber breeding.

\*Corresponding Author: Tel. 02-3408-4376, E-mail: sanglee@sejong.ac.kr

## PA-43

### 펠릿 재료가 카멜리나 종자의 발아에 미치는 영향

박민우<sup>1</sup>, 최충원<sup>2</sup>, 이상협<sup>2,3\*</sup>

<sup>1</sup>현대종묘(주)

<sup>2</sup>서울특별시 광진구 군자동 세종대학교 생명과학대학 식물생명공학전공

<sup>3</sup>서울특별시 광진구 군자동 세종대학교 식물생명공학연구소

본 연구는 캐나다산 봄 재배용 카멜리나 종자에 적합한 펠릿 물질의 탐색과 이들 피복 물질들과 발아에 미치는 영향을 알아보려 수행하였다. 십자화과에 속하는 카멜리나 종자는 오메가3와 같은 지방산이 풍부하여 대체 의료 작물 뿐만 아니라 바이오 디젤용 작물로 각광을 받고 있다. 국내에서는 재배가 활발히 이루어지지 않고 있으나 유럽과 캐나다 등지에서는 오일을 추출하여 의료용, 화장품 그리고 대체 연료를 이용할 목적으로 광범위하게 이루어지고 있다. 카멜리나는 파종 기계를 이용하여 포장에 직파를 하는데 종자의 크기가 매우 작기 때문에 파종시 종자 소요량이 많고 파종밀도가 불균일하여 발아 후 묘소질도 떨어지는 데다 새나 쥐와 같은 동물들이 가해하여 유실되는 문제점이 발생하게 된다. 소립종 종자들에 펠릿 코팅을 하는 주요한 목적은 파종작업을 용이하게 하며 입모주수의 확보 그로인한 입모 주수의 확보와 수량 증대에 있으며 이러한 문제점을 해결하기 위하여 소립종 종자들의 종자표면에 발아에 영향을 미치지 않는 불활성화 물질을 코팅하여 그 크기를 임의로 조절하여 파종하고 있다. LD, MD 그리고 HD의 세 가지 형태별 카멜리나 펠릿종자의 형태적 특성은 MD와 HD 형태의 펠릿 가공종자가 LD형태에 비하여 표면이 더 매끄러우며 펠릿 종자의 경도는 HD 형태의 것이 0.54kg으로 가장 단단하였으며 수분흡수 후 열 개성이 다소 떨어지는 것으로 관찰되었다. 실내 표준발아 시험에서 세 가지 형태의 카멜리나 펠릿종자는 카멜리나 종자들에 비하여 발아율, 발아속도(GR), 발아속도지수(PI)가 모두 낮게 나타났으나 하우스에서 실시한 토양 출현력 검정 시험에서는 카멜리나 종자를 포함한 세가지 형태의 펠릿종자들의 발아율은 비슷한 결과를 보였으나 발아속도(GR)와 발아속도지수(PI)의 값에서는 HD형태의 펠릿종자가 낮은 결과 값을 보였다.

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

## PA-44

### 중부지역 적응 중생 복합내병성 고품질 벼 품종 ‘선품’ 개발

이정희<sup>1\*</sup>, 정응기<sup>1</sup>, 원용재<sup>1</sup>, 양창인<sup>1</sup>, 조영찬<sup>1</sup>, 김명기<sup>1</sup>, 서정필<sup>2</sup>, 최임수<sup>1</sup>, 이상복<sup>1</sup>, 정오영<sup>2</sup>, 안역근<sup>1</sup>, 오세관<sup>1</sup>, 정종민<sup>1</sup>, 홍하철<sup>1</sup>, 현용조<sup>1</sup>, 모영준<sup>1</sup>, 양운호<sup>1</sup>, 이점식<sup>1</sup>, 이점호<sup>1</sup>, 김보경<sup>1</sup>

<sup>1</sup>경기도 수원시 권선구 수인로 126 농촌진흥청 국립식량과학원

<sup>2</sup>전주시 완산구 농생명로 300 농촌진흥청

중부지역 재배에 적합한 중생 품종은 ‘화성’과 ‘하이아미’가 있지만 다양성이 부족하고, 또한 지구온난화에 의한 병해충 발생에 대응하여 재배안정성을 갖춘 품종이 부족하다. 또한 중부지역에 재배되고 있는 외래품종을 대체할 만한 품종이 부족하여 내병충성 및 내재해성을 갖추면서 밥맛이 우수한 품종 육성이 필요하다. ‘선품’은 벼의 3대 주요병해인 도열병, 흰잎마름병 및 줄무늬잎마름병에 강하고, 쌀알은 심복백이 거의 없어 맑고 깨끗하며, 밥맛이 화성과 추정보다 우수한 품종이다. 출수기 화성보다 4일 늦은 8월 12일로 중생종이다. 화성과 비교하여 주당수수는 같고 수당립수는 많으며 등숙비율이 높고 현미치립중은 22.8g으로 비슷한 편이다. 수량성은 지역적응시험 보통기 보비재배(9개소)에서 5.74 MT/ha로 화성대비 9% 증수된 수량성은 보였다. 중부평야지 및 중서부해안지, 남부중산간지와 동남부해안지가 적응지역으로, 중부지역 적응 품종을 다양화하여 생산자부터 도정 및 유통업자와 소비자까지 만족하는 우리 쌀 품질고급화를 통하여 농가소득증대와 쌀 산업 경쟁력 제고가 기대된다.

\*주저자: Tel. 031-695-4032, E-mail: lejehe@korea.kr

---

**PA-45****QTL Mapping for shoot fresh weight in a RIL population developed from a cross of wild and cultivated soybean**

Sovetgul Asekova<sup>1</sup>, Krishnanand P Kulkarni<sup>1</sup>, Jeong Hwa Kim<sup>1</sup>, Minsu Kim<sup>1</sup>, Jiho Park<sup>1</sup>, Hyun-Jee Kim<sup>1</sup>, J. Grover Shannon<sup>2</sup>, Jeong-Dong Lee<sup>1\*</sup>

<sup>1</sup>Department of Applied Bioscience, Kyungpook National University, Daegu 702-701, Republic of Korea

<sup>2</sup>J.G. Shannon: Division of Plant Sciences, University of Missouri- Delta Center, Portageville, MO 63873, USA

Shoot-fresh-weight (SFW) is one of the parameters, used to estimate the total plant biomass yield in soybean. Understanding the genetic and molecular basis of SFW could help increase the total biomass production. In this particular study, we identified QTLs associated with SFW in a Recombinant Inbred Line (RIL) population derived from interspecific cross of PI483463 and Hutcheson. A total of 551 (535 SNP and 16 SSR) markers, were found to be polymorphic between the parental lines and were used to screen the RILs to develop the genetic map. Linkage analysis and QTL mapping were performed using with the software QTL IciMapping version 4.0, with the minimum LOD score of 3.0 and estimating the likelihood of a QTL and its corresponding effects at every 1cM. QTLs with LOD value > threshold LOD, as determined by 1000 permutation tests at  $p > 0.05$  were considered as significant QTLs. The analysis identified a total of 5 QTLs associated with shoot fresh weight over two environments, with the phenotypic variation (PV) ranging from 6.34 to 21.32%, and the additive effect from -0.54 to 0.33. Among these QTLs, *qFW1314\_19\_1* had the largest LOD scores, with PV of 21.32%. Interestingly, three QTLs, *qFW2013\_19\_1*, *qFW2014\_19\_1*, and *qFW1314\_19\_1* identified on chromosome 19(L), showed negative additive effects, indicating the contribution from the wild parent PI483463. The QTLs identified in this study can be the targets to identify the candidate genes for the SFW and can help in developing cultivars with increased biomass potential.

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

**PA-46****옥수수 유망 자식계통들에 대한 잡종강세 및 수량관련 형질의 유전분석**

박종열<sup>1</sup>, 박기진<sup>1</sup>, 사규진<sup>2</sup>, 이주경<sup>2\*</sup>

<sup>1</sup>강원도농업기술원 옥수수연구소

<sup>2</sup>강원대학교 농업생명과학대학 식물자원응용공학과

본 연구는 종실수량과 SSR 마커 사이의 상관분석을 위하여 종실용 옥수수 9개의 자식계통을 이용하여 반이면 교잡 (Half-Diallel Cross)을 통해 얻어진 36개의 F<sub>1</sub> 교잡종들에 대하여 수량과 농업형질 그리고 유전적 거리와의 상관 분석하였다. 그 결과, 농업형질에 의한 유연관계 분석에서 가장 가까운 계통은 Wf9와 ND203으로 0.809를 보였고, BSSS (Iowa Stiff Stalk Synthetic) 그룹인 B73과 B14A가 0.810으로 가까운 것으로 나타났다. 그러나 같은 LSC (Lancaster Sure Crop) 그룹인 Va85와 C103은 가장 거리가 먼 것으로 나타나서 농업형질로 유전적 거리를 측정하는 것은 한계가 있는 것으로 보였다. 따라서 본 연구에서는 92개의 SSR primer들을 가지고 step-by-step 방식으로 옥수수 종실수량에 영향을 미치는 분자마커를 선발하고자 하였다. 선발된 9개의 SSR primer들을 이용하여 옥수수 종실중과 의 상관분석을 수행한 결과, 고도의 정의 상관(R<sup>2</sup>=0.703\*\*)을 보였다. 선발된 SSR 마커를 이용한 유전적 거리와 교잡종의 주요 농업 형질의 상관분석에서 종실중, 이삭장, 이삭경 등 수량관련 형질뿐만 아니라 간장, 착수고도 유의 성을 보였다.

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

---

**PA-47**

## Detection of novel QTLs for foxglove aphid resistance in soybean

Sumin Park<sup>1</sup>, Ju Seok Lee<sup>1</sup>, Sungmin Kim<sup>1</sup>, Kyungryun Kim<sup>1</sup>, Mijung Cho<sup>1</sup>, Eunsil Kim<sup>1</sup>, Jin Kyo Jung<sup>2</sup>, Jeong-Dong Lee<sup>3</sup>, Sungtaeg Kang<sup>1\*</sup>

<sup>1</sup>Department of Crop Science & Biotechnology, Dankook University, Cheonan, 330–714, Korea

<sup>2</sup>National Institute of Crop Science, RDA, 151 Seodun-dong, Suwon 441–857, Korea.

<sup>3</sup>Division of Plant Bioscience, Kyungpook National Univ., Daegu 702–701, Korea

Foxglove aphid, *Aulacorthum solani* (Kaltenbach), is a Hemipteran insect that infected a wide variety of plants worldwide and caused serious yield losses in crops. The objective of this study was to identify the putative QTL for foxglove aphid resistance in wild soybean, PI 366121, (*Glycine soja* Sieb. and Zucc.). One hundred and forty one F<sub>2</sub>-derived F<sub>8</sub> recombinant inbred lines developed from a cross of susceptible Williams 82 and resistant PI 366121, were used. The phenotyping of antibiosis and antixenosis was done through choice and no-choice assays with total plant damage (TPD) and primary infestation leaf damage (PLD); a genome-wide molecular linkage map was constructed with 504 single nucleotide polymorphism markers utilizing a GoldenGate assay. Using inclusive composite interval mapping analysis for foxglove aphid resistance, one major candidate QTL on chromosome 7 and 3 minor QTL regions on chromosome 3, 6 and 18 were identified. The major QTL on chromosome 7 showed both antixenosis and antibiosis resistance responses. However, the minor QTLs showed only antixenosis resistance response. The major QTL mapped to a different chromosome than the previously identified foxglove aphid resistance QTL, *Rasol*, from the cultivar Adams. Also, the responses to the Korea biotype foxglove aphid were different for *Rasol*, and the gene from PI 366121 against the Korea biotype foxglove aphid were different. Thus the foxglove aphid resistance gene from PI 366121 was determined to be an independent gene to *Rasol* and designated to *Raso2*. This result could be useful in breeding for new foxglove aphid resistant soybean cultivars.

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

**PA-48**

## Identification of quantitative trait loci related to grain filling under low temperature condition

Jong-Min Jeong<sup>\*</sup>, Ung-Jo Hyun, Ji-Ung Jeung, Kyung-Ho Kang, Young-Chan Cho, Bo-Kyeong Kim

Crop breeding division, National institute of crop science(NICS), Wan-ju 565–851, Republic of Korea

Low temperature is a major abiotic stress that adversely affects rice production in rice cultivation regions of the world. Low temperature during the rice growing season, can inhibit growth and development at any development stage, from germination to grain filling. Among the rice growth stage, reproductive stage was known as the most sensitive to low temperature, causing sterile grain and lead yield loss. However, low temperature during the grain filling stage also, may cause delay and incomplete grain maturation. In this study QTL analysis were performed to identify the QTLs associated with percent of grain filling under low temperature condition during the grain filling stage. A 139 RIL derived from a cross between ‘Milyang23’ (Tong-il, cold susceptible) and ‘Gihobyeo’ (Japonica, cold tolerance) were exposed to air and water of 17°C at the same time for 14 days during the grain filling stage. One significant QTL associated to percent of grain filling was detected on chromosome 7. This QTL could explain 14.7% of the phenotypic variance for percent of grain filling. We have the plan to confirm the detected QTL through further study.

\*Corresponding Author: Tel. 063-238-5217, E-mail: jjm0820@korea.kr

PA-49

## 경기지역 콩 다수확 선도단지 조성을 위한 품종선발 및 작부체계 연구

장은균<sup>1\*</sup>, 이진구<sup>1</sup>, 한정아<sup>1</sup>, 송경순<sup>1</sup>, 김진영<sup>1</sup>, 강창성<sup>1</sup>, 윤희태<sup>2</sup>

<sup>1</sup>경기도 연천군 경기도농업기술원 소득자원연구소

<sup>2</sup>대구시 달성군 국립식량과학원 남부작물부

경기지역의 콩 다수확 선도단지를 선정하여 경기지역에 적합한 다수확 품종과 각 지역의 작부체계 및 재배 매뉴얼 설정을 추진하였다. 대상지역은 경기 연천 단작지대 1개소, 양평 이모작지대 1개소 및 예비시험지 3개소를 선정하여 선도농가에 다수확품종을 보급하고, 재배매뉴얼을 보급하여 파종에서 수확 후 관리 및 병해충 방제 등을 교육하였다. 지역별 최대 수량은 연천군 연천읍에서 연풍콩이 328kg/10a로 가장 많은 수량을 나타내었고, 양평 지평면에서는 강풍콩이 271kg/10a로 가장 많은 수량을 나타내었다. 파주시 적성면에서는 우람콩이 비닐피복시 360kg/10a로 가장 많은 수량을 나타내었다. 중북부권 콩 작부체계 모형으로 콩 재배면적 6,293ha의 84%(5,281ha)가 단작형태로 재배를 하고 있었고, 단작형태 중 가장 많은 재배면적을 차지하는 곳은 연천, 파주, 화성 순으로 나타났다. 이모작형태는 감자+콩, 맥류+콩, 콩+채소 순이었으며, 감자+콩 재배가 1,012ha로 이모작 중 56%(568ha)를 차지하였으며, 콩+채소, 맥류+콩 및 기타형태의 이모작은 444ha로 전체적으로(또는 감자+콩) 이모작 재배면적은 안성에서 가장 많은 반면 맥류+콩 작부체계는 평택에서 가장 많이 이루어지고 있는 것으로 조사 되었다. 경기지역에서의 이모작 재배 문제점은 감자+콩 작부체계의 경우 감자 수확 후 6월 하순에서 7월 상순 콩 파종시 한발조건이 되면 재파, 3파를 시도하여도 활착이 잘 되지 않아 생육이 균일하지 않았고, 비닐 피복시 타공 구멍이 작으면, 물 부족으로 인해 유효기에 자엽 및 생장부가 고사하는 문제점 등이 발생하여 금후 대책 연구가 필요한 것으로 나타났다.

\*주저자: Tel. 031-229-6194, E-mail: jek0428@gg.go.kr

PA-50

## 강원지역에서 파종량이 호밀 “곡우”의 생육특성에 미치는 영향

조영일<sup>1</sup>, 이동우<sup>1</sup>, 김영호<sup>1</sup>, 안경구<sup>1</sup>, 박덕심<sup>1</sup>, 김인혜<sup>1</sup>, 조용섭<sup>1</sup>, 한옥규<sup>2</sup>, 이종경<sup>1\*</sup>

<sup>1</sup>경기도 수원시 서둔동 농업기술실용화재단 종자사업단

<sup>2</sup>경기도 수원시 서둔동 국립식량과학원 중부작물부

호밀은 척박한 토양환경이나 내한성이 강하고, 단위면적당 생산성이 높은 특성 때문에 우리나라 중부지방에서 조사료나 녹비로서 많이 재배하는 동계 작물이지만, 종자 생산용으로 재배 시 결실기 장마 등으로 인한 도복피해의 발생으로 국내 채종이 어려워 대부분 수입에 의존하고 있다. 따라서 본 시험은 호밀의 국내 채종을 위한 중수요인을 분석하기 위해 국내 육성품종인 “곡우”의 파종량에 따른 생육특성을 조사하였다. 시험장소는 강원도 영월군에 소재한 농가 채종포에서 실시하였다. 토양은 pH가 5.8~6.9, 유기물 함량이 16~20 g/kg, 유기인산은 38~150 mg/kg, 가리, 칼슘, 마그네슘은 각각 0.15~0.50, 2.4~3.5, 0.7~1.6 cmol/kg이었고, 전질소 함량은 0.07~0.10%, 질산태 질소와 암모니아태 질소함량은 각각 1~25, 1~2 mg/kg, 토양수분은 18.5~28.4%로 비옥도가 양호한 사질양토이었다. 시험처리는 파종량에 따라 3, 5, 7kg/10a의 3수준으로 각각 처리하였고, 난괴법 3반복으로 배치하였다. 파종은 2014년 10월 1일에 손으로 세조파(25cm×5cm)하였다. “곡우” 호밀의 출현일수는 6일이었고, 출현양부는 95%이상이었으며, 생육재생기는 2015년 2월 21일이었다. “곡우”의 월동율은 95.3~99.0%로 매우 높게 나타났으나, 3개의 파종량 처리구 간에 유의한 차이는 보이지 않았다. “곡우”의 단위면적당 지상부 건물중은 파종량이 많아질수록 증가하는 것으로 나타났고, 경수, 이삭수 및 개체수 또한 같은 경향을 보였다. 간장 및 수장은 3개의 처리구 간 유의한 차이가 없는 것으로 나타났다.

\*주저자: Tel. 031-8012-7330, E-mail: leejk@efact.or.kr

## Development of QTL-NIL to Blast Resistance Originated from Korean Weedy Rice

Young-Chan Cho\*, Man-Ki Baek, Jung-Pil Suh, Yong-Jae Won, Jong-Min Jeong, Hyun-Su Park, Jeong-Ju Kim, Jeong-Kwon Nam, Ki-Young Kim

National Institute of Crop Science, Suwon 441-857, Korea

Rice blast caused by the fungal pathogen, *Magnaporthe oryzae*, is a serious disease affecting yield loss and decreasing its quality in rice production. Rice breeders in Korea have developed many *japonica* varieties showing resistance to blast. However, the blast resistance in most *japonica* varieties has broken down within a few years after they were released to farmers because of the spread of new virulent races of *M. oryzae*. There is the most effectiveness to look for novel resistant gene(s) that can express the resistance to broad-spectrum races in diverse environmental conditions. We identified a major QTL, *qLB4.1* linked tightly to RM6352 and RM3643 in 52.6 cM region on chromosome 4 related to the resistance for isolate inoculation and nursery test, and neck blast from a Korean weedy rice, Geumleungaengmi33. This QTL explained 26.1 ~ 28.6% and 45.3 ~ 53.1% of total phenotypic variation by the allele of GL33 for isolate inoculation and nursery test, respectively. A line SR30058(52)-1-1 (Suweon545) that containing the QTL *qLB4.1* was developed from Ilpum\*4/GL33 by marker-assisted backcross method. This line showed resistant reactions to blast nursery test across regions and years, and resistance to neck blast at the hot-spot field in Jecheon. Suweon545 showed also durable resistance of lower 10% of diseased leaf areas (DLAs) in sequential planting method. This line screened by graphical mapping using 136 SSR markers that evenly distributed on 12 chromosomes. Suweon545 contained GL33 alleles of donor parent in a total of 12 loci (8.8%) including QTL region on chromosome 4. In future, Suweon545 would be useful to develop the broad-spectrum resistance variety in *japonica* rice breeding program.

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

## Overexpression of CIPK 15 improved tolerance to pre-harvest sprouting in rice

Dal-A Yu<sup>1</sup>, Hye-Jung Lee<sup>1</sup>, Joonki Kim<sup>1</sup>, Me-Sun Kim<sup>1</sup>, Marjohn Nino<sup>1</sup>, Sothea Ouk<sup>1</sup>, Seong-Dong Kim<sup>1</sup>, Ill-sup Nou<sup>2</sup>, Yong-Gu Cho<sup>1\*</sup>

<sup>1</sup>Department of Crop Science, Chungbuk National University, Cheongju 361-763, Korea

<sup>2</sup>Department of Horticulture, Suncheon National University, Suncheon 540-742, Korea

Since global climate changes drastically, pre-harvest sprouting (PHS) is expected to pose serious problems in rice production. CBL-interacting serine/threonine protein kinases (CIPKs) have been implicated to play important role in regulating various abiotic stresses such as cold, salinity and drought. In this study, to understand the function of this gene under pre-harvest sprouting in rice, a cDNA clone encoding CBL-interacting protein kinase 15 was isolated from rice flowers. We constructed a recombinant vector carrying the *CIPK15* under the control of the CaMV 35S promoter and Tnos terminator and transformed into rice using *Agrobacterium tumefaciens*. Insertion of the gene was verified in transformants using HPT resistance test and genomic PCR. Transcriptional profiling using tissues of wild type, Gopum, revealed expression of the gene in whole plant tissues with level of expression highest in the seeds suggesting possible role in dormancy. Comparative expression analysis of the gene in transgenic and wild type through semi-quantitative RT-PCR and real-time PCR showed higher expression in transgenic rice lines. Moreover, screening in the mist chamber showed overexpression lines that were resistant to the PHS. This result suggests the involvement of *CIPK15* in the regulation of pre-harvest sprouting.

This work was supported by a grant from the National Research Foundation (NRF) programs (2014R1A2A1A11052547) funded by the Korean Ministry of Science, ICT and Future Planning, and by iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

\*Corresponding Author: E-mail: ygcho@cbnu.ac.kr

## 중만생 내병 다수성 찰벼 품종 ‘중모1044호’

하기용\*, 박현수, 남정권, 백만기, 김기영, 김우재, 김현순, 김보경, 김정주, 조영찬, 고재권

농촌진흥청 국립식량과학원

‘중모1044호’는 중만생 내병 다수성 품종육성을 목적으로 2003/2004년 동계에 국립식량과학원(구)벼백류부에서 운봉30호(♀) X 익산482호(♂)를 인공교배하여 육성한 다수성 복합내병성 찰벼품종으로 주요특성과 수량성을 요약하면 다음과 같다. ‘중모1044호’의 출수기는 호남 및 영남평야지 보통기 보비재배에서 8월 16일로 신선찰벼보다 8일 정도 늦은 중만생 품종이다. 도열병 저항성은 발못자리 검정에서 신선찰벼보다 약하나 내구저항성에서는 남평벼보다 강한 편이다. 흰잎마름병 레이스 K1, K2 및 K3에 강하며 줄무늬잎마름병에 강하다. ‘중모1044호’는 불시출수와 위조현상은 없고 저온발아성은 신선찰벼보다 우수하다. 내냉성은 신선찰벼보다 강한 편이고 수발아율은 20.6%로 신선찰벼보다 매우 낮다. 도복지수는 신선찰벼보다 낮고 포장도복은 강한 편이다. 수량관련 특성은 주당수수가 13개로 신선찰벼와 비슷하고 수당립수는 많으며, 천립중은 약간 무거운 편이다. 제현율, 도정율은 74.2%로 신선찰벼보다 높으나, 백미완전립율 및 완전미도정수율은 각각 91.5%, 67.9%로 신선찰벼보다 약간 낮은 편이다. 쌀수량은 2012~2014년 3개년간 실시한 지역적응시험 보통기 보비재배에서 5.23MT/ha로 신선찰벼보다 13% 증수되었다.

\*주저자: Tel. 063-238-5234, E-mail: ha0ky04@korea.kr

---

**PA-54****개화기가 빠르고, 내병성 다수성인 구기자 신품종 「청홍」**주정일<sup>1\*</sup>, 박영춘<sup>1</sup>, 윤덕상<sup>1</sup>, 이보희<sup>1</sup>, 최택용<sup>1</sup>, 김현호<sup>2</sup><sup>1</sup>충남 청양군 운곡면 충남농업기술원 인삼약초연구소 청양구기자시험장<sup>2</sup>충남농업기술원 인삼약초연구소

2007년에 내병성이면서 장타원형인 청명(IT232706)과 다수성인 CB04341-286로 인공교배를 실시하였고, CB07423-104 개체를 선발하여 2011년 “청양 17호”로 계통명을 부여하였다. 청양, 예산, 진도 등 3지역에서 2011~2013년까지 3년간 지역적응성을 검정한 후 개화기가 빠르면서, 키가 작고, 내병충성, 지표성분 고함유, 다수성으로 인정되어 우수성을 인정받아 2014년도 “청홍(靑紅, Cheonghong)”으로 명명하였다.

구기자 신품종 “청홍”의 주요 특성은 다음과 같다. 잎은 피침형으로 녹색이고 대비품종인 「청명」에 비하여 가늘다. 개화기는 대비품종에 비하여 약 11일 빨랐고, 수형은 개장형으로 키가 작고 적실에 의한 분지발생이 적은 편이다. 열매는 황적색이면서 장타원형이고 100과중이 약 19g로서 중간크기이다. 병해충 저항성은 무방제 상태인 노지포장에서 자연 발생 정도를 조사하였는데, 탄저병 이병과울과 흑응애 발생률은 대비품종인 「청명」과 비슷하여 저항성이 강하였다. 주요 지표성분으로 베타인 함량 0.85%, 당도 15.4°Brix로서 대비품종에 비하여 높았고, 건과수량은 대비품종에 비하여 생산력 검정시험에서 22%, 지역적응시험에서 16% 증수되었다. 주요 용도는 약용과 식용으로 모두 이용이 가능하였다.

신품종 「청홍」의 수분수는 열매크기가 비슷하고 두 품종의 혼식시 결실률이 높은 「청명」 품종이 가장 적합하였다. 또한 건조 후 외관 품질 향상을 위하여 적기에 수확하고, 건조온도를 준수할 필요가 있다.

\*주저자: Tel. 041-635-6384, E-mail: cnswhbar@korea.kr

**PA-55****Screening for Resistance of Tomato Genetic Resources to Bacterial wilt caused by *Ralstonia solanacearum***

On-Sook Hur<sup>\*</sup>, Sang Gyu Kim, Ho-Cheol Ko, Su Ran Ahn, Jung-Sook Sung, Na-Young Ro, Sukyeung Lee, Yu-mi Choi, Do yoon Hyun, Kyoung-Yul Ryu, Hyung-Jin Baek

National Agrobiodiversity Center, National Academy of Agricultural Science, Rural Development Administration, Jeonju 560-500, Republic of Korea

This study aimed to evaluate 105 tomato accessions conserved in National Agrobiodiversity Center regarding their resistance to *Ralstonia solanacearum*, a soil-borne vascular bacterium that causes lethal wilt diseases of a wide range of crops worldwide. All the accessions are *Solanum lycopersicum* var. *lycopersicum* including cultivar or breeding lines. At the four leaf stage, the seedlings were inoculated by drenching the soil with the bacterial suspension concentrated of 10<sup>8</sup> CFU/ml. Plant roots were wounded before inoculation by cutting with the knife. Seven accessions including IT 32899 were rated as resistant, while other 98 accessions were rated as susceptible. IT 32899 scored 0.1 of disease rate and 0.7 of disease index. The selected accessions will be used as a material to reveal the mechanism of wilt tolerance and to identify the host gene involved in defense response.

\*Corresponding Author: Tel. 063-238-4942, E-mail: oshur09@korea.kr

## **Overexpression of *Brassica rapa* cysteine protease improves rice resistance to bacterial blight**

Marjohn Nino<sup>1</sup>, Sailila E. Abdula<sup>1</sup>, Hye-Jung Lee<sup>1</sup>, Dal-A Yu<sup>1</sup>, Seon-Kyeong Song<sup>1</sup>, Eun-Ju Jeong<sup>1</sup>, Kwon-Kyoo Kang<sup>2</sup>, Ill-sup Nou<sup>3</sup>, Yong-Gu Cho<sup>1\*</sup>

<sup>1</sup>Department of Crop Science, Chungbuk National University, Cheongju 361-763, Korea

<sup>2</sup>Department of Horticulture, Hankyong National University, Ansong 456-749, Korea

<sup>3</sup>Department of Horticulture, Sunchon National University, Suncheon 540-742, Korea

Cysteine protease (CP) is one of the well-studied proteolytic enzymes in plants. This class of protease has been implicated in various physiological aspects of developmental stages in plants including seed germination, senescence, and disease immunity. A handful of studies assigned plants cysteine protease in different molecular battlefield under a few selected pathosystems, and initially extricated complex molecular mechanism of resistance. However, its potential use as an agent of resistance to diseases in rice has never been explored. This study demonstrates the function of CP specifically in rice - *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) pathosystem. The CP -encoding full-length cDNA was cloned from *Brassica rapa* and transformed into japonica rice cv. 'Gopumbyeo'. The gene was overexpressed under the control of CaMV35S promoter in pFLC vector. Blast analysis of the conserved domain of the gene confirmed its affinity to Peptidase\_CIA family. RT-PCR analysis showed that the gene was constitutively expressed in all tissues tested. Regulation of rice resistance through cysteine protease activity is evident in overexpression lines which exhibited an enhanced resistance to four Korean *Xoo* isolates. Further analyses will be carried out to uncover the specific role of CP in rice-*Xoo* interaction.

This research was supported by a grant from the National Research Foundation (NRF) programs (2014R1A2A1A11052547) funded by the Korean Ministry of Science, ICT and Future Planning, and by iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

\*Corresponding Author: E-mail: ygcho@cbnu.ac.kr

## 온도구배하우스를 이용한 기후변화 대응 밀 생육반응 비교

하건수\*, 조수현, 임수정, 변학수, 오혜진, 신은영, 임혜리

강원도 춘천시 총열로 83, 강원도농업기술원

지구전체에서 발생하는 기후변화는 지역적으로 영향이 같지 않다. 기후변화는 기후의 평균적 상태 뿐 아니라 극한적 상태도 변화시킴으로써 기존의 안정적 생산성을 유지하는 작물들에는 다양한 생육 반응이 예측된다. 농촌경제연구원에서는 RCP(Representative Concentration Pathways) 8.5 기반 우리나라 쌀 생산량 예측에서 자급율이 75%에서 41.3%로 감소한다고 하였으며, 최근에는 농업, 기상, 경제 등 모든 분야에서 기후변화 대응 연구가 폭넓게 진행되고 있다. 본 연구에서는 기후 변화 대응 밀 적응 품종 육성의 기초자료를 확보하고자 온도 차이를 유발한 온도구배하우스를 이용하여 몇 가지 밀 품종들의 생육반응을 비교하였다. 시험품종은 춘천지역 적응 추파 장려품종인 조정밀, 금강밀과 춘파 밀 품종인 몽골 수집종을 비교하였으며, 재배법은 휴폭 25cm로 가을 파종하였다. 온도구배하우스의 입구와 출구의 온도 차이는 3°C~4°C이었고, 시험품종별로 입구부터 출구까지 일렬로 재배하였으며 대조구로 포장에서 재배한 금강밀의 생육을 이용하였다. 조사지점을 입구부분(1 지점)과 중간부분(2 지점) 그리고 출구부분(3 지점)으로 나누어 조사하였다. 시험결과 출수기는 추파 품종인 금강밀과 조정밀은 3일의 차이가 났고 춘파 품종인 몽골 수집종은 6일의 차이가 있었으며 성숙기는 모든 품종에서 2일 정도의 차이가 있었다. 종실 수량은 2 지점에서 가장 많았으며 이는 3°C 이하의 온도 상승은 밀의 수량이 증수되나 3°C 이상의 온도 상승이 있는 3 지점은 2 지점보다는 수량이 감소되어 수량에 영향을 주는 온도조건이 3°C 정도인 것으로 예측된다. 다만 3°C 이상의 온도 상승지점인 3 지점 역시 1 지점보다는 증수하여 밀의 경우 벼 등의 다른 작물과 달리 고온조건인 기후변화 시 수량의 증수를 예측할 수 있었다. 따라서 기후변화 적응 밀 품종 육성 시 온도구배하우스의 이용 가능성이 확인 되었으며 주요 계통 선발에 유용할 것으로 생각된다.

\*주저자: Tel. 033-248-6038, E-mail: redclover@korea.kr

## 중북부 고랭지 적응 내냉성 조생 벼 진부61호

현웅조<sup>1\*</sup>, 정종민<sup>2</sup>, 강경호<sup>2</sup>, 정지용<sup>2</sup>, 이상복<sup>3</sup>, 이정희<sup>3</sup>, 성열규<sup>1</sup>, 이점호<sup>2</sup>

<sup>1</sup>강원도 춘천시 총열로 251 국립식량과학원 춘천출장소

<sup>2</sup>전북 완주군 이서면 혁신로 181 국립식량과학원 작물육종과

<sup>3</sup>경기도 수원시 수인로 125 국립식량과학원 중부작물부 중부작물과

우리나라는 최근 몇 년 동안의 풍년과 소비감소로 인해 쌀 재고가 사회문제로 대두되고 있다. 그러나 세계적으로는 식량부족에 대한 우려와 함께 지구온난화, 엘니노 등으로 홍수, 가뭄, 폭설, 여름철 이상저온과 같은 기상이변이 지구촌 곳곳에서 속출하고 있다. 최근 우리나라에서도 봄철 가뭄, 동해안 지역의 잦은 폭설, 주기적으로 찾아오는 여름철 이상저온 등 크고 작은 기상이변이 해마다 발생하고 있어 쌀의 안정적 공급을 강화하기 위한 대비가 필요한 실정이다. 특히 여름철 이상저온이 발생하여 벼의 생육에 알맞은 기온범위인 19°C~33°C보다 기온이 13°C~17°C 이하로 낮아지게 되는 경우, 생육불량·불임·등숙불량 등의 피해를 유발하여 결과적으로 수량감소로 이어진다. 벼 냉해를 막는 가장 좋은 방법은 내냉성이 우수한 벼 품종의 개발이다. ‘진부61호’는 내냉성과 더불어 쌀수량 및 품질이 향상된 중북부 고랭지에 적응하는 조생품종 육성을 목적으로 ‘진부’를 모본으로 하고 ‘운광’을 부분으로 하여 2006년에 인공교배 되었다. 계통육종법에 의해 세대를 진전시킨 후 고정세대에서 실시한 생산력검정 시험에서 쌀수량이 5.49MT/ha로 진부보다 10% 증수하였다. ‘진부59호’의 출수기는 7월 26일로 조생종이며 간장이 69cm 정도로 ‘진부와 비슷하고 수당립수는 80개 정도이다. ‘진부61호’의 13°C 저온발아성은 99%로 우수하고 유묘내냉성이 강할 뿐만 아니라 생식생장기에서도 17°C 포장냉수구 임실율이 높아 생육전시기에 내냉성을 두루 갖춘 계통이다. 향후 지역적응성 검정 후 품종출원 하여 내냉성 품종 다양화 및 수량성 개선에 부응할 것으로 기대된다.

## 고구마뿌리혹선충 저항성 식용 고구마新品种 ‘풍원미’

이형운<sup>1\*</sup>, 이준설<sup>1</sup>, 정미남<sup>2</sup>, 한선경<sup>1</sup>, 김재명<sup>1</sup>, 안승현<sup>2</sup>, 양정욱<sup>1</sup>, 남상식<sup>1</sup>, 송연상<sup>3</sup>, 최규환<sup>4</sup>, 문진영<sup>5</sup>, 최인후<sup>1</sup>, 황엄지<sup>1</sup>, 이경보<sup>1</sup>

<sup>1</sup>전남 무안군 무안로 199 국립식량과학원 바이오에너지작물연구소

<sup>2</sup>전북 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

<sup>3</sup>전북 전주시 완산구 농생명로 300 농촌진흥청

<sup>4</sup>전북 익산시 서동로 413 전라북도농업기술원

<sup>5</sup>경남 진주시 대신로 570 경상남도농업기술원

최근 고구마의 연작, 병해충에 감수성인 품종의 재배면적 확대 및 이상기상 등으로 인해 고구마의 단위면적당 생산량이 '00년 2,136kg/10a에서 '13년 1,484kg/10a으로 30% 이상 감소하였다. 특히 고구마뿌리혹선충(*Meloidogyne incognita*)에 감염된 고구마는 뿌리에 혹이 발생하거나 괴근의 표피가 갈라지고 심하면 부패될 수도 있어 고구마의 수량과 상품성을 현저히 저하시킨다. 따라서 고구마의 생산성과 상품성을 향상시키기 위해서는 선충 등 병해충에 강하고 수량성이 높은 품종의 개발 및 보급이 필요하다. 2014년에 육성된 ‘풍원미’(Pungwonmi)는 육색이 담주황색이고 껍질색은 홍색이며 괴근의 모양은 방추형이다. ‘풍원미’는 ‘베니사즈마’(IT232278)를 모본, ‘Luby3074’(IT232216)를 부분으로 하여 2006년에 교배하였으며 고구마뿌리혹선충에 강하고, 덩굴쪄김병(*Fusarium oxysporum*) 저항성도 ‘중’ 이상으로 주요 병해충에 저항성인 품종이다. 생산력검정시험에서 ‘풍원미’의 상품괴근수량은 표준품종인 ‘올미’ 대비 42%가 많았다('10~'11). 지역적응시험 보통기재배 시 상품괴근수량이 24.1MT/ha으로 ‘올미’ 대비 26% 증수하였고, 주당상저수는 2.8개로 ‘올미’의 2.2개보다 유의적으로 많았다('12~'14). 조기재배 시 ‘풍원미’의 상품괴근수량이 24.3MT/ha으로 ‘올미’ 대비 46%가 많아 조기재배용으로도 적합하였다. ‘풍원미’의 찢고구마 총유리당 함량과 감미도(sweetness)는 각각 31.6g/100g, 16.5로 ‘올미’의 26.1g/100g, 12.7보다 높아 단맛이 더 강하였다. 베타카로틴 함량은 9.1mg/100g으로 높은 편이었으며, 전분의 호화개시온도는 70.0℃로 ‘올미’의 75.3℃보다 5.3℃ 낮아 ‘풍원미’의 전분이 ‘올미’보다 낮은 온도에서 호화되는 것으로 나타났다. ‘풍원미’는 고구마뿌리혹선충과 덩굴쪄김병이 상습적으로 발생하는 포장에서 재배될 경우 수량 증대 및 상품성 향상으로 농가소득 증대에 기여할 수 있을 것으로 기대된다.

\*주저자: Tel. 061-450-0141, E-mail: leehu79@korea.kr

**Association of haplotype variations in *GmCHX1* with salt tolerance in wild and cultivated soybeans.**

Jeong Hwa Kim, Jong-Tae Song, Jeong-Dong Lee\*

School of Applied Bioscience, Kyungpook National University, Daegu 702-701, Republic of Korea

Soybean [*Glycine max* (L.) Merr.] is a major agricultural crop widely used for providing human and animal food owing to its high protein and oil content. For this reason, they have been consumed in Asia and world greatly and demand is ever increasing. Soybean is classified as a moderately salt-sensitive crop and its production is greatly affected due to increasing salinity stress. About 8 % of the world's total land is salt-affected. In Korea, around 9 % of total agricultural land (approximately 130,000ha) was reclaimed since 1960's. In order to meet the demand for soybean and to solve arable land shortage problem, it is unavoidable to cultivate soybean in salt-affected soils. Fortunately, soybean germplasm has been shown to have salt-tolerant phenotypes, which have been used to identify the salt-tolerant genes. *GmCHX1*, a novel ion transporter, is one of the genes known to confer salt tolerance in soybeans. Present study was conducted to understand the effects of sequence variations of *GmCHX1*, on salt tolerance in wild and cultivated soybeans. A total of 1026 (301 lines of *G. max* and 725 lines of *G. soja*) lines were phenotyped for salt tolerance in greenhouse conditions. At the V1-V2 growth stage, the plants were treated with 100mM NaCl solution for two weeks and thereafter the response was measured depending on leaf scorch score (1-health, 3-mid, 5-dead). About 20 lines found to show tolerance to saline conditions and were selected for sequence analysis of *GmCHX1*. Most of the haplotypes detected in this study corresponded with the haplotype patterns in previous studies. However, several lines showed different patterns of polymorphism in the coding region, suggesting that sequencing of more lines and analysis for the polymorphism in *GmCHX1* is needed in order to identify new haplotypes that could confer greater salt tolerance.

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

## 야생벼 이용 총체사료 적성 계통육성

강경호<sup>1\*</sup>, 안억근<sup>2</sup>, 정지웅<sup>1</sup>, 김석만<sup>3</sup>, 정종민<sup>1</sup>, 전재범<sup>1</sup>, 현용조<sup>2</sup>

<sup>1</sup>전북 완주군 이서면 혁신로 농촌진흥청 국립식량과학원 작물육종과

<sup>2</sup>경기도 수원시 서둔동 국립식량과학원 중부작물부 중부작물과

<sup>3</sup>전북 완주군 이서면 혁신로 국립식량과학원 IRRI-Korea Office

총체벼의 곡실수량, 바이오매스 및 병해충저항성은 총체수량과 재배안전성을 높이기 위한 가장 중요한 요소로서, 총체벼 육종효율을 높이기 위해서는 이들 각 요소에 대한 육종소재의 확충이 필수적이다. 이를 위해 AA계놈 야생벼인 *O.glaberrima*, *O.longistaminata*, *O.rufipogon*을 이용하여 밀양23호, 일품, 삼광, 오대, 호품, 화성과 중간교배를 실시하여 야생벼가 보유하고 있는 수량성, 벼멸구저항성 및 고도의 바이오매스를 이전한 육종집단을 육성하였으며 수량성과 바이오매스를 기준으로 세대를 전개하였다. 육종집단의 특성은 야생벼에 따라 달라서 *O.rufipogon*과 *O.lognistaminata*의 교잡후대 선발계통은 간장이 150~180cm인 고도의 바이오매스와 벼멸구저항성을 나타내었으며, *O.glaberrima*집단에서는 고도 수량성을 나타내었다. 특히 *O.glaberrima*와 국내 대표적 다수성 통일형 품종인 밀양23호를 교잡하여 육성된 수원596호의 수량성은 쌀수량이 769kg/10a로 밀양23호 대비 14% 증진된 초다수성이며 총체수량도 1.74톤/10a로 기존 총체품종인 녹양벼 대비 15% 증대되는 총체 계통을 육성하였다. 향후 본 연구에서 야생벼를 이용하여 생산된 초다수성, 고도바이오매스, 내병충성 계통들은 형질복합화를 위해 교잡을 통해 총체벼의 건물수량을 한 단계 증진시킬 수 있는 육종소재로 활용이 가능할 것이다.

\*주저자: Tel. 063-238-5233, E-mail: khkang@korea.kr

## 감마선 처리에 의한 정원장미 돌연변이 유기

고갑천<sup>1\*</sup>, 한태호<sup>2</sup>, 기광연<sup>3</sup>

<sup>1</sup>전남대학교 농업과학기술연구소

<sup>2</sup>전남대학교 농업생명과학대학

<sup>3</sup>전남농업기술원

근래 우리나라에서 정원장미는 가장 인기 있는 화목류로 자리잡아가고 있다. 그러나 국산 정원장미 품종의 육성 및 보급이 미미한 실정이어서 보급되고 있는 품종은 대부분 외국 수입품종이다. 우리나라에서 절화장미의 감마선 처리 돌연변이 육종 방법은 잘 확립되었다(고, 2011). 즉, 감마선을 처리하여 기존의 우수한 품종의 특성은 대부분 유지하되 화색이나 화형 등의 변이를 유발하여 신품종을 매우 효과적으로 육성할 수 있다. 본 연구에서는 정원장미 신품종을 육성하기 위해 정원장미 2품종(‘러브’ 20주, ‘로잔나’ 30주)에 감마선 70Gy 선량을 각각 처리하여 화색 및 화형 돌연변이를 유기하였다. 감마선 처리한 삼목묘는 포장에 심어 3년에 걸쳐 변이발생을 조사하였다. 품종별 화색 및 화형 변이 형태 등을 조사하였고 발생한 변이는 삼목하여 고정변이주로 작성하였다. 감마선 처리로 러브 품종은 주로 화색변이가 발생하였다. 적색인 러브 품종에서 적자색(Lo1), 분홍색(Lo2), 미색(Lo3), 꽃잎 모자의 무늬 변이(Lo4, Lo5)가 발생하였다. 화형 및 화경 크기 변화는 미미 했고, 꽃잎수는 러브품종(37.6장)에 비해 적어지는 계통(4계통, 32.5-25.0장)과 현저히 꽃잎수가 많아지는 계통(1계통 Lo3, 69.0장)이 발생하였다. 잎색은 분홍변이(Lo2)에서 약간 엷어졌다. 로잔나 품종에서 5개의 변이가 발생하였다. 변이의 발생 형태는 화색, 화형, 화경, 꽃잎수 등에 있어 다양한 모습이었다. 로잔나 품종과 화형이 같으면서 화색만 변화한 것(1계통, Ro1), 화형은 같으면서 화색과 화경크기가 변화한 것(1계통, Ro2), 화형과 화색은 같으면서 화경 크기가 줄어든 것(1계통, Ro3), 화형과 화색이 변하고 꽃잎수가 현저히 많아진 것(1계통, Ro4), 화형이 열린컵형태에서 로제트로 변하고 꽃잎수가 현저히 증가한 것(2계통, Ro4, Ro5) 등 다양한 특성이 조합되어 발생하였다.

\*주저자: Tel. 062-530-0624, E-mail: choseongnara@naver.com

## PB-03

### 호밀 왜성 유전자가 외관 형태에 미치는 효과

구자환<sup>1\*</sup>, 황종진<sup>1</sup>, 한옥규<sup>1</sup>, 김대욱<sup>2</sup>, 권순중<sup>1</sup>, 박광근<sup>1</sup>, 이점호<sup>1</sup>

<sup>1</sup>경기도 수원시 서둔동 국립식량과학원 중부작물과

<sup>2</sup>경기도 수원시 서둔동 국립식량과학원 작물재배생리과

왜성 유전자는 보리, 밀, 트리티케일에 있어서 초장을 짧게 하여 도복을 경감시킴으로써 다수성 반왜성 품종 개발에 중요한 역할을 하여 왔다. 반왜성 호밀 품종인 AC Remington에서 유래한 왜성 유전자가 호밀의 외관 형태에 미치는 효과를 알아보기 위하여 시험을 실시하였다. 연구결과를 요약하면 AC Remington을 방임 수분시킨 후 계통분리법으로 전개한 후대의 F<sub>5</sub> 102개 개체를 대상으로 외관 형질을 조사한 결과 왜성계통의 초장은 88.3±12.6cm (n=41), 반왜성계통 초장은 115.2±2.7cm (n=17), 정상계통 초장은 142.1±11.1cm (n=44)의 분포를 보였다. 개체당줄기수는 왜성계통은 67.1개, 반왜성계통은 64.4개, 정상계통은 53.3개로 나타나 왜성계통이 정상계통보다 줄기수가 많은 경향을 보였다. 왜성계통 초장이 정상계통 초장보다 짧은 이유는 상위 제1번째~제4번째 마디사이 길이가 정상계통보다 모두 짧아진 것에서 비롯되었다. 줄기마디수는 왜성계통과 정상계통 간에 동일하였으며, 줄기 굵기는 왜성계통과 정상계통 간에 상위 1번째 마디 굵기는 차이가 없었으나 상위 제2번째부터 제4번째까지의 마디 굵기는 왜성계통이 정상계통보다 가는 경향이 있었다. 상위 제1번 엽(지엽)의 엽장과 제2번 엽의 엽장은 왜성계통이 정상계통보다 짧은 경향이었고 상위 제3번 엽의 엽장은 왜성계통과 정상계통 간에 차이가 없었다. 엽폭에 있어서는 상위 제1번 엽부터 제3번 엽 모두 왜성계통과 정상계통 간에 차이가 없었다. 이삭길이는 왜성계통이 정상계통보다 짧은 경향이었으며, 이삭당영화수도 왜성계통이 정상계통보다 적은 경향이었으나 이삭당착립수는 왜성계통과 정상계통 간에 차이가 없었다. 이러한 결과들로 볼 때 AC Remington에서 유래한 호밀의 왜성 유전자는 초장을 짧게 하고, 엽장, 줄기굵기, 이삭당영화수를 감소시키는 경향이 있는 반면에 줄기수는 증가시키는 효과가 있는 것으로 판단된다.

\*주저자: Tel. 031-695-4053, E-mail: jhku@korea.kr

## PB-04

### 면 가공용 시중밀가루의 품질 분석

김정훈\*, 김경민, 박형호, 현종내, 권영업

경남 밀양시 점필재로 20, 농촌진흥청 국립식량과학원 남부작물부

면 가공용 밀가루 소비자의 기호를 충족하기 위해 현재 시판되고 있는 수입산 시중밀가루와 국내에서 생산한 밀가루의 품질을 비교 확인하고자 한다. 이에 국내에서 수확하고 제분하여 얻어진 조정밀 밀가루와 시중에서 유통되고 있는 시중밀가루 6종류(강력분, 중력분, 박력분)와 가공 공장에서 면 가공시에 사용되는 국내산 백밀가루, 통밀가루, 국수면 등 11종류를 수집하였다. 시험재료의 단백질과 회분 함량을 측정하고 비교 분석하였다. 그 결과, 수입산 시중밀가루의 단백질 함량은 강력분 15.0%, 중력분 12.2%, 박력분 10.5%이었고, 조정밀 밀가루는 13.7%로 중강력분의 특징을 나타냈다. 국수면용 밀가루는 11.3%이었는데, 국수면으로 가공되어 시판되는 국수면의 단백질 함량은 12.5%로 높았다. 그 밖에 갈국수용 밀가루는 12.2%, 라면용 밀가루는 13.7%로 국수면용으로 쓰이는 밀가루보다 단백질 함량이 상대적으로 높았다. 회분 함량의 측정 결과, 시중밀가루는 0.45%로 가장 낮았고, 면 가공용으로 사용되는 밀가루는 0.64%, 국수면은 2.81%로 면 가공 후 회분 함량이 다소 높아졌다. 향후 이 수집한 밀가루를 면으로 가공하고 질감, 식감 등의 특성을 분석하여 면용 품종을 육성하는 적합 품질 기준설정에 자료로 활용할 예정이다.

\*주저자: Tel. 055-290-1173, E-mail: k2h0331@korea.kr

## 감마선 조사에 의한 포인세티아 품종 육성

O Hyeon Kwon, Bong Sik Yoo, Su Young Lee, Hye Jin Lee

농촌진흥청 국립원예특작과학원 화훼과

‘Clara’ 품종은 국립원예특작과학원에서 2005년도에 육성한 포인세티아 품종으로 초장이 작고 컴팩트한 수형으로 포엽의 형태는 난형이며 엽맥 사이 주름의 정도는 약하다. 포엽의 길이와 폭, 잎몸의 길이와 폭, 엽병의 길이는 짧으며 단일처리 후 약 9주일이 경과하면 충분히 착색되어 출하가 가능한 품종이다. 2008년 5월과 10월 ‘Clara’ 품종의 캘러스가 형성된 삼수에 100Gy의 감마선을 24시간 동안 처리하여 유기한 돌연변이를 이용하여 2010년과 2013년에 국립원예특작과학원에서 ‘Clara Pink’와 ‘Clara White’ 품종을 육성하였다. 이 두 품종들은 포엽의 색이 완전히 변한 변이주를 선발하여 계통화 하였으며 2008년 5월에 감마선을 처리한 삼수들 중 포엽의 색이 분홍색인 변이주를 선발하여 2009년에 2차에 걸쳐 특성검정을 실시하였다. 2010년에 ‘원예 D5-2’를 육성한 후 3차 특성검정과 품종평가회를 실시하여 최종선발하였으며, 농작물 직무육성 신품종선정위원회를 거쳐 ‘Clara Pink’로 명명하였다. 2005년 10월에 감마선을 처리한 삼수들중에서는 포엽의 색이 연황색인 변이주를 선발하여 계통화 하였으며, 2012년과 2013년에 1,2차 특성검정을 실시하였다. 2013년에 ‘원예 D5-34’를 육성하여 특성검정과 품종평가회를 실시하고 농작물 직무육성 신품종선정위원회를 거쳐 ‘Clara White’로 명명하였다. ‘클라라 핑크’와 ‘클라라 화이트’ 두 품종 모두 ‘클라라’ 품종과 같은 소형으로 적십하지 않은 상태에서도 분지가 많이 발생하는 컴팩트한 수형이다. 포엽의 형태는 결각이 없는 난형이며, 엽맥 사이에 약한 주름이 있고 단일처리 후 약 9주일 경과하면 완전히 착색된다. 잎몸의 모양은 난형이며, 엽병의 길이는 짧다. 그러나 ‘클라라 핑크’와 ‘클라라 화이트’ 품종의 포엽과 엽맥의 안토시아닌 발현에 차이를 나타내었다. ‘클라라 핑크’의 포엽은 분홍색이며, ‘클라라 화이트’의 포엽은 연황색이다. 또한 ‘클라라 핑크’와 ‘클라라 화이트’ 품종은 ‘클라라’ 품종과 비교해서 잎자루 윗면의 안토시아닌 발현 정도가 약하였으며, 잎몸 윗면의 가운데 맥의 색이 ‘클라라’ 품종은 녹색과 빨강색이 함께 발현되었으나, ‘클라라 핑크’와 ‘클라라 화이트’ 품종은 녹색만 발현되었다.

\*Corresponding Author: Tel. 063-238-6833, E-mail: rkddnjseo01@korea.kr

## **Genome-wide structural variation by different types of ionizing irradiation sources**

Soon-Jae Kwon, Hong-Il Choi, Jung Eun Hwang, Injung Jung, Sung Min Han, Jin-Baek Kim, Joon-Woo Ahn, Sang Hoon Kim, Yeong Deuk Jo, Si-Yong Kang, Dong-Sub Kim\*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580-185, Korea.

To define whole genome-level of structural variation by ionization energies and radiation doses in plant, the seeds of Ilpum rice cultivar were acutely irradiated with gamma rays (100Gy, 200Gy, and 400Gy) and ion-beams (20Gy, 40Gy, and 80Gy), respectively. Six M<sub>1</sub> rice plants were re-sequenced by Hi-Seq2500 with Ilpum cultivar as control. The average sequencing coverage of the individuals was 10.6X, and the average mapping rate to the rice reference genome (IRGSP-1.0) sequence was 96.95%. The individual plants were irradiated with gamma-400Gy and ion-50Gy had highest variation of SNP with 471,837 and 469,147, respectively. The number of insertion/deletion was 77,500 and 77,106, the synonymous and frame-shift were 7,859 and 7,763 in above two individuals. Although high genome variation shown between Ilpum cultivar and irradiated individuals, there were non-correlation between number of variation and radiation doses. However, five individuals, except ion-20Gy, showed 33 common variant blocks (CVBs) spanning 6 Mb in whole rice genome (1.6%). The CVBs were distributed on 12 rice chromosomes, Chromosome 6 had biggest CVB (5 blocks, 1.3Mb), whereas chromosome 9 had smallest CVB (0.01Mb). Total five hundred fifty one genes were in CVBs which can regard radiation sensitive genes or may be regarded as radiation hot spots in rice genome. This study will contribute to the improvement of the radiation mutation breeding research in genetic and genomic aspect.

\***Corresponding Author:** Tel. 063-570-3311, E-mail: bioplant@kaeri.re.kr

## 하얀꽃이 피는 경관용 유채 ‘중모7003’

김광수<sup>1\*</sup>, 이영화<sup>1</sup>, 장영석<sup>1</sup>, 최규환<sup>2</sup>, 강달순<sup>3</sup>, 김성택<sup>4</sup>, 이경보<sup>1</sup>

<sup>1</sup>농촌진흥청 국립식량과학원 바이오에너지작물연구소

<sup>2</sup>전라북도농업기술원

<sup>3</sup>경상남도농업기술원

<sup>4</sup>제주특별자치도농업기술원

유채(*Brassica napus* L.)는 주로 기름을 생산하기 위해 제주도를 비롯한 남부지방에서 재배되어 왔다. 유채는 전초를 나물용 또는 청예사료용으로 이용하고, 종자는 착유하여 식용유와 바이오디젤용으로 이용하며, 부산물인 유채박은 가축사료와 유기질 비료로도 사용되는 용도가 다양한 작물이다. 최근에는 대규모 유채 경관단지 조성을 통한 지역자치단체의 홍보 및 관광수익 창출의 목적으로 남부지방 뿐만 아니라 서울 등 중부지방에서도 경관을 목적으로 유채 재배면적이 크게 증가하고 있어 경관용으로 적합한 유채 품종에 대한 요구가 증가하고 있다. 하지만 유채꽃의 색깔은 노란색으로 단순하기 때문에 경관효과를 높이기 위해서 꽃색의 다양화에 대한 요구가 높아지고 있다. 하얀색 꽃이 피는 경관용 유채 ‘중모 7003’은 국립식량과학원 바이오에너지작물연구소에서 1983년에 ‘Tower’를 모본으로 하고 ‘AB130’을 부분으로 교배하여 고정계통 ‘83025’을 양성하였고, 그 중 하얀색 꽃이 피는 개체를 선발하여 1984년부터 1990년까지 세대를 전개하면서 하얀색 꽃이 고정된 계통 ‘83025-B-1-1-2’를 선발하였다. ‘83025-B-1-1-2’은 2010~2011(2년)에 걸친 생산력검정시험과 2012~2014(3년)에 걸친 지역적응시험 결과, 이형주의 발생이 없고 대비품종인 ‘한라’에 비해 내도복성과 내병성(균핵병)에 강하며 하얀색 꽃이 피어 경관용뿐만 아니라 바이오디젤용으로 적합하여, 중모7003 (Jungmo7003)으로 명명하였다. ‘중모7003’은 개화기(4월 16일)와 성숙기(6월 5일)가 ‘한라’에 비해 5일 빠르다. 수량은 207kg/10a로 ‘한라’에 비해 6%가 적으나 개화 균일성이 좋고 하얀색 꽃이 피어 경관용으로 적합하다. 균핵병에는 강하나 도복저항성이 비교적 약하다. 기름함량(43.8%)과 올레인산 함량(68.4%)로 ‘한라’와 비슷하였고, 에루신산은 전혀 없고 글루코시놀레이트 함량은 1.94g/g으로 국제허용기준치인 3.0mg/g 이하이다.

\*주저자: Tel. 061-450-0133, E-mail: ajuga@korea.kr

## Genetic Diversity of Rice Landraces Collected in Cordillera Region, Philippines

Backki Kim, Sheryl N. Sierra, Hong-Yeol Kim, Hee-Jong Koh\*

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

Banaue Rice Terraces in the Philippines has been a rich source of genetic diversity of untapped rice landraces in the mountainous region of Cordillera. Although some may have been included into modern breeding programs, significant *indica-japonica* differentiation among landraces cultivated in the region is not well known. Thus, Cordillera landraces differentiation across different altitude gradient (458 m to 1830 m) will provide great opportunities for improvement on rice genetics. We analyzed the genetic variation among 166 accessions collected in 17 towns in 6 provinces across different altitudes using Subspecies Specific Sequence Tagged Site (SS-STS) and Insertion-Deletion (InDel) markers. Subspecies Prototype Index (SPI) degree of each landrace was used to calculate the genomic inclination of each variety towards subspecies. The 50 molecular markers (24 SS-STS and 26 InDel) that assayed variation in 166 accessions revealed 116 alleles. Gene diversity ranged from 0.04 (R3M23) to 0.50 (S04058) with an average of 0.40. Polymorphism information content (PIC) ranged from 0.04 (R3M23) to 0.37 (S12030, S07047, R10M40, S10001, S04058 and S09040B) with an average of 0.31. Using the control varieties to assign groups, the larger group of 114 Cordillera landraces corresponds to 71% *japonica* type while the smaller group of 42 corresponds to 26% *indica* and 3% intermediates. A total of 7 (4%) *indica* and 9 (6%) *japonica* type accessions were found above 1500 m. Results of this study suggested that majority of *japonica* type rice landraces were grown in high altitudes of Banaue Rice Terraces and nearby provinces, and interestingly, *indica* type rice landraces were cultivated in areas at much higher altitudes (>1500 m) than those categorized by the traditional methods. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. +82-2-880-4541, E-mail: heejkoh@snu.ac.kr

## Differentially expressed proteins between two Korean inbred lines under drought stress at vegetative stage

Sang Gon Kim\*, Seonghyu Shin, Hwan Hee Bae, Jin-Seok Lee, Jung-Tae Kim, Min Jung Seo, Beom-Young Son, Jeom Ho Lee, Seong-Bum Baek

Department of Central Area Crop Science, National Institute of Crop Science, Rural Development Administration, Suwon 441-707, South Korea

Understanding the response of a crop to water deficiency is the first step towards breeding drought-tolerant varieties. In this study, inbred maize (*Zea mays* L.) lines KS140 and KS141 were subjected to drought stress by withholding water for 10 days at the V5 or V6 leaf stage. Water-deficient plants experienced a decrease in relative leaf water content, stomatal conductance, net CO<sub>2</sub> assimilation rate, and water use efficiency compared to well-watered plants. This was accompanied by a decrease in the relative leaf water content that resulted in severe growth retardation in KS140 and KS141. However, leaf chlorophyll content in KS140 was unchanged. To understand the proteome dynamics during the 10-day drought stress in maize leaves, comparative proteome analysis was carried out between the well-watered and water-withheld leaves. Differential expression was observed for 29 protein spots from KS140 and 14 protein spots from KS141, and these were identified using MALDI-TOF mass spectrometry. Among identified proteins, metabolism and stress related proteins were highly increased by drought stress. This study provides a protein profile of a Korean maize inbred line during drought stress, which will be valuable for future studies of the molecular mechanisms underlying drought resistance and for development of selective breeding markers for drought tolerance in maize.

\*Corresponding Author: Tel. 031-695-4045, E-mail: sen600@korea.kr

## 주성분 분석 및 군집 분석을 이용한 자생국화의 휘발성 향기성분 분류

김수정<sup>1\*</sup>, 하태정<sup>2</sup>, 김종윤<sup>3</sup>, 유동림<sup>1</sup>, 서종택<sup>1</sup>, 김윤희<sup>1</sup>, 홍수영<sup>1</sup>, 남정환<sup>1</sup>, 손황배<sup>1</sup>, 장동철<sup>1</sup>, 김기선<sup>4</sup>

<sup>1</sup>국립식량과학원 고령지농업연구소

<sup>2</sup>농촌진흥청 연구정책과

<sup>3</sup>배재대학교 원예조경학부

<sup>4</sup>서울대학교 원예생명공학과

본 연구는 자생국화 15분류군의 휘발성 향기성분을 다변량 분석을 통해 분류학적 유연관계를 구명하여 그 분류 기준을 제시하고 조경용 및 약용 소재로 이용하기 위한 기초자료로 활용하고자 본 연구를 수행하였다. 국화속 15분류군의 잎을 대상으로 GC/MS 분석 결과, 총 45종의 휘발성 향기성분이 함유된 것으로 나타났으며, camphor, borneol, phytol,  $\alpha$ -pinene, camphene, 1,8-cineole 및 germacrene-D는 모든 분류군에 공통적으로 함유된 것으로 나타났다. 국화속 15분류군은 hydrocarbon류(sabinene, cymene,  $\beta$ -selinene), alcohol류(1-octen-3-ol, cischrysanthenol, hinesol), ketone류(chrysanthenone, camphor), 및 ester류(cis-sabien hydrate, trans-chrysanthenyl acetate)의 휘발성 향기성분을 바탕으로 주성분 분석과 군집 분석 결과 총 3그룹으로 분류할 수 있었다. Group I은 5분류군의 구절초류를 나타내었으며, 주요 성분은 D-limonene와 m-thymol이었다. Group II는 낙동구절초, 남구절초, 넓은잎구절초, 서홍넓은잎구절초 그리고 마키노 국화로 구성되었으며, linalool과 cis-chrysanthenol, eugenol, 및 chrysanthenone이 주요 성분이었다. Group III은 감국, 흰감국, 가는잎감국, 산국, 키큰산국이었다. 특히, Group I과 II에서는  $\alpha$ -terpineol이 공통적으로 함유되었으나, Group III에서는 검출되지 않았다.

---

**PB-11****흑색 찰성 고품질 다수성 겉보리 신품종 ‘흑수정찰’**

김양길<sup>1\*</sup>, 이미자<sup>1</sup>, 박종철<sup>1</sup>, 강천식<sup>1</sup>, 김경호<sup>1</sup>, 김상민<sup>1</sup>, 최인배<sup>1</sup>, 한옥규<sup>1</sup>, 윤건식<sup>2</sup>, 배정숙<sup>3</sup>, 조수현<sup>4</sup>, 최재성<sup>1</sup>, 박광근<sup>1</sup>, 오영진<sup>1</sup>, 정영근<sup>1</sup>, 박기훈<sup>1</sup>

<sup>1</sup>전북 완주군 이서면 혁신로 181 농촌진흥청 국립식량과학원

<sup>2</sup>충청북도 청주시 청원구 오창읍 가곡길 46 충청북도농업기술원

<sup>3</sup>대구광역시 북구 칠곡중앙대로136길 47 경상북도농업기술원,

<sup>4</sup>강원도 춘천시 충열로 83 강원도농업기술원

식생활 변화에 따라 보리는 혼반용에서 점차적으로 보릿가루, 엿기름, 보리차, 새싹, 맥주, 면 등 다양한 용도로 활용될 뿐만 아니라, 건강식품으로 보리 수요가 확대되고 있어 이를 위한 용도별 고품질 기능성 보리 품종개발이 요구되고 있다. 따라서 이에 적합한 품종을 육성하기 위해 2005년에 조숙, 대립, 다수성 품종인 “큰알보리1호(IT213217)”를 모본으로, 흑색 찰성 특성을 가진 “마산과맥(IT268885)/Mortoni(IT111490)” 계통을 부분으로 인공교배하여, 흑색 찰성이고 보리호위축병 저항성이면서 다수성인 취반용 ‘흑수정찰’을 개발하였다. ‘흑수정찰’은 6조이며 파성이 III인 병성 겉보리로 이삭의 형태는 밀수형이고, 종실색은 흑색으로 까락이 길며 탈망성이 좋다. 출수기는 서둔찰에 비해 전작에서 5월 1일로 3일, 답리작에서 4월 27일로 4일 늦었다. 간장은 89cm로 서둔찰보다 7cm 정도 긴 장간형으로 내도복성이며, 수장과 립수는 비슷하였고, 수수는 다소 적은 소열성이다. 천립중(36.0g)은 서둔찰보다 2.0g 무거웠다. 병해저항성 중 보리호위축병은 저항성을 나타냈으며, 내한성은 서둔찰과 비슷하였다. ‘흑수정찰’은 단백질 함량(12.5%)이 서둔찰과 비슷하나 베타글루칸 함량(6.7%)이 높고, 아밀로즈 함량(5.5%)이 낮은 찰성 품종이다. 수량성은 전작에서 4.72톤/ha으로 7% 증수, 답리작 3.75톤/ha으로 서둔찰과 비슷하였다. ‘흑수정찰’은 1월 평균기온이 -8℃ 이상인 지역에 보급 될 것으로 기대 된다.

\*주저자: Tel. 063-238-5225, E-mail: kim5yk@korea.kr

**PB-12****Selection of mutant related to salt and drought tolerance in rice with expression microarray**

Joung Sug Kim<sup>1</sup>, Kyong-Mi Jun<sup>2</sup>, Hyejin Yoon<sup>3</sup>, Songhwa Chae<sup>1</sup>, Yoon Mok Pakh<sup>2</sup>, Yeon-Ki Kim<sup>1</sup>, Baek-hie Nahm<sup>1,2\*</sup>

<sup>1</sup>Division of Bioscience and Bioinformatics, Myongji University, Yongin, Korea

<sup>2</sup>Plant molecular genetics Institute, GreenGene Biotech Inc., Yongin, Korea

<sup>3</sup>Rural Development Administration, Jeonju, Korea

Salt and drought stresses affect virtually every aspect of plant physiology and metabolism and thus limiting the productivity of crop plants worldwide. Salt and drought tolerance and adaptation in rice has been improved by engineering various genes related to transcription, signaling, accumulation of antioxidants and compatible solutes etc. Previously, we have produced 2,000 non-GM mutants induced by *Tos17* in rice. We analyzed >2,000 flanking sequences of newly transposed *Tos17* copies by the adaptor-ligation PCR method. We also identified significantly up- or down-regulated genes under drought, salt, or ABA stress in rice based on expression microarray data, which previously were performed from leaf at different developmental stages and conditions. For screening and characterizing the salt or drought tolerance mutations by extensive phenotypic analysis as well as the functional analysis of genes, we selected 133 mutant lines. To evaluate rice phenotypic traits under abiotic stress condition, we plan to investigate phenomics, which integrates technologies such as photonics, biology, computers, and robotics.

\*Corresponding Author: Tel. 031-330-6193, E-mail: bhnaem@gmail.com

---

**PB-13****Development of the *Tos17*-insertional mutants and functional analysis of transcription factors involved in seed development**

Joung Sug Kim<sup>1</sup>, Songhwa Chae<sup>1</sup>, Kyong-Mi Jun<sup>2</sup>, Yoon Mok Pakh<sup>2</sup>, Yeon-Ki Kim<sup>1</sup>, Baek-hie Nahm<sup>1,2\*</sup>

<sup>1</sup>Division of Bioscience and Bioinformatics, Myongji University, Yongin, Korea

<sup>2</sup>Plant molecular genetics Institute, GreenGene Biotech Inc., Yongin, Korea

Rice, as a model system of monocotyledon plants for genomic studies, is a main staple food for over half of the world population. A rice retrotransposon, *Tos17*, is active during tissue culture and its ability was widely used in insertional mutagenesis. In this study we have produced 2,000 non-GM mutants induced by *Tos17* in rice. We analyzed >2,000 flanking sequences of newly transposed *Tos17* copies by the adaptor-ligation PCR method. The frequencies of *Tos17* insertions in the genic and intergenic regions were 60.3% and 36.6%, respectively. We also selected four *Tos17* insertion mutant lines for three TF genes which can be considered to be involved in rice seed development based on expression microarray data: *osrem3*, *osta1*, *osbhlh1-1*, and *osbhlh1-2* mutant lines. According to Quadruple 9-mer-based protein binding microarray (Q9-UPBM) experiment, we found that the *OsREM3*, *OsTA1*, and *OsbHLH1* bound to the ACACCAC, CACGTG, and GTAACA motifs, respectively. In combination of Q9-UPBM, RiceArrayNet analysis, and expression microarray data, we identified 8, 20, and 9 putative target genes of *OsREM3*, *OsTA1*, and *OsbHLH1*, respectively. We have been screening and characterizing the mutations by extensive phenotypic analysis as well as the functional analysis of genes.

\*Corresponding Author: Tel. 031-330-6193, E-mail: bhnaem@gmail.com

**PB-14****Phenotypic screening and breeding with colored wheat by mutation breeding technique**

Jin-Baek Kim<sup>1\*</sup>, Min Jeong Hong<sup>1</sup>, Young Ha Yoon<sup>1</sup>, Dong Sub Kim<sup>1</sup>, Soon-Jae Kwon<sup>1</sup>, Hong Il Choi<sup>1</sup>, Si-Yong Kang<sup>1</sup>, Yong Weon Seo<sup>2</sup>

<sup>1</sup>Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup, Jeonbuk 580-185, Korea

<sup>2</sup>Korea University, Anam-dong Seongbuk-Gu, Seoul, 136-701 Korea

Anthocyanin, a group of purple or reddish flavonoids, have been recognized as health-promoting functional food ingredients due to antioxidant activity. For this reason, plant breeders are trying to increase the anthocyanin contents using methods such as classical breeding and biotechnological approaches. To broaden the mutants population, seeds of colored wheat variety (K4191) were irradiated by using 250 Gy gamma irradiation. Individual 968 M<sub>4</sub> plants were grown in Korea Atomic Energy Research Institute field. Many mutant phenotypes were shown: seed color variation, abnormal spike shape, awning formation, heading and ripening time, plant height, ripening period, super dwarf, etc. To identify the inheritance traits of colored-wheat, individual lines were maintained the spike base classified by generation. Characteristics per spike and plant were piled up to construct for mutant database. In the future, fixed descent will be analyzed the anthocyanin contents or other phytonutrients by ultra-performance liquid chromatography (UPLC). Expression of seed color-related transcription factors and anthocyanin biosynthetic pathway genes will be examined.

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

---

**PB-15****전정에 의한 다래 과실의 등급별 생산특성**

김철우\*, 박영기, 김만조, 김세현, 김재희

경기도 수원시 권선구 오목천동 국립산림과학원 특용자원연구과

15 cm이하의 결과모지에서 발생한 다래 과실의 무게는 평균  $10.0\pm 3.2$  g이었고, 과실수는 평균  $3.8\pm 2.0$ 개로 나타났다. 이 결과는 30 cm 이상의 결과모지에서 발생한 결과지의 과실수 평균  $13.3\pm 7.8$ 개에 비해 낮은 값이다. 15 cm 이하의 짧은 결과모지는 과실이 적게 착립하며 대부분 하급과실이 생산되므로 과실의 품질향상을 위해선 동계전정시 15 cm이하의 결과모지를 우선 제거해야 할 것으로 판단된다. 전정처리구에서는 과실 총 생산량이 본당 평균  $14.3\pm 1.5$  kg이었으며, 이중 상급과실(15 g이상)이  $8.2\pm 0.9$  kg, 중급과실(10 g에서 15 g)이  $4.0\pm 0.7$  kg 그리고 하급과실(10 g이하)이  $2.1\pm 0.3$  kg 생산되었다. 무처리구에서는 과실 총 생산량이 본당 평균  $26.7\pm 2.1$  kg이었으며, 이중 상급과실이  $2.5\pm 0.5$  kg, 중급과실이  $19.2\pm 1.4$  kg 그리고 하급과실이  $5.0\pm 0.6$  kg 생산되었다. 특히, 전정처리구와 무처리구에서의 15g이상의 상급과실의 무게분포를 보면 무처리구는 대부분 15~16 g의 과실이 분포하였으나, 전정처리구는 15~20 g이상까지 고르게 분포하는 것으로 나타났다. 따라서, 전정을 실시하지 않을 때 17 g 이상의 과실생산이 쉽지 않을 것으로 판단되며, 고품질 다래 생산을 위해서는 적절한 동계전정이 필수적이다.

\*주저자: Tel. 031-290-1186, E-mail: ftree@forest.go.kr

**PB-16****콩 유전자원의 isoflavone 함량변이**김현명<sup>1</sup>, 이지석<sup>1</sup>, 이재원<sup>1</sup>, 김보경<sup>1</sup>, 황세구<sup>2</sup>, 김홍식<sup>1\*</sup><sup>1</sup>충청북도 청주시 서원구 충대로1 충북대학교 농업생명환경대학 식물자원학과<sup>2</sup>충청북도 청주시 청원구 오창읍 가곡길 46 농업기술원

국내외에서 수집된 유전자원 632점에 대한 isoflavone 함량의 변이를 구명하여 기능성 콩 품종개발의 기초자료로 활용하고자 본 연구를 수행하였다.

Isoflavone의 총 함량 평균은  $801.2\mu\text{g/g}$ , 범위는  $162.2\sim 3,569.5\mu\text{g/g}$  이었다. Daidzein의 총 함량의 평균은  $312.6\mu\text{g/g}$ 이었고,  $47.3\sim 2,050.1\mu\text{g/g}$ 의 범위였으며, glycitein은 평균  $121.1\mu\text{g/g}$ , 범위는  $27.1\sim 443.8\mu\text{g/g}$ 이었다. Genistein의 평균함량은  $367.6\mu\text{g/g}$ 이었고,  $19.5\sim 1,404.6\mu\text{g/g}$ 의 범위였다. 총 함량이  $2000\mu\text{g/g}$ 이상 되는 고함량 자원은 IT262889, IT167230, IT100869, IT171009, IT208248, IT142854 및 IT142911이었다. 수집국가에 따른 총 평균함량은 캐나다가 가장 높았으며, 일본, 미국, 북한, 중국, 한국, 러시아의 순이었고, 종실크기에 따른 총 평균함량은 소립종이 가장 높았으며, 중립종, 대립종의 순이었다. 종피색에 따른 총 평균함량은 녹색콩이 가장 높은 함량을 보였으며, 검정콩, 갈색콩, 황색콩의 순서로 나타났다. Daidzein, glycitein 및 genistein과 총 isoflavone함량 간에는 정의 상관이었으며, 각 함량간의 상관관계 또한 정의 상관이었다.

\*주저자: Tel. 043-261-2513 E-mail: hongsigk@chungbuk.ac.kr

---

**PB-17**

## **Chemical Components in the Leaves of Selected Mutant Cultivars of kenaf (*Hibiscus cannabinus* L.)**

Jaihyunk Ryu, Sang-Wook Jeong, Seung Bin Im, Joon-Woo Ahn, Soon-Jae Kwon, Dong Sub Kim, Jin-Baek Kim, Sang Hoon Kim, Si-Yong Kang\*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580-185, Korea.

Kenaf (*Hibiscus cannabinus* L.) native to Africa can be used as fiber, food, feedstock and bio plastic. This study was carried out to evaluate the mineral, amino acid and vitamin contents of six selected kenaf cultivars which are enable to produce seed under Korean circumstance. The leaves of three mutant cultivars (Jangdae, Jeokbong and Baekma), two original cultivars (Jinju, C14) and one Chinese cultivar (Auxu) were harvested at flowering time. Mineral components of kenaf leaves, such as calcium, potassium, and mineral, did not showed significant differences among the cultivars. As major amino acids including proline and phenylalanine, significant differences were found in these kenaf cultivars. The Auxu cultivar contained the highest amount of essential amino acid (Phenylalanine, Leucine, Isoleucine, Valine, Methionine and Lysine). The amount of vitamin displayed significant differences such as vitamin E and vitamin K among these cultivars. Especially, Jangdae cultivar contained the highest amount of vitamin E and vitamin K. Thus, these data suggested that Jangdae and Auxu is the most desirable cultivar containing high amount of vitamin and amino acid.

\*Corresponding Author: Tel. 063-570-3310, E-mail: sykang@kaeri.re.kr

**PB-18**

## **Negative roles of MAPK signaling cascades for nitrogen-fixing nodule formation in *Medicago truncatula***

Wonsil Bae, Jinsoo Lee, Hojin Ryu\*

Department of Biology, Chungbuk National University, Cheongju, 361-763, Korea

Mitogen-activated protein kinase (MAPK) signaling cascades play critical roles in various cellular events including abiotic/biotic stress responses, innate immunity, hormone signaling and cell specificity in plants. The MAPK-mediated stress and ethylene signaling are recently known to be involved in nitrogen-fixing symbiotic interactions; however, the biological role of MAPK for nodule development in legume plants is largely unknown. We here elucidated that MtMKK5-MtMPK3/6 cascade negatively regulate the nitrogen fixing nodule formation in *Medicago truncatula*. MtMKK5, an ortholog of SIMKK, overexpression significantly reduces the nodule formation in *M. truncatula* roots. MtMKK5 directly activates MtMPK3/6 by phosphorylation on the TEY motif within the activation loop in the cytoplasm, which might link to EFD as a negative regulator for nodule formation. EFD has a putative MAPK phosphorylation Thr residue and could be a target of the activated MtMPK3/6 in the nucleus. Consistently, a MAPK specific inhibitor U0126 enhances nodule formation and confers similar nodule phenotypes to the *efd-1* mutant such as lower proliferation and differentiation to symbiotic tissues. Our works thus reveal a key negative signaling module mediated by MtMKK5-MtMPK3/6-EFD for symbiotic nitrogen fixing nodule organogenesis.

\*Corresponding Author: Tel. 043-261-2293, E-mail: hjryu96@chungbuk.ac.kr

---

**PB-19****표피가 매끈하고 육질이 단단하며 근장이 짧은 무 ‘원교10045호’ 육성**

박수형\*, 윤무경, 박민영, 장하영, 채원병, 서명훈

농촌진흥청 국립원예특작과학원 채소과

무는 한국인의 주요 부식인 김치 뿐 아니라, 국, 무침, 찌개 등 다양한 요리의 재료가 되는 전통 채소이다. 70년대 초반에 우수한 일대잡종 품종을 개발하였으며, 70년대 중반부터 일본에 수출을 시작하여 이후 꾸준하게 수출이 증가하여, 2014년에는 일본, 중국, 미국 등에 8,896US\$를 수출하여 전체 채소종자 수출액의 22%를 차지하게 되었다. 최근 중국과 인도의 채소종자 시장이 일대잡종 시장으로 변화되며 우수 품종이라면 고가를 주고라도 구입하려는 농가가 증가하고 있어 국내 뿐 아니라 외국 시장의 수요를 충족할 수 있는 다양한 특성의 품종 개발이 필요하게 되었다. 이를 뒷받침하기 위해 국립원예특작과학원 채소과에서는 다양한 특성의 중간모본을 육성하여 신속하게 민간에 보급코자 연구를 수행하였다.

제주 지역은 단지무, 갯무 등 다양한 무 자원이 자생하는 곳으로 육종 적으로 중요하다. 따라서 2005년에 제주 지역에서 수집된 자원을 2006년에 수원에서 평가 후 뇌수분을 통한 세대진전을 지속적으로 수행하였다. 2010년 가을 노지에서 재배하며 그 원예적 특성을 민간 육종가와 공동 평가한 결과 우수한 계통으로 선발되었다. 2010년엔 무 파종 직후 태풍이 강하게 발생하여 성숙모본의 상태가 불량하여 당해연도엔 종자의 증식이 원활치 못하여 2011년부터 2014년까지 종자 증식 및 증식된 종자의 순도 검정을 수행하였다. 2015년에 증식 완료된 종자를 국립종자원에 ‘원교 10045호’(출원 2015-398)로 품종등록 하였다.

‘원교 10045호’는 지상부와 지하부 전체 무게가 593g으로 대조인 ‘서호무’의 2,231g보다 작았으며, 뿌리 무게도 479g으로 대조의 1,862g보다 작았고, 뿌리의 길이는 16.3cm로 대조의 22.1cm보다 짧았다. 근폭은 잎과 닿는 부위인 상부의 지름이 41mm로 대조의 67mm보다 좁았으며, 가장 두꺼운 부위의 지름은 9cm로 대조의 14cm보다 좁았고, 끝부분인 하부의 지름은 20mm로 대조의 29mm보다 좁았다. 엽수는 20.5매로 대조인 ‘서호무’의 24.1매보다 적었으며, 잎의 길이는 23.5cm로 대조의 39.3cm보다 짧았다

\*주저자: Tel. 063-238-6622, E-mail: psh@korea.kr

**PB-20****Breeding of new walnut cultivar, “Golden-ball”**

Youngki Park\*, Chul-Woo Kim, Sea-Hyun Kim, Mahn-Jo Kim, Jae-Hee Kim

Division of Special Purpose Trees, Korea Forest Research Institute, Suwon 441-350, Republic of Korea

A new cultivar of walnut (*Juglans sinensis*) was developed through selection from Korea Forest Research Institute. The goals of this research were to evaluate the yielding of walnut and their fruit characteristics of walnut selected from different regions in Korean Wild. Different varieties of walnut grown in Korea, were investigated in what concerns fruit weights, fruit length and their yielding. The walnut belongs to the family Juglandaceae. It is one of the most important nut crops grown in temperate regions. Walnuts, the seeds of *J. sinensis* are a highly nutritious food. They are also used as a traditional remedy for treating cough, stomach ache and cancer in Asia. The present investigations were undertaken during 2000-2009 in five walnut growing areas. In the present study a wide range of variation was observed in walnut characters from different locations. From these varieties, we have been regularly investigated the fruiting characteristics, which are the average of Fruit Length (FL) and Width (FW), and Weight of Fruit (WF) and Individual Yields (IY), during 10 years to select good quality walnut trees.

\*Corresponding Author: Tel. 031-290-1196, E-mail: woodpark@korea.kr

---

**PB-21****Identification of genus *Vigna* using ITS2 and *matK* as a two-locus DNA barcode**

Jae-Wan Park, Sebastin Raveendar, Jung-Ro Lee, Gi-An Lee, Young-Ah Jeon, Eun Seong Park, Yang-Hee Cho, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung\*

National Agrobiodiversity Centre, National Academy of Agricultural Science, Rural Development Administration, Jeonju 560–500, Republic of Korea

DNA barcoding is the use of short DNA sequences of the genome for large scale species identification. The Consortium for the Barcode of Life (CBOL) plant-working group recommended the 2-locus combination as the standard plant barcode. The evolutions of the chloroplast regions combine with nuclear genes are sufficiently rapid to allow discrimination between closely related species. We evaluated the efficacy of the proposed plant barcoding loci *matK* along with ITS2 for barcoding *Vigna* species. To assess the discrimination ability of barcoding loci to resolve *Vigna* species, we sampled 52 of the taxonomically best known groups in the genus. Topologies of the phylogenetic trees based on ITS2 and *matK* analyses were similar but a few accessions were placed into distant phylogenetic groups. Neither ITS2 nor *matK* analyses were able to discriminate some closely related *Vigna* species alone. Thus, we used concatenated data to increase the resolving power of ITS2 and used *matK* as an additional tool for phylogenetic analysis in *Vigna* because characterization of the nucleotide sequences of *matK* region was easier to recover and more cost-effective than those of the ITS region.

\*Corresponding Author: Tel. +82-63-238-4872, E-mail: jwchung73@korea.kr

**PB-22****A New Peanut Variety “Daan” with High Yield and Disease Resistance**

Suk-Bok Pae\*, Myung-Hee Lee, Sung-Up Kim, Chung-Dong Hwang, Ki-Won Oh, Chan-Sik Jung, Deuk-Young Song, In-Youl Baek, Young-Hee Lee

Department of Southern Area Crop Science, NICS, RDA, Miryang 627–803, Korea

Peanut is grown worldwide in the tropics and temperate zones primarily as an oilseed crop (38-54%) and protein source(25-30%). A new peanut variety “Daan”( *Arachis hypogaea* ssp. *fastigiata* L.) with the high yield potential was developed at the Department of Southern Area Crop Science, NICS, in Milyang in 2014. This was developed from the crossing line between cultivar “Sangpyeong” with short stem and high quality and “Dakwang” with large grain. “Daan” which is Shinpung plant type has 44cm of main stem length and 13 branch number per plant. Each pod has two grains with long ellipse shape of brown testa and yield components is composed of 34 mature pods of per plant, 127g of 100-seed weight, 75% of pod shelling ratio in the regional yield trials(RYT). Seed quality showed 47.8% of crude oil and 28.3% of protein content. This variety also showed more resistant to early leaf spot, late leaf spot, web blotch, stem rot and lodging compared with check variety “Daekwang”.

In the regional yield trials “Daan” outyielded check variety by 16% with 5.00 MT/ha for kernel yield.

\*Corresponding Author: Tel. 055-350-1215, E-mail: paesb@korea.kr

## A New Dark Purple Peanut Variety “Heuksaeng”

Suk-Bok Pae\*, Chan-Sik Jung, Ki-Won Oh, Sung-Up Kim, Myung-Hee Lee, Chung-Dong Hwang, Deuk-Young Song, In-Youl Baek, Young-Hee Lee

Department of Southern Area Crop Science, NICS, RDA, Miryang 627–803, Korea

Anthocyanin has antioxidant and radical-scavenging effects which may protect cells from oxidative damage and reduce risk of cardiovascular diseases and cancer. A new peanut variety “Heuksaeng” (*Arachis hypogaea* ssp. *hypogaea* L.) with dark purple peanut skin was developed at the Department of Southern Area Crop Science, NICS, in Milyang in 2014. This variety was developed from the crossing line between cultivar “Iksan 31” with short stem and erect plant type and “Iksan35” with large grain and purple skin. “Heuksaeng” which is semi erect Virginia plant type has 32cm of main stem length and 25 branch number per plant. This also show more resistant to late leaf spot, web blotch and lodging, compared with check variety “Daekwang”. Each pod has two grains with ellipse shape of purple testa and its yield components is composed of 60 mature pods of per plant, 69g of 100-seed weight, 77% of pod shelling ratio in the regional yield trials(RYT). For 3 year regional yield trials the average kernel yield of “Heuksaeng” had 4.25 MT/ha similar to that of check variety.

Its seed quality show 26.9% of crude protein and 46.0% of crude oil and 53.4% of oleate in fatty acid composition. Peanut skin of variety “Heuksang” consist of 2 kind of anthocyanin compounds such as 4.67mg/100g of delphinidine-3-glucoside (D3G) and 1.18mg/100g of cyanidine-3- glucoside(C3G). Peanut variety with high anthocyanin conent in skin will be useful to the recent preference of colorful food with healthful functional compounds.

\*Corresponding Author: Tel. 055-350-1215, E-mail: paesb@korea.kr

## 무 모식물체의 광 환경 조절을 통한 소포자 유래 배 발생효율 증진

배은지<sup>1</sup>, 나해영<sup>1,2\*</sup>

<sup>1</sup>목포대학교 원예과학과

<sup>2</sup>목포대학교 자연자원개발연구소

소포자 유래 배 발생 효율을 높이기 위해 무 모식물체의 광질 처리에 따른 개화까지 소요되는 기간, 화기구조, 소포자 밀도와 소포자 유래 배 발생 효율 및 활력을 조사하였다. 공시재료로 소포자 유래 배 발생 효율이 높은 태백무를 선정하였으며, 4.0±0.5mm길이의 화뢰를 선별하여 실험을 수행하였다. 광질 처리는 각각 LED 단독광(Red), LED 혼합광(Red+Blue+White) 그리고 형광등으로 처리하였으며, 광량은 50μmolm<sup>-2</sup>s<sup>-1</sup>로 설정하여, 16/8시간(명/암)의 광 주기 조건에서 생육하였다. 광질 처리에 따른 무의 개화시기는 형광등 처리구에서 다른 처리구에 비하여 평균 20일로 가장 빨랐다. 처리별로 화뢰 구조를 관찰한 결과, LED 단독광(Red)과 LED 혼합광(Red+Blue+White)에서 재배된 모식물체의 화뢰가 소포자 유래 배 발생 효율이 높은 단계로 보고된 주두의 길이가 꽃잎의 길이보다 긴 화뢰가 형성된 것을 확인할 수 있었다. 광질 처리에 따른 소포자의 밀도는 LED 단독광(Red)에서 화뢰당 약 3,579,000개로 가장 많이 조사 되었으며, 소포자 유래 배 발생 효율 역시 약 2.46개로 가장 높았다. 또한 LED 단독광(Red)에서 재배한 모식물체의 화뢰가 소포자 활력 유지 비율이 가장 높았다. 무 모식물체를 형광등에서 재배하였을 때, 개화까지 소요 되는 기간을 가장 많이 단축시킬 수 있었으며, 또한 LED 단독광(Red)에서 소포자 밀도 및 소포자 유래 배 발생효율 그리고 활력 또한 다른 처리구에 비하여 높은 결과를 보였다. 소포자 유래 배 발생 효율을 높이기 위한 방법으로 무 모식물체에 LED를 이용한다면 소포자 배양에 적합한 단계의 화뢰를 단기간에 생산할 수 있으며, 소포자 유래 배 발생 효율을 증가시킬 수 있을 것으로 기대된다. 또한 위의 결과는 다른 작물의 반수체 육종을 이용한 신품종 육성에도 적용 가능할 것으로 판단된다.

\*주저자: Tel. 061-450-2371, E-mail: somerze@mokpo.ac.kr

## 미나리 종자의 저온 증적처리 및 세척방법

배은지<sup>1</sup>, 황순임<sup>1</sup>, 나해영<sup>1,2\*</sup>

<sup>1</sup>목포대학교 원예과학과

<sup>2</sup>목포대학교 자연자원개발연구소

미나리의 종자번식을 위해 각 기간에 따라 증적처리 한 후 세척 방법에 따른 발아율을 조사하였다. 증적처리 유무에 따른 발아율을 조사한 결과 증적처리를 하였을 때 69.3%로 증적처리를 하지 않았을 때 보다 약 1.4배 높게 발아 되었다. 증적처리 전, 수확한 종자를 음건 처리한 후 발아율을 비교한 결과, 음건처리를 하지 않은 종자의 발아율이 더 높게 조사되었다. 음건처리 하지 않은 종자를 저온저장고와 노지에 각각 2, 4, 8, 12주 동안 증적처리하여 저장한 결과, 노지에서 8주 동안 처리하였을 때 발아율이 평균 88%로 가장 높았다. 개화 후 40일 된 종자를 수확하여 모래증적처리 한 후 증류수와 농도 수준이 다른 sodium hypochlorite, vital oxide로 세척시간을 달리하여 발아율을 조사한 결과 증류수는 세척시간에 따른 발아율을 차이를 보이지 않았으나, sodium hypochlorite의 경우 0.5~1.0% 용액으로 약 3~5분 동안 세척하였을 때 발아율이 향상되었고, 2.0% 용액으로 세척하였을 때는 발아율이 저하되는 경향을 나타내었다. 또한 vital oxide 0.0005%의 농도로 60분 동안 세척하였을 때 발아율이 향상되었다. 본 연구 결과 기존의 열악한 환경에서 악성노동이 요구되는 영양번식에서 종자번식으로 전환하여 악성노동을 탈피하고, 기계화를 통한 노동력 감소 및 청정재배를 가능하게 하는 기초자료로 사용 가능할 것이며, 또한 종자발아가 어려워 재배화가 불가능한 많은 식물의 재배법 연구에 도움이 될 것으로 기대된다.

사사: 본 연구는 농림축산식품부 종자번식을 이용한 미나리 주년 생산과 유통체계 확립 및 종자 산업화 지원에 의해 이루어진 것임.

\*주저자: Tel. 061-450-2371, E-mail: somerze@mokpo.ac.kr

## Glycoalkaloids content in tuber peel and cortex of 24 potato cultivars of Korea

Hwang-Bae Sohn<sup>1</sup>, Su-Jeong Kim<sup>1</sup>, Yu-Young Lee<sup>2</sup>, Hyang-Mi Park<sup>3</sup>, Manjulatha Mekapogu<sup>1</sup>, Su-Young Hong<sup>1</sup>, Jeong-Hwan Nam<sup>1</sup>, Jin-Cheol Jeong<sup>1</sup>, Kibum Kweon<sup>1</sup>, Yul-Ho Kim<sup>1\*</sup>

<sup>1</sup>Highland Agriculture Research Institute, NICS, RDA, Pyeongchang 232-955, Republic of Korea

<sup>2</sup>Department of Central Area, NICS, RDA, Suwon 441-770, Republic of Korea

<sup>3</sup>Headquarters, NICS, RDA, Wanju-gun 565-851, Republic of Korea

Potato glycoalkaloids(PGAs) are potentially toxic to humans at high levels and current safety regulations have recommended that PGAs content in tubers of potato cultivars should not exceed 20 mg/100g-FW. Accordingly, it is important to determine the PGAs composition and levels on potato cultivars for food safety and the breeding for new cultivars with low levels of PGAs. The main aim of this study was to evaluate  $\alpha$ -chaconine,  $\alpha$ -solanine and total PGAs content in the peel and cortex portions in 24 cultivars including 'Haryoung', 'Goun', 'Hongyoung' and 'Jayoung', recently released by Highland Agricultural Research Institute. The total PGAs ranged from 3.1 to 10.1 mg/100g-FW. 75-94% of total PGAs was existed in the peel part of all cultivars. We selected two cultivars, which can be eaten with the skin on tubers, and so used for soy sauce braised potatoes and baby potatoes for the rest area. These results will provide consumers and breeders with fundamental information about the content of PGAs in Korea major cultivars.

\*Corresponding Author: Tel. 033-330-1840, E-mail: kimyuh77@korea.kr

---

**PB-27****단간 내도복 중생 메조 ‘단아메’ 육성**

고지연\*, 이재생, 송석보, 최명은, 우관식, 고종철, 김기영, 정태욱, 오인석

농촌진흥청 국립식량과학원

조는 균형 잡힌 영양소와 풍부한 미량원소로 인하여 건강기능성 곡식의 하나로 최근 관심이 증가하고 있는 밀렛류 대표작물이다. 새로 개발된 조 ‘단아메’는 키가 97cm로서 대조품종에 비하여 20cm나 작은 단간종으로 쓰러짐에 강하여 기계수확하기에 적합한 품종이다. 평균 출수기는 ‘13년~’14년 8월 7일로 대조품종인 황금조에 비하면 4일 정도 늦으나, ‘삼다찰’ 등의 만생종 품종에 비하면 10일 정도 출수가 빠른 중생종이다. 수량성은 2013~2014년 2년간 밀양에서 실시한 생산력검정시험 결과 평균수량은 286 kg/10a으로 대비품종인 ‘황금조’에 비하여 5% 감소되었으며, 같은 해 전국 5개 지역에서 2년간 실시한 지역적응시험 평균수량은 381 kg/10a로 대비품종 ‘황금조’보다 4% 증수되어 ‘황금조’와 수량이 비슷하였다. 주당수수는 1.8개, 수당이삭무게는 10.9g, 등숙비율 68.3%로 황금조와 비슷한 편이고, 천립중은 조곡 2.95g, 현곡 2.38 g으로 ‘황금조’ 보다 약간 무거운 편이다. 조는 배유특성에 따라 밥에 넣어먹거나 떡으로 이용하는 찰기가 있는 차조와 찰기가 없는 메조로 나뉜다. ‘단아메’는 주황색 종피를 지닌 메조로서 죽이나 제과, 선식 등의 가공에 이용하기 좋고, 밥에 넣어 먹어도 좋은데 특히, 찰기가 없어 식감이 좋은 볶음밥, 리조또 등에 사용하면 잘 들러붙지 않고, 밝은 노란색의 조 알갱이가 흰 쌀밥과 잘 어울리므로 새로운 조의 소비확대에 기여할 것으로 생각된다.

\*주저자: Tel. 055-350-1225, E-mail: kjeeyeon@korea.kr

**PB-28****흰앙금 제조특성이 우수한 팔 신품종 ‘흰나래’ 육성**

송석보<sup>1\*</sup>, 이재생<sup>1</sup>, 고지연<sup>1</sup>, 우관식<sup>1</sup>, 최명은<sup>1</sup>, 정태욱<sup>1</sup>, 문중경<sup>1</sup>, 고종철<sup>1</sup>, 오인석<sup>1</sup>, 최유미<sup>2</sup>

<sup>1</sup>농촌진흥청 국립식량과학원

<sup>2</sup>농촌진흥청 국립농업과학원 농업유전자원센터

팔은 전통음식인 팔죽을 비롯, 떡, 빵, 과자, 팔빙수 등의 앙금 및 양갱 재료 이용 뿐만 아니라, 최근 현대인의 건강식품, 천연색소, 다이어트 음료, 미백용 화장품 등 다양한 분야에서 사업화 되고 있다.

이러한 제품의 원료곡으로 주로 적색팥이 사용되었으나 팔 재배면적 및 소비 확대를 위해서 가공 특성이 우수하고 기능성분이 높은 다양한 색상의 팔 신품종 개발이 요구되고 있다.

지금까지 흰앙금은 붉은 팥의 종피를 제거하여 제조하는 가공과정이 필요하였다. 또한 붉은 팥은 소비자 및 가공업체에서 원하는 다양한 색깔의 양갱 및 앙금 제품 개발에 한계가 있다.

새로 개발된 팔 신품종 ‘흰나래’는 이러한 가공단계 생략 및 제품 다양화에 알맞은 흰앙금 제조가 가능한 황백색 종피를 가진 품종이다. ‘흰나래’는 2003년에 흰앙금 제조 팔 품종개발을 목표로 Gyeongwonpat와 Sodubaenggei 3을 교배육종법을 통해 2014년 육성된 신품종이다. 2010~’13년에 강원, 충북, 전북, 밀양 등 4개소에서 실시한 지역적응 시험에서 수량은 1.86MT/ha 이며 ‘흰나래’의 성숙시기는 충주팥 보다 10일 늦은 10월 12일로 만생종이다. 백립중은 16.6g으로 대립이며 흰앙금 제조 가공특성과 품질이 우수하다.

흰앙금 제조특성이 우수한 ‘흰나래’는 팔의 용도 다양화, 신수요 창출, 부가가치 향상 및 소비확대에 기여 할 것으로 기대된다.

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

---

## 안면도 소나무 채종원 종자생산 진단을 위한 구과분석

송현진\*, 배태웅, 문병호, 이성기, 이병실

충북 충주시 수안보면 국립산림품종관리센터 종묘관리과

종자생산기지의 주기적인 구과분석은 산림종자의 안정적 생산·공급을 위한 채종원의 종자생산성 및 관리상태 진단 기준설정에 요구되는 기술이다. 본 연구에서는 2013-2014년 안면도 채종원의 소나무 구과분석을 통해서 종자생산성 및 관리상태를 진단하고자 연구를 수행하였다. 연구방법은 안면도 채종원 4개 단지에서 40본의 채종목을 선정하였고, 각각 4~6개의 구과를 채취하여 특성을 조사하였다. 구과분석은 구과의 외형적 특성(크기, 무게, 인편수)과 종자개수, 충실종자 및 고사배주 등을 조사하여 채종원의 종자생산성 및 관리실태를 검토하였다. 그 결과 개체별 구과의 길이 43.52~43.64mm, 폭 23.09~23.70mm, 무게(FW) 11.68~12.01g으로 개체별·단지별 구과크기에는 유의차가 없었다. 종자생산량의 경우 2013년 384.60kg, 2014년 267.70kg로 단지별·년도별 종자생산량에 차이를 보였다. 2013년 구과의 종자생산 잠재성(Seed potential)은 평균 156.12개(최고 165.06개, 최저 136.26개), 총 종자생산 평균 36.77개(최고 42.63개, 최저 30.41개), 충실종자 평균 30.18개(최고 36.34개, 최저 25.15개) 이었고, 종자충실율은 82.1%로 나타났다. 2014년 종자생산 잠재성은 평균 175.09개(최고 178.52개, 최저 170.72개), 총 종자생산 평균 42.37개(최고, 51.49개, 최저 34.98개)로 전년도에 비해서 증가하였고, 충실종자 평균 33.64개(최고 42.96개, 최저 26.45개)로 유사하였으나, 종자충실율은 79.4%로 전년도에 비해서 조금 낮았다. 년도별 1차 및 2차 고사배주를 조사한 결과 2013년도에는 각각 1.03과 4.07로 나타났고, 2014년도는 각각 3.08과 0.50로 나타나 수분(pollination), 충해 및 영양결핍 등에 의한 영향으로 사료된다. 이와같이 구과분석을 통한 채종원 종자생산 진단기술은 주기적인 종자 예찰조사(개화시기 특성조사, 유구과 특성조사)와 기상자료 분석을 수행하여 종자생산에 관련된 수분(pollination) 생리, 병해충 방제 및 영양상태 점검 등을 검토할 수 있는 정보를 제공할 수 있을 것으로 사료된다.

\*주저자: Tel. 043-850-3346, E-mail: hyunjinkfsv@gmail.com

## 홍화 집단교배 및 유전자지도 작성을 위한 수집자원의 선발

이정훈\*, 안찬훈, 이윤지, 허목, 안태진, 김영국, 차선우

충청북도 음성군 소이면 비산로92 농촌진흥청 국립원예특작과학원 인삼특작부 약용작물과

홍화의 집단교배를 통한 품종 육성 및 유전자지도 작성에 대한 연구가 요구되고 있지만, 이를 위해서는 유전 분리 집단 육성이 선행되어야 한다. 홍화의 육종은 주로 자가수분식물의 방법이 적용되어 격리채종 등의 방법으로 이루어져왔다. 현재까지 육종된 청수홍화(1999년), 진선홍화(2000년), 의산홍화(2000년)와 화선홍화(2002년)는 수집종의 선발 방법을 이용하였으며, 집단교배를 통한 육종은 이루어지지 않았다. 타가교배 방법을 통하여 새로운 품종의 육종은 교배대상 모본과 부분의 자원 선발이 선행되어야 한다. 본 연구는 홍화 집단교배 및 유전자지도 작성을 위하여 수집자원으로부터 교배대상 모본과 부분 자원을 선발하고자 수행되었다. 대상 자원은 국내·외 지역 재래종과 품종 등 34자원을 수집하여 시험포장에 증식한 식물체를 대상으로 수행하였다. 증식된 자원은 각각 종자를 격리 채종하여 파종 후 개화시기, 두화수 및 형태적 특성평가를 실시하여 선발하였다. 식재된 자원의 개화시기는 6월 11일에서 7월 1일로 최대 20일 가량의 차이를 보였으며, 개화율은 90% ~ 100%로 나타났다. 두화수는 개체 당 8.3개 ~ 37.7개로 최대 4.5배 가량 차이를 보였다. 모본은 개화시기가 가장 빠르며 개화시작 후 20일 이내에 90%이상 개화가 이루어진 육성품종 의산홍화를 선발하였다. 부분은 한 개체 당 두화수가 37.7개로 꽃수가 가장 많으며 초장이 가장 작아 단간의 형태로서 도복에 아주 강한 미얀마 수집자원 MMR-STs-2011-11039를 선발하였다. 선발된 모본과 부분의 잎은 모두 난상피침형이나, 모본에 비해 부분의 잎은 폭이 좁으며 매우 강한 가시가 잎과 줄기에 나타나 형태적으로 현저한 차이가 나타났다. 선발된 자원은 형태적 다양성이 높고 유사도가 낮아 집단교배 및 F1 세대 육종을 통한 유전자 지도 작성 연구에 적합한 자원으로 판단된다.

\*주저자: Tel. 043-871-5578, E-mail: artemisia@korea.kr

## A Genetic Linkage Map based on AFLP markers in China type Tea Plant

Yali Chang<sup>1</sup>, Eun-Ui Oh<sup>1</sup>, Min-Seuk Lee<sup>2</sup>, Kwan-Jeong Song<sup>1\*</sup>

<sup>1</sup>Faculty of Bioscience & Industry, SARI, Jeju National University, Jeju 690-756, Korea

<sup>2</sup>Sulloc Cha R & D Center, Jangwon Co.,Ltd, Jeju 697-922, Korea

Based on double pseudo-testcross theory, a population of 76 F1 clones, which were derived from a cross of China type tea plants (*Camellia sinensis* var. *sinensis*) with a Korean tea cultivar, 'Kemsull' for female parent and a Japanese tea cultivar, 'Houshun' for male parent, was used to construct a genetic linkage map with AFLP markers. Totally, 2,360 markers were detected by 26 pairs of primers and 90.8 markers for each pair on average. Among these, 481 markers (20.3%) were polymorphic, 392 markers (81.5%) of which showed Mendelian segregation ratio ( $p=0.01$ ). Of these Mendelian segregated markers, 139 (35.5%) were segregated in 3:1 ratio and 253 (65.5%) were segregated in 1:1 ratio. The construction of AFLP molecular marker based linkage map were carried out by Joinmap 4.0 version. The linkage map of 'Kemsull' contained 227 markers which distributed into 18 linkage groups. The linkage map of 'Kemsull' covered 1,382.2 cM with the average distance between two markers of 6.0 cM. The linkage map of 'Houshun' contained 154 markers which were distributed into 17 linkage groups and were spanned with the total map length of 1,540.9 cM and the average distance between two markers of 10 cM. However, these AFLP markers were not distributed evenly and further even saturation is additionally required.

\*Corresponding Author: Tel. 064-754-3328, E-mail: kwansong@jejunu.ac.kr

## **Radiation impacts on morphological and qualitative properties in common buckwheat (*Fagopyrum esculentum*) and tartary buckwheat (*Fagopyrum tataricum*) seeds**

Je-Hyeok Yu<sup>1</sup>, Min-Heon Yun<sup>1</sup>, Seon-Mo Yang<sup>1</sup>, Dong-Seop Kim<sup>2</sup>, Young-Ho Yun<sup>3</sup>, Kyung-Ho Ma<sup>4</sup>, Eun-Ho Son<sup>4</sup>, Sok-Young Lee<sup>4</sup>, Hong-Sig Kim<sup>1</sup>, Sun-Hee Woo<sup>1\*</sup>

<sup>1</sup>Dept. of Crop Science, Chungbuk National University, Cheong–ju 361–763, Korea

<sup>2</sup>KAERI Advance Technology Radiation Laboratory, 580–185, Jeong–eup, Korea

<sup>3</sup>Dept. of Functional Crop, National Institute of Crop Science, RDA, Gyeongnam 627–803, Korea

<sup>4</sup>National Agrobiodiversity Center, NAAS, RDA, Wanju–gun 565–851, Korea

Breeding and cultivation techniques are being treated very severely regarding ecological and physiological development in buckwheat. This study was conducted to focus on the diversity occurring in the cultivated and tartary buckwheat and provide an overview of the characteristics and genetic resources activities. Morphological results showed that the height of common buckwheat ranges from 82-90cm, common buckwheat induced by 200Gy ranges from 52-75cm, common buckwheat induced by 300Gy ranges from 43-56cm, common buckwheat induced by 400Gy ranges from 33-60cm whereas the tartary buckwheat height ranges from 65-87cm, and while it exposed to various radiation (200Gy, 300Gy and 400Gy), the obtained height ranges from 73-92cm, 55-80cm and 60-75cm respectively. However, the stems from the both cultivar are hollow and that's why, the plant is very prone to lodging. The leaf color of common buckwheat was green, 200Gray, 300Gy 400Gy common buckwheat light green and green, whereas the tartary buckwheat green and bottle-green, 200Gray 300Gy 400Gy tartary buckwheat bottle-green, common buckwheat (control, 200Gy, 300Gy, 400Gy) stem color is light green and pink, flower color is white, tartary buckwheat (control, 200Gy, 300Gy, 400Gy) flower color is light green. The stem color from tartary buckwheat showed (200Gy, 300Gy, 400Gy) light green and light red color. The results revealed that the two buckwheat cultivars showed diversified characteristics.

Acknowledgements: This work was supported by a grant (code ;PJ010369012014) from the National Agrobiodiversity Center through Rural Development Administration (RDA), Republic of Korea

\*Corresponding Author: Tel. 043-261-2515, E-mail: shwoo@chungbuk.ac.kr

## Heterogeneity of CMA Banding Patterns in Jeju Citrus Landraces

Kyunguk Yi<sup>1</sup>, Chi-Won Chae<sup>2</sup>, Young-Chul Park<sup>3</sup>, Ho-Bang Kim<sup>4</sup>, Kwan-Jeong Song<sup>1\*</sup>

<sup>1</sup>Faculty of Bioscience and Industry, Jeju National University, Jeju 690–756, Republic of Korea

<sup>2</sup>Jeju Provincial Office, Korea Seed & Variety Service, Seoqwipo 669–940, Republic of Korea

<sup>3</sup>Citrus Breeding Center, Jeju Special Self–Covering Province Agricultural Research and Extension Service, Seoqwipo 697–828, Republic of Korea

<sup>4</sup>Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 420–852, Republic of Korea

CMA banding patterns of chromosomes of eleven Jeju citrus landraces were characterized and compared by means of sequential staining using fluorochromes of chromomycin A3 (CMA) and 4',6-diamidino-2-phenylindole (DAPI). The somatic metaphase chromosomes examined in this study were all diploids ( $2n = 18$ ). Chromosomes were classified into five types based on the number and distribution of CMA positive bands; A: two telomeric and one proximal bands, B: one telomeric and one proximal bands, C: two telomeric bands, D: one telomeric band, E: no band. Four to five types of chromosomes and unique chromosome compositions were observed from each accession. The CMA banding patterns of Jeju citrus landraces were 1A+1B+1C+9D+6E in jinkyul, 1A+1B+1C+8D+7E in cheongkyul, 1B+1C+10D+6E in hongkyul, 2A+1B+3C+6D+6E in sadoogam, 1A+2B+1C+8D+6E in dangyooza, 1A+1B+3C+7D+6E in dong-geongkyul, 2B+2C+7D+7E in pyunkyul, 2A+2B+2C+6D+6E in gamza, 1A+2B+1C+7D+7E in byungkyul, 1A+1B+1C+9D+6E in jigak, 1A+1C+10D+6E in binkyul. Type D and E chromosomes were predominant in all Jeju citrus landraces. The chromosome composition with an even number distribution in gamza was observed, hence it could be recognized as a non-hybrid species. The results indicated all Jeju citrus landraces except gamza seemed to be hybrids, but might be diverged from species originated or cultivated in Jeju, Korea and other countries.

\*Corresponding Author: Tel. 064-754-3328, E-mail: kwansong@jejunu.ac.kr

## Antioxidant activity and total phenolic and flavonoid contents of 10 *Vicia* species

Kyung Jun Lee<sup>\*</sup>, Gi-An Lee, Young-Ah Jeon, Jung-Ro Lee, Sok-Young Lee, Kyung-Ho Ma, Jong-Wook Chung

National Agrobiodiversity Center, NAAS, RDA, Jeonju 560–500, Republic of Korea

Flavonoids and total polyphenols are important secondary plant metabolites, as they play a role in reducing the oxidative stress caused by ROS. In this study, we investigated for flavonoid contents, total polyphenol contents, and antioxidant activities in 27 accessions from 10 *Vicia* species. Among 27 *Vicia* accessions, NAC17 (*V. monantha*) and NAC14 (*V. hircanica*) had the highest total flavonoid ( $1.42 \pm 0.09$  mg/g) and total polyphenol ( $124.2 \pm 0.5$  µg/GAE mg) contents, respectively. In four flavonoids, naringenin showed the highest concentrations in *Vicia* species. The DPPH and ABTS were the range from 0.2 (NAC24, *V. sativa* subsp. *nigra*) to 18.5 (NAC13, *V. faba*) µg/ASC mg and 19.1 (NAC7, *V. cracca*) to 253.4 (NAC13, *V. faba*) µg/Trolox mg, respectively. Among the 10 *Vicia* species, *V. monantha* and *V. hircanica* had the highest flavonoid ( $1.31 \pm 0.09$  mg/g) and total polyphenol ( $116.5 \pm 2.0$  µg/GAE mg) contents, respectively. The highest antioxidant activity was detected in *V. faba*. These results will expand the flavonoid database and provide information on *Vicia* species valuable for development of functional foods or feed-additives resources.

\*Corresponding Author: Tel. +82 63 239-4871, E-mail: jwchung73@korea.kr

## **Genetic diversity base on agrinomial traits and SSR markers in Korean rice landraces**

Kyung Jun Lee\*, Jong-Ro Lee, Gi-An Lee, Sebastin Raveendar, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung

National Agrobiodiversity Center, NAAS, RDA, Jeonju 560–500, Republic of Korea

In order to assess the genetic diversity, phylogenetic relationships and population structure of Korean rice landraces, 76 accessions were estimated using agronomical traits and SSR markers. Among 11 agronomical traits, amylose content (AC) was the trait with the largest variance with values ranged from 4.9 to 28.39 %, while grain length (GL) was the lowest variance ranged from 4.4 to 5.9 cm. In the result of PCA, the first PC with Eigen value of 217.5 explained 60.3% of the total variance. Culm length (CL) was the variable with the largest positive loadings. Growth period (GP) was the positive variances, while AC was the negative variance. The second PC with Eigen value of 80.6 explained an additional 22.4% of the total variance. Growth period (GP) was variable with highest positive loading. Amylose content (AC) was variable with high positive, while CL was the negative variance. The 49 SSR markers produced a total of 473 alleles with an average of 9.6 alleles. The polymorphism information content (PIC) was in the range 0.11 to 0.93. The observed heterozygosity ranged from 0.12 to 0.39, with an average of 0.61. 76 rice accessions showed two subpopulations and three groups based on SSR markers. Group I and Gropu II appertained Pop-2 and Pop-1 subpopulation, respectively. They showed similar agronomical traits. Group III consisted 7 rice accessions predominantly appertained to Pop-1. These results provide insight into the characters of Korean rice landraces and help to improve our knowledge of rice breeding

\*Corresponding Author: Tel. +82 63 239-4871, E-mail: jwchung73@korea.kr

## **Variation of pre-harvest sprouting and ABA content in rice germplasm**

Gi-An Lee\*, Young-Ah Jeon, Ho-Sun Lee, Jong-Wook Chung, Do-Yoon Hyun, Jung-Ro Lee, Myung-Chul Lee, Kyung-Ho Ma, Sok-Young Lee

National Agrobiodiveristy Center, NAAS, RDA, Jeonju–si, Jeollabuk–do, Republic of Korea

Among the diverse crops, rice (*Oryza sativa* L.) has been domesticated as a staple carbohydrate sources mainly in Asia region, and RDA Genebank at the National Agrobiodiversity Center (NAAS) has conserved about 37 thousand rice accessions accordingly. Seed dormancy, one of domesticated traits, prevents pre-harvest sprouting (PHS) which causes degradation of grain quality in cereal crop. In previous study, we surveyed the variation of seed germinability of diverse 200 rice germplasm and detected the three distinguished groups besides admixed types; the first group (G-1) revealed high germinability at harvesting time, and the second group (G-2) and third group (G-3) acquired high germnability subsequent to after-ripening and dormancy breaking process, respectively. To reduce environmental effects on detected variation of germinability, we selected representative 14 accessions which have similar heading date of each group and measured the degree of PHS using freshly harvested panicles. Variation of PHS showed similar tendency of germinability group; generally, high PHS for G-1, low PHS for G-2 and no PHS for G-3. To resolve genetic and physiological factors concerning on PHS and seed dormancy, we checked the change and variation of ABA known for critical regulator for seed dormancy, and high PHS accessions interestingly revealed high ABA content in 10 DAF. Based on these study, we plan to analyze genetic factors affecting the degree of seed germinability and PHS.

\*Corresponding Author: Tel. 063-238-4883, E-mail: gkntl1@korea.kr

## ***Brachypodium distachyon* mutants induced by gamma radiation contain reduced lignin content**

Man Bo Lee, Yong Weon Seo\*

Dept. of Biotechnology, Korea University, Seoul 136–713, Republic of Korea

It is necessary to alleviate environmental and economic disadvantages of fossil fuels for global warming. Among the conceivable options, the use of plant biomass for the production of bioethanol is considered as a potential alternative for fossil fuels. Plant biomass that contains lignocellulose for bioethanol production has recently emerged as biofuel feedstock because of its sustainable and environment-friendly properties. However, lignin inhibits the hydrolysis process and the lignin recalcitrance in ethanol conversion remains in a problem. The attempt for down-regulating enzymes involved in lignin biosynthesis is one of attractive strategy to reduce the lignin contents. Recently, *Brachypodium distachyon* has been proposed as an alternative monocotyledon model species. The close phylogenetic relationship of *Brachypodium* with other grasses suggests that the *Brachypodium* may be useful for structural and functional genomic studies in these species. *Brachypodium*, standard line Bd21, was subjected to irradiation at doses of 50, 100, 150, 200, and 250 Gy. Phenotypes were investigated using M<sub>0.2</sub> population. Through histochemical analysis using phloroglucinol, 25 M<sub>2</sub> putative lignin deficient mutants were selected. Depend on the phenotypic and histochemical data, mutants were selected and used for measuring lignin content. Total lignin content was measured using the acetyl bromide (AcBr). Mutant #142-3-1 contains 16.9 (mg/g dry cell wall) of total lignin and the lignin level was significantly reduced (87.9%) compared to wild-type (19.23 mg/g dry cell wall). Additionally, Mutant line #2259-1-2 reduced lignin level at 94.4% (18.15 mg/g dry cell wall) in comparison to wild-type. The enzymatic hydrolyses in lignin deficient lines have been performing with the time courses. Lignin composition, cell wall carbohydrates, and genetic analysis in mutant lines will be discussed.

This work was supported by the National Research Foundation of Korea(NRF) grant funded by the Korea government(MSIP) (No. 2012M2A2A6035566).

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

## Development and characterization of endophyte free tall fescue variety Greenmaster3ho

Sang-Hoon Lee\*, Ki-Won Lee, Ki-Yong Kim, Hee Jung Ji, Tae Young Hwang, Hyung Soo Park, Hyun Seok Chae

Grassland and Forages Division, National Institute of Animal Science, Rural Development Administration, Cheonan, 330-801, Republic of Korea

In order to improve high persistence and forage quality, through selection of various superior parental varieties for breeding and synthesis of them with new lines, there are ongoing worldwide studies aiming to enhance the quality of tall fescue through a traditional breeding method by selection and hybridization. A new tall fescue variety (*Festuca arundinacea* Schreb.), named Greenmaster3ho, was developed by the National Institute of Animal Science, Rural Development Administration in Korea from 2010 to 2014. For synthetic seed production of this new variety, five superior clones, 09XFa02, 09XFa03, 09XFa11, 09XFa13, and 09XFa14 were selected and polycrossed. The agronomic growth characteristics and forage production capability of the seeds were studied at Cheonan from 2010, and regional trials were conducted in Cheonan, Hoengseong, Jeju, and Jinju from 2012 to 2014. Greenmaster3ho showed enhanced disease resistance, persistence, and regrowth ability as compared to Fawn. The dry matter yield of Greenmaster 2 was 29% higher (15,119 kg/ha) than that of Fawn. However, the nutritive value of both varieties was similar. This study developed a new tall fescue variety with excellent environmental adaptability, aiming to make a contribution to the vitalization of the Korean grassland industry.

This work was carried out with the support of Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ008599022015)

\*Corresponding Author: Tel. 041-580-6754, E-mail: sanghoon@korea.kr

## 딸기 동양계와 미국 품종간 여교잡 횟수에 따른 분리집단의 변화

이선이<sup>1</sup>, 김승유<sup>1</sup>, 김대영<sup>1</sup>, 노일래<sup>2\*</sup>

<sup>1</sup>국립원예특작과학원

<sup>2</sup>경상대학교 농학과(농업생명과학연구원)

현재 국내 품종들은 일본품종을 소재로 육성되었기 때문에 형태적으로 일본품종과 매우 유사할 뿐만 아니라 새롭게 육성된 품종도 변이의 형태가 매우 적어 품종간의 차이가 크게 나타나지 않는다. 따라서 딸기에서 여교잡 육종기술을 이용하여 동양계와 미국 품종의 우수한 유전 형질을 도입하여 gene-pool을 확대하고자 연구를 수행하였다.

동양계와 미국 품종간 여교잡을 위해 수량성이 높고 과실크기가 크지만 당도가 낮은 미국 품종 ‘Gaviota’를 이용하였고, 동양계 품종으로는 당도는 높지만 수량과 과중이 미국품종에 비해 떨어지는 ‘매향’을 이용하여 교배조합을 작성하였다. 이들 교잡 후대(F<sub>1</sub>) 중에서 다수성이면서 대과성이고, 고당도에 가까운 실생개체를 선발하고 선발된 실생개체는 동양계 품종을 반복친으로 이용하여 여교잡(BC<sub>1</sub>F<sub>1</sub>, BC<sub>2</sub>F<sub>1</sub>...BC<sub>3</sub>F<sub>1</sub>)을 반복 실시하여 발아율 및 후대 실생개체들에 대한 과실특성을 조사하였다.

교잡후대(F<sub>1</sub>)와 여교잡을 수행한 BC<sub>1</sub>F<sub>1</sub>세대에서의 발아율은 큰 차이를 나타내지 않았으나 여교잡 횟수가 증가할수록 발아율은 점차 낮아졌으며 특히 BC<sub>3</sub>F<sub>1</sub> 이후 세대에서는 현저히 감소하였다. 교잡후대 개체의 과실 무게, 수량, 경도, 당도 등은 대체로 원 품종들의 중간형질을 나타내었으나, 당도 향상을 위해 ‘매향’을 반복친으로 이용하여 여교잡을 실시하였을 경우, 과실 경도는 큰 차이가 없었으나 과중과 수량은 감소하고 당도는 다소 향상되는 효과를 나타내었다. 그리고 BC<sub>3</sub>F<sub>1</sub> 이후 세대부터는 변이가 아주 적어 반복친에 의한 당도 고정효과가 나타나는 것으로 보여진다.

## **Evaluation of genetic diversity of Asian landrace wheat based on HMW glutenin subunit and maturity**

Sukyeung Lee, Yu-mi Choi, Do yoon Hyun, Myung-chul Lee, Sejong Oh, On sook Hur, Hocheol Ko, Na-Young Ro

National Agrobiodiversity Center, NAAS, RDA, 560–500, Korea.

Glutenin is the major factor responsible for the unique viscoelastic dough characteristics of wheat flour, which determine mixing and bread baking performance (X. Shan et al, 2007). And early maturity is one of the most important cultural characteristic in Korea because of its winter cropping system. This study is to reveal the genetic properties of Asian wheat landrace collection originated from 6 separate regions such as Korea, China, Japan, Afghanistan, Iran, Pakistan, Caucasus, and Middle East. Using germplasms maintained in National Agrobiodiversity Center, RDA, Korea, the variations in morphological character and HMW glutenin subunit composition were investigated.

In this study, Glu-A1c(null), Glu-B1b(7+8) and Glu-D1a(2+12) alleles are the most frequent in Asian landrace wheats. When it comes to unique composition, Glu-B1aj(8) and Glu-D1q(2+11) subunits are only in Afghanistan wheat. And Glu-B1k(22), Glu-D1l(12), Glu-D1m(10) subunits are only in accessions from Pakistan, Korea, and China, respectively.

The accessions from Iran and Caucasus have the highest PIC value(0.57), which shows wheat origin region has high genetic diversity. Grouping by UPGMA analysis of combination of Glu-1 allele, most accessions from Afghanistan, Korea, and Japan were in the same group despite of geological distance. Contrastively, many germplasms originated from China, Caucasus, and Middle East were in the other same group.

The evaluation of bread baking quality by Glu-1 scoring system, 34 accessions are perfect 10. 16 samples from China and 1 Afghanistan among them were also matured before early June, suitable to Korean cropping system. Especially, 3 accessions(K151847, K151865, K151962) had extremely early maturity, ripened before late May. These genetic resources having good gluten quality and early maturity are expected to be used for Korea wheat breeding system.

Keywords: Wheat, Asia, landrace, genetic variation, HMW-glutenin, Glu-1 score, early maturity

## **Analysis of genetic diversity and cytoplasm male-sterility types in radish germplasm**

O New Lee, Hyo Joung Kwon, Mi Kyung Han, Han Yong Park\*

Department of Bioresource Engineering, Sejong University, Seoul 143–747, Republic of Korea

Radish (*Raphanus sativus* L.) is a widely-consumed root vegetable that is grown worldwide. To utilize the radish genetic resources for breeding research, we collected radish germplasms and evaluated their morphological and genetical characteristics. Here, phylogenetic relationship of 288 accessions were analyzed using 16 SSR markers and classified cytoplasm male sterility (CMS) types using cpDNA-based molecular markers. To create a collection of 288 accessions, 188 and 73 accessions were selected from RDA-Genebank (Korea) and NIAS-Genebank (Japan), respectively, after generation advancement for the accessions with low uniformity. In addition, 27 elite lines currently used for commercial radish breeding programs were included. In the result of phylogenetic analysis, 288 accessions were clustered into 5 major groups corresponding to the morphological traits and origins at the similarity coefficient value of 0.51. Analysis of CMS types revealed that majority of accessions were determined as DBRMF1 and DBRMF2 mitotypes, 15 accessions to Ogura and 4 accessions to DCGMS mitotypes. Further genetic analysis for radish germplasm will be valuable in assisting radish fl hybrid breeding.

\*Corresponding Author: Tel. 02-3408-4376, E-mail: hypark@sejong.ac.kr

## 녹색자엽 검정콩 유전자원의 농업형질 및 품질관련 성분 평가

이은자<sup>1\*</sup>, 최홍집<sup>1</sup>, 배정숙<sup>1</sup>, 한윤열<sup>1</sup>, 김세중<sup>1</sup>, 이정동<sup>2</sup>

<sup>1</sup>대구광역시 북구 동호동189 경상북도농업기술원 작물육종과

<sup>2</sup>대구광역시 북구 산격동 경북대학교 농업생명과학대학 응용생명과학부

본 연구는 녹색자엽 검정콩 유전자원의 다양한 농업형질 조사와 품질관련 성분을 분석하고, 더불어 우수 유전자원을 선발하여 검정콩 신품종 육성을 위한 기초자료로 활용코자 수행하였다. 시험재료는 국립농업유전자원센터에서 분양받은 유전자원 458점과 경북지역에서 수집한 유전자원 15점에 대해 특성평가를 하였다. 가변특성인 성숙기는 68% 이상이 만생종이었으며, 이 중 24% 정도가 극 만생종이었다. 청자콩 3호(10월 7일)와 비교했을 때, 숙기가 열흘 이상 빨랐던 자원은 29점으로 전체의 6% 정도였다. 경장은 90cm 이상이 44%, 60cm 이하가 15% 정도였다. 백립종은 소립종 9%, 중립종 5%, 대립종 18%, 극대립종은 68%이었다. 이 중 55점은 백립종이 45g 이상인 극대립이었다. 고유특성인 화색의 경우 10점이 흰색이었고, 나머지는 모두 자색이었다. 엽형은 75% 이상 난형을 보였으며, 25%는 4가지의 다양한 형태를 보였다. 안토시아닌의 평균함량은 72.0mg/g이었고, 최소 3.5mg/g에서 최대 167.6mg/g의 함량을 보였다. 청자콩 3호 보다 안토시아닌 함량이 높은 유전자원은 61%였다(청자콩 3호: 65mg/g). 조지방의 평균함량은 18.9%였으며, 최저 14.1%에서 최대 23.5%의 함량을 보였다. 녹색자엽의 진한 정도를 평가하기 위해 색차값( $\Delta E$ )을 분석한 결과 유전자원 중 청자콩3호와 구별되는 진한 녹색자엽을 가진 개체는 407점이었고(NBS units 3 이상), 이중 매우 진한 녹색자엽을 가진 자원은 186점이었었다(NBS units 12 이상). 이상의 품질특성 평가를 통해 백립종이 35g 이상이고, 조지방 함량이 20% 이상이며, 매우 짙은 녹색자엽을 가진 44점의 유전자원을 선발하였다. 추후 이들 녹색자엽 검정콩의 대표 집단 작성을 위해 분자유전학적 기법을 추가하여 실험을 진행할 예정이다.

\*주저자: Tel. 053-320-0283, E-mail: dock0409@korea.kr

## 벼의 수형과 도정특성간의 관계

이정희\*, 원용재, 안억근, 정국현, 이상복, 전용희, 장재기, 하운구, 정응기, 이점호

농촌진흥청 국립식량과학원 증부작물과

기후온난화에 따른 온도상승으로 벼는 등숙기간 중 고온에 의한 벼 품질과 수량이 저하될 것으로 예상되고 있다. 이에 따라 기후온난화에 대처하기 위한 고온 적응형 품종개발이 요구되고 있다. 이러한 고온 적응형 고품질 품종개발을 위해서는 등숙률 향상과 도정수율이 향상된 우량계통을 육성하는 것이 무엇보다 중요하다. 본 실험은 국내 품종 및 계통에 대하여 수형과 관련 있는 항목 및 도정특성들 간의 상관관계를 분석하여 등숙률과 도정수율에 관계하는 특성과 우수계통을 선발하고자 수행되었다. 11품종 및 계통을 보통기 보비 재배하여 1, 2차 지경수, 지경별 등숙률, 수당립수, 수수 등 농업형질과 제현율, 현백률, 도정률, 완전미율 등 도정특성을 조사하였다. 시험결과, 전체적으로 1차 지경에 달린 알맹이의 등숙률이 2차 지경에 달린 알맹이의 등숙률보다 높았으며 품종간 편차도 1차 지경보다 2차 지경에 달린 알맹이의 등숙률 변이가 더 큰 경향이였다. 1차 지경수는 1차 지경 등숙률과 부의상관, 수당립수와 정의상관이 인정되었고 2차 지경수는 수당립수와 정의 상관, 현백률과 부의 상관이 인정되었다. 현백률과 도정률은 1차/2차 지경비율 및 1차/2차 지경립 비율과 정의 상관이 인정되었고 수당립수와 2차 지경수는 현백률과 고도의 부의 상관을 나타내었다. 분상질립율은 등숙률, 2차 지경 등숙률과 부의상관이 인정되었다. 1차지경에 달린 알맹이의 현미 정상립율이 2차 지경에 비해 높았고 1차 지경과 2차 지경에 달린 알맹이의 현미 정상립율 차이가 적은 품종은 추청, 일미, 운미 등으로 도정수율과 등숙률 향상을 위한 재료로서의 이용성이 높을 것으로 사료된다.

\*주저자: Tel. 031-695-4032, E-mail: lejehe@korea.kr

---

**PB-44****Genetic diversity of super-sweet corn inbred lines using SSR and SSAP markers.**

Woo Ri Ko<sup>1</sup>, Hong-Jib Choi<sup>2</sup>, Kyu Jin Sa<sup>1</sup>, Ju Kyong Lee<sup>1\*</sup>

<sup>1</sup>Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200–701, Korea

<sup>2</sup>Gyeongsangbuk-do Agricultural Research and Extension Services, Daegu 702–320, Korea

In this study we evaluate the informative and efficiency of Simple Sequence Repeat (SSR) and Sequence Specific Amplified Polymorphism (SSAP) markers for genetic diversity, genetic relationship and population structure among 87 super sweet corn inbred lines generated by different origins. The SSR showed relatively higher level of the average gene diversity and shannon's information index value than that of the SSAP. To assess genetic relationship and to characterize among 87 super sweet corn inbred lines using the SSR and SSAP markers. The dendrogram using SSR marker divided into nine groups of clusters were observed at the genetic similarity value 53.0%. For SSAP marker, Total three main clusters were confirmed in genetic similarity value at 50.8%. Result of combine data for SSR and SSAP markers showed six subgroup were detected in genetic similarity at 53.5%. To confirm population structure, the total 87 super sweet corn inbred lines were divided into groups I, II and admixed group based on membership probability 0.8 for SSR and SSAP markers. However population structure using combine data was K=3 and divided into group I, II, III and admixed group. This study has demonstrated the comparative analysis of SSR and SSAP for the study of genetic diversity and the genetic relationship for super sweet corn inbred lines. Thus, the results of this study will be useful to maize breeding programs in Korea.

\*Corresponding Author: Tel. 033-250-6415, E-mail: [jukyonglee@kangwon.ac.kr](mailto:jukyonglee@kangwon.ac.kr)

**PB-45****Genetic diversity and relationships among rice accessions (*Oryza Sativa* L.) of cultivated and weedy types using CACTA-TD and AFLP markers**

Rahul Vasudeo Ramekar<sup>1</sup>, Muhammad Qudrat Ullah Farooqi<sup>1</sup>, Kyu Jin Sa<sup>1</sup>, Kyong-Cheul Park<sup>2</sup>, Ju Kyong Lee<sup>1\*</sup>

<sup>1</sup>Department of Applied Plant Sciences, College of Agriculture and Life Sciences, Kangwon National University, Chuncheon, 200–701, Korea

<sup>2</sup>Department of Molecular Biosciences, Kangwon National University, Chuncheon 200–701, Korea

For understanding the genetic diversity and genetic relationship between cultivated and weedy types, we evaluated genetic variation of 80 accessions of rice (*O. Sativa*). This included 42 cultivated accessions and 38 weedy accessions with the help of AFLP and CACTA-TD. A total of 542 loci were analyzed (255 for AFLP and 287 for CACTA-TD) of which AFLP markers exhibited 75% of polymorphism and transposon based CACTA-TD markers exhibited 93% of polymorphism. The average genetic diversity value for all 80 accessions, using AFLP markers was 0.226 (Cultivated – 0.210; Weedy 0.241) and based on CACTA-TD markers was 0.281 (Cultivated – 0.294; Weedy 0.269). A UPGMA phylogenetic tree revealed three major groups for both the marker system. The average polymorphic content value obtained with AFLP and CACTA-TD markers were 0.21 and 0.232, Effective multiplex ratio (AFLP – 47.50; CACTA-TD – 66.75), Marker Index (AFLP – 9.94; CACTA-TD – 21.13) and Resolving power (AFLP – 19.53; CACTA-TD – 34.62) indicated that the CACTA-TD markers were relatively efficient than AFLP markers.

\*Corresponding Author: Tel. 033-250-6415, E-mail: [jukyonglee@kangwon.ac.kr](mailto:jukyonglee@kangwon.ac.kr)

## Genetic diversity, population structure, and association mapping of biomass traits in maize with simple sequence repeat markers

Jong Yeol Park<sup>1,2</sup>, Rahul Vasudeo Ramekar<sup>1</sup>, Kyu Jin Sa<sup>1</sup>, Ju Kyong Lee<sup>1\*</sup>

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

<sup>2</sup>Maize Experiment Station, Gangweon Agricultural Research and Extension Services, Hongcheon 250-823, Korea

Assessing genetic diversity, population structure, and linkage disequilibrium is important in identifying potential parental lines for breeding programs. In this study, we assessed the genetic and phenotypic variation of 174 normal maize (*Zea mays*) inbred lines and made association analyses with respect to nine agronomical traits, using 150 simple sequence repeats (SSR). From population structure analysis, the lines were divided into three groups. Association analysis was done with a mixed linear model and a general linear model. Twenty one marker-trait associations involving 19 SSR markers were observed using the mixed model, with a significance level of  $P < 0.01$ . All of these associations, as well as 120 additional marker-trait associations involving 77 SSR markers, were observed with the general model. Two significant marker-trait associations (SMTAs) were detected at  $P \leq 0.0001$ . In the mixed linear model, one locus was associated with water content, two loci were associated with 100-kernel weight, setted ear length, ear thickness and stem thickness; three loci were associated with ear height, four loci were associated with total kernel weight and five loci were associated with plant height. These results should prove useful to breeders in the selection of parental lines and markers.

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

## 고품질 복합내병성 벼 신품종 “새신”

이지윤<sup>1\*</sup>, 이종희<sup>2</sup>, 조준현<sup>1</sup>, 오성환<sup>1</sup>, 손영보<sup>1</sup>, 황운하<sup>3</sup>, 박수권<sup>3</sup>, 신동진<sup>1</sup>, 송유천<sup>1</sup>, 박동수<sup>1</sup>, 김상열<sup>4</sup>, 박인희<sup>1</sup>, 여운상<sup>1</sup>, 최대식<sup>1</sup>, 남민희<sup>1</sup>, 이영희<sup>1</sup>

<sup>1</sup>경남 밀양시 점필재로 20 국립식량과학원 남부작물부

<sup>2</sup>전라북도 전주시 완산구 농생명로 300, 농촌진흥청 연구정책국

<sup>3</sup>전라북도 완주군 이서면 갈산리 혁신로 181 국립식량과학원

<sup>4</sup>경상북도 영덕군 병곡면 원황길 44 국립식량과학원 영덕출장소

‘새신’은 밥맛이 양호하면서 복합내병성 특히, 흰잎마름병  $K_{3a}$ 에 강한 벼를 육성하고자 2007/2008년 동계에 중만생종이고 쌀알이 맑은 고품질 새누리를 모본으로, 흰잎마름병  $K_{3a}$ 에 강하고 수량성이 높은 품종인 신백을 부분으로 교배하였다. 2008년 하계에 양성한  $F_1$ 개체로 약배양을 실시하여 96개의 재분화 개체를 얻었으며, 이 중에서 줄무늬 잎마름병과  $K_{3a}$ 에 저항성이며, 농업적특성이 우수한 YR27906Acp84를 선발하여 2년간의 생산력검정시험 실시 후 밀양273호의 계통명이 부여하였다. 3년간의 지역적응시험 결과 복합내병성, 내도복성 및 수량성 등의 우수성이 인정되어 농작물 직무육성 신품종 선정위원회에서 ‘새신’으로 명명되었다.

\*주저자: Tel. 055-350-1164, E-mail: minitia@korea.kr

## 카로티노이드를 함유한 노랑찰옥수수 ‘황미찰’ 육성

이진석<sup>1\*</sup>, 손범영<sup>1</sup>, 신성휴<sup>1</sup>, 김정태<sup>1</sup>, 배환희<sup>1</sup>, 서민정<sup>1</sup>, 김상곤<sup>1</sup>, 백성범<sup>1</sup>, 박장환<sup>1</sup>, 이점호<sup>1</sup>, 김성국<sup>1</sup>, 정태욱<sup>2</sup>, 권영업<sup>3</sup>

<sup>1</sup>경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부

<sup>2</sup>전라북도 전주시 완산구 농생명로 300 농촌진흥청

<sup>3</sup>경상남도 밀양시 점필재로 20 국립식량과학원 남부작물부

‘황미찰’은 자식계통 KY30을 종자친(모본)으로 하고 KY9를 화분친(부본)으로 하는 단교잡종 노랑찰옥수수이다. 황미찰은 2010년 생산력검정시험을 거쳐 2012~2014년 3년간 전국 5개 지역에서 지역적응시험을 하였으며 그 우수성이 인정되어 2014년 농촌진흥청 직무육성 신품종으로 선정되었다.

‘황미찰’은 이삭의 색이 황색인 찰옥수수로 이삭의 형태는 중간형이고 일미찰(표준품종)과 달리 옹수 영의 기부에 약하게 안토시아닌 색소를 발현한다. 출사일수는 71일, 간장은 211 cm로 일미찰과 유의한 차이가 없었으며 일미찰보다 착수고는 낮고 분지는 적으며 이삭은 작은 편이다. 황미찰은 일미찰보다 깨씨무늬병과 도복에 강하다. 3년간 지역적응시험에서 황미찰은 일미찰보다 10a당 이삭수는 많았으나 이삭중은 적었다. 품질특성에서는 일미찰보다 과피두께가 45 $\mu$ m로 얇았고 카로티노이드를 32.2 $\mu$ g/g 함유하고 있었으며 관능평가 결과 전체기호도가 6.1로 식미가 우수하였다. 황미찰은 강원도 및 제주도를 제외한 전국에서 재배가 가능하고 1대 교잡종이므로 매년 종자를 갱신하여 사용해야 하며 찰옥수수 열성인자를 보유하고 있어 다른 종류의 옥수수와 200m 이상 격리 재배가 반드시 필요하다. 또한 조명나방에 감수성이어서 적기 방제가 필요하고 밀식 재배시 이삭이 작아지고 이삭 끝달림이 불량해짐으로 가급적 표준 재배(60×25cm)보다 넓게 심기를 권장하며 강풍을 동반한 우기에는 배수 관리에 유의하여야 한다.

\*주저자: Tel. 031-695-4043, E-mail: z9813139@korea.kr

## Mutation induced with gamma-ray irradiation in Rose cultivar (*Rosa Hybrid* Hort.)

Hyo-Jeong Lee<sup>\*</sup>, Sang Hoon Kim, Ye-Sol Kim, Yeong Deuk Jo, Dong Sub Kim, Si-Yong Kang<sup>\*</sup>

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

Rose (*Rosa Hybrid* Hort.) are of a high symbolic value and a great cultural importance in different societies. They are widely used as garden ornamental plants and as cut flowers. For the induction of mutation, gamma-rays are widely used as a mutagen. This study was carried out to establish a system for mutation breeding by irradiation of gamma-ray in rose. The rooted cuttings of five cultivar roses (Lovelydia, Vital, Aqua, Yellowbabe and Haetsal) are grown by in a greenhouse. They were two difference treatment (Before rooting gamma-ray irradiation, After rooting gamma-ray irradiation) were exposed to dose of 70 Gy using a <sup>60</sup>Co gamma-irradiator (150 TBq of capacity ; ACEL, Canada) at the Korea Atomic Energy Research Institute. The irradiated plants were planted in a greenhouse, and investigated survival rate, mutation rate, flower buds number, and shoot length were planted after 80days. The two treatments of and growth characters was significantly reduced to 20% to 40% compared with the control. In addition, survival rate and mutation rate were ‘after rooting  $\gamma$ -ray irradiation (37.4~67.3% and 0.5~5.6%)’ higher than ‘before rooting  $\gamma$ -ray irradiation (18.3~50.8% and 0.3~3.4%)’. Mutation types were solid type, chimeric and mosaic petal mutants with various colors were induced from five rose. These results indicate that efficiency of mutation induction in rose by gamma-ray irradiation on petal colors and petal shapes in two difference treatment with rooted cutting system.

\*Corresponding Author: Tel. 063-570-3310, E-mail: sykang@kaeri.re.kr

## **Study of anthocyanin accumulation in lettuce cultivars by different environments with digital phenotyping and next generation sequencing (NGS) technologies**

Sungyul Chang<sup>1</sup>, Eun-Hee Soh<sup>2</sup>, Chee Hark Harn<sup>3</sup>, Hyoung Seok Kim<sup>1\*</sup>

<sup>1</sup>Biomodulation Team, Natural Products Research Center, Korea Institute of Science and Technology (KIST), 679 Saimdang-ro, Gangneung, Gangwon-do 210-340, Republic of Korea.

<sup>2</sup>Seed Testing & Research Center, Korea Seed & Variety Service, Ministry for Food, Agriculture, Forestry & Fishery, 6-43 Kimcheon Hyuksindosi, Kimcheon City, Gyeongsangbuk-do 740-220, Republic of Korea.

<sup>3</sup>Biotechnology Institute, Nongwoo Bio. Co., Ltd., Yeosu, Gyeonggi-do, 469-885, Republic of Korea.

Anthocyanin is known for positive health beneficial effects that including reduces age related oxidative stress and inflammatory responses. It was produced by vegetable crops and a lettuce is one of the crops. The general pathway of anthocyanin expression is well defined but it is not clear how environments effects on anthocyanin accumulation in a lettuce. Therefore we initiated to study interaction between anthocyanin expression and environment factors. Frist, we applied RGB leaf images in a lettuce to calculate anthocyanin areas in a leaflet with two different cultivars, different developmental stages, and different environments. Later, we attempted to capture RNA expression level with next generation sequence (NGS) RNA sequencing method called RNA-seq. As a result, combined two technologies showed that quantitate phenotypic data help to understand the gene expression of anthocyanin in lettuce cultivars.

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

## **Identification of Hybrids using SSR markers from Polyembryonic Citrus Breeding Lines.**

Sun-Yung Yoon<sup>1</sup>, Hyo-Min Ahn<sup>1</sup>, Hyun-Jeong Oh<sup>1</sup>, Kyung-Hwan Boo<sup>1</sup>, Ho-Bang Kim<sup>2</sup>, Gyoeng-Lyong Jeon<sup>1\*</sup>

<sup>1</sup>Bio-Agr. Co., Ltd., 102-1 Shinkwang-ro, Jeju 690-813, Republic of Korea

<sup>2</sup>Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 420-852, Republic of Korea

Polyembryony in many citrus varieties is an impediment in breeding because it makes hard to identify hybrids after crossbreeding. So, it has become imperative for developing efficient methods to distinguish zygotic seedling generated from polyembryonic seed depending on citrus variety. Simple sequence repeat(SSR) marker is one of useful systems for such purpose. However, SSR markers to separate zygotic seedlings derived from the crossbreeding between 'Marita unshiu' (Citrus unshiu) 'Seongjeon' and 'Shiranuhi mandarin' [(C. unshiu x C. sinensis) x C. reticulata] 'Hallabong' have not been developed yet. In this study we tried to identify an effective SSR marker to screen zygotic seedling after crossbreeding between 'Seongjeon' and 'Hallabong'. For this investigation, 387 seedlings were generated from 114 seeds produced from crossing those two varieties. A total of 116 SSR markers were tested to identify a special marker for distinguishing origin, zygotic or nucellar seedling. As a result, two markers, SSR012 and SSR093, were found to be more effective than other markers. These two SSR markers might be useful to select zygotic individuals in crossbreeding between 'Seongjeon' and 'Hallabong'.

This research was supported by Golden Seed Project (Center for Horticultural Seed Development, 213003-04-3-SBT30 Gyoeng Lyong Jeon, Bio-Agr Co. Ltd), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS)

**\*Corresponding Author:** Tel. 064-721-0399, E-mail: bbjeon0@gmail.com

---

**PB-52**

## **Assessment of Growth Characteristics and Cell Wall Components in Mutant Cultivars of Kenaf (*Hibiscus cannabinus*)**

Sang Wook Jeong<sup>1</sup>, Jaihyunk Ryu<sup>1</sup>, Seung Bin Im<sup>1</sup>, Soon-Jae Kwon<sup>1</sup>, Joon-Woo Ahn<sup>1</sup>, Jin-Baek Kim<sup>1</sup>, Sang Hoon Kim<sup>1</sup>, Hee-Bong Lee<sup>2</sup>, Si-Yong Kang<sup>1\*</sup>

<sup>1</sup>Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580–185, Korea

<sup>2</sup>Chungnam National University Dept. of Applied Botany

This study was carried out to determine the amount of lignin, cellulose, and hemicellulose in six kenaf cultivars during different harvesting stages. Three mutant cultivars (Jangdae, Jeokbong and Baekma), two original cultivars (Jinju, C14), and one Chinese cultivar (Auxu) were planted on May 14, 2013. Four harvesting times were made at intervals of 20 days from 15 July to 16 September, 2013. The overall growth characters of mutant cultivar ‘Jeokbong’ such as plant height, stem diameter, flowering time, and dry mass were similar with those of the original variety. The mutant cultivar ‘Baekma’ occurred 10-day late flowering in comparison with the original variety and also displayed higher dry mass than the original variety. Jinju, Auxu and Jangdae, mid-late maturing kenaf cultivars, had high dry weight compared to early maturing cultivars such as Jeokbong, Baekma and C14. In all cultivars, the lignin contents were increased by a late harvest. The Mid-late maturing kenaf cultivars showed high lignin content in comparison with those of the early maturity cultivars. There were no significant differences of cellulose, and hemicellulose content between the cultivars, however cellulose content in stems of these kenaf cultivars were significantly decreased by a late harvest. These results may provide valuable information to assist the parental selection of kenaf breeding.

\*Corresponding Author: Tel. 063-570-3310, E-mail: sykang@kaeri.re.kr

**PB-53**

## **Complete chloroplast genome sequence of *Capsicum baccatum* var. *baccatum***

Tae-Sung Kim<sup>1</sup>, Jung-Ro Lee<sup>2</sup>, Sebastin Raveendar<sup>2</sup>, Gi-An Lee<sup>2</sup>, Young-Ah Jeon<sup>2</sup>, Ho-Sun Lee<sup>2</sup>, Eun Seong Park<sup>1</sup>, Kyung-Ho Ma<sup>2</sup>, Sok-Young Lee<sup>2</sup>, Jong-Wook Chung<sup>2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan, 340–702, Korea

<sup>2</sup>National Agrobiodiversity Centre, National Academy of Agricultural Science, Rural Development Administration, Jeonju 560–500, Korea

The chloroplast (cp) is an organelle with its own genome that encodes a number of cp-specific components. Resequencing technology via next-generation sequencing has recently been successfully applied to cp genome characterization. The field of cp characterization is rapidly growing due to its wide versatility and two complete chloroplast (cp) genome sequences of *Capsicum* species have been reported. We herein report the complete chloroplast genome sequence of *Capsicum baccatum* var. *baccatum*, a wild *Capsicum* species. The total length of the chloroplast genome is 157,145 bp with 37.7% overall GC content. One pair of inverted repeats, 25,910 bp in length, was separated by a small single-copy region (17,974 bp) and large single-copy region (87,351 bp). This region contains 86 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Eleven genes contain one or two introns. Pair-wise alignments of cp genome were performed for genome-wide comparison. Analysis revealed a total of 134 simple sequence repeat (SSR) motif and 282 insertions or deletions variants in the *C. baccatum* var. *baccatum* cp genome.

\*Corresponding Author: Tel. +82-63-238-4872, E-mail: jwchung73@korea.kr

## 황색 반겹꽃 대륜화 절화용 거베라 ‘레몬비치’ 육성

정용모<sup>1\*</sup>, 황주천<sup>1</sup>, 진영돈<sup>1</sup>, 이병정<sup>1</sup>, 이상대<sup>2</sup>, 이영병<sup>3</sup>, 권오창<sup>3</sup>

<sup>1</sup>경남 창원시 경남농업기술원 화훼연구소

<sup>2</sup>경남 진주시 경남농업기술원 연구개발국

<sup>3</sup>부산시 사하구 하단동 동아대학교 생명자원과학대학

경상남도농업기술원 화훼연구소에서 2014년 화색이 선명한 황색 절화용 거베라 ‘레몬비치’를 육성하였다. 교배조합 육성을 위하여 2005년부터 국내 재배농가에서 유전자원 수집 후 특성을 검정하였다. 2010년 4월 교배 후 우수개체를 선발하여 2012년부터 2014년까지 3회의 특성검정을 거친 다음, 화색과 화형이 우수한 계통 경남교G-52호를 선발하였다. 이 계통은 절화특성이 우수하고 화색 등 소비자의 기호도가 높아 2014년 10월 농촌진흥청 농작물 직무육성 신품종 선정 심의회의 심의를 거쳐 ‘레몬비치(Lemon Beach)’로 명명하였다. ‘레몬비치’ 품종의 생육 및 개화특성 조사를 위하여 대조품종으로 ‘포커스(CFG0072)’를 사용하였다. ‘레몬비치’ 품종은 핑크색 대륜계의 ‘프렌드(IT 2811414)’와 황색 대륜계의 ‘오존’(IT 281149)과의 교잡에서 육성된 품종으로, 화색이 선명한 황색(RHS, 9-A) 반겹꽃으로, 화폭이 12.8cm 정도인 절화용 대륜화이다. 또한 포기당 연간 평균절화수량은 49.8송이 정도이며, 절화수명은 약 12.8일 정도이다. 개화소요일수는 91.4일로 대비품종 ‘포커스’의 93.7일에 비하여 약 2일 정도 빠르며 이때 개화엽수는 약 9.6매 정도이다. ‘레몬비치’ 품종의 설상화의 길이는 5.7cm 정도로 대조품종 ‘포커스’의 5.5cm에 비하여 길며, 설상화의 폭은 1.3cm 정도로 대조품종 ‘포커스’와 비슷하다. 화경 직경은 상부와 하부는 각각 0.6cm, 0.8cm 정도로 대조품종 ‘포커스’의 상부 0.6cm, 하부 0.7cm와 비슷한 편이다. 재배상의 유의사항은 지온의 관리 및 양·수분의 흡수가 쉽도록 가능한 이랑을 높게 만들고, 여름철 고온기의 생리장해 및 고온에 의한 꽃봉오리의 유실 방지를 위하여 차광재배하여 온도상승을 막아주고 환기에 주의하는 것이 좋다.

\*주저자: Tel. 055-254-1614, E-mail: ymchung@korea.kr

---

**PB-55**

## **The Complete Chloroplast Genome Sequence of Korean Landrace “Subicho” (*Capsicum annuum* var. *annuum*)**

Sebastin Raveendar, Young-Ah Jeon, Jung-Ro Lee, Gi-An Lee, Kyung Jun Lee, Yang-Hee Cho, Kyung-Ho Ma, Sok-Young Lee, Jong-Wook Chung\*

National Agrobiodiversity Centre, National Academy of Agricultural Science, Rural Development Administration, Jeonju 560–500, Republic of Korea

Chloroplast DNA sequences are a versatile tool for species identification and phylogenetic reconstruction of land plants. Different chloroplast loci have been utilized for phylogenetic classification of plant species. However, there is no evidence for a short sequence that can distinguish all plant species from each other. Molecular markers derived from the complete chloroplast genome can provide effective tools for species identification and phylogenetic resolution. Thus, the complete chloroplast genome sequence of Korean landrace “Subicho” pepper (*Capsicum annuum* var. *annuum*) has been determined here. The total length of the chloroplast genome is 156,878 bp, with 37.7% overall GC content. A pair of IRs (inverted repeats) of 25,801 bp was separated by a small single copy (SSC) region of 17,929 bp and a large single copy (LSC) region of 87,347 bp. The chloroplast genome harbors 132 known genes, including 87 protein-coding genes, 8 ribosomal RNA genes, and 37 tRNA genes. A total of seven of these genes are duplicated in the inverted repeat regions, nine genes and six tRNA genes contain one intron, while two genes and a *ycf* have two introns. Analysis revealed 144 simple sequence repeat (SSR) loci and 96 variants, mostly located in the non-coding regions. The types and abundances of repeat units in *Capsicum* species were relatively conserved and these loci will be useful for developing molecular markers.

\*Corresponding Author: Tel. +82-63-238-4872, E-mail: jwchung73@korea.kr

**PB-56**

## **The complete chloroplast genome of *Capsicum annuum* var. *glabriusculum* using Illumina sequencing**

Sebastin Raveendar<sup>1</sup>, Jung-Ro Lee<sup>1</sup>, Donghwan Shim<sup>2</sup>, Kyung Jun Lee<sup>1</sup>, Kyung-Ho Ma<sup>1</sup>, Sok-Young Lee<sup>1</sup>, Jong-Wook Chung<sup>1</sup>\*

<sup>1</sup>National Agrobiodiversity Centre, National Academy of Agricultural Science, Rural Development Administration, Jeonju 560–500, Republic of Korea

<sup>2</sup>The Agriculture Genome Center, National Academy Agriculture Science, RDA, Jeonju, Jeonbuk, Republic of Korea

Chloroplast (cp) genome sequences provide a valuable source for DNA barcoding. Molecular phylogenetic studies have concentrated on DNA sequencing of conserved gene loci. However, this approach is time consuming and more difficult to implement when gene organization differs among species. Here we report the complete re-sequencing of the cp genome of *Capsicum* pepper (*Capsicum annuum* var. *glabriusculum*) using the Illumina platform. The total length of the cp genome is 156,817 bp with a 37.7% overall GC content. A pair of inverted repeats (IRs) of 50,284 bp were separated by a small single copy (SSC; 18,948 bp) and a large single copy (LSC; 87,446 bp). The number of cp genes in *C. annuum* var. *glabriusculum* is the same as that in other *Capsicum* species. Variations in the lengths of LSC, SSC and IR regions were the main contributors to the size variation in the cp genome of this species. A total of 125 simple sequence repeat (SSR) and 48 insertions or deletions variants were found by sequence alignment of *Capsicum* cp genome. These findings provide a foundation for further investigation of cp genome evolution in *Capsicum* and other higher plants.

\*Corresponding Author: Tel. +82-63-238-4872, E-mail: jwchung73@korea.kr

## The Complete Chloroplast Genome of *Capsicum frutescens* L.

Jung-Ro Lee<sup>1</sup>, Donghwan Shim<sup>2</sup>, Gi-An Lee<sup>1</sup>, Sebastin Raveendar<sup>1</sup>, Na-Young Ro<sup>1</sup>, Young-Ah Jeon<sup>1</sup>, Yang-Hee Cho<sup>1</sup>, Kyung-Ho Ma<sup>1</sup>, Sok-Young Lee<sup>1</sup>, Jong-Wook Jeong<sup>1\*</sup>

<sup>1</sup>National Agrobiodiversity Centre, National Academy of Agricultural Science, Rural Development Administration, Jeonju 560–500, Republic of Korea

<sup>2</sup>The Agriculture Genome Center, National Academy Agriculture Science, RDA, Jeonju, Jeonbuk, Korea

The chloroplast (cp) is an organelle with its own genome encoding a number of cp-specific components. The membrane-bound organelles are mainly involved in the photosynthetic conversion of atmospheric CO<sub>2</sub> into carbohydrates in which light energy is stored as chemical energy. Resequencing technology via next-generation sequencing has recently been successfully applied which results the field of cp genome characterization is growing fast. Here, we report the complete sequence of the chloroplast genome of *Capsicum frutescens*, a species of chili pepper. The total length of the genome is 156,817 bp, and the overall GC content is 37.7%. A pair of 51,584-bp inverted repeats (IRs) is separated by a small (17,853 bp) and a large (87,380 bp) single-copy region. The *C. frutescens* chloroplast genome encodes 103 unique genes, including 79 protein-coding genes, 20 tRNA genes, and four rRNA genes. Of these, 19 genes are duplicated in the IRs and 18 genes contain one or two introns. Comparative analysis with reference cp genome revealed 125 simple sequence repeat (SSR) motif and 34 variants, mostly located in the non-coding regions. These microsatellite markers will facilitate the studies of genetic diversity, population genetic structure, and sustainable conservation for *C. frutescens*.

\*Corresponding Author: Tel. +82-63-238-4872, E-mail: jwchung73@korea.kr

## Content of *Trans*-Resveratrol in Soybean Mature Seed

Sang-Woo Choi, Sung-Jin Han, Jong-Il Chung\*

Division of Applied Life Science, Graduate School, Gyeongsang National University, Chinju 660–701, Republic of Korea

Soybean [*Glycine max* (L.) Merr.] seed is one of the major food sources for protein, oil, carbohydrates, isoflavones, and many other nutrients to humans and animals. *Trans*-resveratrol produced by plants is a polyphenol phytoalexin and displays a wide range of biological effects like as anti-cancer activities, cardio-protective properties, anti-inflammatory, anti-oxidation, neuroprotective, antidiabetic and phytoestrogenic properties. Content of *trans*-resveratrol in soybean seed may depend on genotype and environment. Genotype with high *trans*-resveratrol content is valuable in breeding project. One hundred eighty three soybean genotypes were cultivated in the field. After harvesting, *trans*-resveratrol content was analyzed. Content (ug/g) of *trans*-resveratrol was from 0.199 to 5.447. Thirty genotypes with high *trans*-resveratrol content were selected.

\*Corresponding Author: Tel. 055-772-1872, E-mail: jongil@gnu.ac.kr

## 토마토 잎 추출물의 항염증 활성 검정 및 steroid glycoalkaloids 분석

김효정<sup>1</sup>, 이경준<sup>1</sup>, 이기안<sup>1</sup>, 전영아<sup>1</sup>, 이호선<sup>1</sup>, 마경호<sup>1</sup>, 이석영<sup>1</sup>, 이동진<sup>2</sup>, 정중욱<sup>1\*</sup>

<sup>1</sup>전라북도 전주시 중동 국립농업과학원 농업유전자원센터

<sup>2</sup>충청남도 천안시 안서동 단국대학교 생명자원과학대학 식량생명공학과

토마토는 남아메리카 서부 고원지대가 원산지이며 전 세계적으로 재배 및 생산되고 있는 가지과 작물로 토마토에 함유된 steroid glycoalkaloids 화합물은 미생물이나 곤충에 독성을 나타내지만 최근 항염증, 항균 등의 생리활성을 나타내는 것으로 밝혀졌다. 따라서 토마토 42자원 잎 추출물의 항염증 활성을 검정하고 steroid glycoalkaloids 함량을 비교하고자 하였다. 토마토 잎 추출물이 RAW 264.7 세포주에 미치는 독성 효과를 알아본 결과, 추출물 처리 농도 범위 (20~100 ug/ml) 안에서 RAW 264.7 세포주가 50%이상 생존하였고, 추출물의 농도가 증가할수록 세포 생존율이 감소하는 것을 확인할 수 있었다. 이것은 추출물 자체가 세포에 독성으로 작용하지 않아 세포가 생존 가능한 범위 안에서 실험이 가능함을 의미하여 같은 농도 범위의 추출물로 항염증 활성을 검정하였다. 20 ug/ml의 추출물을 처리한 경우 14.1%의 낮은 nitric oxide (NO) 생성 저해율을 보였고 50 ug/ml을 처리 시 79.4%까지 증가하였으며 100 ug/ml 처리 시 98.9%의 높은 저해율을 보였다. 각 자원의 IC<sub>50</sub> 값을 비교한 결과 IT173907 (BRA, 84.0 ± 0.1 ug/ml)이 가장 높은 저해 활성을 보였고 IT211836 (JPN, 130.7 ± 2.5 ug/ml)이 가장 낮았다. 또한 steroid glycoalkaloids를 분석한 결과, tomatine 함량은 IT203466 (AUS, 8.2 ± 0.6 100 ug/mg)이 가장 높았고 IT229711 (KOR, 2.5 ± 0.5 100 ug/mg)가 가장 낮았다. 또한 tomatidine의 경우, IT173906 (BRA, 1.41 ± 0.22 100 ug/mg)이 가장 높았고 IT235444 (THA, 0.28 ± 0.07 100 ug/mg)가 가장 낮았다. 토마토 잎 추출물의 항염증 활성과 steroid glycoalkaloids 함량의 상관관계를 분석한 결과, tomatine과 tomatidine은 높은 정의 상관관계를 보였으나 두 물질과 nitric oxide (NO) 생성 저해 활성은 유의적 상관관계를 보이지 않았다. 본 연구의 결과를 통해 토마토 잎 추출물의 tomatine, tomatidine 함량과 항염증 활성의 상관관계를 확인할 수는 없었지만, 토마토 잎의 천연 항염증제로의 활용 가능성을 확인하였고 토마토 부산물의 다양한 활용 방안 수립에 도움이 될 것으로 사료 된다.

\*Corresponding Author: Tel. +82 63 239-4871, E-mail address: jwchung73@korea.kr

## 토마토 잎 추출물의 항산화 활성 검정 및 flavone aglycones 분석

김효정<sup>1</sup>, 이경준<sup>1</sup>, 이기안<sup>1</sup>, 전영아<sup>1</sup>, 이정로<sup>1</sup>, 박은성<sup>1</sup>, 이호선<sup>1</sup>, 조양희<sup>1</sup>, 마경호<sup>1</sup>, 이석영<sup>1</sup>, 이동진<sup>2</sup>, 정중욱<sup>1\*</sup>

<sup>1</sup>전라북도 전주시 중동 국립농업과학원 농업유전자원센터

<sup>2</sup>충청남도 천안시 안서동 단국대학교 생명자원과학대학 식량생명공학과

토마토는 남아메리카 서부 고원지대가 원산지이며 전 세계에 널리 재배되고 있는 가지과 작물이다. 최근 토마토의 건강 증진 효과에 대한 연구와 소비의 다양성으로 인해 재배 및 생산량이 증가함과 동시에 다량으로 발생하는 부산물 활용 방안 수립에 대한 관심이 증가하였다. 따라서 토마토 42자원 잎 추출물의 항산화 활성과 flavone aglycones를 분석하여 기능성 소재의 활용 가능성을 보고자 하였다. 토마토 잎 추출물의 DPPH 라디칼 소거 활성 검정 결과, IT191046 (CHN,  $130.9 \pm 1.2$  ug/ml)이 가장 높았고 IT207234 (BTN,  $376.7 \pm 14.1$  ug/ml)가 가장 낮았으며 ABTS의 경우 IT189949 (IND,  $1348.6 \pm 36.4$  ug/ml)이 가장 높았고 IT259255 (TWN,  $3789.3 \pm 84.4$  ug/ml)가 가장 낮았다. 총 폴리페놀 함량은 IT207214 (NPL,  $59.9 \pm 0.0$  mg GAE g<sup>-1</sup>)이 가장 높았고 IT203262 (RUS,  $16.8 \pm 0.3$  mg GAE g<sup>-1</sup>)가 가장 낮았다. 토마토 잎 추출물의 총 flavone aglycones 함량을 분석한 결과, IT229711 (KOR,  $78.9 \pm 1.0$  ug/mg)가 가장 높았다. myricetin, quercetin, naringenin, kaempferol, isorhamnetin 함량은 각각 0.08 ~ 0.28 ug/mg, 0.6 ~ 24.1 ug/mg, 1.4 ~ 53.1 ug/mg, 0.19 ~ 4.73 ug/mg, 0.06 ~ 0.42 ug/mg 이었으며 특히 isorhamnetin은 88% (37 자원)가 검출한계치 (0.05 ug/mg) 미만이었다. 토마토 잎 추출물의 항산화 활성과 flavone aglycones 함량의 상관관계를 분석한 결과, DPPH와 ABTS 라디칼 소거 활성은 높은 정의 상관관을 보였으며, 이 두 활성 모두 myricetin과 정의 상관관을 나타냈다. 또한 총 flavone aglycones 함량은 quercetin, naringenin, isorhamnetin과 높은 정의 상관관을 보였다. 이 연구 결과를 토대로 토마토 잎의 기능성 소재로의 이용 가능성을 확인 할 수 있었고 토마토 부산물 활용을 위한 다양한 활용 방안 수립에 도움이 될 것으로 사료 된다.

\*Corresponding Author: Tel. +82 63 239-4871, E-mail: jwchung73@korea.kr

## Seed traits of *y9ti* genotype in soybean

Sang-Woo Choi, Sung-Jin Han, Jong-Il Chung\*

Division of Applied Life Science, Graduate School, Gyeongsang National University, Chinju 660-701, Republic of Korea

Soybean [*Glycine max* (L.) Merr.] protein is a high quality source for food and feed. But, antinutritional factors in the raw mature soybean are exist. Kunitz trypsin inhibitor (KTI) protein of mature soybean seed is a main antinutritional factor in soybean seed. The *Le* gene controls a lectin protein and *Ti* gene controls the KTI protein in soybean. *Ti* locus has been located on molecular linkage group A2 (chromosome 8) of soybean. The *y9* type found in T135 is yellow at emergence, becoming greenish-yellow by maturity. Although this type is considered chlorophyll-deficient, it is fairly vigorous in growth. The objective of this research was to exam an agronomic traits of *y9ti* genotype selected from the breeding line. The seeds of *y9ti* genotype were planted in the field. Traits of maturity date, seed weight, and seed coat color were checked.

\*Corresponding Author: Tel. 055-772-1872, E-mail: jongil@gnu.ac.kr

## 대추나무 품종식별을 위한 Microsatellite DNA표지 개발

조아르나<sup>1</sup>\*, 신유승<sup>1</sup>, 김영미<sup>1</sup>, 김종환<sup>2</sup>, 정지희<sup>1</sup>

<sup>1</sup>국립산림품종관리센터 종묘관리과

<sup>2</sup>주세종농원

본 연구에서는 대추나무 육종 연구 및 품종식별 등에 활용 가능한 microsatellite DNA표지를 개발 하였다. 또한 개발된 표지를 이용하여 국내 대추 3품종 8점(복조, 이조, 슈퍼왕대추)과, 중국에서 수집된 11품종을 분석하여 품종별 고유 DNA profile를 작성하고 품종 간 유연관계를 분석하였다. 대추나무 엽시료에서 DNA를 분리하고, Glenn과 Schable(2005)의 방법에 따라 microsatellite enrichment 라이브러리를 작성하였다. 작성된 라이브러리로부터 microsatellite repeat을 가지는 62개 contig 서열(Genebank Acc. No. KJ156642 - KJ156703)을 확보하고 이로부터 총 22개의 primer를 디자인 하였다. 이 중 품종 간 변이가 있고 재현성이 높은 15개 primer를 최종 선정하여 분석에 사용하였다. 대추나무 14품종 19점 시료를 분석한 결과 유전자좌에 따라 2개에서 7개의 대립유전자가 관찰되어 모든 유전자좌에서 다형성이 확인되었다. 국내 품종인 복조, 이조 및 슈퍼왕대추는 품종 내 개체 간 변이는 전혀 관찰되지 않았고, 품종 간에는 유전적 거리가 0.43-0.63사이 값을 보여 품종 식별에 활용 가치가 높은 것으로 판단되었다. UPGMA dendrogram을 통한 품종 간 유연관계를 분석한 결과 최근 우리나라에서 인기 있는 ‘슈퍼왕대추’는 중국에서 수집된 다른 대립종들과 유전적으로 유사한 경향을 보였다. 우리나라에서 널리 재배되는 ‘복조’ 품종은 중국 심서성에서 수집된 ‘대백령’과 유전적으로 가장 가까웠다. 본 연구에서 개발된 microsatellite 표지는 대추나무 품종 유전·육종 연구 뿐 아니라, 품종 식별을 통한 유통단속에도 널리 활용될 수 있을 것으로 기대된다.

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

## Classification of Korean rice varieties based on growth characteristics

Me-Sun Kim, Hye-Jung Lee, Dal-A Yu, Joonki Kim, Franz Nogoy, Eun-Ju Jeong, Jang-Hwan You, Yong-Gu Cho\*

Department of Crop Science, Chungbuk National University, Cheongju 362-763, Korea

The International Union for the Protection of New Varieties of Plants (UPOV) promotes an effective system of plant variety protection and encourages the development of new varieties of plants. International convention was initiated to standardized the system efforts and strengthen the policy. This study was conducted to establish a database for rice identification using morphological characters which include number of tillers and panicle per plant, spikelets per panicle, yield, plant maturity, height, leaf pigments, flag leaf angles, and rice bran. The whole rice population was grouped into three based on leaf angles, majority members of which retained the flag leaf angle-character until maturity stage. Most rice accessions did not exhibit anthocyanin pigments on the leaves particularly on the first leaf, leaf blade, leaf sheath and auricle, except for varieties classified as black rice. In the case of grain, many accessions produced secondary branching, and showed no awn. For agronomic traits, productive tiller and panicle per plant were higher in early flowering varieties, while spikelets per panicle and ripened grain were higher in late flowering varieties, and yield was higher in medium flowering varieties. All data were then pooled for cluster analysis which revealed three major independent clusters and four minor clusters.

This research was supported by iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

\*Corresponding Author: Tel. 043-261-2514, E-mail: ygcho@cbnu.ac.kr

## High tryptophan rice with an improved eating quality

Franz Marielle Nogoy<sup>1</sup>, Hye-Jung Lee<sup>1</sup>, Marjohn Nino<sup>1</sup>, Me-Sun Kim<sup>1</sup>, Sothea Ouk<sup>1</sup>, Yu-Jin Jung<sup>2</sup>, Kwon-Kyoo Kang<sup>2</sup>, Ill-sup Nou<sup>3</sup>, Yong-Gu Cho<sup>1\*</sup>

<sup>1</sup>Department of Crop Science, Chungbuk National University, Cheongju 361–763, Korea

<sup>2</sup>Department of Horticulture, Hankyong National University, Ansong 456–749, Korea

<sup>3</sup>Department of Horticulture, Suncheon National University, Suncheon 540–950, Korea

Geneticists and rice breeders are continuing to address solutions to high cases of undernutrition and malnutrition in many parts of the world. Fortification with vitamins in rice is a feasible solution to directly reach consumers who suffer nutritional problems. In this study, we are working on tryptophan, a limiting amino acid in almost all protein sources which are of importance for human nutrition. The present high tryptophan rice lines are much higher tryptophan level in mature seeds than wild type, however, the grain quality is very low. We try to improve the eating quality of the current high tryptophan rice lines by crossing them to popular Korean varieties, Hopumbyeo and Samgwangbyeo. Insensitive lines for tryptophan feedback inhibition are screened by growing in medium containing amino acid analogues, 5-methyl tryptophan. *In vitro* screening of each progenies enables us to select in each generation the rice lines with tolerance to 5-methyl tryptophan. After a series of *in vitro* screening and phenotypic selection in the field, the F4 progeny containing the same mutation in ASA2 gene from its parent showed an improvement in its grain quality.

This research was supported by iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

\*Corresponding Author: E-mail: ygcho@cbnu.ac.kr

## Protein expression pattern of soybean sprouts at different germination temperatures

Man-Soo Choi<sup>\*</sup>, Sung-Cheol Koo, Hyun-Tae Kim, Beom-Kyu Kang, In-Seok Oh, Hong-Tai Yun

Upland Crop Breeding Research Division, Department of Southern Area Crop Science, NICS, Miryang, 627–803, Korea

Soybean sprouts have been used as a year round vegetable and become increasingly popular among people as a functional food because of their nutrient values. This study was conducted to investigate the effects of growth temperature for sprouting soybean. Soybean sprouts showed different growth characteristics, nutrient composition and secondary metabolite depending on temperature. Sprout qualities such as whole length, hypocotyl length and yield increased at high temperature condition (25°C) than at low temperature condition (20°C). Total protein also increased at 25°C, while total fatty acid decreased at 20°C. Total phenolic content of pungwongkong sprout was higher at 25°C, while total phenolic content of pungsankong sprout was lower at 25°C. The antioxidant activity increased temperature dependently. Both DPPH activity and ABTS activity were higher at 25°C. To understand proteomic profiles from soybean sprouts germinated at different temperature, proteomic analysis was conducted and protein compositions were compared. 33 spots were differentially expressed and were identified using MALDI-TOF mass spectrometer. They were mainly involved in storage proteins, stress related proteins and metabolism related proteins. The results suggest that growth temperature could affect on protein profile change related to secondary metabolite in sprouts and consequently could alter sprout characteristics.

This work was supported by a grant from Rural Development Administration (No. PJ009291), Republic of Korea.

\*Corresponding Author: Tel. 053-663-1109, E-mail: mschoi73@korea.kr

**Modification of starch composition using RNAi targeting of *SSS1* gene in rice**

Hye-Jung Lee<sup>1</sup>, Moo-Geun Jee<sup>1</sup>, Dal-A Yu<sup>1</sup>, Me-Sun Kim<sup>1</sup>, Joonki Kim<sup>1</sup>, Seon-Kyeong Song<sup>1</sup>, Kwon-Kyoo Kang<sup>2</sup>, Yong-Gu Cho<sup>1\*</sup>

<sup>1</sup>Department of Crop Science, Chungbuk National University, Cheongju 362–763, Korea

<sup>2</sup>Department of Horticulture, Suncheon National University, Suncheon 540–950, Korea

<sup>3</sup>Department of Horticulture, Hankyong National University, Ansong 456–749, Korea

An increasing preference for good eating quality of rice among consumers has become one of the important considerations in rice breeding. Amylose content is a leading factor affecting eating quality of rice. Amylose composition is determined by the relative activity of soluble starch synthase (SSS) and granule-bound starch synthase (GBSS). This study focused on modifying the expression of SSSI gene which is responsible for amylopectin and amylose synthesis in rice by using RNA interference (RNAi) technology. The transgenic rice plants showed various amylose content in rice grains. Favorable rice lines were selected according to genomic PCR, transgene expression and amylose contents analysis. A semi-quantitative RT-PCR was carried out to determine the expression level of SSSI gene after flowering of transgenic rice and wild type. Down-regulation of SSSI gene in transgenic plants was evident in the decreasing expression in rice grains. Accordingly, scanning electron microscopy (SEM) analysis revealed uniform size with smooth curves starch granules in down-regulation rice lines, in contrast with the non-uniform granules in wild type. Results indicated that RNAi-SSSI transgenic lines produced low amylose contents that fell between glutinous and non-glutinous rice. This study showed that down-regulation of endogenous SSSI may improve the eating quality in rice.

This work was supported by a grant from the Next-Generation BioGreen 21 Program, RDA and iPET, Ministry for Food, Agriculture, Forestry and Fisheries, Republic of Korea.

**\*Corresponding Author:** E-mail: ygcho@cbnu.ac.kr

## Growth and Yield characteristics of Orchardgrass ‘Onnuri 2 ho’ Variety

Hee Chung, Ji<sup>1\*</sup>, Ki Yong, Kim<sup>1</sup>, Tae Young Hwang<sup>1</sup>, Hyun Seok Chae<sup>1</sup>, Seong Tae Lee<sup>2</sup>

<sup>1</sup>Grassland & Forages Research Center, National Institute of Animal Science, RDA, Cheonan 331–808, Republic of Korea

<sup>2</sup>Agricultural Research & Extension Services, Gyeongsangnam–Do, 660–985, Republic of Korea.

Orchardgrass (*Dactylis glomerata* L.) is a Gramineae perennial grass species and commonly used as a forage crop and developed to be used for pasture.

In Korea, in order to improve high persistence and forage quality, through selection of various superior parental varieties for breeding and synthesis of them with new lines, there are ongoing worldwide studies aiming to enhance the quality and environmental adaptability of Orchardgrass.

Between 2010 and 2014, a Orchardgrass variety named Onnuri 2ho was developed by the Grassland & Forages Division, National Institute of Animal Science, Rural Development Administration (RDA), Republic of Korea. For the production of synthetic seeds for Onnuri 2ho 4 superior clones, Dg7506, Dg9508, Edg215 and Edg218 were selected and polycrossed. Between 2010 and 2011, the agronomic growth characteristics and forage production capability of the seeds were studied at Cheonan, and between 2012 and 2014, regional trials were conducted in Cheonan, Hoengseong, Jinju, and in Jeju.

The main growth characteristic of Onnuri 2ho is a tetraploid variety, a medium-late maturity variety, the heading stage of which is around May 17, which is four days later than that of Amba. This study tested the regional adaptability of Orchardgrass in Cheonan, Hoengseong, Jeju, and in Jinju. The average dry matter yield of Onnuri 2ho in the four regions was 15,814 kg/ha, which is greater than that of Amba by 34%. These differences show that Onnuri 2ho is more resistant to environmental stresses than Amba and that this growth characteristic directly led to dry matter yield. Thus, Onnuri 2ho is a suitable variety for the establishment of grasslands as it has enhanced disease resistance and persistence, compared to Amba.

The forage quality of Onnuri 2ho was similar to that of Amba in crude protein (11.5%), total digestible nutrients (59.2%), neutral detergent fiber (62.7%), and acid detergent fiber (37.6%), whereas the forage quality of Ongreen was higher than that of Amba in (71.0%).

The new variety was selected and named Onnuri 2ho from Composite 34 by the RDA in November 2014, and the application for the protection of the new variety by the Korea Seed and Variety Service is currently pending. In this study, a new variety of Orchardgrass with excellent environmental adaptability was developed, in order to contribute to the vitalization of the Korean grassland industry.

\*Corresponding Author: Tel. 041-580-6749, E-mail: cornhc@korea.kr

---

**PB-68**

## **Agricultural Characteristics and SSR Profiling of Soybean from Korea, China, Japan and Southeast Asia**

Yu-Mi Choi\*, Sukyeung Lee, Do yoon Hyun, Sejong Oh, Myung-Chul Lee, Hocheol Ko, On-Sook Hur, Na-Young Ro, Yeon-Ju Jeong

National Academy of Agricultural Science, RDA, Jeonju 560–500, Rep. of Korea

This experiment was carried out to compare the morphological traits of Korean, Chinese, Japanese and Southeast Asian(SEA) soybeans from RDA genebank. Days to flowering were ranged from 51 to 125 days with an average of 75 days. Those of China were the shortest with an average of 58 days and those of SEA were the longest with an average of 99 days. Growth days were the shortest with 94 days from China, and longest with 188 days from Korea and SEA. The 100 seed weight of soybeans was ranged from 3.4g to 46.4g, with an average 22.2g. The 100 seed weight was the lightest with an average 11.8g from SEA and the heaviest with an average 24.6g from Korea. In growth habit, over 50% of being collected from Korea, Japan and China were erect type, but 94% from SEA were intermediate type. The highest percentage of seed coat color was yellow(66.1%), followed by yellowing green(10.0%). As a result of cotyledon color in 760 black seed was 76.1% with yellow, 23.9% with green. Green cotyledon was much more in Korea(38.6%) and Japan(33.3%) than other countries. One thousand seven accessions from Korea, Japan, China and SEA were analyzed using 7 SSR markers. One hundred eighty alleles were detected with a lowest 16 at the Satt537 and a highest 35 at the Satt390. The average polymorphism information content(PIC) was 0.68, the highest with 0.7 in Japan. Gene diversity was the highest with 0.73 in China and Japan, while the lowest in SEA with 0.68.

Keywords: soybean, days to flowering, cotyledon color, 100 seed weight, seed coat color, PIC, SSR,

\*Corresponding Author: Tel. +82-63-238-4911, E-mail: cym0421@korea.kr

**PB-69**

## **A Red Single Freesia ‘Cutie Red’ for Pot Plant**

Youn Jung Choi\*, Hyang Young Jeoung, Dae Hoe Goo, Yun Im Kang, Hae Ryong Cho

Floriculture Division, National Institute of Horticultural and Herbal Science, RDA, Suwon, 440–441, Korea

A freesia (*Freesia hybrida* Hort.) ‘Cutie Red’ was developed for the pot flower in the National Institute of Horticultural Herbal Science in 2014. This hybrid was crossed and selected from a seedling of three-way crossing the seedling of ‘Volcano’ and ‘Sailor’ with ‘Figaro’, and ‘Suzy’ in 2006 and 2010, respectively. Morphological characteristics of the selected freesia hybrid were investigated for 3 years from 2011 to 2013, and then it was named ‘Cutie Red’ in 2014. ‘Cutie Red’ has single and red petals (RHS, R45A) with yellow-orange color of center (RHS, YO21B). The average flower width is 5.3 cm and the average yield is 4. The growth of the plant is vigorous and the average height is 70.3 cm, and it is shorter than about 15.4 cm that of control cultivar ‘Red Race’. The average number of floret per stalk and stalk length, 10.7, and the stalk was 9.6 cm length, shorter than ‘Red Lace’, 13 and 11.7 cm length, respectively. The first flowering, in average, of ‘Cutie Red’ takes about 141 days, and it’s average vase life and yield is 9.7 days and 5 cornlets per plant, respectively.

\*Corresponding Author: Tel. 063-238-6823, E-mail: lillium@korea.kr

## 수량많고 껍질 벗김성이 뛰어난 잎자루 채소용 고구마 우수계통 선발

한선경<sup>1\*</sup>, 안승현<sup>2</sup>, 김재명<sup>1</sup>, 송연상<sup>3</sup>, 이형운<sup>1</sup>, 양정욱<sup>1</sup>, 이준철<sup>1</sup>, 남상식<sup>1</sup>, 이정보<sup>1</sup>

<sup>1</sup>전라남도 무안군 무안로 199 국립식량과학원 바이오에너지작물연구소

<sup>2</sup>전라북도 완주군 이서면 혁신로 181 국립식량과학원 기획조정과

<sup>3</sup>페루 국제감자연구소

고구마는 주로 괴근(덩이뿌리)을 식용으로 이용하지만 최근 고구마 지상부에 대한 영양성분 및 기능성이 밝혀지면서 다양한 식품소재로 이용되고 있다. 고구마 줄기에는 탄수화물, 당류, 단백질 등의 에너지원과 칼슘, 철 등의 여러 무기질이 함유되어 있으며, 비타민 함량은 괴근보다 더 많다고 알려져 있다. 현재 농가에서 주로 재배하고 있는 잎자루 채소용 고구마 품종은 국립식량과학원에서 육성한 ‘신미’ 품종으로, 그 이외에 잎자루 채소용 고구마의 품종 육성은 미흡한 실정이다. 따라서 본 시험은 수량이 많고 껍질 벗김성이 뛰어난 우수 계통을 선발하여 품종으로 개발하고자 수행하게 되었다. 고구마는 ‘신미’(잎자루색 녹색)와 ‘하얀미’(자주색+녹색)를 대조품종으로 하여 ‘MI2011-31-09’, ‘MI2010-05-03’는 2014년 3월 중순에 유리온실에 파종(주간 0.5m, 조간 0.5m)하고 파종 후 60일부터 15~20일 간격으로 9차례 수확한 후 생육 및 품질특성을 조사하였다. ‘MI2011-31-09’는 ‘신미’에 비하여 10a당 잎자루 평균수량이 47% 증수되었으며, 잎자루 길이는 평균 6cm 정도 길었다. 또한 잎자루 두께도 평균 1.3mm 더 두꺼우며 껍질 벗김성은 ‘신미’ 5에 비하여 7.3으로 용이하였다. 잎자루를 삶았을 때 경도는 ‘신미’의 0.54kg 보다 낮은 0.45kg으로 삶는 시간이 절약되며 총폴리페놀 함량도 신미 949mg/100g보다 985mg/100g으로 더 높았다. ‘MI2010-05-03’은 ‘신미’에 비하여 10a당 평균수량이 61%, 잎자루 개수는 50% 증수되었고, 잎자루 길이는 평균 2.5cm 더 길었다. 껍질 벗김성은 ‘신미’ 5에 비하여 7.0으로 쉽게 벗길 수 있었고 생잎자루의 경도와 삶았을 때의 경도는 각각 0.86kg, 0.48kg으로 신미 1.05kg, 0.54kg보다 낮아 삶는 시간이 절약되며 총폴리페놀 함량도 ‘신미’ 949mg/100g보다 1,078mg/100g로 더 높음을 알 수 있었다.

\*주저자: Tel. 061-450-0120, E-mail: skhan92@korea.kr

## 절화 알스트로메리아 ‘씨엔알스호프’의 육성과 특성

한수범<sup>1</sup>, 박성화<sup>1</sup>, 김정석<sup>1</sup>, 박형빈<sup>2</sup>, 안주희<sup>3</sup>, 한태호<sup>1,2,3,4\*</sup>

<sup>1</sup>광주광역시 북구 용봉로 77 전남대학교 농업생명과학대학 원예학과

<sup>2</sup>광주광역시 북구 용봉로 77 전남대학교 농업생명과학대학 식물생명공학부 원예생명공학전공

<sup>3</sup>광주광역시 북구 용봉로 77 전남대학교 농업과학기술연구소

<sup>4</sup>광주광역시 북구 용봉로 77 전남대학교 기술지주회사 연구소기업 (주)가든플란트

남아메리카 원산종인 알스트로메리아(*Alstroemeria* spp. L)는 2012년 기준 재배 면적 9ha 시장규모 15억, 2013년 기준 재배면적 10.7ha 시장규모 21억으로 재배 면적과 시장 규모가 매년 증가하고 있는 인기 품종이다. 양재동 화훼공판장에서 거래되는 품종은 에베레스트, 핑크, 켈거리 등 17품종이 있지만 모두 수입 품종으로 로열티를 지불하고 있다. 이를 개선하고자 전남대학교에서는 2009년부터 알스트로메리아 육종을 시작하였고, 수정 후 종자의 퇴화를 극복하기 위해 미숙아 배양을 통하여 2014년도에 국내육성 첫 품종인 씨엔알스호프(no. 5192)를 국립 종자원에 등록하였다. 본 연구에서는 씨엔알스호프의 특징을 소개하고자 한다. 초장, 꽃 크기, 분지수, 화색, 꽃 모양, 줄무늬 수를 측정하여 외양적 특질을 통해 상품 가치를 알아보고, 화분의 크기 및 모양, 염색체 관찰을 통해 임성을 알아보았다. 씨엔알스호프는 분지수가 평균 5개 이상이며 꽃의 크기가 가로 4.5cm 세로 4cm 이상, 초장이 평균 90cm 이상으로 외형에서 수입 품종에 비해 손색이 없으며, 흰색 바탕에 노란색과 보라색이 어우러져 있고 줄무늬가 많으며 둥근 달걀형의 화형으로 씨엔알스호프만의 아름다움이 있어 시장에서 소비를 기대해 볼 수 있다. 염색체 관찰 결과 씨엔알스호프는 4배체로 3배체인 품종에 비해 임성이 있음을 확인할 수 있었고, 화분 관찰 결과 모양과 크기가 균일한 타원형의 화분으로 높은 임성을 기대할 수 있었다. 씨엔알스호프는 외형적 아름다움과 높은 임성으로 농가 소득 향상에 기여할 수 있는 품종이 될 수 있다.

사사: 본 연구는 농림수산식품부 생명산업기술개발사업과 농촌진흥청 농업유전자원관리기관사업과 미래창조과학부 연구개발특구기술사업화 지원에 의해 이루어진 것임.

## 정원용 장미 대목으로 사용되는 짚레 경지삼 발근 효율 증진 연구

김정석<sup>1</sup>, 강성환<sup>2</sup>, 한수범<sup>1</sup>, 박성화<sup>1</sup>, 안주희<sup>3</sup>, 한태호<sup>1,2,3\*</sup>

<sup>1</sup>광주광역시 북구 용봉로 77 전남대학교 농업생명과학대학 원예학과

<sup>2</sup>광주광역시 북구 용봉로 77 전남대학교 농업생명과학대학 식물생명공학부 원예생명공학전공

<sup>3</sup>광주광역시 북구 용봉로 77 전남대학교 농업과학기술연구소

현재 절화용 장미는 국가기관에서 주관하여 품종을 육성하고 있으나, 정원용 장미는 미진한 실정이다. 우리나라에 수입판매 되는 장미 묘는 주당 1,000원~30,000원으로 로열티가 포함되어 있어 단가가 높으며, 대부분이 영국, 독일, 일본 등 외국에서 수입되고 있다. 우리나라에서 정원용 장미의 판매액은 80억 원에 달하고 이중 50억 원에 이르는 양이 수입되고 있으며, 수입량도 계속 늘어가는 추세이다. 또한 대형공원 조성 및 아파트 단지화, 학교, 도로변의 울타리용 등으로 크고 작은 정원들이 생겨나고 있어서 정원용 장미의 수요도 그만큼 증가하고 있다. 국내 정원장미 번식은 대부분 눈접묘를 사용하고 있다. 하지만 짚레 실생을 사용한 눈접묘 생산 시스템이 노동집약적이고 접사들의 고령화로 인하여 눈접묘 생산 시스템의 개선이 요구되었다. 본 실험에서는 눈접묘에 사용되는 짚레를 삼목 번식하여 대목으로 사용하기 위해 삼목 최적화 조건을 구명하고자 하였으며, 삼목 배지와 시기에 따른 경지삼 발근율 효율을 조사하였다.

무가시 품종인 짚레원예1호를 시료로 사용하였고, 삼수는 2년생 가지 중 목질화가 상당히 진행된 가지를 20cm 정도 길이로 절단하여 1시간 정도 물에 침지한 후 저온창고(섭씨 4도)에 1주일 보관하였다. 배지는 질석과 펠라이트 1:1, 질석, 펠라이트를 사용하였고 시기는 2013년 9월부터 2014년 3월까지 수행 하였다. 본 실험 결과 질석과 펠라이트를 동비율로 혼합하여 사용한 배지가 발근율이 가장 좋았고 뿌리무게는 다른 두 종류 배지보다 낮았으며 그 외 줄기무게, 잎수, 신초무게, 신초길이, 줄기 두께, 뿌리 건물중은 대동소이하였다. 시기적으로는 11월에 60% 정도의 가장 높은 발근율을 보였으며 2월에 12% 정도로 가장 낮은 발근율을 보였다. 짚레원예1호 외에도 여러 다양한 대목품종들의 실험이 요구되며 그 외에도 다양한 배지에서의 발근 효율을 알아볼 필요성이 제기되었다.

사사: 본 연구는 농림수산식품부 생명산업기술개발사업과 농촌진흥청 농업유전자원관리기관사업과 미래창조과학부 연구개발특구기술사업화 지원에 의해 이루어진 것임.

## 황기의 유효성분 대량생산을 위한 기내배양 조건정립

허목\*, 엄유리, 안태진, 이정훈, 김영국, 차선우

충북 음성군 소이면 비산로92 국립원예특작과학원 인삼특작부 약용작물과

황기는 콩과에 속하는 다년생 초본으로 단너삼이라고도 불리며 한국을 비롯한 중국, 몽고 등 아시아 지역에서 자생한다. 한국에서는 한약재와 식품을 주 목적으로 재배하며 주 이용부위인 뿌리는 독성이 없어 안정하면서도 다양한 약리효능 때문에 소비가 증대되고 있다. 하지만 황기는 뿌리작물로써 연작장해가 심하고 재배 시 노동력과 비용이 많이 소모되기 때문에 이러한 문제점을 극복하기 위해 기내배양 조건을 구축하고자 하였다. 실험재료는 황기품종인 아성과 풍성을 이용하였다. 각 종자를 기내에서 발아시키기 위해 1% NaOCl에 5분동안 침지하고 다시 70% Et-OH에 3분간 침지하여 표면살균 후 멸균수에서 3회 세척하였다. 종자발아를 유도하기 위해 30g/L sucrose가 함유된 1/2MS 배지를 25℃ 인큐베이터에서 16시간의 광조건 3,000룩스(lux) 광량으로 배양하였다. 부정근을 유도하기 위하여 발아된 유식물의 잎, 줄기, 뿌리 절편을 0.5×0.5 mm 로 절취하여 3~5 mg/L 3-indolybutyric acid(IBA)가 첨가된 1/2MS 고체배지를 사용하였으며 25℃, 암조건의 인큐베이터에서 3주간 배양하였다. 부정근의 증식은 고체배양 할 때에는 1~5 mg/L IBA가 첨가된 MS 배지에 캘러스를 치상하여 25℃, 암조건의 인큐베이터에서 3주간 배양하였고 액체배양은 0.5와 1.0mg/L IBA가 첨가된 MS 배지에 부정근 생체를 0.2g으로 정량하여 25℃, 120rpm, 암조건의 진탕배양기에서 배양하였다. 그 결과 캘러스의 유도는 아성뿌리절편에서 IBA 3 mg/L, 풍성뿌리절편에서 IBA 4 mg/L 일 때 가장 높은 유도율을 보였다. 캘러스의 유도율이 가장 우수한 조건에서 얻어진 부정근을 이용하여 고체배양을 실시하였으며, 아성은 IBA 3 mg/L, 풍성은 IBA 5 mg/L에서 높은 증식률을 나타냈다. 액체배지의 증식은 MS액체배지에 IBA 0.5와 1.0mg/L 농도로 수행하였다. 그 결과 IBA 1.0mg/L의 MS배지에서 대조군에 비해 약 2배의 부정근 생산량을 보였다. 따라서 본 연구에서 얻어진 결과를 바탕으로 황기의 유효성분 대량생산을 위한 기내배양 시스템을 구축할 수 있을 것이라 사료된다.

\*주저자: Tel. 043-871-5562, E-mail: mok0822@korea.kr

## 발아자극물질 Strigolactone 혼합물의 발아자극활성

김현일<sup>1\*</sup>, 샤 시오난<sup>2</sup>, 키스기 타카야<sup>2</sup>, 요네야마 카오리<sup>2</sup>, 요네야마 코이치<sup>2</sup>

<sup>1</sup>전라북도 완주군 이서면 농생명로 100, 국립원예특작과학원 과수과

<sup>2</sup>Center for Weed and Wildlife Management, 350 Mine-machi, Utsunomiya University, Utsunomiya 321-8505, Japan

뿌리기생식물 종자의 발아를 유도하는 대표적인 물질로 알려진 Strigolactone은 토양균의 하나인 *Arbuscular mycorrhizal* 균과의 공생적 작용은 물론, 식물 지상부의 결가지 생성을 억제하는 식물 호르몬으로서도 알려져 있다. 최초의 Strigolactone이 목화에서 확인되어 Strigol로 명명된 이후, 지금까지 약 15종 이상의 Strigolactone이 숙주 식물과 비숙주 식물로부터 확인되었다. 대부분의 Strigolactone은 모핵이 되는 tricyclic-lactone(ABC-ring)에 methyl butenolide(D-ring)이 enol ether 결합된 구조를 이루고 있다. 이러한 구조적 특징이 뿌리기생식물 종자의 발아를 자극하는 활성으로 작용한다. 특히, Strigolactone의 C-D ring구조와 AB ring의 치환기가 뿌리기생식물의 발아자극활성과 밀접한 관계가 있는 것으로 나타났다. 지금까지 뿌리기생식물 종자의 발아자극활성에 관한 많은 연구가 이루어졌으나, 이는 Strigolactone 단독처리를 통한 활성을 측정하는 것이다. 대부분의 식물은 두 종류 이상의 Strigolactone을 분비하는 것으로 알려져 있다. 따라서 Strigolactone 혼합물에 대한 뿌리기생식물 종자의 발아자극활성을 조사할 필요가 있다 하겠다. 그러므로 본 연구에서는 대표적인 뿌리기생식물로 알려진 *Orobancha minor*와 *Phelipanche ramosa* 종자를 이용하여, solanacol, solanacyl acetate, orobanchol, orobanchyl acetate 및 각각의 입체이성질체 혼합물에 대한 발아자극활성을 조사하였다.

두 종류의 뿌리기생식물 종자는 평상시 휴면 상태로 존재하므로, 실험 전에 휴면 타파처리인 Conditioning을 실시한 수 실험에 사용하였다. 또한, 각각의 Strigolactone 혼합물은  $10^{-13}$ M~ $10^{-7}$ M로 처리하였으며, positive control 과 negative control로는 합성 Strigolactone인 GR24와 Milli-Q를 각각 사용하였다. 뿌리기생식물 *orobancha minor* 종자에 대한 발아자극활성을 측정한 결과, Strigolactone 혼합물의 활성에 큰 차이가 확인되지 않았다. 그러나 2'-*epi*-solanacyl acetate 혼합물의 경우 다른 혼합물에 비해 낮은 활성을 나타내었다. 또 다른 뿌리기생식물 *phelipanche ramosa* 종자에 대한 발아자극활성에서도 각 처리구에서 뚜렷한 차이는 확인되지 않았다.

\*주저자: Tel. 063-238-6751, E-mail: hyunil81@korea.kr

## 국내 블루베리 품종 구분을 위한 형태적 특성 비교

김수진\*, 고상욱, 남종철, 정성민, 허운영

전라북도 완주군 이서면 농생명로 100, 국립원예특작과학원 과수과

국내에 다양한 블루베리 품종이 재배되고 있으나 품종 도입이 묘목업자들에 의해 주도됨으로써 정확한 품종의 판별이 어렵고 구입한 품종의 특성이 상이하여 재배자들이 고충을 겪는 일이 많아 국내 도입된 블루베리 품종의 형태학적 특성을 파악하기 위해 연구를 수행하였다. 블루베리 신초 마디의 길이는 대부분 품종이 10~20mm 정도인 것으로 나타났다. 북부 하이부쉬블루베리 품종 계통의 마디가 길고 래빗아이블루베리 품종의 마디가 짧은 편으로 나타났으나 품종에 따라 차이가 많이 나타나 일관적인 특성으로 볼 수는 없었다. 잎의 종경은 품종에 따라 3~8cm으로 나타났으며, 횡경은 1~4cm로 다양하게 나타났다. 잎은 하이부쉬블루베리의 경우 짙고 빛나는 왁스층을 띠는 녹색을 띠는 특징을 지닌 것들이 대부분이었으며 래빗아이블루베리나 남부 하이부쉬블루베리의 경우에는 하얀 분가루가 있는 듯한 연녹색 잎색을 띠는 특징을 보였으나 품종별로는 뚜렷한 차이를 보이지는 않았다. 하이부쉬블루베리의 경우 화기의 색은 하얀색이 대부분이었으며 래빗아이블루베리 계통은 붉은색을 띠는 것이 많았으며 그 중간교잡종인 남부 하이부쉬블루베리에서도 붉은색을 띠는 품종이 많은 것으로 조사되었다. 화기의 종경은 대부분 5~9mm, 횡경은 8~13mm로 나타났으며 화관 크기는 2~6mm로 다양하게 조사되었다. 과실의 무게는 품종에 따라 1~3g으로 나타났으며 과실의 종경은 14~20mm, 횡경은 10~15mm으로 나타났다. 과실의 경도는 0.4~0.6N으로 대부분은 0.5~0.6N으로 비슷하게 나타났다. 당도는 11~16°Brix으로 조사되었으나, 대부분 품종의 당도는 11~12°Brix로 나타났다. 과실의 산도는 0.3~1.3%로 ‘Bladen’, ‘Duke’, ‘Friendship’, ‘Georgiagem’, ‘Northsky’, ‘Polaris’가 산도 0.3%로 가장 낮아 반수고 하이부쉬블루베리 품종의 산도가 대부분 낮은 것으로 조사되었다. 수확기는 북부 하이부쉬블루베리 조생종인 ‘Weymouth’가 5월 23로 가장 빨랐으며 래빗아이블루베리인 ‘Tifblue’와 ‘Southland’의 수확이 8월 초순으로 가장 늦었다. 수확 기간은 짧게는 2주일부터 길게는 품종에 따라 7주 정도가 소요되었다. 이와 같이 블루베리 품종별 형태적 특성 조사를 군집 분석한 결과, 종에 따른 차이는 항목에 따라 나타나기도 하였으나 뚜렷한 차이를 보이지 않아 형태적 차이에 따른 품종의 구분은 어려울 것으로 판단되어 품종 구분을 위해서는 형태적 특성 외에 분자 마커의 개발이 필요할 것으로 판단되었다.

\*주저자: Tel. 063-238-6750, E-mail: himssem@hanmail.net

## Gibberellin Application at Pre-bloom in Grapevines Alters GABA-shunt Resulting in Accumulation of GABA ( $\gamma$ -aminobutyric acid) at Full Bloom

Chan Jin Jung, Youn Young Hur\*, Sung-Min Jung, Sang-Uk Koh, Jong-Chul Nam

Fruit Research Division, National Institute of Horticultural and Herbal Science, RDA, Wanju 565–850, Korea

The GA application on grapevines induces parthenocarpy, fruit set without fertilization, and the inhibition of pollen tube growth. But the molecular mechanism underlying this inhibition is not understood. Similar defective pollen tube growth within the transmitting tract has been reported in the mutant of GABA transaminase (GABA-T), referred to as *pollen-pistil-interaction2 (pop2)* in *Arabidopsis*. In spite of the similarity of pollen tube growth inhibition observed in GA-applied grapevines with that of *pop2*, only the effects of GABA on stress responses in grapevines have been reported. In present study, transcriptional changes of *Vitis* GABA metabolic genes, together with changes in GABA levels with or without GA application were analyzed to define how GA application restrained the pollen tube growth in grapevines. A GA solution (Dongbu, Seoul, Korea) at 100 ppm was onto inflorescence clusters 14 days before full bloom (DBF) and clusters were harvested at 0, 1, 2, 4, 7, 9, 12, 14, 16, and 19 days after GA application. Harvested inflorescence samples were immediately frozen in LN<sub>2</sub> and extracted RNA and amino acid. The GABA contents were analyzed using high-performance liquid chromatography (Agilent 1100 HPLC, Agilent Technologies, Inc., Santa Clara, USA) equipped with a C18 column (4.6 mm×150 mm, 3.5  $\mu$ m/VDS optilab, Berlin, Germany), according to the manufacturer's instructions. Without GA application, the simultaneous high expressions of *VvGAD1*, *VvGAD4* and *VvGABA-T2* during 10 to 5 days before full bloom (DBF) showing the activation of GABA metabolism. But the contents of GABA were low before 2 DBF, and it peaked only at near full bloom when expression levels of *VvGABA-T2* remained low. After GA application, the contents of GABA were constant during 10 to 5 DBF, although transcription levels of both *VvGAD1* and *VvGABA-T2* rapidly declined less than 30% of the levels observed without GA application. However, the GABA levels increased more than 2-fold only at near full bloom, compared to those without GA application, and at that time, expression levels of *VvGAD1* up-regulated more than 3-fold and those of *VvGABA-T2* kept low. But other amino acid contents did not show significant changes. In case of *VvSSAHDs*, their transcriptional changes with or without GA application were not correlated with GABA levels. These results indicates that GABA levels before pollination is tightly regulated, but GA application alters the GABA-shunt to accumulate excess GABA more than needed for proper pollen tube growth at full bloom. Gibberellin application alters the GABA-shunt to accumulate excess GABA resulting in inhibition pollen tube growth in grapevines.

\*Corresponding Author: Tel. 063-238-6743, E-mail: yyhur76@korea.kr

## 국내 블루베리 품종 구분을 위한 형태적 특성 비교

김수진\*, 고상욱, 남종철, 정성민, 허운영

전라북도 완주군 이서면 농생명로 100, 국립원예특작과학원 과수과

국내에 다양한 블루베리 품종이 재배되고 있으나 품종 도입이 묘목업자들에 의해 주도됨으로써 정확한 품종의 판별이 어렵고 구입한 품종의 특성이 상이하여 재배자들이 고충을 겪는 일이 많아 국내 도입된 블루베리 품종의 형태학적 특성을 파악하기 위해 연구를 수행하였다. 블루베리 신초 마디의 길이는 대부분 품종이 10~20mm 정도인 것으로 나타났다. 북부 하이부쉬블루베리 품종 계통의 마디가 길고 래빗아이블루베리 품종의 마디가 짧은 편으로 나타났으나 품종에 따라 차이가 많이 나타나 일관적인 특성으로 볼 수는 없었다. 잎의 종경은 품종에 따라 3~8cm으로 나타났으며, 횡경은 1~4cm로 다양하게 나타났다. 잎은 하이부쉬블루베리의 경우 짙고 빛나는 왁스층을 띠는 녹색을 띠는 특징을 지닌 것들이 대부분이었으며 래빗아이블루베리나 남부 하이부쉬블루베리의 경우에는 하얀 분가루가 있는 듯한 연녹색 잎색을 띠는 특징을 보였으나 품종별로는 뚜렷한 차이를 보이지는 않았다. 하이부쉬블루베리의 경우 화기의 색은 하얀색이 대부분이었으며 래빗아이블루베리 계통은 붉은색을 띠는 것이 많았으며 그 중간교잡종인 남부 하이부쉬블루베리에서도 붉은색을 띠는 품종이 많은 것으로 조사되었다. 화기의 종경은 대부분 5~9mm, 횡경은 8~13mm로 나타났으며 화관 크기는 2~6mm로 다양하게 조사되었다. 과실의 무게는 품종에 따라 1~3g으로 나타났으며 과실의 종경은 14~20mm, 횡경은 10~15mm으로 나타났다. 과실의 경도는 0.4~0.6N으로 대부분은 0.5~0.6N으로 비슷하게 나타났다. 당도는 11~16°Brix으로 조사되었으나, 대부분 품종의 당도는 11~12°Brix로 나타났다. 과실의 산도는 0.3~1.3%로 'Bladen', 'Duke', 'Friendship', 'Georgiagem', 'Northsky', 'Polaris'가 산도 0.3%로 가장 낮아 반수고 하이부쉬블루베리 품종의 산도가 대부분 낮은 것으로 조사되었다. 수확기는 북부 하이부쉬블루베리 조생종인 'Weymouth'가 5월 23로 가장 빨랐으며 래빗아이블루베리인 'Tifblue'와 'Southland'의 수확이 8월 초순으로 가장 늦었다. 수확 기간은 짧게는 2주일부터 길게는 품종에 따라 7주 정도가 소요되었다. 이와 같이 블루베리 품종별 형태적 특성 조사를 군집 분석한 결과, 종에 따른 차이는 항목에 따라 나타나기도 하였으나 뚜렷한 차이를 보이지 않아 형태적 차이에 따른 품종의 구분은 어려울 것으로 판단되어 품종 구분을 위해서는 형태적 특성 외에 분자 마커의 개발이 필요할 것으로 판단되었다.

\*주저자: Tel. 063-238-6750, E-mail: himssem@hanmail.net

## 발아자극물질 Strigolactone 혼합물의 발아자극활성

김현일<sup>1\*</sup>, 샤 시오난<sup>2</sup>, 키스기 타카야<sup>2</sup>, 요네야마 카오리<sup>2</sup>, 요네야마 코이치<sup>2</sup>

<sup>1</sup>전라북도 완주군 이서면 농생명로 100, 국립원예특작과학원 과수과

<sup>2</sup>Center for Weed and Wildlife Management, 350 Mine-machi, Utsunomiya University, Utsunomiya 321-8505, Japan

뿌리기생식물 종자의 발아를 유도하는 대표적인 물질로 알려진 Strigolactone은 토양균의 하나인 *Arbuscular mycorrhizal* 균과의 공생적 작용은 물론, 식물 지상부의 결가지 생성을 억제하는 식물 호르몬으로서도 알려져 있다. 최초의 Strigolactone이 목화에서 확인되어 Strigol로 명명된 이후, 지금까지 약 15종 이상의 Strigolactone이 숙주 식물과 비숙주 식물로부터 확인되었다. 대부분의 Strigolactone은 모핵이 되는 tricyclic-lactone(ABC-ring)에 methyl butenolide(D-ring)이 enol ether 결합된 구조를 이루고 있다. 이러한 구조적 특징이 뿌리기생식물 종자의 발아를 자극하는 활성으로 작용한다. 특히, Strigolactone의 C-D ring구조와 AB ring의 치환기가 뿌리기생식물의 발아자극활성과 밀접한 관계가 있는 것으로 나타났다. 지금까지 뿌리기생식물 종자의 발아자극활성에 관한 많은 연구가 이루어졌으나, 이는 Strigolactone 단독처리를 통한 활성을 측정하는 것이다. 대부분의 식물은 두 종류 이상의 Strigolactone을 분비하는 것으로 알려져 있다. 따라서 Strigolactone 혼합물에 대한 뿌리기생식물 종자의 발아자극활성을 조사할 필요가 있다 하겠다. 그러므로 본 연구에서는 대표적인 뿌리기생식물로 알려진 *Orobancha minor*와 *Phelipanche ramosa* 종자를 이용하여, solanacol, solanacyl acetate, orobanchol, orobanchyl acetate 및 각각의 입체이성질체 혼합물에 대한 발아자극활성을 조사하였다.

두 종류의 뿌리기생식물 종자는 평상시 휴면 상태로 존재하므로, 실험 전에 휴면 타파처리인 Conditioning을 실시한 수 실험에 사용하였다. 또한, 각각의 Strigolactone 혼합물은  $10^{-13}$ M~ $10^{-7}$ M로 처리하였으며, positive control 과 negative control로는 합성 Strigolactone인 GR24와 Milli-Q를 각각 사용하였다. 뿌리기생식물 *orobancha minor* 종자에 대한 발아자극활성을 측정한 결과, Strigolactone 혼합물의 활성에 큰 차이가 확인되지 않았다. 그러나 2'-*epi*-solanacyl acetate 혼합물의 경우 다른 혼합물에 비해 낮은 활성을 나타내었다. 또 다른 뿌리기생식물 *phelipanche ramosa* 종자에 대한 발아자극활성에서도 각 처리구에서 뚜렷한 차이는 확인되지 않았다.

\*주저자: Tel. 063-238-6751, E-mail: hyunil81@korea.kr

## Analysis of transcriptional regulation of Arabidopsis *PIF* family genes in response to abiotic stresses

Jin-Seok Moon<sup>1,3\*</sup>, Satoshi Kidokoro<sup>1</sup>, Daisuke Todaka<sup>1</sup>, Sayuri Igusa<sup>1</sup>, Junya Mizoi<sup>1</sup>, Kazuo Shinozaki<sup>2</sup>, Kazuko Yamaguchi-Shinozaki<sup>1</sup>

<sup>1</sup>Grad. Sch. Agr. Life Sci., Univ. Tokyo

<sup>2</sup>Center for Sustainable Resource Science, RIKEN

<sup>3</sup>Fruit Research Division, National Institute of Horticultural and Herbal Science, RDA, Wanju 565–850, Korea

As one of the most severe stress conditions, drought strongly affects the plant growth and productivity. *OsPIL1*, a gene encoding a rice Phytochrome Interacting Factor (PIF)-Like transcription factor, was found to be down-regulated under drought stress condition. *OsPIL1* shows a diurnal expression pattern and known to be involved in regulation of plant height. However, the mechanisms of down-regulation of *OsPIL1* expression under stress conditions are remained unclear. In this study, the expression of *PIF4* and *PIF5*, the most homologous genes of *OsPIL1* in Arabidopsis, was analyzed and the expression of these genes were found to be oscillated in circadian manner and down-regulated in response to drought and low temperature similar to that of *OsPIL1*. To identify the regions involved in the responses to drought, low temperature and diurnal cycle, the promoter analysis of *PIF4* was performed using transgenic Arabidopsis. Further promoter analysis is ongoing to specify regulatory regions in more detail.

\*Corresponding Author: Tel. 063-238-6743, E-mail: gsmoon@chol.com

## Characterization of the Koji (*Aspergillus oryzae*) in four wheat varieties

Jong-Nae Hyun<sup>1\*</sup>, Hyung-ho Park<sup>1</sup>, Kyung-Hun Kim<sup>1</sup>, Kyung-Min Kim<sup>1</sup>, Jee-Yeon Ko<sup>1</sup>, Young-Up Kweon<sup>1</sup>, Chon-Sik Kang<sup>2</sup>, Sang-Jong Lim<sup>2</sup>, Jae-Hyun Kim<sup>3</sup>

<sup>1</sup>Department of Southern Area, NICS, Miryang, 627–803, Republic of Korea

<sup>2</sup>National Institute of Crop Science, Jeonju, 560–500, Republic of Korea

<sup>3</sup>National Academy of Agricultural Science, Jeonju, 560–500, Republic of Korea

Koji (*Aspergillus oryzae*) is used to ferment crude cereals of wheat to make a traditional alcoholic drink called Makkolli and industrial materials. It's quality varies depending on the wheat quality. Four domestic wheat varieties (Kosomil, Jokyungmil, Geumgangmil, Baegjungmil) were characterized. They were found similar in pH (6.02 to 6.08) and total acid (0.105 to 0.120%) contents. However, amino acid content of Gemgangmil was the highest (4.46%) and that of Baegjungmil was the lowest (3.72%). The total bacillus number was highest in Kosomil ( $333 \times 10^3$ CFU/ml) and lowest in Gemgangmil ( $60 \times 10^3$ CFU/ml). On the other hand, the fungus number was  $47 \times 10^5$ CFU/ml in Gemgangmil and the other varieties had similar quantity. The content of Alpha-amylase was the highest (500.01unit/g) in Kosomil followed by Jokyungmil and Gemgangmil, and the lowest was in Baegjungmil (353.32unit/g). The content of Glucoamylase was the highest in Geumgangmil (5105.0unit/g) followed by Jokyungmil and Kosomil, and the lowest was in Baegjungmil (3880.0unit/g). Acid protease was the highest in Kosomil (3515.15unit/g) followed by Geumgangmil and Baegjungmil, and the lowest in Jokyungmil (1280.5unit/g). From the result, Koji made from Kosomil was found to be of superior quality.

\*Corresponding Author: Tel. 055-350-1171, E-mail: hyunjn@korea.kr

## A high tocopherol content rice cultivar ‘Tocomi-1’

Jung Eun Hwang\*, In Jung Jung, Sung Min Han, Hong-Il Choi, Soon-Jae Kwon, Jin-Baek Kim, Si-Yong Kang, Dong Sub Kim

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongseup 580–185, Republic of Korea

‘Tocomi-1’, a new japonica rice cultivar derived from a 200 Gy gamma ray irradiation with high tocopherol content and red pericarp. The local adaptability test of MRXII-1001-1 was carried out from 2012 to 2014 and it was named as ‘Tocomi-1’ in 2014. This variety is medium matured with heading date of August 12 in honam plain area of Korea. This variety is about 80 cm tall culm length and 106 spikelets per panicle. Its 1,000 grain-weight of rice seeds is 25.4 g. The yield potential of this variety is about 5.15 MT/ha in local adaptability test for three years. This variety exhibited greater seed longevity than the Donganbyeo, indicating a crucial role for tocopherols in maintaining viability during quiescence, and displayed faster seedling growth during the early growth stage. Tocopherol contents was 50% higher than the Donganbyeo. To study the molecular mechanism underlying vitamin E biosynthesis, we examined the expression patterns of seven rice genes encoding vitamin E biosynthetic enzymes. Accumulation levels of the *OsVTE2* transcript and OsVTE2 protein in the ‘Tocomi-1’ were significantly higher than in the Donganbyeo. Sequence analysis revealed that the ‘Tocomi-1’ harbored a point mutation in the *OsVTE2* promoter region, which resulted in the generation of MYB transcription factor—binding *cis*-element. These results help identify the promoter regions that regulate *OsVTE2* transcription, and offer insights into the regulation of tocopherol content in ‘Tocomi-1’.

\*Corresponding Author: Tel. 063-570-3311, E-mail: bioplant@kaeri.re.kr

## 고생장성의 복색 홑꽃 절화용 스프레이국화 ‘매직발라드’ 육성

황주천<sup>1\*</sup>, 진영돈<sup>1</sup>, 정용모<sup>1</sup>, 안동춘<sup>1</sup>, 이병정<sup>1</sup>, 이상대<sup>2</sup>, 정병룡<sup>3</sup>

<sup>1</sup>경남 창원시 의창구 대산면 경남농업기술원 화훼연구소

<sup>2</sup>경남 진주시 경남농업기술원 연구개발국

<sup>3</sup>경남 진주시 가좌동 경상대학교 농업생명과학대학 원예학과

스프레이국화 ‘매직발라드’는 2010년 10월에 경남농업기술원 화훼연구소에서 복색 홑꽃인 ‘Hansome’을 모본, 생장성이 좋고 흰녹병에 강한 복색 홑꽃 화형의 ‘Magic(CFC0072)’을 부분으로 인공교배하여 획득한 474개의 종자로부터 실생계통을 양성하여 화색이 좋고 화형이 안정되며, 생장성이 우수한 홑꽃 화형의 복색(RP64A/WNN155C)인 스프레이국화 ‘HM11-141’을 개체 선발하였다. 삼목에 의해 개체증식 후 화훼연구소 비닐온실 내에 정식하였으며, 2012년부터 2013년까지 2년간에 걸쳐 1~2차 생육특성검정을 통해 안정성, 균일성과 흰녹병 저항성 등을 조사하였고, 2014년에는 계통번호 ‘경남교CS-42호’를 부여하여 3차 특성검정을 수행해 안정성과 균일성에 대한 연차별 재현성 그리고 주년생산성(자연, 축성, 억제재배) 및 품평회와 시장출하 등을 통해 생산자와 소비자의 기호성 평가를 받았다. 그 결과 고생장성이면서 착화성이 좋고 흰녹병에도 비교적 강해 재배자들이 선호하고 또한 화형·화색이 우수하여 소비자들의 기호성이 아주 높을 뿐만 아니라 품질이 우수하다고 판단되어 2014년 농작물 직무육성신품중심의회의 심의를 거쳐 ‘매직발라드’로 명명하고 12월말 국립종자원에 품종보호출원 하였다. 국화 ‘매직발라드’ 품종의 자연 개화기는 10월 하순이며, 선명한 자주색(RP64A) 꽃잎의 가장자리 부분에 깊게 백색(WNN155C) 테를 아주 조화롭게 두른 복색 홑꽃 화형인 스프레이국화이다. 화형이 안정되고 화색이 우수하며, 생육이 균일하고 동시개화한다. 초장 125.5cm, 줄기 직경 7.2mm로 대조품종인 ‘Hansome’의 114.7cm, 6.4mm 보다 11cm, 0.8mm 정도 길고 굵으며, 꽃 크기는 6.4cm로 대조품종 보다 약간 크다. 턱잎 크기는 중간 정도이고 잎은 대조품종 보다 약간 크다. 잎 최하단의 열편 깊이가 얇은 편이고 기부 주된 모양이 대조품종은 둥근 반면에 심장형이며, 잎의 광택은 약하다. 잎자루 길이는 11.3cm로 약간 길지만 견고하여 부러짐이 없어 절화시 작업성이 좋다. 설상화의 주된 형태는 선단모양이 둥근 모양이고 꽃잎 수는 29.8개로 많다. 평균 착화수는 14.8개로서 대조품종 보다 1~2개 적고 절화수명은 21.9일로 대조품종 보다 3일정도 길다. ‘매직발라드’ 품종은 비닐하우스 내에서 연중재배 할 수 있으며, 재배상 유의사항은 하계 고온기에는 화색 발현을 위해 한 낮엔 차광을 30% 정도의 한랭사로 차광하여 온도상승을 막아주고 환기도 충분히 해 주는 것이 좋다.

\*주저자: Tel. 055-254-1622, E-mail: gypso@korea.kr

---

**PC-01****Genetic Analysis and Fine Mapping of Panicle Tip Mutant *pnt* in rice (*Oryza sativa* L.)**

Abebe Megersa Diriba, Dongryung Lee, Jeonghwan Seo, Backki Kim, Zhuo Jin, Hee-Jong Koh\*

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

In the rice inflorescence development, timing of inflorescent meristem abortion, conversion of the rachis branch meristem to the terminal spikelet meristem and shift to lateral meristem identity determine the overall architecture of the rice panicle (keda-Kawakatsu et al. 2009). Cheng et al. (2011) reported that quantitative trait loci (QTLs) have major effects on panicle apical abortion in rice. However, there have been very few reports about panicle tip mutants. Therefore, this research is conducted to fine map mutant gene and perform functional analysis of mutant gene. Hwacheongbyeon (japonica rice) seed was treated with ethyl methane sulfonate (EMS) for inducing mutation. Two F<sub>2</sub> population (Japanica mutant crossed with wild type and Japanica mutant crossed with Milyang 23, Indica type) were established for Phenotyping and genomic analysis. STS markers in crop molecular Breeding laboratory. Additional STS markers for fine mapping were developed based on the Nipponbare genome sequence (<http://rgp.dna.affrc.go.jp/blast/runblast.html>). All F<sub>2</sub> generations showed the segregation of normal plants and mutant following a ratio of 3:1 suggesting the mutant phenotype is caused by a single recessive gene. Initial BSA test made using STS markers confirmed the mutant gene is found in the long arm of chromosome 8. Panicle tip mutant gene, *pnt* has pleiotropic effect which has been manifested in significant reduction of tiller development starting from late stage of vegetative growth and pronounced effect on possession of stay green nature of the rice during the vegetative stage of development. The only significant difference observed within panicle traits is the number of spikelet on primary branch and spikelet fertility. The first primary branch which contain aborted spikelet and elongated distance between spikelet is the most affected structure in the panicle. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. +82-2-8804541, E-mail: heejkoh@snu.ac.kr

**PC-02****Phylo rice transcription factor database: a resource for phylogenomics based systematic analysis of rice transcription factor for functional studies**

Anil Kumar N.C, Yo-Han Yoo, Ki-Hong Jung\*

Graduate School of Biotechnology, Kyung Hee University, Yongin 446–701, Korea

Rice gene functional annotation is greatly hindered due to functional redundancy. Based on OGRO database information, function of only 1022 genes were characterized previously where estimated expressed genes is approximately 50000. TFs protein class consist of 80 families and function of only 211 were reported. To address this issue, we developed web resource using MySQL, PHP and related frame work. Database integrates expression pattern and diverse data in phylogenomic contest. Since TFs plays diverse role in plants, meta-expression analysis would provide putative function of remaining genes. Using this approach and in-house database, we have identified featured expression groups: 228 belongs to anatomy, 224 to abiotic stress, 202 to biotic stress and hormone responsive group includes 267 genes. Out of 315 known genes through loss of functional studies, 294 genes have no closely related family members. Among 12 pairs with probes in database, 6 genes have PCC value with more than 0.5 among closely related genes. These data suggest that TFs showing more than 0.5 PCC value among closely relating family members more likely have functional dominancy. This study will provide useful functional information for whole rice TFs and suggest promising functional genomic studies.

\*Corresponding Author: E-mail: khjung2010@khu.ac.kr

---

**PC-03****Map-based cloning to identify gene involving in male gametophyte development in Arabidopsis**

Thi Hoai Thuong Nguyen, Hyo-Jin Park, Tien Dung Nguyen, Sung Aeong Oh, Soon Ki Park\*

School of Applied Biosciences, Kyungpook National University, Korea

In the course of map-based cloning, mutant genes are identified through linkage to specific region on genetic map. Here, we demonstrated gametophytic mutant line, named as *AP-28-23*, in which mutant gene was mapped on chromosome 2. Based on phenotypic analysis of mature pollen, mutant phenotype of *AP-28-23* was classified into three classes, wild-type showing 2-4%, moderate 35-53% and severe type 97-100% on aberrant pollen frequencies, respectively. The severe type is completely sterilized with 100% unfertilized ovules. We also revealed that the transmission was reduced through male gametophyte in the *AP-28-23* line. The transmission efficiency (TE) through the male gametophyte is only 0.67%, whereas in the female gametophyte is 89.87%.

\*Corresponding Author: Tel. 053-950-7751, E-mail: psk@knu.ac.kr

**PC-04****Molecular characterization and functional analysis of the UDP-glucose 4-epimerase (*BrUGE*) gene family in response to biotic and abiotic stress in Chinese cabbage (*Brassica rapa*)**

Yu Jin Jung<sup>1,2</sup>, Boo Min Yun<sup>1</sup>, Hyun Ji Kim<sup>1</sup>, Yong Gu Cho<sup>3</sup>, Ill Sup Noh<sup>4</sup>, Kwon Kyoo Kang<sup>1,2\*</sup>

<sup>1</sup>Department of Horticulture, Hankyong National University, Ansong, 456-749, Korea

<sup>2</sup>Institute of Genetic Engineering, Hankyong National University, Ansong 456-749, Korea

<sup>3</sup>Department of Crop Science, Chungbuk National University, Cheongju, 361-763, Korea

<sup>4</sup>Department of Horticulture, Sunchon National University, Sunchon, 540-742, Korea

UDP-glucose 4-epimerase (UGE; EC 5.1.3.2) is an enzyme that plays an essential role in the interconverts UDP-D-glucose (UDP-Glc) and UDP-Dgalactose (UDP-Gal). Five members of the Chinese cabbage (*Brassica rapa*) UDP-glucose 4-epimerase gene family, designated *BrUGE1* to *BrUGE5*, have been cloned and characterized. Quantitative PCR shows that the *BrUGE1* and *BrUGE4* mRNA are most abundant among other *BrUGE* genes, accounting for more than 55% of total *BrUGE* transcripts in most of the tissues examined. All genes showed organ specific expression pattern, two of which (*BrUGE1* and *4*) actively responded after *Pectobacterium carotovorum* subsp. *carotovorum* infection, while four genes (*BrUGE-1*, *-3*, *-4* and *-5*) were shown to respond considerably against salt, drought and abscisic acid (ABA) treatments. To better understand the function of the UGE gene, we constructed a recombinant pART vector carrying the *BrUGE1* gene under the control of the CaMV 35S promoter and nos terminator and transformed using *Agrobacterium tumefaciens*. We then investigated *BrUGE1* overexpressing rice lines at the physiological and molecular levels under biotic and abiotic stress conditions. Bioassay of T<sub>3</sub> progeny lines of the transgenic plants in Yoshida solution containing 120 mM NaCl for 2 weeks, confirmed that the *BrUGE1* enhances salt tolerance to transgenic rice plants. Also T<sub>3</sub> progeny lines of the transgenic plants, when exposed to infection caused by *Xanthomonas oryzae* pv *oryzae*, showed tolerance to bacterial blight. These results showed that *BrUGE1* can be used as potential genetic resource for engineering *Brassica* with multiple stress resistance.

## **A Map-based Cloning Approach for the Identification of a Low Temperature Sensitive Gene *sy-2* in Chilli pepper (*Capsicum chinense*)**

Li Liu<sup>1</sup>, Min-Young Kang<sup>1</sup>, Jin-Ho Kang<sup>1</sup>, Yeong Deuk Jo<sup>1</sup>, Sota Koeda<sup>2</sup>, Munetaka Hosokawa<sup>2</sup>, Doil Choi<sup>3</sup>, Byoung-Cheorl Kang<sup>1\*</sup>

<sup>1</sup>Department of Plant Science and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151–921, Korea

<sup>2</sup>Department of Agronomy and Horticultural Science, Graduate School of Agriculture, Kyoto University, Sakyo-ku, Kyoto 606–8502, Japan

<sup>3</sup>Department of Plant Science, College of Agriculture and Life Sciences, Seoul National University, Seoul 151–921, Korea

*sy-2* (*Seychelles-2*) is a temperature sensitive natural mutant of *Capsicum chinense* and native to Seychelles Island in Africa. Previously we showed that *sy-2* leaves were irregularly shaped and defective in chlorophyll development at temperatures below 24°C. A segregation test revealed that the *sy-2* gene is controlled by a single recessive gene. To identify the *sy-2* gene, we performed a map-based cloning approach using a total 600 individual F<sub>2</sub> plants derived from crossing *sy-2* and the wild type *C. chinense* ‘No.3341’. Fine-mapping of the locus allowed us to position *sy-2* to an approximately 170-kb region flanked by markers IN2-1-1 and SNP-3-7 on chromosome 1. Among the approximately 36 hypothetical genes in this region several candidate genes including: HSP90-like ATPase family proteins, lipid-transfer proteins, calmodulin-domain protein kinases, and zinc finger proteins (ZFPs) were identified. RT-PCR and sequencing of the hypothetical genes are under way to identify *sy-2*.

Keywords: *Capsicum chinense*, map-based cloning, single nucleotide polymorphism, *sy-2*

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

## **Characterization and interaction analysis of two QTLs, *QTL5-1* and *QTL5-2*, controlling *Phytophthora capsici* resistance in *Capsicum annuum* using near-isogenic lines**

Hyeon-Seok Jeong<sup>1</sup>, Muhammad Irfan Siddique<sup>1</sup>, Jeong-Tak An<sup>1</sup>, Ki-Taek Kim<sup>2</sup>, Gyung Ja Choi<sup>3</sup>, Darush Struss<sup>4</sup>, Byoung-Cheorl Kang<sup>1\*</sup>

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

<sup>2</sup>The Foundation of Agricultural Technology Commercialization and Transfer, 441-100 Suwon, Republic of Korea

<sup>3</sup>Chemical Biotechnology Research Center, Green Chemistry Division, Korea Research Institute of Chemical Technology, 305-600 Daejeon, Republic of Korea

<sup>4</sup>Biotechnology group East West Seed, Hortigenetics Research, Chiang Mai, 50290 Thailand

*Phytophthora capsici* an Oomycete pathogen is a major challenge to the pepper (*Capsicum spp.*) production around the world. Control measures are proved ineffective, so breeding resistant cultivars are the most promising strategy against the pathogen. Resistance against *P. capsici* is governed by quantitative trait loci (QTL). According to previous studies on QTL detection, the QTL on pepper chromosome 5 is a major contributor to resistance. In this study, to exploit the involvement of this QTL and identify its contributing genes, the F<sub>2</sub> population derived from a cross between ECW30R and CM334 was inoculated with a medium virulence *P. capsici* strain JHAI1-7 zoospores at the 6-8 leaf stage. Composite interval mapping revealed two major QTLs; *QTL5-1* from 7 days post inoculation (dpi) and *QTL5-2* from 16 dpi on chromosome 5. To characterize and detect interactions of the two QTLs, near isogenic lines (NIL) were constructed by crossing Tean and recombinant inbred line (RIL) derived from a cross between YCM334 and Tean. RILs were screened with *P. capsici* strain MY-1 and resistant lines were selected. Among the resistance RILs most closely related to Tean were selected using AFLP and SSR genotyping data. These RILs were named as YT39-2 and YT143-2. To develop more advanced NILs, two rounds of marker-assisted backcrossing were done using a high-throughput SNP genotyping system (EPI Fluidigm, USA). Among the NILs derived from YT39-2, YT39-2-64 contains only *QTL5-1* whereas YT39-2-61 and YT39-2-69 were identified to have both QTLs. On the other hand, YT143-2-55-7 with the highest Tean genetic background contains *QTL5-1* only. In the next step, the 3 different NILs having *QTL5-1*, *QTL5-2* individually and both QTLs will be identified. Furthermore, phenotyping and fine mapping will be done for the analysis of individual and interaction effects of QTLs.

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

## 한국 들잔디에서의 $\beta$ -1,3-glucanase 유전자의 cloning

강소미<sup>1</sup>, 강지남<sup>1</sup>, 강홍규<sup>2</sup>, 선현진<sup>2</sup>, 권용익<sup>2</sup>, 고석민<sup>2</sup>, 이효연<sup>1,2</sup>

<sup>1</sup>제주대학교 생명공학부

<sup>2</sup>제주대학교 아열대원예산업연구소

한국형 잔디는 다른 병에 비해 진전 속도가 빠르고 주로 뿌리에서부터 발병하여 잔디를 고사시키고 발병 후 구제하기 매우 어려운 라이족토니아잎마름병(라지패취)이 큰 문제로 대두되고 있다. 라이족토니아잎마름병(라지패취)은 *Rhizoctonia solani* AG2-2(IV)병원균에 의해 발생하는데, 이 병원균에 강한 내병성 들잔디를 개발하기 위해 식물방어 반응에 중요한 역할을 하는 것으로 알려진 PR-Protein 중 하나인  $\beta$ -1,3-glucanase를 들잔디로부터 cloning 하였다.  $\beta$ -1,3-glucanase는 바이러스나 균의 감염으로 인해 식물조직이 과민반응을 일으킬 때 세포내에서 생성되고 세포외로 분비되어 세포 사이 공간에서 주로 기능을 하는 것으로 알려져 있다.  $\beta$ -1,3-glucanase의 기능분석이 되어있는 단자엽식물 중 옥수수, 밀, 보리, 벼의 염기서열에서 공통으로 보존되어 있는 부분을 이용해 degenerate PCR을 수행하고 얻어낸 sequence를 통해 3' RACE와 5' RACE를 진행하였다.

그 결과 1,228 bp, 399개의 아미노산으로 구성된 *ZJGlu1*과 1,179 bp, 340개의 아미노산으로 구성된 *ZJGlu2*의 Full-sequence 얻어냈다. *ZJGlu1*과 *ZJGlu2*와의 염기서열 상동성은 76%이며, *ZJGlu1*의 경우 VISESGWPSAG서열을 보존하고 있고 *ZJGlu2*의 경우 VSESGWPSA서열을 보존하고 있어 glycosyl hydrolase motif(LGIVISESGWPSAG)와 비교해 봤을 때 상당부분 일치하는 것을 보였다.

*ZJGlu1*과 *ZJGlu2* 유전자의 기능을 해석하기 위해 각각의 유전자를 도입한 식물형질전환용 벡터를 제작하여 모델식물인 애기장대와 잔디 형질 전환체는 현재 진행 중에 있으며, *E.coli* over-expression을 수행하여 목표 단백질을 정제하고 *in vitro* 활성을 측정할 예정이다.

사사: 한국연구재단 대학중점연구소 지원사업으로 수행된 연구임(2009-0094059)

\*주저자: Tel. 064-754-3347, E-mail: hyoyeon@jejunu.ac.kr

## PC-08

### 환경스트레스 내성 들잔디 (*Zoysia japonica* Steud.)의 형질전환체 개발

박미영<sup>1</sup>, 선현진<sup>1</sup>, 이동희<sup>2</sup>, 류기중<sup>3</sup>, 이효연<sup>1,3\*</sup>

<sup>1</sup>제주대학교 아열대원예산업연구소

<sup>2</sup>(주)제노마인

<sup>3</sup>제주대학교 생명공학부

한국들잔디(Korean Lawngrass, *Zoysia japonica* Steud.)는 한국잔디류 중 답압성, 내한성, 내서성이 가장 강하며, 관리가 용이하여 정원, 공원, 묘지, 경사면 녹화 등에 폭넓게 이용되고 있다. 최근 잔디의 이용범위가 확대되면서 다양한 용도의 잔디 품종 개발이 요구되고 있어 개량할 수 있는 형질이 제한되어 있는 전통육종법 대신 분자유종에 의한 신품종 개발이 활발하게 진행되고 있다.

본 연구에서는 건조, 산화스트레스 내성, 노화지연 등의 형질을 제공하는 것으로 알려진 애기장대 유래의 *ATPG10* (AT-hook protein of Genomine 10) 유전자를 *Agrobacterium* 형질전환방법을 이용하여 도입시켰다. *Agrobacterium* 배양액을 최종 O.D.600 값이 0.1이 될 때까지 현탁하여 재분화가 잘되는 형태의 캘러스를 24시간 감염, 3일간 공동배양, PPT 항생제가 첨가된 선발배지에서 신초유도 및 선발, 2~3cm 이상 성장한 shoot를 뿌리유도 및 선발과정을 거쳐 11개체의 형질전환 식물을 생산하였다. 확보된 형질전환체는 순화/증식하여 유전자의 도입 및 발현을 확인하고 기능분석을 수행하고 있다. *ATPG10* 유전자가 도입된 형질전환식물은 생산성 증대, 건조 스트레스 내성, 산화 스트레스 내성, 노화 지연 등의 기능을 가질 것으로 기대된다.

사사: 농촌진흥청 차세대 바이오그린21사업(PJ011244012015); 한국연구재단 기초연구사업(2009-0094059)

\*주저자: Tel. 064-754-3347, E-mail: hyoyeon@jejunu.ac.kr

## PC-09

### 제초제저항성 GM들잔디 유래 초형개선 신품종 잔디(JG21-MJ) 계통의 분자생물학적 특성 평가

정하나<sup>1</sup>, 좌지방<sup>2</sup>, 선현진<sup>1</sup>, 권용익<sup>1</sup>, 강홍규<sup>1\*</sup>, 이효연<sup>1,2</sup>

<sup>1</sup>제주특별자치도 제주시 아라2동 제주대학교 아열대원예산업연구소

<sup>2</sup>제주특별자치도 제주시 아라2동 제주대학교 생명공학부

잔디는 스포츠 경기장, 골프장, 조경분야, 공원, 묘지, 사방건설, 개인주거지 등 광범위하게 활용되고 있는 고부가가치의 경제성 작물이다. 본 연구는 제초제저항성 들잔디 JG21의 화분(pollen)과 금잔디(*Z. meliloti*) 암술(carpel)의 중간인공수분을 통해 육성된 제초제저항성 교배종 잔디 계통(JG21-MJ)의 분자생물학적 특성을 평가하기 위해 수행되었다. genomic Southern blot분석에서 제초제저항성 교배종 잔디들은 모두 *bar* 유전자가 확인되었고, JG21과 동일한 혼성화 패턴(hybridization pattern)을 보여 주었다. PCR을 이용하여 교배종 가운데 제초제저항성이 없는 대조군 품종과 제초제저항성 품종에서 도입유전자 주변염기서열을 분석하였다. 이 실험은 들잔디(JG21)와 금잔디의 교배(F1)와 자가수분(F2) 과정에서 도입유전자 삽입위치 주변의 염기서열에서 상동재조합이 발생하였는가를 조사하기 위해 수행하였다. 제초제저항성 교배종의 도입유전자 주변염기서열은 JG21과 동일하였고, 제초제저항성이 없는 대조군의 삽입위치 주변의 염기서열은 금잔디의 염기서열과 동일하였다.

사사: 본 연구는 농촌진흥청 차세대바이오그린21 프로그램(과제번호 PJ011244022015)의 지원에 의해 수행되었음.

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

**Cloning of *WRKY* genes, induced by stresses in *Zoysia japonica* Steud.**Woo-Nam Kim<sup>1</sup>, Yong-Ik Kwon<sup>2</sup>, In-Ja Song<sup>2</sup>, Bo-Hwa Hwang<sup>2</sup>, Dong-Sun Lee<sup>1</sup>, Hyo Yeon Lee<sup>1,2\*</sup><sup>1</sup>Faculty of Biotechnology, Jeju National University, 690–756, Korea<sup>2</sup>Subtropical Horticulture Research Institute, Jeju National University, Jeju 690–756, Korea

All kinds of crops including foods, feeds and turf grasses are damaged frequently by various environmental stresses such as drought, salt, cold, and high temperature, which cause the loss of agronomic productivity. Plants cannot escape from environmental stresses. Thus, plants were evolving in the direction of overcoming environmental stresses. Some genes such as *ARF*, *AB13*, *NAC*, *HSF*, *WRKY* respond to environmental stresses have been reported in plants. The genes play a role in stress responses pathway of plants, the transcription factor in response to environmental stress. Typically *OsWRKY76* increased the low temperature resistance, *AtWRKY28* been reported to be related to the environmental stress. Zoysiagrass (*Zoysia japonica* Steud.) is used primarily useful for the garden or the golf course. But *WRKY*, environmental stress-related gene, is unknown in zoysiagrass. Here, we report the analyzing of *WRKY* genes and response by cold, dehydration and senescence stresses in zoysiagrass. Three *WRKY* gene (*ZjWRKY3*, *ZjWRKY5*, *ZjWRKY7*) cloning from zoysiagrass. It was transformed in Arabidopsis and zoysiagrass. It will be a function analysis.

This work was supported by a grant from the Next-Generation BioGreen 21 Program (PJ011244012015), Rural Development Administration, Republic of Korea.

This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (grant number 2009-0094059)

\*Corresponding Author: Tel. 064-754-3347, E-mail: hyoyeon@jejunu.ac.kr

---

**PC-11****Antifungal activities of zoysiagrass (*Zosia japonica* Steud.) chitinases against *Rhizoctonia solani* and analysis of fungus responsive cis-elements in chitinase genes promoter**

Ji-Nam Kang<sup>1</sup>, So-Mi Kang<sup>1</sup>, Hong-Gyu Kang<sup>2</sup>, Hyeon-Jin Sun<sup>2</sup>, Yong-Ik Kwon<sup>2</sup>, Suk-Min Ko<sup>2</sup>, Hyo-Yeon Lee<sup>1,2</sup>

<sup>1</sup>Faculty of Biotechnology, Jeju National University, Jeju 690–756, Korea

<sup>2</sup>Subtropical Horticulture Research Institute, Jeju National University, Jeju, 690–756, Korea

Zoysiagrass are damaged by fungi diseases such as large patch, dollar spot, pythium blight and brown patch. Large patch is one of the major diseases caused by *Rhizoctonia solani* AG2-2 on zoysiagrass fields e.g. golf courses. Plant chitinases have been known PR (Pathogen related)-protein. In this study, we isolated two chitinase genes (*Zjchi1* and *Zjchi2*) from zoysiagrass. Antifungal activity analysis revealed that *Zjchi2* protein inhibited mycelium extension of fungi. A further study, we cloned 5' upstream region from two chitinase genes for investigating transcription regulatory mechanism that inducing of two chitinase genes dependent *R. solani*. -818 bp and -799 of upstream region from *Zjchi1* and *Zjchi2* successfully isolated using *in vitro* LA (Long and Accurate) PCR system. And then, we generated promoter-GUS reporter constructs with deletion construct based on W-boxes. Constructs were introduced into *Arabidopsis thaliana* by *Agrobacterium*-mediated transformation for stable expression of GUS reporter gene.

This research was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (grant number 2009-0094059)

\*Corresponding Author: Tel. 064-754-3347, E-mail: hyoyeon@jejunu.ac.kr

**PC-12****The Karyotype Analysis of *Lilium* Species Native to China**

Ge Guo, Ki-Byung Lim\*

Department of Horticultural Science, Kyungpook National University, Daegu 701–702, Korea

The karyotype analysis of various *Lilium* species native to Yun nan, Northeast China, viz., *L. sulphureum*, *L. nepalense* var., *L. wenshanense*, *L. nepalense* and *L. brownii* var. were observed through ordinary tablet compressing method. The results indicated that the chromosome number was  $2n=2x=24$  in all the species studied. The karyotype formula was  $2n=2x=24=2m + 6sm (2SAT) + 4st+12t (4SAT)$  for *Lilium sulphureum*;  $2n=2x=24=2m + 10st (2SAT) + 12t (4SAT)$  for *Lilium nepalense* var.;  $2n=2x=24=2m + 2sm+8st (6SAT) +12t (2SAT)$  for *Lilium wenshanense*;  $2n=2x=24=4m (4SAT) + 10st (4SAT) + 10t$  for *Lilium nepalense*;  $2n=2x=24=2m + 2sm+10st + 10t$  for *Lilium brownii* var. The As.K value (the ratio between long arm and total chromosome length) and the ratio of the length of the longest and the shortest chromosome were recorded as 78.25%~83.71% and 1.83~2.18 respectively. The karyotype of all the species was 3B except for *L. nepalense* which was 3A. Comparatively, the karyotype analysis of *Lilium nepalense* var. and *Lilium nepalense* were similar and genetically close to each other. A great diversity in chromosome morphology was existed among different populations or cultivars of the same species. The genetic diversity of different species or populations could be discriminated thru the number and position of different kinds of chromosomes, as well as the difference of satellite number and positions.

“This work was supported by a grant from Regional Subgene Bank Support Program of Rural Development Administration, Republic of Korea.”

**Bio assay of DNP 7, 9 Response in Rice Screening with Whitebacked planthopper**

Sopheap Yun<sup>1</sup>, Vicheka Than<sup>1</sup>, Kyung-A kim<sup>1</sup>, Hyun-Suk Lee<sup>1</sup>, Gi-Hwan Yi<sup>2</sup>, Byung-Wook Yun<sup>1</sup>, Kyung-Min Kim<sup>1\*</sup>

<sup>1</sup>Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 702-701, KOREA

<sup>2</sup>Department of Farm Management, College of Agriculture and Life Science, Kyungpook National University, Gunwi-gun, Gyeongbuk 716-821, KOREA

The objectives of this study were to investigate the diversity of natural products (DNP7, 9) in responding to Whitebacked planthopper (WBPH) feeding. Resistant rice (cv. Cheongcheong), susceptible rice (cv. Nagdong) and susceptible control rice (cv. TN1) were used as materials for WBPH infestation in seedling stage. The treatment was conducted by spraying DNP 7 and 9 for 100 ppm to materials before being fed to 2<sup>nd</sup> and 3<sup>rd</sup> instar WBPH while control group was not sprayed DNP 7 and 9. The density of WBPH was 7 insect per plant. As a result, WBPH survival rate of 57% was found in the DNP 7 treatment, whereas those in DNP 9 and control were 27% and 71%, respectively. Resistance score of Cheongcheong, Nagdong, and TN1 in DNP 7 treatment were 3.4±0.8, 5.9±1.9, and 6.8±1.6, respectively, while those in DNP 9 treatment were 1.6±0.8, 4.7±1.6, and 7.9±1.4, respectively. The plant heights of Cheongcheong, Nagdong, and TN1 in DNP 7 treatment after 3 week infestation were 19.7±3.0, 23.4±7.5, and 15.8±8, respectively while those in DNP 9 treatment were 32.4±4, 26.3±12.7, and 25.9±8.5, respectively. Moreover, chlorophyll content was examined 3 week post infestation. In both DNP 7 and DNP 9 treatment, the chlorophyll levels of Cheongcheong and Nagdong in were higher than that in control. Based on observation and bio-scoring, plant with DNP 9 was strongly resistant to WBPH feeding and the survival rate of WHPB was lower than plant with DNP7.

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ011257012015), Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. +82-10-2650-5414, E-mail: kkm@knu.ac.kr

## **Timing screening effects and QTLs analysis of Whiteback planhopper Resistance Cheongcheong/Nagdong Double haploid Rice**

Sopheap Yun<sup>1</sup>, Hyun-Suk Lee<sup>1</sup>, Than Vicheka<sup>1</sup>, Gi-Hwan Yi<sup>2</sup>, Kyung-Min Kim<sup>1\*</sup>

<sup>1</sup>Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 702-701, KOREA

<sup>2</sup>Department of Farm Management, College of Agriculture and Life Science, Kyungpook National University, Gunwi-gun, Gyeongbuk 716-821, KOREA

In total, 120 'Cheongcheong/Nagdong' doubled haploid (CNDH) populations was developed by F<sub>1</sub> derived from a crossing whitebacked planthopper (WBPH, *Sogatella furcifera*) resistance 'Cheongcheong' and susceptible 'Nagdong' lines. The main objective of this research was to determine the rice resistance optimum screening after infesting by WBPH and identify quantitative trait loci (QTLs) associated with rice resistance in order to provide consistent information for marker-assisted selection (MAS) and develop new varieties. The genetic map with average 9.6 centimorgans (cM) between markers was constructed from 120 CNDH populations using 217 SSR markers. In this study, The result of determine rice with WBPH infestation showed that the rice damage and resistance at 7, 14, and 21 days, were 100%, 76%, and 10% resistance lines of 120 CNDH population. Four QTLs were detected on four regions of the chromosomes 1 and chromosome 8, which contained qWBPH1 and qWBPH8 for resistance rice. The markers were found to be contained in identification the genetic markers RM3482, RM1196, RM3709, RM11694, RM11669, RM17699 and RM264 for marker assisted selection. These markers efficiently were shown to be very useful for MAS in breeding populations of crossing lines associated simple sequence repeat (SSR) marker with WBPH resistance in 120 CNDH populations.

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ011257012015), Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

## **QTLs for detecting DNA markers related to alkali digestion value in rice grain using doubled haploid population**

Hyun-Suk Lee<sup>1</sup>, Gyu-Ho Lee<sup>1</sup>, A-Ra Cho<sup>1</sup>, Gihwan Yi<sup>2</sup>, Kyung-Min Kim<sup>1\*</sup>

<sup>1</sup>Division of Plant Biosciences, School of Applied Biosciences, Kyungpook National University, Daegu, 702–701, Korea

<sup>2</sup>Department of Farm Management, College of Agriculture & Life Science, Kyungpook National University, Gunwi-gun, Gyeongbuk, 716–821, Korea

Improving rice high-quality potential is to suffice the food demand of the rapid decreasing consumption, and is a major breeding target recently. We calculated the alkali digestion value (ADV), used to indirectly measure gelatinization temperature, to evaluate the quality of cooked rice in 2013 and 2014. The ADV score of frequency distribution was higher milled rice than brown rice. In total, nine different quantitative trait loci (QTLs) were found on chromosomes 1, 3, 5, 6 and 8 in 2013 and 2014. Also, chromosome 5, 8 were detected over two years. The polymorphism using RM223, RM3530, and RM18130 markers can be used to select lines that have a good trait for breeding of high-quality rice. We conclude that selected molecular markers from this QTL analysis could be exploited in future rice quality.

Acknowledgements: This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ011257012015), Rural Development Administration, Republic of Korea.

\***Corresponding Author:** Tel. 053-950-5711, E-mail: kkm@knu.ac.kr

## Practical use of standard set of microsatellites based classification of primary pears and Korean native pears (*Pyrus* spp.)

Keumsun Kim<sup>1,2</sup>, Hyunsuk Shin<sup>1,2</sup>, Youngjae Oh<sup>1,2</sup>, Sewon Oh<sup>1,2</sup>, Jungyeon Won<sup>1,2</sup>, Hyeondae Han<sup>1,2</sup>, Yoon-Kyeong Kim<sup>3</sup>, Seolah Kim<sup>1,2</sup>, Sung-Il Oh<sup>4</sup>, Mingi Lee<sup>1</sup>, Daeil Kim<sup>1,2\*</sup>

<sup>1</sup>Department of Horticulture, Chungbuk National University, Cheongju 361–763, Korea

<sup>2</sup>Brain Korea 21 Center for Bio–Resource Chungbuk National University, Cheongju 361–763, Korea

<sup>3</sup>Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 520–821, Korea

<sup>4</sup>Division of Special–purpose Trees, Korea Forest Research Institute, Suwon 441–350, Korea

In this study, we sought to identify primary pears species and Korean native pears, without the use of morphological characteristics. In addition, this study was to establish pear DNA fingerprinting data for Korean native pears using 12 microsatellite markers, and to accurately classify a database for management of the Korean pear collection. Forty two pear accessions (7 primary pears, 5 Asian pears, 29 Korean pears, and 2 reference pears) were analyzed with twelve primers covering whole pear genome. In the present study, all pear accessions were successfully classified along with their pedigrees, and the distribution of primary pears was parallel to those of the previous taxonomic results. Korean pears were divided into 3 groups. Group I was characterized by *Pyrus calleryana*, and included Korean pea pears. Group II was characterized by *P. pyrifolia*, and was classified into 2 small groups. The first small group comprised of ‘Najucheonbae’, ‘Sunchanggulimdolbae’, ‘Andongmookbae’, ‘Andongdangsilri’, and ‘Najucheonbae’ and was presumed to be cultivars of *P. pyrifolia*. The second small group consisted of ‘Cheongdangrori’ and ‘Pyeongchangsuhyangri’. These two accessions were assumed to be a hybrid of *P. pyrifolia* and the other cultivar. Group III was characterized by *P. ussuriensis*. ‘Goesanhwangbae’, ‘Andongcheongsilri’, ‘Gongjucheongsilri’, and ‘Yecheoncheonbae’ were assumed to be cultivars of *P. ussuriensis*. Contrary to ‘Ulreungdocheonbae A’, ‘Ulreungdocheonbae B’ was classified as belonging to the *P. ussuriensis* group. It is possible that this is a consequence of *P. ussuriensis* genes being transferred into ‘Ulreungdocheonbae B’. The result of this research reaffirmed the efficiency of a standard set of microsatellite markers and provides data, which will be useful for developing a core collection of pears.

\*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

## **Distinct roles of *E3*-parologue genes promote early flowering in late flowering soybean cultivars**

Kil Hyun Kim<sup>1</sup>, Min-Jung Seo<sup>1</sup>, Jin-Seok Lee<sup>1</sup>, Hwan Hee Bae<sup>1</sup>, Jung-Tae Kim<sup>1</sup>, Beom-Young Son<sup>1</sup>, Seong-Bum Baek<sup>1</sup>, Jeom-Ho Lee<sup>1</sup>, Jung-Kyung Moon<sup>2</sup>, Chang-Hwan Park<sup>1\*</sup>

<sup>1</sup>National Institute of Crop Science, RDA, Suwon, 441–857, Republic of Korea

<sup>2</sup>National Institute of Crop Science, RDA, Wangju, 565–238, Republic of Korea

Soybean (*Glycine max* (L.) Merr) is a short day plant and has been adapted to various climates and environments during cultivation. However, the cultivation area is restricted to a very narrow range of latitudes. To date, nine major genes (*E1* to *E8* and *J*) have been reported to control the flowering time and maturity. Here, we evaluated the role of *E2*, *E3*, *E4*, and their parologue genes in late flowering soybean cultivars under long day (LD) conditions using *Soybean yellow common mosaic virus* (SYCMV)-based virus-induced gene silencing (VIGS) system. A total of nine VIGS constructs were infiltrated into two fully expanded cotyledons and primary leaves. After inoculation with these VIGS constructs on Jangyeobkong, which is a late-flowering cultivar, phenotypic traits were evaluated for the first flowering dates (FFDs) and pod maturities under LD conditions. The FFDs of the silenced plants occurred 50-56 days after sowing (das), while the non-silenced plants bloomed on 60-61 days. We found that the *E3* parologue-silenced plants flowered the fastest and responsive genes were identified to be associated with the promotion of flowering time. As the knock-down of *E3* parologue, expression of *E1* was up-regulated, *E2* was no difference, *E3* and *E4* genes were down-regulated in the silenced plants. Expression of *GmFT2a* and *GmFT5a* is known to be controlled by *E3* and *E4*. Interestingly, *GmFT5a* were highly expressed in SYCMV:*E3* parologue-silenced plants, whereas the expression of *GmFT2a* was not significant. These results support that *GmFT5a* is able to independently promote flowering under LD conditions.

\*Corresponding Author: Tel. 031- 695-4046, E-mail: park6725@korea.kr

**Evidence of whole genome duplication in *Panax ginseng* draft sequence**

Nam-Hoon Kim<sup>1</sup>, Woojong Jang<sup>1</sup>, Murukarthick Jayakodi<sup>1</sup>, Sang-Choon Lee<sup>1</sup>, Yun Sun Lee<sup>1</sup>, Junki Lee<sup>1</sup>, Beom-Soon Choi<sup>2</sup>,  
Tae-Jin Yang<sup>1\*</sup>

<sup>1</sup>Department of Plant Science and Plant Genomics and Breeding Institute, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea

<sup>2</sup>PHYZEN Genomics Institute, Seoul, 151-836, Korea

The generation and analysis of genomic resources information are essential to understand genomic features of crops. Even though medicinal component and its effect of *Panax ginseng* was well studied, the genomic study has been recently started. The ginseng genome has been known to undergo two rounds of whole genome duplication (WGD), therefore we investigated an evidence of WGD in ginseng draft sequence for understanding current ginseng genome structure. Four paralogous gene-rich genome blocks were found, consisted by eight scaffolds, using about 3.0 Gb whole genome draft sequence and 48,821 unigenes of *P. ginseng* generated by whole genome shotgun sequencing. The eight scaffold sequences were ordered and connected into four genomic blocks, using zig-zag extension within scaffold sequences recently duplicated. The paralogous scaffold pairs that were recently duplicated showed high sequence conservation in genic and non-genic regions. However, paleo duplicated paralogue scaffold sequences showed little conservation only in genic regions. Finally, a total of 110 paralogous gene pairs and its expression were identified from recently and paleo duplicated scaffold pairs, which were co-linear among four genomic blocks. This study provides the first insight into duplicated genome structure of ginseng and will be a valuable information for further ginseng genomics including improvement of draft sequence quality, chromosome anchoring of scaffolds, and genetic mapping. This research was supported by “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01100801)” Rural Development Administration, Republic of Korea.

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

## Identification and characterization of novel phosphate starvation signaling mutant in *Arabidopsis*

Hyun Jin Chun, Mi Suk Park, Byung-Jun Jin, Min Chul Kim\*

Division of Applied Life Science (BK21 Plus), Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 660–701, Korea.

To identify novel signaling components involved in regulation of plant responses to phosphate (Pi) starvation, we screened an *Arabidopsis* T-DNA activation tagging library for mutants with altered Pi-starvation responses. Here, we report the identification and characterization of novel activation-tagged mutant involved in Pi starvation signaling in *Arabidopsis*. The *hpd* (hypersensitive to Pi deficiency) mutant exhibits enhanced phosphate uptake and altered root architectural change under Pi starvation compared to wild type. Expression analysis of auxin-responsive *DR5::GUS* reporter gene in *hpd* mutant indicated that both auxin biosynthesis and auxin translocation under Pi starvation are suppressed in *hpd* mutant plants. Impaired auxin translocation in roots of *hpd* mutant was attributable to abnormal root architecture changes in Pi starvation conditions. Mis-regulation of auxin translocation in *hpd* mutant was further confirmed by analysis of expression patterns of auxin efflux carrier proteins, PIN-FORMED (PIN) 1, 2, and 3 fused with GFP. Not only expression levels but also expression domains of PIN proteins were altered in *hpd* mutant in response to Pi starvation. Molecular genetic analysis of *hpd* mutant revealed that the mutant phenotype is caused by the lesion in *ENHANCED SILENCING PHENOTYPE4 (ESP4)* gene whose function is proposed in mRNA 3'-end processing. The results propose that mRNA processing plays crucial roles in Pi homeostasis as well as developmental reprogramming in response to Pi deprivation in *Arabidopsis*.

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

**Metabolic analysis of high salt-adapted *Arabidopsis* suspension cultured cells**

Hyun Jin Chun<sup>1</sup>, Wook-Hun Jung<sup>1</sup>, Mi Suk Park<sup>1</sup>, Hyun Min Cho<sup>1</sup>, Dae-Jin Yun<sup>1</sup>, Young-Shick Hong<sup>2</sup>,  
Min Chul Kim<sup>1\*</sup>

<sup>1</sup>Division of Applied Life Science (BK21 Plus), Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 660–701, Korea.

<sup>2</sup>Department of Food and Nutrition, Chonnam National University, 77 Yongbong-ro, Buk-gu, Gwangju 500–757, Korea

To understand molecular mechanisms underlying adaptation of plant cells to saline stress and stress memory, we developed *Arabidopsis* callus suspension-cultured cells adapted to high salt. Adapted cells to high salt exhibited enhanced tolerance compared to control cells. Moreover, the salt tolerance of adapted cells was stably maintained even after the stress is relieved, indicating that the salt tolerance of adapted cells was memorized. Salt-adapted and stress memorized cells were densely aggregated and formed multi-layered cell lump. Cell morphology analysis using transmission electron microscopy indicated that cell wall thickness of salt-adapted cells was significantly induced compared to control cells. In order to characterize metabolic responses of plant cells during adaptation to high salt stress as well as stress memory, we compared metabolic profiles of salt-adapted and stress-memorized cells with control cells by using NMR spectroscopy. A principle component analysis showed clear metabolic discrimination among control, salt-adapted and stress-memorized cells. Compared with control cells, metabolites related to shikimate metabolism such as tyrosine, and flavonol glycosides, which are related to protective mechanism of plant against stresses were largely up-regulated in adapted cell lines. Moreover, coniferin, a precursor of lignin, was more abundant in salt-adapted cells than control cells. The results provide new insight into metabolic level mechanisms of plant adaptation to saline stress as well as stress memory.

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

## Integrating Omics Analysis of Salt Stress-Responsive Genes in Rice

Seo-Woo Kim, Hee-Jeong Jeong, Ki-Hong Jung

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

The detrimental effect of high salinity on crop production is a serious problem. However, the number of genes with known functions relating to salinity tolerance is very limited in rice. To effectively address this limitation, selection of useful candidate genes and identification of major regulatory factors through global approaches are necessary. To this end, we used three data series of affymetrix array data produced with salt-treated samples from NCBI Gene Expression Omnibus (<http://www.ncbi.nlm.nih.gov/geo/>) and identified 653 rice genes commonly differentially expressed under three salt-stress conditions. While evaluating the quality of selected candidate genes for salt-stress responses, Gene ontology enrichment analysis revealed that responses to salt and water stresses of biological process category are highly overrepresented in salt-stress conditions. In addition, the major salt stress-responsive metabolism process and regulatory gene modules are classified through MapMan analysis, and detailed elements for further studies are suggested. Based on this, we proposed a salt stress-responsive signaling pathway in rice. The functional analysis of the main signal transduction and transcription regulation factors identified in this pathway will shed light on a novel regulatory metabolism process that can be manipulated to develop crops with enhanced salinity tolerance.

Keywords: gene ontology enrichment analysis, MapMan analysis, meta-expression analysis, rice, salt stress

\*Corresponding Author: E-mail: khjung2010@khu.ac.kr

## Development of a simple PCR marker linked to the gene conferring resistance to downy mildew (*Peronospora destructor*) in onion (*Allium cepa* L.)

Seongjun Kim, Sunggil Kim\*

Department of Plant Biotechnology, Chonnam National University, Gwangju 500-757, Republic of Korea

For efficient introgression of the downy mildew resistance gene from a resistant cultivar into domestic breeding lines, molecular markers used for marker-assisted backcrossing (MAB) were developed in onion (*Allium cepa* L.). The resistance gene (*Pd*) was originally introgressed from a wild species, *A. roylei*, by interspecific hybridization, and the resistant gene was known to be positioned at the end of chromosome 3. Therefore, cDNA sequences of loci located at the ends of chromosome 3 of two linkage maps were obtained from a transcriptome database. Primer pairs were designed on exon sequences of eight loci. Among them, the PCR products of the i25255 locus showed length polymorphism between *A. roylei* and onions, and both large and small-sized PCR products were observed in the resistant cultivar. Sequence analysis showed that a 67-bp indel existed in the intron sequences. Based on this indel polymorphism, a simple PCR marker, designated DMR1, was developed. Analysis of diverse onion accessions showed that no accessions contained the *A. roylei*-specific marker genotype except for the resistant cultivar. These results indicated that the DMR1 marker was successfully tagging the *A. roylei* fragment harboring the downy mildew resistance gene, and the resistant cultivar was heterozygous for the resistance gene. After further analysis of multiple loci positioned at chromosome 3, a range of the *A. roylei* fragment introgressed in the resistant cultivar was determined in two linkage maps. On the basis of the range of the *A. roylei* fragment, three molecular markers used for recombinant selection in MAB were also developed.

\*Corresponding Author: Tel. 062-530-2061, E-mail: dronion@jnu.ac.kr

## nSSR 표지를 이용한 안면도지역 곰솔 채종원과 자연집단의 교배양식 유전모수 연간 변이

김영미<sup>1\*</sup>, 홍경낙<sup>2</sup>, 박유진<sup>2</sup>, 홍용표<sup>2</sup>, 박재인<sup>3</sup>

<sup>1</sup>충북 충주시 수안보면 국립산림품종관리센터 종묘관리과

<sup>2</sup>경기도 수원시 오목천동 국립산림과학원 산림유전자원과

<sup>3</sup>충북 청주시 개신동 충북대학교 산림학과

11개 nSSR 표지를 이용하여 안면도지역 곰솔 채종원 '81단지과 내륙과 해안집단의 화분유동과 교배양식 유전모수를 추정하였다. 이형접합도 관측치( $H_o$ )와 Shannon의 유전다양성지수( $I$ )는 안면도 곰솔 채종원(클론:  $H_e = 0.680$ ,  $I = 1.608$ ; 종자:  $H_e = 0.636 \sim 0.646$ ,  $I = 1.472 \sim 1.508$ )과 내륙집단(성목:  $H_e = 0.690$ ,  $I = 1.691$ ; 종자:  $H_e = 0.658 \sim 0.685$ ,  $I = 1.573 \sim 1.636$ ), 해안집단(성목:  $H_e = 0.683$ ,  $I = 1.641$ ; 종자:  $H_e = 0.665 \sim 0.685$ ,  $I = 1.595 \sim 1.669$ ) 간에 유의한 차이는 없으며, 각 집단의 생산년도간에 뿐 만 아니라 세대간에 유의한 차이가 없었다( $P > 0.05$ ). MLTR로 분석으로 추정된 교배양식 유전모수를 추정한 결과 다수 유전자좌 타가교배율(채종원: 0.887~0.919, 내륙: 0.948~0.972, 해안: 0.850~0.932)과 양친 근친교배(채종원: 0.003~0.006, 내륙: 0.038~0.066, 해안: 0.034~0.099)는 집단간에 유의한 차이가 없는 반면, 2009년 생산된 종자에서 추정된 부계상관(채종원: 0.022, 내륙집단: 0.010, 해안집단: 0.047)은 집단간에 유의한 차이가 있다( $P < 0.05$ ). 안면도 지역 곰솔 집단 전반은 화분수의 유전다양성이 높고 교배의 대부분이 다수의 화분수가 기여하는 타가수정으로 이루어지기 때문에 각 집단의 공간구조와 유전구조의 차이에도 불구하고 세대간 유전변이의 감소가 없으며, 집단간에 유전다양성의 유의한 차이가 없는 것으로 생각된다. 반면 임분의 밀도와 규모 등에 따라 생산년도간에 유전모수의 변이를 달리하며, 그중 곰솔 해안집단은 연간 변이에 큰 차이를 보이고 있어 다른 집단에 비해 교배환경의 변화에 반응이 크게 나타나는 것으로 생각된다.

\*주저자: Tel. 043-580-3355, E-mail: sugarmayple2015@gmail.com

## 백합나무 (*Liriodendron tulipifera*) 체세포배 유래 순화묘의 활착을 향상을 위한 몇가지 황산화제 처리 효과

김용욱\*, 김지아, 문홍규, 정수진, 이나눔

경기도 수원시 권선구 온정로 39 국립산림과학원 산림생명공학과

백합나무의 건전 순화묘 생산을 위해 체세포배 유래 발아체를 여러 종류의 황산화제로 전처리 후 토양이식 한 결과 500mg/L Citric acid 처리구에서 가장 높은 87.9%의 순화묘 생존율을 보였으며, 그 외 처리구에서는 대조구(수돗물)보다 다소 높거나 낮은 현상을 보여 별 생존율 차이가 없었다. 묘고 생장의 경우 500mg/L Citric acid를 처리한 처리구에서 44.5cm를 보여 가장 높았으며, 근원경 비교의 경우에서도 마찬가지로 500mg/L Citric acid를 처리한 처리구에서 4.38mm를 보여 가장 높았다. 그러나 엽면적의 경우 수돗물 처리구 유래 순화묘가 66.03cm<sup>2</sup>으로 가장 높게 나타났으나 생중량 비교에서는 500mg/L Citric acid 유래 처리구에서 8.79g으로 가장 높게 나타났다.

\*주저자: Tel. 031-290-1171, E-mail: dragonkim@forest.go.kr

## QTL-seq analysis of flowering time in radish

Youn-Sung Kim<sup>1\*</sup>, Chan-Sup Ko<sup>1,2</sup>, Eun-Ju Lee<sup>1</sup>, Jeong-Pal Suh<sup>1</sup>, Jae-Yong Lee<sup>1</sup>, Hye-Sun Cho<sup>2</sup>

<sup>1</sup>Department of Biotechnology, NH Seed, An-Seong, 456-824, Republic of Korea

<sup>2</sup>Sustainable Bioresource Reserach Center, KRIBB, Daejeon, 305-806, Republic of Korea

To develop molecular markers for late flowering time in radish we performed QTL-seq analysis in which whole genomes are sequenced and SNPs between two groups showing opposite phenotypes in F2 population are analyzed to find regions or QTLs involved in a trait of interest. Two inbred lines (NH-JS1 and NH-JS2) showing opposite phenotypes of flowering time were selected to generate F2 population for the analysis. NH-JS1 showed late flowering time whereas NH-JS2 early flowering time. Genomic DNA from the two lines were extracted and sequenced. In addition F2 population from F1 between NH-JS1 and NH-JS2 was generated and flowering time phenotypes of 180 F2 plants were analyzed. We selected 11 plants with late flowering time and 12 plants showing early flowering time. We extracted DNA from each individuals from the two groups and bulked them to generate two bulked DNA samples that are subject to whole genome resequencing. Preliminary analysis of SNP data from the resequencing showed that there may be several QTLs involved in flowering time control in radish.

\*Corresponding Author: Tel. 031-652-5526, E-mail: yskim0907@hanmail.net

## 다양한 농도의 사과, 감자 및 바나나 추출물 처리가 형질전환 팔레놉시스 원괴체유사체 성장 및 증식에 미치는 영향

노희선\*, 박선경, 김중보

충청북도 충주시 단월동 건국대학교 의료생명대학 생명공학과

팔레놉시스는 최근 심비디움과 더불어 주요 수출화훼작물로 자리잡고 있으며, 국내 화훼시장에서 중요성이 증대되고 소비자들로부터 많은 인기를 받고 있는 실정이다. 이에 반해 국내 팔레놉시스 우량묘 생산체계는 대만, 네덜란드 및 일본 등 난 생산 선진국들과 비교해서 변이발생 및 우량형질 유지 측면에서 부족한 점이 많으며 최근 화훼류 신품종 육성에 많이 도입되고 있는 식물형질전환 기술을 이용한 사례도 국내에는 거의 없는 실정이다. 본 연구는 노화지연 유전자가 삽입된 팔레놉시스 형질전환 식물체의 원괴체유사체 (PLB: protocorm-like bodies)의 증식 및 신초 재분화에 있어서 다양한 천연산물 처리가 어떠한 효과를 나타내는 지 구명하고자 실시하였다. 팔레놉시스 조직배양 및 형질전환 유래 식물체들은 banana powder, apple powder 및 potato powder 이 3가지 천연 산물들을 VW배지에 1, 5, 10, 20, 30, 40 그리고 50 g/l 농도로 각각 첨가하여 생체중 측정 및 신초 분화효율을 측정하여 최적의 형질전환 팔레놉시스 PLB 대량증식 체계를 확립하고자 하였다. 그 결과 apple powder 30 g/l 및 banana powder 40 g/l을 혼용한 처리구에서 PLB 생체중이 대조구 대비 2.2배 이상 증가하여 처리구 중 가장 좋은 결과를 보였으며, 또한 PLB로부터 신초 발생율도 80-85%의 고효율을 나타내었다. 그리고 PLB 조직의 갈변율도 3% 미만으로 양호한 결과를 보여 주었다. 또한 이 두 천연산물의 조합은 형질전환 팔레놉시스 PLB 뿐만 아니라 조직배양 유래 팔레놉시스 PLB 성장과 증식에도 유사한 효과를 나타내었다. 이러한 천연산물의 적절한 첨가는 향후 형질전환 팔레놉시스 식물체 대량증식 체계 확립에 기여할 수 있을 것이다.

\*주저자: Tel. 043-840-3549, E-mail: jbhee1011@kku.ac.kr

---

**PC-27****A highly sensitive real-time PCR systems for detecting rice grain-derived food ingredients in commercial mixed-flour Products**

Ju-Hee Kim, Sun-Goo Hwang, Cheol Seong Jang\*

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

Recently, the increased consumption of mixed-grain flour products have led to improved human health in busy modern life. For this reason, the verification of commercial food authenticity is one of important subjects. The development of DNA techniques such as real-time PCR has led to the increasing efficiency of illegal food product detection. Here, we have developed a comprehensive method for detecting the grain flour of various rice cultivars in commercial food products derived from different plant species. In the genetic variation analysis of different protein coding genes on various chloroplast genomes, we found the high numbers of segregating sites in *rpoB* and *rpoC2* more than in other genes. Thus, we have attempted to develop chloroplast DNA (cpDNA) markers, which were Os\_m\_rpoB in *rpoB*, and Os\_m1\_rpoC2 and Os\_m2\_rpoC2 in *rpoC2*. To assess the applicability of three cpDNA markers, we have identified the appropriate statistical measurements of each marker in various mixed-grain flour samples derived from rice cultivars and different plant species by real-time PCR. In addition, the three cpDNA markers successfully applied for detecting of nonexistent rice flour in different commercial food products.

\*Corresponding Author: Tel. 033-250-6416, E-mail: csjang@kangwon.ac.kr

**PC-28****Profiling of differentially expressed genes with space environments exposed Brachypodium seeds**

Jin-Baek Kim\*, Min Jeong Hong, Young Ha Yoon, Dong Sub Kim, Sang Hoon Kim, Joon-Woo Ahn, Yeong Deuk Jo, Si-Yong Kang

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup, Jeonbuk 580–185, Korea

Space has many distinguishable characteristics from earth such as strong cosmic radiation, microgravity, supervacuum and weak magnetic field. For this reason, space environments can be used an efficient mutagen for plant breeding nowadays. To identify the affected genes by condition in space with outer space, *Brachypodium distachyon* seeds were placed in the Russia Segment (RS) Biorisk module of International Space Station (ISS). *Brachypodium distachyon* is a model system for temperature grass, because they represent the characteristics for annual winter grass. Seeds and organs of plants carried by satellite or spacecraft to space can be genetically mutated by exposing space environment. We performed a duplicated RNA sequencing to profile the differentially expressed genes. As a results, about 700 genes were upregulated and 250 genes were downregulated by cosmic environments, respectively. In the molecular function category, protein kinase and transcription activity related genes were upregulated. Among the many transcription factors (TFs), stress related TFs such as ERF, NAC and WRKY were differentially expressed in space exposed samples. In the future, their expression will be identified by using qRT-PCR.

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

---

**PC-29****Complete chloroplast genome of *Codonopsis lanceolata* and *Platycodon grandiflorus*: insight into evolution of the Asterales and development of molecular marker.**

Jin-hyuk Kim, Sun-Goo Hwang, Cheol-Seong Jang\*

Plant Genomics Lab, Department of Applied Plant Sciences, Kangwon National University, Chuncheon 200–713, Republic of Korea

Asterales are dicotyledonous flowering plants and are one of the Asterid clade, including many species as well as *Codonopsis* and *Platycodon*. Here, we have determined the complete chloroplast genome sequences of *C. lanceolata* and *P. grandiflorus* by using the targeted *denovo* assembly method of short reads derived from whole genome resequencing. The total lengths of each chloroplast genome sequence are 156,180 bp for *C. lanceolata* and 155,453 bp for *P. grandiflorus*. In their chloroplast genomes, 106 genes (75 protein-coding genes, 4 rRNA genes, 23 tRNA genes, and 4 hypothetical chloroplast open reading frames [*ycf*s]) exhibited the relatively similar positions. Also, 7 protein-coding genes commonly showed to contain introns in both *C. lanceolata* and *P. grandiflorus* chloroplast genome, while *psaA* gene contain intragenic regions only in *P. grandiflorus* chloroplast genome. In further analysis, we identified the codon usage bias to A or T and found the different simple sequence repeat (SSR) loci of each chloroplast genome (18 SSR loci of *C. lanceolata* and 16 SSR loci of *P. grandiflorus*). In the phylogenetic trees based on 72 protein-coding genes, *C. lanceolata* is more closely related to *P. grandiflorus* than the other plant species order Asterales. Also, we found the highest sequence diversities of 12 protein-coding genes in small single copy (SSC) region than in the inverted repeat (IRs) and large single copy (LSC) region, and 3 genes such as *rpoC2* (LSC region), *ndhB* (IRs region), and *ndhF* (SSC region) showed the highest number of segregating sites in each region. Additionally, we developed the molecular markers for phylogenetic applications of *C. lanceolata* and *P. grandiflorus* chloroplast genome.

\*Corresponding Author: Tel. 033-250-6416, E-mail: csjang@kangwon.ac.kr

**PC-30****MAB SNP marker development to accelerate the breeding of Chinese cabbage**

Jinhee Kim\*, Do-Sun Kim, Hye-Eun Lee, Yul-Kyun Ahn, Jeong Ho Kim

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

The goal of marker-assisted backcrossing is to reduce the number of generations significantly by using genome-based molecular markers. Among other types of molecular markers, SNP (single nucleotide polymorphism) is mostly used in genetic diversity analysis due to its abundance. To develop high-throughput SNP marker for MAB system, we selected 20 Chinese cabbage lines each represent traits as inner leaf color, disease resistance, head type and maturity etc. Then, we sequenced the transcriptomes of 20 lines by using Illumina Hiseq2000. The average transcriptome size was 1.37 Gbase, and the average of short reads mapping rate was about 62.15% (30xcoverage). We identified 13,976 SSR markers and 380,198 SNPs by aligning contigs of 20 Chinese cabbage lines. To develop SNP marker set, we chose 409 SNPs that covers the whole *Brassica rapa* transcriptome. The filtering criteria were depth, polymorphism, segregation ratio, lack of adjacent SNP and copy number. We positioned the selected SNP markers to the Chinese cabbage linkage map. Clustering dendrogram was produced using SNP marker and three different clusters were generated. The result showed that the genotyping data is partially linked to the phenotyping data. We assume that the developed SNP marker set can be applied in the Chinese cabbage MAB system soon.

## **CSGM Designer: a convenient platform for designing cross-species intron-spanning genic markers**

Jin-Hyun Kim<sup>1</sup>, Chaeyoung Lee<sup>1</sup>, Joo-Seok Park<sup>2</sup>, Douglas R. Cook<sup>3</sup>, Hong-Kyu Choi<sup>4\*</sup>

<sup>1</sup>Department of Medical Bioscience, Dong-A University, Busan, Republic of Korea

<sup>2</sup>Department of Applied Bioscience, Dong-A University, Busan Republic of Korea

<sup>3</sup>Department of Plant Pathology, University of California, Davis, CA 95616, USA

<sup>4</sup>Department of Genetic Engineering, Dong-A University, Busan Republic of Korea

Genetic markers are tools that can facilitate molecular breeding, even in species lacking genomic resources. An important class of genetic markers is those based on orthologous genes, because they can guide hypotheses about conserved gene function. For under-studied species a key bottleneck in gene-based marker development is the need to develop molecular tools that reliably access genes with orthology to the genomes of well-characterized reference species. Here we report an efficient platform for designing cross-species gene-derived markers in legumes. The automated platform, named CSGM Designer (URL: <http://tgil.donga.ac.kr/CSGMdesigner>), facilitates rapid and systematic design of cross-species genic markers. The underlying database is composed of genome data from five legume species whose genomes are substantially characterized. Use of CSGM designer is enhanced by graphical displays of query results, which we describe as “circular viewer” and “search-within-results” functions. CSGM platform provides a virtual PCR representation, called eHT-PCR, that predicts the specificity of each primer pair simultaneously in multiple genomes. CSGM Designer output was experimentally validated for the amplification of orthologous genes using 16 genotypes representing 12 crop and model legume species, distributed among the galegoid and phaseoloid clades. Successful cross-species amplification was obtained for 85.3% of PCR primer combinations. CSGM Designer spans the divide between well-characterized crop and model legume species and their less well-characterized relatives. The outcome is PCR primers that target highly conserved genes for polymorphism discovery, enabling functional inferences and ultimately facilitating trait-associated molecular breeding.

**\*Corresponding Author:** Tel. 051-200-7508, E-mail: [hkchoi@dau.ac.kr](mailto:hkchoi@dau.ac.kr)

**Molecular mapping of QTLs related to cold tolerance at seedling stage in rice**

Tae Heon Kim<sup>1</sup>, Yeon-Jae Hur<sup>1</sup>, Saisbeul Lee<sup>1</sup>, Ji-Yoon Lee<sup>1</sup>, Youngbo Son<sup>1</sup>, Sung Hwan Oh<sup>1</sup>, Sang-Ik Han<sup>1</sup>, Jun-Hyun Cho<sup>1</sup>, You-Chun Song<sup>1</sup>, Jong-Hee Lee<sup>2</sup>, Min-Hee Nam<sup>1</sup>, Dong-Soo Park<sup>1</sup>, Yeong-Up Kwon<sup>1</sup>, Dongjin Shin<sup>1\*</sup>

<sup>1</sup>Department of Southern Area Crop Science, Paddy Crop Research Division, National Institute of Crop Science, RDA, Miryang, 627–803, Korea

<sup>2</sup>Research Policy Bureau, RDA, Jeonju, 560–500, Korea

Rice is a staple food crop for more than half of the world population. Severe losses of rice production was caused by various environmental conditions such as cold, heat and flooding annually. Rice is a highly sensitive to low temperature below 15-20 °C because of originating from tropical or subtropical climates. Especially, seedling of rice is easily damaged to low temperature and result in seedling yellowing, growth retardation, reduced tillering and yield losses at last. We used a recombinant inbreeding lines (RIL) population of 384 individuals derived from a cross between Hanareum 2, a highly cold sensitive variety and Unkwang, a cold tolerant variety for molecular mapping of QTLs related to cold tolerance. Seedling discoloration of each lines and parents caused by cold response were investigated in field condition after transplanting. And leaf samples of RIL population were collected for evaluation of chlorophyll content using 80% acetone extraction. The seedling of each lines and parents was subjected to low temperate by 5~13 °C during 14 days. The cold recovery score (CRS) of RILs was recorded after 4 days recovery period according to standard evaluation system (SES, IRRI). Total of eight QTLs were detected on chromosome 1, 7, 8, 10, 11 and 12 using cold tolerance traits, chlorophyll content, seedling discoloration and cold recovery score in 384 RILs. The *qCRS12*, which detected on chromosome 12 between two flanking markers id12002113, id12002563 (1.1 Mbp) showed 25 LOD score with 26% of phenotypic variation of cold recovery score in RILs population. The positive allele contributing to cold tolerance came from the cold tolerant parent Unkwang. The result may provide useful information for a marker-assisted breeding program to improve cold tolerant in rice.

\*Corresponding Author: Tel. 055-350-1185, E-mail: jacob1223@korea.kr

**Up-dating of new dCAPS markers for mapping yield-related traits using MGRIL**

Ye-Ji Lee<sup>1</sup>, Hyun-Ju Lee<sup>1</sup>, In-Seon Jeong<sup>1</sup>, Seon-Hwa Bae<sup>1</sup>, Hyeon-So Ji<sup>2</sup>, Gang-Seob Lee<sup>3</sup>, Ung-Han Yoon<sup>1</sup>, Jang-Ho Hahn<sup>1</sup>, Tae-Ho Kim<sup>1\*</sup>

<sup>1</sup>Genomics Division, National Academy of Agricultural Science, RDA, Jeonju, 560–500, Republic of Korea

<sup>2</sup>Molecular Breeding Division, National Academy of Agricultural Science (NAAS), RDA, Jeonju, 560–500, Republic of Korea

<sup>3</sup>Biosafety Division, National Academy of Agricultural Science (NAAS), Jeonju, 560–500, Republic of Korea

The next-generation sequencing(NGS) technology is being used for more effective genetic mapping. In previous study, we obtained 60x coverage of sequence from Milyang23 and Gihobyeeo on average comparing with Nipponbare reference genome. Also, we developed new derived cleaved amplified polymorphic sequence(dCAPS) markers based on the single nucleotide polymorphisms(SNPs) in coding region sequence(CDS) between these varieties. Totally, 1,726,798 SNPs between Milyang23 and Gihobyeeo were detected. Among them, 146 SNP were selected for making dCAPS markers and located on genetic map with previously reported 219 PCR-based DNA markers. The map was applied to the detection of quantitative trait loci(QTLs) for stem internode diameters, culm length and panicle length within MGRIL population, and six QTLs with relatively high LOD score were found at three chromosomes; culm length and stem diameter including the first internode diameter, third and fourth internode diameter.

This study showed that the NGS allowed the rapid discovery of a large number of SNPs for dCAPS marker. So, we tried to find out more single nucleotide polymorphisms(SNPs) which were located on the whole genome sequence, such as un-translated region(UTR), intron, Inter-region and coding region sequence(CDS) between Milyang23 and Gihobyeeo varieties. And we collected phenotypic information about culm length, panicle length, four stem internode diameters and panicle number in rice MGRIL population for QTLs. Furthermore, results of QTL analysis described above will shows relevance of molecular markers in mapping genes for useful breeding.

## **Development of simple sequence repeat (SSR) markers from ramie (*Boehmeria nivea* L.) and application to the genetic resources**

Yoon Kyung Uhm<sup>1</sup>, Hye-young Lee<sup>1</sup>, Jinkyu Woo<sup>1</sup>, JiHyeon Kim<sup>1</sup>, Young-Mi Kim<sup>2</sup>, Yong-Su Jung<sup>2</sup>, Hyun Sam Lee<sup>2</sup>, Sanghyun Lee<sup>3</sup>, Ho Bang Kim<sup>1\*</sup>

<sup>1</sup>Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 420–852, Republic of Korea

<sup>2</sup>Yeong–Gwang Agricultural Technology Center, Yeong–Gwang 513–842, Republic of Korea

<sup>3</sup>Department of Integrative Plant Science, Chung–Ang University, Anseong 456–756, Republic of Korea

Ramie (*Boehmeria nivea* L.) is a hardy perennial herbaceous plant of the Urticaceae family and has been grown as a fiber crop in several countries including Korea for many centuries. Ramie leaves also have been traditionally used as a major ingredient of a type of rice cake called ‘Song-pyun’ in the Southwest area of Korea, especially Yeong-Gwang province. Despite its economic importance, the molecular genetics of ramie have not been studied in detail yet. Genetic resources of ramie were widely collected from domestic local sites by Bioenergy Crop Research Center (RDA) and Yeong-Gwang Agricultural Technology Center. For the systematic and efficient management of the genetic resources, we developed SSR (simple sequence repeat) markers of ramie. To do this, we generated microsatellite-enriched genomic DNA libraries using magnetic bead hybridization selection method. 247 non-redundant contigs containing SSR motif were generated using nucleotide sequences of 376 clones from the libraries. Primer sets were designed from the flanking sequences of the repeat motif. Finally, we selected 10 SSR markers, possibly showing polymorphism among the genetic resources. Results on the genotype analysis of the ramie genetic resources using the SSR markers will be presented.

**Acknowledgments:** This work was supported by the Bio-Industry Technology Development Program grant, funded by IPET, Republic of Korea (grant no. 112139-03-1-HD030 to Ho Bang Kim).

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

## **Functional analysis of a stress-related gene *BrTSR53* conferred salt tolerance in Yeast**

A-Ram Kim, Hyemin Lim, Hyun-Ju Hwang, Sung Han Park, Chang-Kug Kim, Hyeonso Ji, Jung-Il Cho, Soo-Chul Park, Gang-Seob Lee\*

National Academy of Agricultural Science, Rural Development Administration, Jeonju, Jeonlado, Korea

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

\***Corresponding Author:** Tel. 031-299-1656, E-mail: kangseoblee@korea.kr

## **A conserved oligomeric Golgi complex component-related protein is essential for pollen development in Arabidopsis**

Tien Dung Nguyen, Binbin Li, Sung Aeong Oh, Soon Ki Park\*

School of Applied Biosciences, Kyungpook National University, Korea

To identify genes that play critical roles during male gametogenesis in Arabidopsis, we have isolated several pollen morphological mutants from a mutagenized seed pool generated with a T-DNA activation vector. In this study, we have focused on a mutant plant producing ~50% abnormal pollen grains including high levels of collapsed pollen at maturity. The pollen developmental analysis showed that the mutant pollen phenotype was first observed at tricellular stage. Interestingly, the mutation was only maintained as a heterozygote due to the severely reduced genetic transmission through both sexes. TAIL PCR analysis led to the identification of the responsible gene which encodes a conserved oligomeric golgi complex component-related protein (COGCC). RT-PCR analysis showed predominant expression of the gene in reproductive organs including developing spores. The gene identity was confirmed by the result that mutant plants harboring a T-DNA containing corresponding wild type gene produced less level of mutant pollen grains. Furthermore, confocal laser scanning microscopy using mature pollen expressing COGCC-RFP driven under the native promoter showed small punctate signals, which are likely to be from the Golgi complex. Further experiments for co-localization of the COGCC-RFP with the Golgi markers are underway.

\***Corresponding Author:** Tel. 053-950-7751, E-mail: [psk@knu.ac.kr](mailto:psk@knu.ac.kr)

## Identification of microspore-active promoters using transgenic rice and *Arabidopsis*

Tien Dung Nguyen<sup>1</sup>, Moe Moe Oo<sup>1</sup>, Sung Aeong Oh<sup>1</sup>, Thi Hoai Thuong Nguyen<sup>1</sup>, Hyo-Jin Park<sup>1</sup>, Jong Tae Song<sup>1</sup>, Moon-Soo Soh<sup>2</sup>, Ki-Hong Jung<sup>3</sup>, Soon Ki Park<sup>1\*</sup>

<sup>1</sup>School of Applied Biosciences, Kyungpook National University, Korea.

<sup>2</sup>Department of Molecular Biology, Sejong University, Korea.

<sup>3</sup>Department of Plant Molecular Systems Biotechnology & Crop Biotech Institute, Kyung Hee University, Korea.

We recently reported rice promoters that are active in late stages of pollen development. However, rice promoters that allow manipulation of gene expression at earlier stages of pollen development are still very limited to date. In this study, we have chosen 10 putative microspore promoters, *OsMSP1* through *OsMSP10*, based on publicly available transcriptomic datasets in rice (*Oryza sativa* L.). Sequence analysis of these promoter regions revealed some *cis* regulatory elements involved in pollen-specific expression. We also examined promoter activities using the promoter-GUS reporter constructs in both transgenic rice and *Arabidopsis*. In rice, all of the 10 promoters directed GUS signals from the microspore stage throughout the all stages of pollen development. In addition, while GUS signals from 4 promoters, *OsMSP2*, *OsMSP7*, *OsMSP9* and *OsMSP10*, seem to be expressed preferentially during pollen development, those from other six promoters were observed in vegetative tissues such as leaves, stems, and roots of seedlings. Similarly, in *Arabidopsis*, all of the 10 promoters directed GUS signals during pollen development. In detail, 8 promoters, *OsMSP1* ~ *OsMSP8* directed GUS signals from the microspore stage, whereas 2 promoters, *OsMSP9* and *OsMSP10*, exhibited GUS signals from tricellular stage. Furthermore, seven promoters, except for *OsMSP1*, *OsMSP2* and *OsMSP10*, showed GUS signals in shoot apical region or root tissues of seedlings. Furthermore, we verified microspore activity of four promoters, *OsMSP1*, *OsMSP2*, *OsMSP3* and *OsMSP6*, by complementation analysis of the *sidecar pollen* (*scp*) mutant which displays microspore-specific defects. Currently, further analyses are underway for GUS expression of T<sub>2</sub> generation in transgenic rice and *scp* complementation with remaining promoters.

\*Corresponding Author: Tel. 053-950-7751, E-mail: psk@knu.ac.kr

## **Development of Multiplex PCR for Species-Specific Identification of the Poaceae family Based on chloroplast *rpoC2* genes**

Jun-Cheol Moon<sup>1,2</sup>, Ju-Hee Kim<sup>1</sup>, Cheol Seong Jang<sup>1\*</sup>

<sup>1</sup>Plant Genomics Lab., Department of Applied Plant Sciences, Kangwon National University, Chuncheon 200–713, Republic of Korea

<sup>2</sup>Agriculture and Life Sciences Research Institute, Kangwon National University, Chuncheon 200–713, Republic of Korea

In this study, we report that the development of a multiplex PCR method using species-specific primers for the simultaneous detection of *Poaceae* family members, including adlay, barley, maize, rice and wheat, based on the sequence polymorphism of the DNA-directed RNA polymerase beta" chain (*rpoC2*) genes. Species-specific primers were constructed with common forward primer and each reverse primers which have differences on the basis of sequences. Each primer pairs could amplify PCR products of 443 bp for rice, 346 bp for barley, 278 bp for adlay, 221 bp for wheat and 96 for maize, respectively, from the five chloroplast DNAs. The series of template DNA concentrations were identified by the sensitivity of multiplex PCR. The band of products were clearly amplified from the DNA concentration range of 0.01 to 10 ng/μL. In addition, the species-specific primers were examined for the detection of seven commercial flour mixed products. The combination of the sensitivity of a multiplex PCR with the specificity of the primers for the detection of species would allow to be applied in analyses of processed foods.

**\*Corresponding Author:** Tel. 033-250-6416, E-mail: csjang@kangwon.ac.kr

**Development of marker-free transgenic rice expressing wheat storage protein, *TaGlu-Ax1*, for increasing quality processing of bread and noodle**

Soo-Kwon Park, So-Hyeon Baek, Dool-Yi Kim, Myoung-Ryoul Park, Na-Ra Lee, Kyoung Soon Shin, Su-Kyoung Jeon, Eun-Jae Kim, Sun-Lim Kim, Jung-Kyoung Moon\*

National Institute of Crop Science (NICS), Wanju-gun, Jeollabuk-do, 565-851, Korea

Rice flour is used in many food products. However, dough made from rice lacks extensibility and elasticity, whereas that of wheat is suitable for many food products including breads. We have produced marker-free transgenic rice plants containing a wheat *TaGlu-Ax1* gene encoding the HMG-GS from the Korean wheat cultivar 'Jokyeong' using the *Agrobacterium*-mediated co-transformation method. The *TaGlu-Bx7*-own promoter was inserted into a binary vector for seed-specific expression of the *TaGlu-Ax1* gene. Two expression cassettes comprised of separate DNA fragments containing only *TaGlu-Ax1* and hygromycin phosphotransferase II (*HPTII*) resistance genes were introduced separately to the *Agrobacterium tumefaciens* EHA105 strain for co-infection. Each EHA105 strain harboring *TaGlu-Ax1* or *HPTII* was infected to rice calli at a 3:1 ratio of *TaGlu-Ax1* and *HPTII*, respectively. Then, among 210 hygromycin-resistant T<sub>0</sub> plants, we obtained 20 transgenic lines with both *TaGlu-Ax1* and *HPTII* genes inserted into the rice genome. We reconfirmed integration of the *TaGlu-Ax1* gene into the rice genome by Southern blot analysis. Transcripts and proteins of the wheat *TaGlu-Ax1* were stably expressed in the rice T<sub>1</sub> seeds. Finally, the marker-free plants harboring only the *TaGlu-Ax1* gene were successfully screened at the T<sub>1</sub> generation.

\*Corresponding Author: Tel. +82-63-238-53214, E-mail: moonjk@rda.go.kr

## Delimitation of Genomic Location for *Frl* locus Conferring Resistance to Fusarium Crown Root Rot in Tomato

Bichsaem Kim<sup>1</sup>, Jihyun Hwang<sup>1</sup>, Joon Young Kim<sup>2</sup>, Byung Sup Kim<sup>2</sup>, Sung Ran Min<sup>3</sup>, Huijung Jung<sup>4</sup>, Ill-Sup Nou<sup>4</sup>, Younghoon Park<sup>1</sup>

<sup>1</sup>Department of Horticultural Bioscience, Pusan National University, Miryang, Korea

<sup>2</sup>Department of Plant Science, Gangneung–Wonju National University, Gangneung, Korea

<sup>3</sup>Plant Systems Engineering Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon, Korea

<sup>4</sup>Department of Horticulture, Suncheon National University, Suncheon, Korea

Fusarium crown root rot (FCRR) is a severe fungal disease caused by *Fusarium oxysporum* f. sp. *radicis-lycopersici* (FORL) in tomato. Resistance to FORL is conferred by single dominant locus *Frl* on chromosome 9, but its precise genomic location is not clearly determined. In this study, detailed location of *Frl* was assessed by using a set of molecular markers physically anchored on Chr.9 and F<sub>2</sub> and RIL population derived from FORL-resistant inbred AV107-4 (*S. lycopersicum*) x susceptible L3708 (*S. pimpinellifolium*). Bioassay of the two populations with a FORL strain isolated from Korea resulted in single dominant inheritance of the resistance. Two SCAR and 11 CAPS markers encompassing 3.6Mb~72Mb of Chr.9 were developed from the Tomato-EXPEN 2000 map and SolCAP SNP-array analysis. These markers were genotyped on 345 F<sub>2</sub> plants. A high level of cosegregation with the resistance were observed for 5 markers which were mapped at a large physical interval of 5.1Mb (T1212) to 46.4Mb (SSR237), indicating that genetic recombination was highly suppressed in this region. Cosegregation of these markers with *Frl* was confirmed by using 126 RILs. The results implied that, in contrast with the previously reported long arm, *Frl* is present on a pericentromeric region of short arm of Chr. 9, in which crossing-over is severely suppressed. The marker set was further tested on 12 FORL-resistance or susceptibility commercial cultivars. Unlike the biparental populations, frequent linkage break was observed for T1212 and D4 in commercial cultivars. T1212 and D4 showed 50% and 100% match with the phenotype, respectively. D4, a CAPS, was converted to a high resolution melting (HRM) marker and tested on 55 breeding lines from private seed companies (Fig.3). All breeding lines showed the HRM genotype for resistance allele, indicating that D4 can be useful for selecting FORL-resistance tomato plants.

## A new approach for detecting natural selection signature among rice in-paralogs

Kyu-Won Kim<sup>1,2</sup>, Tae-Sung Kim<sup>1,2</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

Ratio of functional changes from orthologous genes is being widely used for detecting the signature for natural selection between species. However, one to one orthologous genes allows only for the analysis due to methodological limitation. A number of genes have in-paralogs as a result of gene expansion in crops. Here, we report a new approach for detecting accelerated evolution, which includes in-paralogs as well as one to one orthologs. This new approach can detect many novel accelerated genes among rice in-paralogs, which have not been investigated yet.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## Transcriptome changes in rice (*Oryza sativa* L.) for high zinc content at the early milky stage

Eun-Beom Heo<sup>1</sup>, Min-Young Yoon<sup>1</sup>, Buung Choi<sup>1</sup>, Donghwan Shim<sup>2</sup>, Beom-Seok Park<sup>2</sup>, Won-Il Kim<sup>3</sup>, Yong-Jin Park<sup>1,4\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>The Agricultural Genome Center, National Academy of Agricultural Science, Rural Development Administration, Jeonju, Republic of Korea

<sup>3</sup>Chemical Safety division, National Academy of Agricultural Science, Rural Development Administration, Jeonju, Republic of Korea

<sup>4</sup>Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

Zinc (Zn) deficiency is one of the important abiotic factors limiting rice productivity world-wide and also a widespread nutritional disorder affecting human health. Zinc is one of the most important essential micronutrient for human. About thirty percentage world's population doesn't still get enough zinc through their diets. As a staple food of over half world's population, rice should take the responsibility to provide much more zinc in the future. We analyzed the transcriptome profiles for rice grain from high zinc content and low zinc content lines at the early milky stage using the Illumina Sequencing method. The analysis results for the sequencing data indicated that many transcripts showed different expressions between high zinc content and low zinc content in early milky stage of rice and RT-qPCR analyses confirmed the expression patterns of selected transcripts. Functional analysis of the differentially expressed transcripts indicated that genes have functional annotation and their functions are mainly involved in oxidation-reduction, metabolic, transport, transcript regulation, defense response and photosynthetic processes. Based on the functional annotation of the differentially expressed genes, the possible process that regulates these differentially expressed transcripts in rice grain responding to Zinc at the early milky stage was further analyzed. The functional classification of those genes indicated their connection with various metabolic pathways, Zinc transport, signal transduction, transcriptional regulation, and other processes related to growth and development in early milky stage of rice. Using Illumina sequencing technology, the differences between the transcriptomes of high zinc content and low zinc content lines the early milky stage was described here for the first time. The candidate transcripts may provide genetic resources that may be useful in the improvement of Zinc concentration of rice. The model proposed here is based on differences in expression and transcription between two rice lines. In addition, the model may support future studies on the molecular mechanisms underlying plant responses to Zinc.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## Resequencing reveals different domestication rate for *BADH1* and *BADH2* in rice (*Oryza sativa*)

Qiang He<sup>1</sup>, Jie Yu<sup>1</sup>, Tae-Sung Kim<sup>1</sup>, Yoo-Hyun Cho<sup>1,2</sup>, Young-Sang Lee<sup>3</sup>, Yong-Jin Park<sup>1,4\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Science, Yesan 340–702, Kongju National University, Republic of Korea

<sup>2</sup>Seedpia, 85, Maesil-ro, Kwonsun-ku, Suwon, 441–882 Republic of Korea

<sup>3</sup>Department of Medical Biotechnology, Soonchunhyang University, Asan 336–745, Republic of Korea

<sup>4</sup>Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

*BADH1* and *BADH2* are two homology genes, encoding betaine aldehyde dehydrogenase in rice. In the present study, we scanned *BADHs* sequences of 295 rice cultivars, and 10 wild rice accessions to determine the polymorphisms, gene functions and domestication of these two genes. A total of 16 alleles for *BADH1* and 10 alleles for *BADH2* were detected in transcription region of cultivars and wild species. Association study showed that *BADH1* has significant correlation with salt tolerance in rice during germination stage, the SNP P1<sub>1483</sub>(T/A) is highly correlated with salt tolerance index (STI) ( $P < 10^{-4}$ ). While, *BADH2* was only responsible for rice fragrance, of which two *BADH2* alleles (P2<sub>3036</sub>, P2<sub>5390</sub>) explain 97% of aroma variation in our germplasm. It indicated that there are no overlapping functions between the two homology genes. In addition, a large LD block was detected in *BADH2* region, however, no large LD blocks in a 4-Mb region of *BADH1*. Only *BADH2* region shown significant bias Tajima's D value from the balance. Extended haplotype homozygosity study revealed fragrant accessions had a large LD block that extended around the mutation site (P2<sub>3036</sub>) of *BADH2*, while both of the *BADH1* alleles (SNP P1<sub>1483</sub>(T/A)) did not show large extended LD block. All these results suggested that *BADH2* was identified as a domesticated gene during rice evolution, while *BADH1* was not selected by human beings.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## **Discovery of a novel fragrant allele and development of functional markers for fragrance in rice**

Qiang He<sup>1</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

Aroma in rice (*Oryza sativa* L.) results from the loss of function of the betaine aldehyde dehydrogenase (*Badh2*) gene on chromosome 8. An 8-bp deletion in exon 7 of *Badh2* was reported to be the main allele functionally associated with fragrance. The discovery of new functional alleles will provide additional genetic resources to improve fragrant rice. In this study, we sequenced the *Badh2* gene in 30 rice accessions and filtered the *Badh2* polymorphisms from whole genome re-sequence data of 295 rice accessions. Seven alleles were detected from the sequence data. Six of the seven were known alleles and one was a novel allele (*badh2-E12*). The novel allele was a 3-bp deletion in exon 12. Five functional markers, targeting six of the seven alleles, were identified. Fourteen accessions were selected to test the utility of these markers. The five molecular markers reliably distinguishing this fragrant rice from other fragrant or non-fragrant rice accessions. Analysis of two F2 rice population validated the genetic markers FME12-3 and FME14I as functional markers. These two markers co-segregated with the fragrance phenotype. These markers will be used in a *Badh2* diversity study and to breed improved fragrant rice accessions via marker-assisted selection.

\***Corresponding Author:** Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## Orthologous based study to detect the fast evolutionary genes related to rice pre-harvest sprouting

Wei Tong<sup>1</sup>, Tae-Sung Kim<sup>1,2</sup>, Kyu-Won Kim<sup>1,2</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

Pre-harvest sprouting (PHS) results in lower yields for rice and other crops, especially in rainy season before harvest. By using gene based functional studies to reveal the mechanism of PHS related pathways can be a good way in breeding for more PHS resistant accessions. Orthologous genes, which are homologous genes that diverged after a speciation event, generally maintain a similar function in different species to that of the ancestral gene in which they evolved from. Applied with a McDonald-Kreitman Test (MKT), we examined more than 10,000 orthologous genes between rice (*Oryza sativa*) and *Brachypodium* (outgroup) based on different phenotypic groups in order to find some fast evolutionary genes in rice PHS. Three groups which represented the PHS susceptible (group 1), PHS medium (group 2) and PHS resistant (group 3) were separated based on the phenotype and each group was examined with the outgroup for MKT. Total 60 fast evolutionary genes that have a positive selection with  $FDR \leq 0.05$  were found in the three groups, and 19, 5 and 8 genes were specific existed in group 1, 2 and 3, respectively. Annotation of these genes were conducted and the predicted functions were investigated, leading that one Ethylene receptor-like gene that may related to PHS based on the previous studies, which need to be validated later, however. In addition, network analysis of these characterized genes were also investigated, which could reveal the connection of genes between each other. Moreover, the association study between the candidate gene ethylene receptor and the PHS phenotype was performed and indicated that this gene is significantly correlated with PHS in rice. All these above indicated that with this orthologous based method, we can find some important candidate genes that may play an important role in some traits.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## **A chloroplast variation map generated using whole genome re-sequencing of Korean landrace rice reveals phylogenetic relationships among *Oryza sativa* subspecies**

Wei Tong<sup>1</sup>, Qiang He<sup>1</sup>, Xiao-Qiang Wang<sup>1</sup>, Min-Young Yoon<sup>1</sup>, Won-Hee Ra<sup>1</sup>, Feng Peng Li<sup>1</sup>, Jie Yu<sup>1</sup>, Win Htet Oo<sup>1</sup>, Sun-Kyung Min<sup>1</sup>, Buung Choi<sup>1</sup>, Eun-Beom Heo<sup>1</sup>, Byoung-Kook Yun<sup>2</sup>, Kyu-Won Kim<sup>1</sup>, Tae-Sung Kim<sup>1</sup>, Chang-Yong Lee<sup>2</sup>, Yong-Jin Park<sup>1,3\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Department of Industrial & Systems Engineering, Kongju National University, Cheonan 330–717, Republic of Korea

<sup>3</sup>Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

Although the overall structure of the chloroplast genome is generally conserved, a number of sequence variations have been identified, which are valuable for plant population and evolutionary studies. Here, we constructed a chloroplast variation map of 30 landrace rice strains of Korean origin, using the *Oryza rufipogon* chloroplast genome (Genbank: NC\_017835) as a reference. Differential distribution of single nucleotide polymorphisms (SNPs) and indels across the rice chloroplast genome is suggestive of a region-specific variation. Population structure clustering revealed the existence of two clear subgroups (*indica* and *japonica*) and an admixture group (*aus*). Phylogenetic analysis of the 30 landrace rice strains and six rice chloroplast references suggested and supported independent evolution of *O. sativa indica* and *japonica*. Interestingly, two “*aus*” type accessions, which were thought to be *indica* type, shared a closer relationship with the *japonica* type. One hypothesis is that “Korean *aus*” was intentionally introduced and may have obtained *japonica* chloroplasts during cultivation. We also calculated the nucleotide diversity of 30 accessions and compared to six rice chloroplast references, which shown a higher diversity in the *indica* and *aus* groups than in the *japonica* group in lower level substitution diversity.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## Evolutionary study for rice iron uptake from Korean authentic rice core set

Buong Choi<sup>1</sup>, Min-Young Yoon<sup>1</sup>, Tae-Sung Kim<sup>1,2</sup>, Kyu-Won Kim<sup>1,2</sup>, Donghwan Shim<sup>3</sup>, Beom-Seok Park<sup>3</sup>, Won-Il Kim<sup>4</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

<sup>3</sup>The Agricultural Genome Center, National Academy of Agricultural Science, Rural Development Administration, Jeonju, Republic of Korea

<sup>4</sup>Chemical Safety division, National Academy of Agricultural Science, Rural Development Administration, Jeonju, Republic of Korea

Iron is an essential mineral found in every cell of the human body to make the oxygen-carrying proteins hemoglobin and myoglobin. More than 2 billion people face Fe deficiency. Rice can be a potentially valuable source to supplement that mineral since it is staple food for two-thirds of the world's population. To bring the nutritional level of the milled product up to that of the whole grain (brown), rice should be enriched with thiamin, niacin and iron. Also iron has important role that absorption from the photosynthetic cells proceeds, chlorophyll synthesis and the growth process of the plant. Orthologous genes, which are homologous genes that diverged after a speciation event, generally maintain a similar function in different species. We applied a McDonald-Kreitman Test (MKT) to examine more than 10,000 orthologous genes between rice (*Oryza sativa*) and *Brachypodium* (outgroup) based on different phenotypic groups. This analysis was undertaken to find fast evolutionary genes in rice iron uptake. Three groups were separated based on the phenotype and each group was examined with the outgroup for MKT. Fast evolutionary genes that have a positive selection with  $FDR \leq 0.05$  were detected at each groups. Annotation of these genes were conducted and the predicted functions were also discussed here. And also, the association study between the candidate gene related to iron uptake phenotype was performed. These results support that using this orthologous based method, we may find some important candidate genes underlying the iron uptake in rice.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## A computer program for combining SNP information and estimating SNP-related statistics

Chang-Yong Lee<sup>1\*</sup>, Yong-Jin Park<sup>2,3</sup>

<sup>1</sup>Department of Industrial and Systems Engineering, Kongju National University, Cheonan 330–717, Republic of Korea

<sup>2</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>3</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

We report the C language implementation of a program that merges SNP data from all samples and estimates various statistical quantities related to SNP. The software combines the SNP information from different samples according to the SNP position in the nucleotide sequence. The combined SNP information is converted into HapMap format that can be used as an input for genome-wide association analysis for quantitative traits. The software additionally provides estimates of the minor allele frequency, the heterozygosity ratio, and the In/Del frequency. The software is prepared as a stand-alone program and is downloadable from <http://info.kongju.ac.kr/snpmerge/>.

\*Corresponding Author: Tel. 041-521-9432, E-mail: clee@kongju.ac.kr

## Evolutionary study for rice flowering time genes in Korean authentic rice core set

Min-Young Yoon<sup>1</sup>, Tae-Sung Kim<sup>1,2</sup>, Kyu-Won Kim<sup>1,2</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

In rice (*Oryza sativa* L.), there is a diversity in flowering time that is strictly genetically regulated by plenty of genes. The floral transition from vegetative to reproductive development is a very important step in the life cycle of a flowering plant. Orthologous genes, which are homologous genes that diverged after a speciation event, generally maintain a similar function in different species. with a McDonald-Kreitman Test (MKT), we examined more than 10,000 orthologous genes between rice (*Oryza sativa*) and *Brachypodium* (outgroup), based on different phenotypic groups, to find some fast evolutionary genes of rice flowering time. Three groups with early flowering time (group 1), midium flowering time (group 2) and late flowering time (group 3) were separated and each group was examined for McDonald-Kreitman Test (MKT). Total 70 fast evolutionary genes under a positive selection were found in the three groups, and 14, 42 and 14 genes were specific existed in group 1, 2 and 3, respectively. Annotation of these genes were conducted and the predicted functions were also surveyed. In addition, network analysis of these characterized genes were also investigated to infer related pathways. And also, the association study between the one early flowering factor and the flowering time phenotype was performed and indicated that this gene is significantly correlated with flowering time in rice. These results suggest that using this orthologous based method, we could find some important candidate genes underlying flowering time regulations.

\***Corresponding Author:** Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## Evolution related genes of salt tolerance in rice revealed by McDonald-Kreitman Test

Jie Yu<sup>1</sup>, Tae-Sung Kim<sup>1,2</sup>, Kyu-Won Kim<sup>1,2</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340-702, Republic of Korea

<sup>2</sup>Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340-702, Republic of Korea

Salt is the major factor limiting crop productivity in saline soils. Development of genetic basis of high salt-tolerant rice is necessary to satisfy urgent needs in rice breeding. In this study, 295 rice accessions from a Korean authentic core set were used to identify the evolution associated genes regarding salt tolerance. By using McDonald-Kreitman Test (MKT), we detected orthologous genes in rice (*Oryza sativa*) using *Brachypodium* as an outgroup to investigate fast evolved genes that express differentially based on distinct phenotypic groups. Three groups which represented the salt sensitive (group 1), salt medium tolerant (group 2) and salt tolerant (group 3) were separated and each group was examined with the outgroup in neutral and non-neutral polymorphism together with the divergence levels. Total 53 fast evolutionary genes that have a positive selection with  $FDR \leq 0.05$  were found in the three groups. Among them, 15, 31 and 7 genes were included exclusively in group 1, 2 and 3, respectively. Annotation of these genes showing the predicted functions were checked. Two genes were found to be related to high salt tolerance based on the previous studies. Besides, association study of the candidate gene alleles and salt tolerance phenotype was carried out, indicating that these genes were correlated with salt tolerance. All these result support that using this type of evolution study, we may find some important candidate genes which are related to important traits in rice, such as the salt tolerance, providing important information for future gene based molecular breeding and functional analysis in rice.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

---

**PC-51**

## **Transcriptome changes of rice(*Oryza sativa* L.) in oil accumulation at the early milky stage**

Win Htet Oo<sup>1</sup>, Tae-Sung Kim<sup>1,2</sup>, Donghwan Shim<sup>3</sup>, Beom-Seok Park<sup>3</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

<sup>3</sup>The Agricultural Genome Center, National Academy of Agricultural Science, Rural Development Administration, Jeonju, Republic of Korea

Rice bran has been reckoned as a potential source of edible oil contained 15-20 % of oil, in its natural state, also contains several constituents of potential significance in diet and health. Interest has focused primarily upon gamma-oryzanol, tocotrienols, and tocopherols, all of which demonstrate antioxidant properties. We analyzed the transcriptome profiles for rice grain from high and low oil content lines at the early milky stage using the Illumina sequencing method. This analysis indicated that many transcripts showed different expressions level between high and low oil content rice. The functional classification of those genes indicated their connection with various metabolic pathways, oil transport, signal transduction, transcriptional regulation, and other processes. The results obtained here will enable to understand how changes in oil concentration or availability are interpreted into adaptive responses in early milky stage of rice. Based on the functional annotation of the differentially expressed genes, the possible processes that regulate these expressed transcripts in rice grain was further analyzed. The candidate transcripts may provide genetic resources that may be useful in the improvement of oil contents of rice.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

**PC-52**

## **A pipeline for genome assisted breeding to efficiently exploit useful alleles from rice germplasm**

Tae-Sung Kim<sup>1,2</sup>, Kyu-Won Kim<sup>1,2</sup>, Yong-Jin Park<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340–702, Republic of Korea

<sup>2</sup>Legume Bio–Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340–702, Republic of Korea

Rice (*Oryza sativa* L.) is one of the most important staple crops in the world, providing main energy source for more than half of the world's population. It is even closely associated with economic and political stability in many developing countries of Asia and Africa. These days, moreover, amount of land suitable for the agriculture is shrinking due to a variety factors, such as rapid climate changes and industrializations, while rice eating human populations keeps growing. To meet the nutritional and socio-economic demands worldwide, dedicated efforts in developing superior rice varieties need to be reinforced, accumulating and combining beneficial alleles as much as possible from rice germplasm. Here, we propose a pipeline for genome assisted breeding where new genomic technologies including GWAS, omics and evolutionary studies together with follow-up breeding programs are integrated. Once pinpointing candidates genes, the integrated genomics approach allows informed choice of parents for the following breeding program based on the haplotype information, in addition to providing precise molecular marker information. We also conducted proof-of-concept analysis, using various agriculturally important phenotypes for rice improvements.

\*Corresponding Author: Tel. 041-330-1201, E-mail: yjpark@kongju.ac.kr

## **Generation and characterization of T-DNA insertion population for genetically-modified rice**

Hyemin Lim, A-Ram Kim, Hyun-Ju Hwang, Jung-Il Cho, Hyeonso Ji, Chang-Kug Kim, Soo-Chul Park, Gang-Seob Lee\*

National Academy of Agricultural Science, Rural Development Administration, Jeonju 565–851, Republic of Korea

We have generated 383 independent transgenic lines for genetically modified (GM) rice that contained *PsGPD* (*Glyceraldehyde-3-Phosphate Dehydrogenase*), *ArCspA* (*Cold Shock Protein*), *BrTSR15* (*Triple Stress Resistance 15*) and *BrTSR53* (*Triple Stress Resistance 53*) genes over-expression constructs under the control of the constitutive (CaMV 35S) promoter. TaqMan copy number assay was determined inserted T-DNA copy number. Also flanking sequence tags (FSTs) analysis was isolated from 203 single copy T-DNA lines of transgenic plants and sequence mapped to the rice chromosomes. In analyzing single copy lines, we identified 157 flanking sequence tags (FSTs), among which 58 (36%) were integrated into genic regions and 97 (62%) into intergenic regions. About 27 putative homozygous lines were obtained through multi-generations of planting, resistance screening and TaqMan copy number assay. To investigate the transgene expression patterns, quantitative real-time PCR analysis was performed using total RNAs from leaf tissue of single copy, intergenic region of T-DNA insertion and homozygous T2 plants. The mRNA expression levels of the examined transgenic rice were significantly increased in all of the transgenic plants. In addition, myc-tagged 35S:BrTSR15 and 35S:BrTSR53 transgenic plants were displayed higher levels of transgene protein. These results may be useful for producing of large-scale transgenic plants or T-DNA inserted mutants in rice.

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

## Molecular dissection of a rice RING finger protein induced by salt and drought treatments

Yong Chan Park, Cheol Seong Jang\*

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

As sessile organisms, plants have evolved mechanisms that allow them to adapt and survive periods of various environmental stresses including high salinity and drought. The ubiquitin-proteasome system (UPS) is an integral player in plant response and adaptation to various abiotic stresses. Understanding UPS function has centered mainly on defining the role of E3 ubiquitin ligases, which are the substrate-recruiting component of the ubiquitination pathway. Here, we report on Ring finger E3 ligase, *Oryza sativa* salt- and drought-induced RING finger protein1 gene (*OsSDRFP1*) in defense responses to osmotic stresses. Results of qRT-PCR and *In vitro* ubiquitination assay demonstrated that OsSDRFP1 act as an E3 ligase in response to salt and drought stresses. In this study, Subcellular localizations showed that the OsSDRFP1 was observed in cytosol (66%) and nucleus (34%) under non-treated conditions. However, the fluorescence signals of rice protoplasts after salt treatments detected in nucleus (60%) higher than in cytosol (30%). The Arabidopsis plants overexpressing OsSDRFP1 clearly exhibited hypersensitive responses to salt stress, whereas, OsSDRFP1-overexpressing plants were more tolerant to both drought- and ABA-stresses than the wild-type plants. These results might suggest that OsSDRFP1 has a dual function as a regulator of high salt- and drought-stresses.

Keywords: RING E3 ligase, Abiotic stress, Ubiquitin-proteasome system

\*Corresponding Author: E-mail: csjang@kangwon.ac.kr

## Dissection of Korean landrace chamoe (*Cucumis melo* var. *makuwa*) genome

Inkyu Park<sup>1,2</sup>, Jae-Pil Choi<sup>1</sup>, Jungeun Kim<sup>1</sup>, Jeongyeo Lee<sup>1</sup>, Soohwan Lim<sup>1</sup>, Mi-Ye Lee<sup>1,2</sup>, Hey-Ran Kim<sup>1\*</sup>

<sup>1</sup>Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 305–806, Republic of Korea

<sup>2</sup>College of Agriculture and Life Science, Chungnam National University, 99 Daehak-ro, Yuseong-gu, Daejeon 305–764, Republic of Korea

The oriental melon (*C. melo* var. *makuwa*), called ‘Chamoe’ in Korean, is a popular fruit crop cultivated mainly in Asia and a high-market value crop in Korea. To provide a genomic resource as a reference genome for the *Cucurbitaceae* crop improvement, we performed whole genome sequencing of Korean landrace, Gotgam chamoe. We used Illumina HiSeq2000 sequencing platform to generate 89 Gb (205X) of paired and mate pair sequence reads. The pre-processed reads were de novo assembled resulting in 4,764 scaffolds with a N50 scaffold length of 249kb. This assembly represented 379.8Mb which was 84.7% of the 448Mb of the whole genome. The assembled draft was predicted 26,634 genes of which 80% were predicted by known protein or *C. melo* unigene homology. Approximately 20% of predicted genes were hypothetical. A total of 1,885 non-coding RNA was detected including rRNA. The transposable elements were accounted for 21% (71.6Mb) of the total assembly. All the marker candidates including SSR, INDEL, SNP were mined and presented. The draft genome will provide a useful platform for genomic research and improvement for *Cucurbitaceae* crops.

\*Corresponding Author: Tel. 042-860-4345, E-mail: kimhr@kribb.re.kr

---

**PC-56****Profile of econdary metabolites and related gene expressions of *Panax ginseng* adventitious roots induced from 5 korean ginseng cultivars cultured in bioreactors**

Hyun-Seung Park<sup>1</sup>, Dong-Kyu Lee<sup>2</sup>, Yun Sun Lee<sup>1</sup>, Sang-Choon Lee<sup>1</sup>, Murukarthick Jayakodi<sup>1</sup>, Sung Won Kwon<sup>2</sup>, Tae-Jin Yang<sup>1\*</sup>

<sup>1</sup>Department of Plant Science, Plant Genomics and Breeding Institute, and Research Institute for Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Republic of Korea

<sup>2</sup>College of Pharmacy, Seoul national university, Seoul Korea

*Panax Ginseng* is a perennial medicinal plant originated from North-east asia. Because of its well-known tonic effects mainly from ginsenosides, various types of processed ginseng products have been distributed around the world. Here, we analyzed secondary metabolite profiling of adventitious roots of 5 korean ginseng cultivars, Chunpoong (CP), Sunhyang (SH), Gopoong (GO), Sunun (SU), and Cheongsun (CS). At the same time, the profiles of relative gene expressions related to ginsenoside biosynthesis pathway were compared among ginseng cultivars. Secondary metabolite profiles were revealed by UPLC/Q-TOF-MS from extracts of bioreactor derived adventitious roots of five ginseng cultivars. Using principal component analysis, secondary metabolite profiles of ginseng cultivars were categorized into three groups. Metabolites with high VIP values were annotated using known database and standards compounds. Relative gene expression of ginsenoside related gene were analyzed using realtime PCR. The three groups had distinct metabolite contents. Furthermore, gene expression profiles related to ginsenoside were also different, which might contribute diverse secondary metabolite composition of ginseng cultivars. Further integrated analysis would provide a relationship between genetic background of ginseng cultivars and secondary metabolite profiles. This research was supported by “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01100801)” Rural Development Administration, Republic of Korea.

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

**PC-57****Gene identification of *Arabidopsis* gametophytic mutation showing aberrant pollen phenotype using map-based cloning approach**

Hyo Jin Park, Nguyen Thi Hoai Thuong, Tien Dung Nguyen, Sung Aeong Oh, Soon Ki Park\*

Division of Plant Biosciences, Kyungpook National University, Deagu, South Korea

Map-based cloning is a basic method for identifying the mutated gene in plants. We selected the gametophytic mutant, named as AP-26-09, in activation-tagging pool. Mutant plant showed various kinds of pollen phenotype, such as the different number of nucleus or abnormal shapes. For the map-based gene cloning, we conducted phenotypic analysis of F2 mapping population through the screening of DAPI-stained pollen using fluorescence microscopy. Genomic DNA of F2 plants is prepared from leaves of approximately 1000 plants. In order to define chromosomal region where mutation is located, we designed SSLP markers and performed PCR amplification. In this study, we characterized gametophytic mutant and determined the chromosomal location using map-based approach.

\*Corresponding Author: Tel. 053-950-7751, E-mail: psk@knu.ac.kr

## Mapping QTLs of resistance to head splitting in cabbage (*Brassica oleracea* L. var. *capitata* L.)

Wenxing Pang, Xiaonan Li, Seong Ho Lee, Dasom Kim, Sang Heon Oh, Su Ryun Choi, Yong Pyo Lim\*

Molecular Genetics and Genomics Lab, Department of Horticulture, Chungnam National University, Daejeon 305–764, Republic of Korea.

Cabbage head splitting can greatly affect both the quality and commercial value of cabbage (*Brassica oleracea*). To detect the genetic basis of head-splitting resistance, a genetic map was constructed using an F2 population derived by crossing “748” (head-splitting-resistant inbred line) and “747” (head-splitting-susceptible inbred line). The map spans 830.9cM and comprises 270 markers distributed in nine linkage groups, which correspond to the nine chromosomes of *B. oleracea*. The average distance between adjacent markers was 3.6cM. A total of six quantitative trait loci (QTLs) conferring resistance to head splitting were detected in chromosome 2, 4, and 6. Two QTLs, *SPL-2-1* and *SPL-4-1*, on chromosomes 2 and 4, respectively, were detected in the experiments over 2 years, suggesting that these two potential loci were important for governing the head-splitting resistance trait. Markers BRPGM0676 and BRMS137, which were tightly linked with head-splitting resistance, were detected in the conserved QTL *SPL-2-1* region using bulked segregant analysis. Synteny analysis showed that *SPL-2-1* was anchored to a 3.18Mb genomic region of the *B. oleracea* genome, homologous to crucifer ancestral karyotype E block in chromosome 1 of *Arabidopsis thaliana*. Moreover, using a field emission scanning electron microscope, significant differences were observed between the two parental lines in terms of cell structures. Line “747” had thinner cell wall, lower cell density, larger cell size, and anomalous cell wall structure compared with the resistant line “748”. The different cell structures can provide a cytological base for assessing cabbage head splitting.

\*Corresponding Author: Tel. 042-821-5739, E-mail: yplim@cnu.ac.kr

---

**PC-59**

## **Characterization and analysis of *OsUPS*, a U-box containing E3 ligase that respond to phosphate starvation in rice.**

Ki-Deuk Bae, Doh-Hoon Kim\*

Department of Genetic engineering, College of Natural Resources and Life Science, Dong-a University, Busan 604-714, Republic of Korea

The ubiquitin-26S proteasome system is important in the quality control of intracellular proteins. The ubiquitin-26S proteasome system includes the E1 (ubiquitin activating), E2 (ubiquitin conjugating) and E3 (ubiquitin ligase) enzymes. U-box proteins are a derived version of RING-finger domains, which have E3 enzyme activity. Here, we present the isolation of a novel U-box protein, *OsUPS*, from rice (*Oryza sativa*). The cDNA encoding the *O. sativa* U-box protein (*OsUPS*) comprises 1338bp, with an open reading frame of 445 amino acids. The open reading frame of the *OsUPS* protein is comprised of notable domains: a single ~70-amino acid domain and a GKL domain that contains conserved glycine, lysine/ arginine residues and leucine-rich feature. We found that full-length expression of *OsUPS* was up-regulated in both rice plants and cell culture in the absence of inorganic phosphate (Pi). A self-ubiquitination assay indicated that the bacterially expressed *OsUPS* protein had E3 ligase activity, and subcellular localization results showed that *OsUPS* was located in the chloroplast. Suppression of *OsUPS* resulted in severe signs of toxicity caused by the over-accumulation of Pi. These results support the notion that *OsUPS* plays an important role in the Pi signaling pathway through the ubiquitin-26S proteasome system.

\*Corresponding Author: Tel. 051-200-7507, E-mail: dhkim@dau.ac.kr

**PC-60**

## **Cloning and identification of the partial major ampullate silk protein gene from the spider *Araneus ventricosus* in rice.**

Ki-Deuk Bae, Doh-Hoon Kim\*

Department of Genetic engineering, College of Natural Resources and Life Science, Dong-a University, Busan 604-714, Republic of Korea

Fibroin silk proteins from spider or silkworm are attractive biomaterials that are of particular biotechnological interest for industrial and medical purposes because of their unique physical and mechanical properties. In this study, we generated and characterized the transgenic rice plant expressing a spider silk protein. Spider silks have great potential as biomaterials with extraordinary properties. Here, we report the cloning and characterization of the major ampullate silk protein gene from the spider *Araneus ventricosus*. A cDNA encoding the partial major ampullate silk protein (*AvMaSp*) was cloned from *A. ventricosus*. An analysis of the cDNA sequence shows that *AvMaSp* consists of a 240 amino acid repetitive region and a 99 amino acid C-terminal non-repetitive domain. The peptide motifs that were found in the spider major ampullate silk proteins, (A)<sub>n</sub>, (GA)<sub>n</sub>, and (GGX)<sub>n</sub>, were conserved in the repetitive region of *AvMaSp*. Phylogenetic analysis further confirmed that *AvMaSp* belongs to the spider major ampullate spidroin family of proteins. Recombinant *AvMaSp-R* was degraded abruptly by trypsin. However, *AvMaSp-R* was stable at 100 °C for at least 30 min. Additionally, the *AvMaSp-R* was stable at pH values from 2 to 12 for at least 1 h. Taken together, our findings describe the molecular structure and biochemical properties of the *A. ventricosus* major ampullate silk protein and demonstrate its potential as a biomaterial.

\*Corresponding Author: Tel. 051-200-7507, E-mail: dhkim@dau.ac.kr

---

**PC-61****Identification and analysis of *osgasd* gene.**

Ki-Deuk Bae, Doh-Hoon Kim\*

Department of Genetic engineering, College of Natural Resources and Life Science, Dong-a University, Busan 604-714, Republic of Korea

We used an efficient system to create rice mutant by Ac/Ds transposon insertion mutagenesis, such as selected homozygous mutant in dwarf phenotypes. We reported here the identification of function of dwarf *OsGASD* gene (*Oryza sativa* Gibberellin Acid Sensitive Dwarf). *OsGASD* gene encodes a 344 amino acid polypeptide and no homology proteins in Gene Bank. The *osgasd* mutant was sensitive to exogenous gibberellic acid (GA) level. We performed experiment to controlled expression the *OsGASD* gene, its role in plant development, a quantitative analysis of endogenous GA content and sensitivity to GA. The *osgasd* mutant includes smaller amount of active GAs than wild-type. *osgasd* mutant plant of GA biosynthesis pathway causes GA deficiency and dwarf plants, and endogenous GA suppliance can restore the wild type phenotype in this mutant. There result indicated that *OsGASD* gene regulated the elongation of shoot, stem and plant height. The increased expression of *OsGASD* gene dramatically induces expression of the factors associated with GA biosynthesis, whereas *osgasd* mutant suppression of the factors associated with GA biosynthesis, loading to dwarf phenotypes. That applied GA3 at the plant development stage to survey the response of *OsGASD* gene to GA3. We suggest that *OsGASD* gene is related to factors of GA biosynthesis pathway regulating rice internodes development.

\*Corresponding Author: Tel. 051-200-7507, E-mail: dhkim@dau.ac.kr

**PC-62*****OsMYB4p*, an R2R3-type MYB transcription factor, improves phosphate uptake in rice**

Ki-Deuk Bae, Doh-Hoon Kim\*

Department of Genetic engineering, College of Natural Resources and Life Science, Dong-a University, Busan 604-714, Republic of Korea

R2R3 MYB transcription factors play regulatory roles in plant responses to various environmental stresses and nutrient deficiency. In this study, we isolated MYB-like gene respond to phosphorus deprivation in rice and designated *OsMYB4P*, an R2R3 MYB transcription factor, from rice under low-phosphate conditions. *OsMYB4P* is 993bp long and encodes a 330 amino acid polypeptide. *OsMYB4P* was localized in the nucleus and acted as a transcriptional activator. Transcriptional levels of *OsMYB4P* in cell suspension, shoots, and roots of rice increased under low phosphate conditions. Shoots and roots of *OsMYB4P* overexpressing plants grew well in high and low phosphate conditions. In addition, root system architecture was altered considerably as a result of *OsMYB4P* overexpression. Under both phosphate sufficient and deficient conditions, more Pi accumulated in shoots and roots of *OsMYB4P* overexpressing plants than in the wild type. Overexpression of *OsMYB4P* led to greater expression of Pi transporter-family proteins *OsPT1*, *OsPT2*, *OsPT4*, *OsPT7*, and *OsPT8* in shoots, and to decreased or unchanged expression of these proteins in roots, with the exception of *OsPT8*. These results demonstrate that *OsMYB4P* may be associated with efficient utilization of Pi in rice.

\*Corresponding Author: Tel. 051-200-7507, E-mail: dhkim@dau.ac.kr

---

**PC-63**

## **Characterizataion and histological analysis of leaf development related gene in rice.**

Ki-Deuk Bae, Doh-Hoon Kim\*

Department of Genetic engineering, College of Natural Resources and Life Science, Dong-a University, Busan 604-714, Republic of Korea

Establishment of rice library is an essential approach for rice functional genomics study. Utilizaing maize transposable element Ac/Ds is a promising method to construct insertional mutagenesis library of rice. Ac/Ds tagging system has received extensive application in rice during the past several years. The maize Ds element is one of the main tagging vehicles used in rice. Narrow leaf mutant have short height, narrow leaf width and large angle. To compare with wild type and narrow leaf mutant in detail, we observed the leaves under microscope. In specific portion(large and small vein), no significantly reduce cell size and number of cell. Knock-out of the *OsNLR*(narrow leaf ribokinase) gene inhibits internodes, panicles, angle(between leaf and stem), leaf, seed. *OsNLR* was shown to specifically expressed on leaf. In real time PCR analysis with mature leaf of wild type and mutant, there might be a functional association between *OsAGO7*, *NRL1*, *NAL1* and *NAL7* in regulating leaf development. We tested on the experimental field using wild type and mutant plants. In agricultural traits that contain leaf and seed related traits(except angle) significantly reduce in mutant plants. These results demonstrate that *OsNLR* gene may be associated with leaf development.

\***Corresponding Author:** Tel. 051-200-7507, E-mail: dhkim@dau.ac.kr

**PC-64**

## **Study of transgenic rice plants in rich expressed sheep serotonin N-Acetyltransferase**

Yeong Byeon, Hyoung Yool Lee, Kyoungwhan Back\*

Department of Biotechnology, Bioenergy Research Center, Chonnam National University, Gwangju, Republic of Korea

Serotonin N-acetyltransferase (SNAT), the penultimate enzyme in melatonin biosynthesis, catalyzes the conversion of serotonin into N-acetylserotonin. Plant SNAT is localized in chloroplasts. To test SNAT localization effects on melatonin synthesis, we generated transgenic rice plants overexpressing a sheep (*Ovis aries*) SNAT (OaSNAT) in their chloroplasts and compared melatonin biosynthesis with that of transgenic rice plants overexpressing OaSNAT in their cytoplasm. To localize the OaSNAT in chloroplasts, we used a chloroplast targeting sequence (CTS) from tobacco protoporphyrinogen IX oxidase (PPO), which expresses in chloroplasts. The purified recombinant CTS:OaSNAT fusion protein was enzymatically functional and localized in chloroplasts as confirmed by confocal microscopic analysis. The chloroplast-targeted CTS:OaSNAT lines and cytoplasmexpressed OaSNAT lines had similarly high SNAT enzyme activities. However, after cadmium and butafenacil treatments, melatonin production in rice leaves was severalfold lower in the CTS:OaSNAT lines than in the OaSNAT lines. Notably, enhanced SNAT enzyme activity was not directly proportional to the production of N-acetylserotonin, melatonin, or 2-hydroxymelatonin, suggesting that plant SNAT has a role in the homeostatic regulation of melatonin rather than in accelerating melatonin synthesis.

\***Corresponding Author:** Tel. 062-530-0441, E-mail: kback@chonnam.ac.kr

---

**PC-65****Presence of melatonin 2-hydroxylase in rice (*Oryza sativa*) plants**

Yeong Byeon, Kyoungwhan Back\*

Department of Biotechnology, Bioenergy Research Center, Chonnam National University, Gwangju, Republic of Korea

Although melatonin biosynthetic genes from plants have been cloned, the melatonin catabolism mechanisms remain unclear. To clone the genes responsible for melatonin metabolism, we ectopically expressed 35 fulllength cDNAs of rice 2-oxoglutarate-dependent dioxygenase (2-ODD) in *Escherichia coli* and purified the corresponding recombinant proteins. In vitro 2-ODD assays showed four independent 2-ODD proteins that were able to catalyze melatonin into 2-hydroxymelatonin, exhibiting melatonin 2-hydroxylase (M2H). These M2H proteins had peak activities at pH 8.0 and 30°C. The  $K_m$  ranged from 121  $\mu$ M to 371  $\mu$ M with the  $V_{max}$  ranging from 1.7 to 18.5 pkat/mg protein, respectively. The M2H enzyme activities were dependent on cofactors such as  $\alpha$ -ketoglutarate, ascorbate, and  $Fe^{2+}$ , similar to the 2-ODD enzymes. M2H activity was inhibited by prohexadione-Ca, an inhibitor of 2-ODD, in a dose-dependent manner. M2H activity was high in the roots of rice seedlings, concurrent with high transcription levels of 2-ODD 21, suggesting that 2-ODD 21 was a major gene for M2H activity. Analogous to the high M2H activity in the roots, 2-hydroxymelatonin was found in large quantities in roots treated with melatonin. These results suggest that melatonin was metabolized into 2-hydroxymelatonin by the M2H genes in plants, but the physiological significance of 2-hydroxymelatonin remains to be examined in the future.

\*Corresponding Author: Tel. 062-530-0441, E-mail: kback@chonnam.ac.kr

**PC-66****Production of doubled haploids through micropore culture in F<sub>1</sub> hybrids of yellow sarson and turnip rape of *Brassica rapa***

Mi-Suk Seo, Mi-Sun Moon, Kyung-gin Lee, So Youn Won, Sangho Kang, Seong-Han Sohn, Jung Sun Kim\*

Department of Agricultural Biotechnology, National Academy of Agricultural Science, RDA, JeonJu, 560–500, Korea

*Brassica rapa* subspecies show morphological variability, containing vegetable types and oilseed types. The yellow sarson types (*Brassica rapa* ssp. *tricoloris*) have distinct morphology, yellow seeded and contain some lines with very unique character of tetralocular ovary. For genetic studies on tetralocular ovary related to high seed yields, we produced genetic segregation population with F<sub>2</sub> and double haploid (DH) population. The yellow sarson LP8 (YS-033, CGN06835) with character of tetralocular ovary used as a maternal plant and crossed by LP21 of turnip rape type with bilocular ovary as paternal plant. We took on the micropore cultures on immature bud which is collected on sizing from 2mm to 3.2mm for DH population. The regenerations DH plants are analyzed by ploidy determination using flow cytometer and selected on diploid plants. These regenerated DH and F<sub>2</sub> plants are doing bud pollination and measuring the phenotype traits. Also, these populations will be used for identify of genetic locus relate to tetralocular ovary using genotyping by sequencing.

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

---

**PC-67**

## **RNA-seq analysis on tetralocular ovary and high seed yields in yellow sarson of *Brassica rapa***

Mi-Suk Seo, So Youn Won, Sangho Kang, Seong-Han Sohn, Jung Sun Kim\*

Department of Agricultural Biotechnology, National Academy of Agricultural Science, RDA, JeonJu, 560–500, Korea

In *Brassica* as matter of seedling manner, they have the bilocular ovary and 20–28 seeds per silique after fertilization. Rarely some of *B. juncea* and yellow sarson (*Brassica rapa* ssp. *tricoloris*) have multilocular ovary. In this study, the LP8 (YS-033, CGN06835) is shown tetralocular ovary as well as high seed yields. As microscope study for the different size of immature bud sections and we have known the floral meristem with already four locules in immature buds less size than 1mm of LP8. To identify of determining of tetralocular ovary formation, RNA-seq was carried out on the isolated RNA from less than 1mm and from 1mm of bud size respectively. By contrast tetralocular ovary and bilocular ovary, Chiifu is used. A total of 994 differentially expressed genes(DEGs) are detected in only LP8. Among the DEGs, we identify 18 DEGs in only immature buds of less size than 1mm. The expression patterns of 18 DEGs are validated by real time quantitative PCR and these genes are cloned and the sequence analyzed. At present, 12 candidate gene are analyzed by sequencing and there are detected by large fragment insertion as well as SNPs in sequence comparison to Chiifu. We will perform the genetic transformation of these DEG genes in Arabidopsis for relation between genes and tetralocular ovary. Our results will be helpful in understanding for mechanisms of tetraovular ovary in *Brassica rapa*.

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

**PC-68**

## **Genome-wide identification of pepper NB-LRR gene family and their evolutionary history in Solanaceae**

Eunyoung Seo<sup>1</sup>, Seon-In Yeom<sup>2</sup>, Seungill Kim<sup>1</sup>, Joohyun Lee<sup>1</sup>, Saet-Byul Kim<sup>1</sup>, Eunbi Choi<sup>1</sup>, Eun Hye Choi<sup>1</sup>, Doil Choi<sup>1</sup>

<sup>1</sup>Department of Plant Science, Seoul National University, Seoul, Korea.

<sup>2</sup>Department of Agricultural Plant Science, Gyeongsang National University, Jinju, Gyeongnam, Korea.

Plants have evolved elaborate innate immune systems against invading pathogens, such as bacteria, fungi, oomycetes, viruses and insects. Among them, intracellular immune receptors known as nucleotide-binding site and leucine-rich repeat (NB-LRR) play critical roles in effector-triggered immunity (ETI) regarding to plant defense. Here, we identified potential NB-LRR coding sequences from pepper genome using bioinformatics analysis and performed comparative analysis with Solanaceae plants. As a result, we identified 267, 443, and 755 NBS-encoding genes in the genome of tomato, potato, and pepper, respectively. These may indicate that the Solanaceae NB-LRRs were evolved through species-specific unequal-duplication event. Further phylogenetic and clustering analyses revealed that Solanaceae NB-LRRs were classified into the 14 subgroups with 1 TNL and 13 CNL types. We found that the genes in CNL-G1 and CNL-G2 subgroup were highly expanded compared to other subgroup showing a large portion of NB-LRR in pepper genome. Among 755 NB-LRRs in pepper genome, 623 were physically mapped on all 12 pepper chromosome pseudomolecules. Furthermore, a number of NB-LRRs in the same group were physically clustered by tandem array in the specific chromosome. Genome-wide identification of pepper NB-LRR family and their evolutionary analysis could provide an important resource for identification and characterization of genes for breeding of disease resistance crops.

## Suitability of Fourier Transform Infrared Spectroscopy as a screening method for the production of useful mutant lines in *Panax ginseng*

Javzandulam Ulziisaikhan<sup>1</sup>, Jun-Ying Zhang<sup>1</sup>, Hong-Yu Li<sup>1</sup>, Hyeon-Jin Sun<sup>2</sup>, Somi Kim<sup>1</sup>, Sung-Jun Song<sup>3</sup>, Hyo-Yeon Lee<sup>1,2</sup>

<sup>1</sup>Department of Biotechnology, Jeju National University, Jeju 690–756, Korea

<sup>2</sup>Subtropical Horticulture Research Institute, Jeju National University, Jeju, 690–756, Korea

<sup>3</sup>Institute for Nuclear Science and technology, Jeju National University, Jeju, 690–756, Korea

*Panax ginseng* C.A Meyer is commonly used in Asian traditional medicine to treat a variety of diseases. Ginsenosides are glycosylated triterpenes, referred to saponins, have been especially noted as active compounds contributing to the various efficacy of ginseng. In this study, we are trying to select high saponin content of ginseng lines from the gamma irradiated adventitious roots. Recently, we have generated several mutant ginseng lines improving ginsenoside content by gamma radiation. The mutant lines were selected by phenotypes and ginsenoside content (HPLC analysis) of the irradiated adventitious root lines. However, the ginsenoside content of the mutant lines was not sufficient for commercial use and the selection method was not suitable for large scale of mutant line selection. In this study, we are testing Fourier transfer infrared spectroscopy (FT-IR) as a new selection method of mutant lines in *Panax ginseng*. About 5,000 pieces of *Panax ginseng* adventitious roots were exposed to gamma radiation (<sup>60</sup>Co). Irradiation dosages were 0, 25, 50 and 70Gy. Survival rate of the irradiated samples was evaluated by counting the number of survival main roots after 5 weeks culture in the solid MS medium with NAA, IAA and 5% sucrose. In present, we are collecting the survived adventitious root lines (about 900 lines) from the gamma irradiated ginseng roots for FT-IR and HPLC analysis. After analysis of FT-IR and HPLC, we will assess the suitability of the FT-IR as a screening method for the preparation of mutant lines in ginseng.

Acknowledgement: This work was supported by Basic Science Research Program through the National Research Foundation (NRF) (2009-0094059)

\*Corresponding Author: Tel. 064-754-3347, E-mail: hyoyeon@jejunu.ac.kr

## Gene transferability between herbicide-resistant *B. napus* and Korean varieties of *B. rapa*

Soo-In Sohn<sup>1\*</sup>, Young-Ju Oh<sup>2</sup>, Si-Myung Lee<sup>1</sup>, Sung-Dug Oh<sup>1</sup>, Gang-Seob Lee<sup>1</sup>, Doh-Won Yun<sup>1</sup>, Hyun-Suk Cho<sup>1</sup>

<sup>1</sup>National Academy of Agricultural Science, Jeonju, 560–500, Republic of Korea

<sup>2</sup>Institute of Future Environmental Ecology, Jeonju, 561–842, Republic of Korea

It is necessary to carry out a risk assessment to determine the consequences of releasing a particular plant species containing specific transgenes before transgenic plants can be grown under field conditions. Gene flow from transgenic plants to wild closely related species has raised concern recently. Since transgenic crops were released in 1996, the global area of transgenic crops has been increasing rapidly. The transgene introgression from transgenic crops to their wild relatives is unavoidable in some species. Transgene introgression is of concern because the crop–wild plant hybrids might be conferred with a selection advantage to increase their performance, which could result in negative ecological consequences to natural ecosystems. The genus *Brassica* has 159 species, including a number of wild species that are of great importance to the economy. Most transgenic *Brassica* gene flow research has focused on the most successful cross between transgenic oilseed rape *Brassica napus* and its wild relatives *Brassica rapa*, a widely distributed weed in the farming system in Europe and America, since the hybridization can spontaneously happen and the generations can backcross to *B. rapa* easily in the wild conditions. In this study, we aimed to characterize transgene introgression, segregation, and expression in backcrossed generations between transgenic *B. napus* and *B. rapa*. These results will contribute to the environmental risk assessment and assist in biosafety management.

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

## Molecular marker evaluated for heat tolerance in wheat

Jae-Han Son<sup>1\*</sup>, Kyeung-Hoon Kim<sup>2</sup>, Chon-Sik Kang<sup>1</sup>, Young-Keun Cheong<sup>1</sup>, Jong-Chul Park<sup>1</sup>, Kyong-Ho Kim<sup>1</sup>, Yang-Kil Kim<sup>1</sup>, Young-Jin Oh<sup>1</sup>, Jong-Ho Park<sup>1</sup>, Tae-Hwa Song<sup>1</sup>, Jae-Seong Choi<sup>1</sup>, Bo-Kyeong Kim<sup>1</sup>

<sup>1</sup>Crop Breeding Division, National Institute of Crop Science, RDA, 565–851, Korea

<sup>2</sup>Department of Southern Area, National Institute of Crop Science, RDA, 627–803, Korea

High temperature is one of major environmental stress. Some of molecular markers related heat stress or tolerance have been reported by many researchers. Heat tolerance managing is difficult through the phenotypic selection, so marker assisted selection (MAS) using molecular markers like as RAPD, SSR ect. was tried to selection of useful traits for heat tolerance. Fourteen SSR markers reported by previous research were selected for this research. These markers were linked to important traits including grain filling duration, HIS (Heat susceptibility index) grain filling duration. In this study, we tried to evaluate 14 SSR markers for MAS using 31 useful wheat resources including 24 crossing line from Turkey and six Korean wheat cultivars using 14 SSR markers. The average of the number of alleles and PIC values in this study were 6.14 and 0.63, respectively. Two major clades and six sub clades were grouped by phylogenetic tree using UPGMA program. Six Korean wheat cultivars were distinct from other Turkey resources in the phylogenetic dendrogram. From the results, we expected that these markers were able to adapt to screening wheat genotyping for heat tolerance.

\*Corresponding Author: Tel. 063-238-5209, E-mail: pathfinder1@korea.kr

## **Meta-analysis of QTL involved in drought tolerance and grain yield of maize**

Kitae Song<sup>1</sup>, Hyochul Kim<sup>1</sup>, Seungho Shin<sup>1</sup>, Kyung-Hee Kim<sup>1</sup>, Jun-Cheol Moon<sup>2</sup>, Jae Yoon Kim<sup>3</sup>, Byung-Moo Lee<sup>1\*</sup>

<sup>1</sup>Department of Life Science, Dongguk University–Seoul, Seoul 100–715, Korea

<sup>2</sup>Agriculture and Life Sciences Research Institute, Kangwon Nat'l Univ., Korea

<sup>3</sup>College of Life Science and Biotechnology, Korea Univ., Seoul 136–713, Korea

The maize genome is complex with exceeding the levels of intra-specific variation, repetitive DNA content, and allelic content observed between many species. Because of tremendous diversity and variants, maize is considered as a forefront crop development and estimation of molecular markers for agricultural trait in genetics and breeding. Using quantitative trait loci (QTL) and marker assisted breeding (MAS), molecular breeders are able to development of drought tolerance and grain yield in maize genotype. To study QTL congruency, a meta QTL analysis including results from eight-teen QTL publications for grain yield and drought tolerance were considered. Among them, we assembled 420 QTLs for abscisic acid (ABA) concentration, anthesis silking interval (ASI), days to flower, days to silk, ear number, kernel number, grain number and grain yields, involved in drought tolerance and grain yield. The meta QTL analysis revealed significant evidence for linkage of these traits to 39 different segments as candidates regions on maize genome. A total of 571 marker was selected as QTL or integrated QTL markers for narrowing down the QTL region into specific functionally relevant candidates. The results of meta QTL analysis helped to refine the genomic regions of agricultural traits, interest described and provided the closest flanking markers.

**Acknowledgment:** This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ0099392015)” Rural Development Administration, Republic of Korea.

This research was supported by 213001-04-3-SB920, Ministry of Agriculture, Food and Rural Affairs(MAFRA), Ministry of Oceans and Fisheries(MOF), Rural Development Administration(RDA) and Korea Forest Service(KFS).

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

---

**PC-73****Screening of rice drought tolerant germplasms and drought tolerant QTL mapping**

Dongjin Shin<sup>1\*</sup>, Tae-Heon Kim<sup>1</sup>, Sang-Ik Han<sup>1</sup>, Ji-Yoon Lee<sup>1</sup>, Youngbo Son<sup>1</sup>, Sung Hwan Oh<sup>1</sup>, Yeon-Jae Hur<sup>1</sup>, Saisbeul Lee<sup>1</sup>, Jun-Hyun Cho<sup>1</sup>, Jong-Hee Lee<sup>2</sup>, You-Chun Song<sup>1</sup>, Min-Hee Nam<sup>1</sup>, Dong-Soo Park<sup>1</sup>, Yeong-Up Kwon<sup>1</sup>

<sup>1</sup>Department of Southern Area Crop Science, Paddy Crop Research Division, National Institute of Crop Science, RDA, Miryang, 627–803, Korea

<sup>2</sup>Research Policy Bureau, RDA, Jeonju, 560–500, Korea

In here, we screened drought tolerant varieties with modified leaf water loss rate assay and visual drought tolerant phenotype in the greenhouse conditions with more than 800 varieties. Among these varieties, Samgang, Gumei4 and Apo showed the lowest of leaf water loss rate and strong drought tolerant phenotype. To identify drought QTLs with Samgang variety, we developed the doubled-haploid (DH) population consist of 101 lines derived from a cross the drought tolerant cultivar Samgang and the drought sensitive cultivar Nagdong. To score the drought phenotype degrees of this population, we withheld water for 6 weeks and treated the watering for 7 days. After watering, visual phenotype was observed 1 to 9 degree according to the standard evaluation system for rice, IRRI. Drought sensitive parent Nagdong was almost died and was scored as 9 degree, while tolerant parent Samgang showed slightly leaf tip drying phenotype and was scored as 3 degree in our experimental conditions. Three main QTLs were detected on chromosome 2, 6, and 11 with this visual phenotype. We also measured relative water content of these population under drought stress conditions, and got one main QTL on chromosome 11. The QTL loci on chromosome 11 with flanking markers RM26755-RM287 has a function for visual phenotype and relative water content under drought conditions.

\***Corresponding Author:** Tel. +82-55-350-1185, E-mail: jacob1223@korea.kr

**PC-74****DNA Profiling and Variety Identification using Insertion–Deletion (InDel) Polymorphisms in Cultivated Tomato**

Minkyung Kim, Sung-Chur Sim

Sejong University, Dept. of Bioresources Engineering, Seoul, 143–747, Korea

Cultivated tomato (*Solanum lycopersicum* L.) is an economically important vegetable and has a narrow genetic base due to intensive human selection through domestication and breeding. The low level of genetic variation between cultivated tomatoes has made it difficult to develop molecular markers for elite breeding lines. Recently, genome-wide 145,695 InDels were identified from *in silico* analysis of two tomato genome sequences, Heinz 1706 (*S. lycopersicum*) and LA1589 (*S. pimpnellifolium*). Of these, 2,272 InDels were validated and 717 InDels showed polymorphism in cultivated tomatoes. In the present study, we selected 48 out of 717 InDels based on PIC value (> 0.3) and size (> 10 bp) to develop a DNA database for commercial tomato cultivars. We also used an additional set of 28 InDels that have been previously reported. These markers were distributed across 11 chromosomes with an average of 6.6 markers. A total of 48 F1 hybrid cultivars were collected from 20 seed companies and a subset of eight cultivars were used to test polymorphism of the InDel markers. The 37 InDel markers were polymorphic in these cultivars and were used to genotype additional 40 cultivars. Genetic distances and relationships between cultivars were assessed using the InDel genotypes of 48 cultivars. This analysis revealed that the InDel markers detected genetic variations to identify 46 cultivars. Our results demonstrate that the InDel markers will be a useful resource to construct a DNA database for tomato cultivars and to protect tomato breeder's rights via variety identification.

## **Proline accumulation and related gene expression in response to higher temperatures during deacclimation in peach shoot tissues**

Hyunsuk Shin<sup>1,2</sup>, Sewon Oh<sup>1,2</sup>, Keumsun Kim<sup>1,2</sup>, Youngjae Oh<sup>1,2</sup>, Jungyeon Won<sup>1,2</sup>, Hyeondae Han<sup>1,2</sup>, Daeil Kim<sup>1,2\*</sup>

<sup>1</sup>Department of Horticulture, Chungbuk National University, Cheongju 361–763, Korea,

<sup>2</sup>Brain Korea 21 Center for Bio–Resource Chungbuk National University, Cheongju 361–763, Korea

Proline (Pro) accumulation is a common physiological reaction in response to abiotic stresses in many plants. Accumulation of Pro is believed to play the important role in protecting cellular components from dehydrating effects due to such stresses. The study was performed to investigate the relationship between cold hardiness and Pro content or expression of related genes in peach cultivars during a constant experimental deacclimation. Changes in cold hardiness were determined using electrolyte leakage method in the shoots of 10 peach cultivars (*Prunus persica* ‘Aikawanakajima’, ‘Chiyomaru’, ‘Daewol’, ‘Janghowon Hwangdo’, ‘Kiraranokiwami’, ‘Mihong’, ‘Misshong’, ‘Soomee’, ‘Suhong’, and ‘Sun Gold’). Pro content was analyzed using the ninhydrin method and related gene expressions were examined using quantitative real-time RT-PCR. While cold hardiness of 10 peach cultivars decreased, Pro contents of those increased during the deacclimation. Notably, at the same time, expression of *P5CS* ( $\Delta^1$ -pyrroline-5-carboxylatesynthase) decreased in 10 peach cultivars, whereas expressions of *P5CR* ( $\Delta^1$ -pyrroline-5-carboxylatereductase) and *OAT* (ornithine- $\delta$ -aminotransferase) increased. Our results demonstrate that Pro responds positively to higher temperature in the shoots of 10 peach cultivars and expression of both *P5CS* and *P5CR* genes could show contrasting patterns during the deacclimation. Furthermore, our results suggest that ornithine pathway, which has been suggested to be important during seedling development, could serve as an alternative pathway in Pro synthesis process during the deacclimation in peach.

\*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

## **Fine Mapping of the Root-Knot Nematode (*Meloidogyne incognita*) Resistance Gene (*Me7*) using an F<sub>2</sub> Population in Pepper**

Amornrat Changkwian<sup>1</sup>, Ji-Woong Han<sup>1</sup>, Jong-Ho Lee<sup>1</sup>, Gyung-Ja Choi<sup>2</sup>, Byoung-Cheorl Kang<sup>1\*</sup>

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

<sup>2</sup>Research Center for Biobased Chemistry, Korea Research Institute of Chemical Technology, Daejeon 305-600, Republic of Korea

Root-knot nematode, *Meloidogyne incognita* is a virulent pest of solanaceous crops worldwide. The *M. incognita* resistance gene *Me7* derived from *Capsicum annuum* CM334, is located on chromosome 9. In the present study, an F<sub>2</sub> population derived from a cross between ECW03R and CM334 was used to locate the *Me7* gene. An F<sub>2</sub> population was inoculated using approximately 1,000 second-stage juveniles per individual plant. Phenotype screening was done 45 days after inoculation by using gall index system. The phenotype study of 503 F<sub>2</sub> individual showed 391 resistant and 112 susceptible plants. The 3:1 phenotypic ratio confirmed that resistance phenotype is controlled by a single dominant gene. Previously reported two markers were tested to reveal the linkage of markers to phenotype. Two markers, CAPS\_F4R4 and SCAR\_PM6a were located at 4.3 and 2.7 cM from the resistance gene, respectively. Additional SNP markers were developed using CM334 reference genome information to narrow down the position of the gene, but no closer markers could be developed due to errors of DNA sequence assembly. The closest marker was positioned on telomere of the chromosome 9 long arm, where tens of other NB-LRR genes are clustered. NB-LRR genes are being used as candidates to identify the *Me7* gene.

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

## 알스트로메리아의 환경위해성 평가를 위한 생물학적 특성평가 방법

안주희<sup>1\*</sup>, 문초아<sup>2</sup>, 한수범<sup>3</sup>, 박성화<sup>3</sup>, 김정석<sup>3</sup>, 박태성<sup>4</sup>, 한태호<sup>1,2,3</sup>

<sup>1</sup>광주광역시 북구 용봉로 77 전남대학교 농업과학기술연구소

<sup>2</sup>광주광역시 북구 용봉로 77 전남대학교 기술지주회사 연구소기업 (주)가든플란트

<sup>3</sup>광주광역시 북구 용봉로 77 전남대학교 농업생명과학대학 원예학과

<sup>4</sup>전라북도 완주군 이서면 농생명로 100 국립원예특작과학원 원예작물부 채소과

알스트로메리아의 환경위해성 평가를 하기 위한 생물학적 특성평가 방법을 제시하고자 본 연구를 수행하였다. 환경위해성 평가를 위해 전남대학교 격리 포장 및 격리온실에서 원예 형질 표현형 지표 비교, 격리 포장에서의 번식성과 월동성, 무성번식을 통한 차세대 표현형적 후대 안정성 등 4항목의 생물학적 특성 조사를 하였으며, 또한 알스트로메리아의 실질적 동등성 평가를 하는데 필요한 적정 실험 개체 수를 제시하고자 하였다. 격리 포장 및 격리 온실에서 원예형질 표현형 지표 비교 조사 결과 줄기 굵기, 잎의 길이와 너비, 꽃차례 분지 길이 및 꽃의 꽃자루 길이 등 5항목에서 포장보다 온실에서 크거나 굵은 차이를 보였다. 자연환경에서 번식성 조사방법은 알스트로메리아 rhizome의 개수를 조사한 결과 7.0에서 10.2개로 계통에 따라 차이가 나타났으며, 월동성은 토양 표면에서의 깊이를 10cm, 20cm, 30cm로 다르게 하여 월동 후 생존력을 조사한 결과 계통에 따라 10~75%로 조사되었다. 무성번식을 통한 차세대 표현형적 후대 안정성 조사에서는 양적 형질 6가지를 조사하였으며, 씨방에서 안토시아닌의 유무를 조사한 결과 ‘씨엔알스호프’(품종등록번호 5192)는 안토시아닌이 있고, ‘파이네세’는 안토시아닌이 없었던 차이를 제외하고 다른 항목에서는 차이를 발견할 수 없었다. 실질적 동등성 평가를 하는데 필요한 적정 실험 개체 수는 전남대학교 온실에서 표준재배법에 따라 재배된 알스트로메리아 96주를 대상으로 하였으며 양적 형질 9항목의 특성을 실측하여, 각 조사항목의 실측치를 로그함수에 의한 비선형회귀모형을 사용하여 분석하여 기울기 값이 0.03이 되는 점을 정하였으며, 조사결과 실질적 동등성 평가를 하기 위한 개체 수는 항목에 따라 13주 이상에서 60주 이상으로 조사되었다.

\*주저자: Tel. 062-530-0624, E-mail: annie65@naver.com

## Development of gene-based markers for pink fruit peel color in tomatoes

Marina Lee<sup>1</sup>, Jungsu Jung<sup>1</sup>, Hyun Jung Kim<sup>2</sup>, Je Min Lee<sup>3</sup>, Inhwa Yeam<sup>1</sup>

<sup>1</sup>Department of Horticulture and Breeding, Andong National University, Andongsi, Gyeongsangbukdo, 760-749

<sup>2</sup>Department of Eco-Friendly Horticulture, Cheonan Yonam College, Cheonansi, Chungcheongnamdo, 331-709

<sup>3</sup>Department of Horticultural Science, Kyungpook National University, Daegu, 702-701

Tomato fruit color, which is the most visible characteristic among the other fruit traits, is considered to have a substantial influence on consumers. The pink-colored tomatoes with high soluble solids content are considerably preferred especially in Asia compared to the other colors. Generally the pink fruit trait of tomatoes is easily determined by visual examination of intact fruit, however, it is technically determined by the characteristic of the fruit peel. The pink trait is regulated by variations of the *SIMYB12(y)* gene located on chromosome 1, which controls the accumulation of the naringenin chalcone, which comprises a large proportion of flavonoids. In this study, we developed a derived Cleaved Amplified Polymorphic Sequences (dCAPS) marker and a sequence characterized amplified regions (SCAR) marker in order to discriminate of pink/non-pink-tomatoes in the domestic breeding lines. Quantitative RT-PCR analysis indicated that the *SIMYB* gene is highly expressed in non-pink fruit peel, whereas the expression is significantly lowered in the pink fruit peel. These gene based markers are expected to enhance the efficiency and accuracy of selection pink-tomatoes in tomato breeding programs.

---

**PC-79****Biosafety assessment and molecular biological characteristics for  $\beta$ -carotene biofortified transgenic rice**

Sung-Dug Oh, Soo-Yun Park, Doh-Won Yun, Soo-In Sohn, Hyun Suk Cho, Si Myung Lee\*

National Academy of Agricultural Science, Jeonju, 560–500

The  $\beta$ -carotene biofortified transgenic rice was developed by transforming rice cv. Nakdongbyeo with phytoene synthase (*Psy*) and carotene desaturase (*Crt I*) genes isolated from *Capsicum* and *Pantoea*. The aim of this study was to perform molecular characterization of rice transformants of T5-T7 generation harboring *Psy* and *Crt I* genes driven by endosperm specific globulin promoter for biosafety evaluation of  $\beta$ -carotene biofortified transgenic rice. The structure and sequence of T-DNA in the transformation vector and the insertion sites, flanking sequences and generational stability of inserted T-DNA in transgenic rice lines were analyzed. The transformation vector consisted of right border, MAR gene, carotenogenic genes unit, herbicide resistance selectable marker unit, MAR gene and left border in sequential order. T-DNA was introduced at the position of 30,363,938-30,363,973 bp of chromosome No. 2 by adaptor-ligation PCR. Stable integration of T-DNA and stable expression of *bar* gene was confirmed in T5 to T7 generations. It was also confirmed that the backbone DNA of transformation vector containing antibacterial gene was not present in the genome of  $\beta$ -carotene biofortified transgenic rice. HPLC analysis confirmed that carotenoids were consistently detected through T5-T7 generations.

\***Corresponding Author:** Tel. 063-238-4711, E-mail: tataby@korea.kr

**PC-80****Assessment of gene flow from disease resistant (OsCK1) genetically modified rice to its non-GM rice and weedy rice**

Sung-Dug Oh, Si Myung Lee, Soo-In Sohn, Hyun Suk Cho, Doh-Won Yun\*

National Academy of Agricultural Science, Jeonju, 560–500

Genetically modified (GM) crops have never been cultivated commercially in Korea, it is necessary for a thorough assessment of the risks associated with their environmental release. We determined the frequency of pollen mediated gene flow from disease resistant GM rice (OsCK1) to non-GM rice (Nagdongbyeo) and weedy rice (R55). A total of 449,711 or 164,604 seeds were collected from non-GM and weedy rice, respectively which were planted around OsCK1. Resistance of the hybrids was determined by repeated spraying of herbicide and DNA analysis using specific primer to confirm hybrids. Though non-GM rice and weedy rice have similar flowering time, the hybrids were found only in non-GM rice and out-crossing ranged from 0.018% at 0.3 m to 0.013% at 0.6 m. All of hybrids were located within 0.6 m distance from the GM rice plot in southerly direction. The meteorological factors including temperature and relative humidity during flowering time were found to be the most important factors for determining rice out-crossing. It should be considered many factors like the local weather condition and flowering time to set up the safety management policy to prevent pollen mediated gene flow between GM and conventional crop.

\***Corresponding Author:** Tel. 063-238-4713, E-mail: dwyun@korea.kr

---

**PC-81****Changes in proline content and related gene expression under artificial deacclimation and reacclimation during ecodormant state in *Prunus persica***

Sewon Oh<sup>1,2</sup>, Hyunsuk Shin<sup>1,2</sup>, Keumsun Kim<sup>1,2</sup>, Youngjae Oh<sup>1,2</sup>, Jungyeon Won<sup>1,2</sup>, Hyeondae Han<sup>1,2</sup>, Daeil Kim<sup>1,2\*</sup>

<sup>1</sup>Department of Horticulture, Chungbuk National University, Cheongju 361–763, Korea,

<sup>2</sup>Brain Korea 21 Center for Bio–Resource Chungbuk National University, Cheongju 361–763, Korea,

Proline has been shown to accumulate in plant under various type of stresses. In our previous study, changes in cold hardiness and proline content showed contrasting patterns during a constant deacclimation. This study was performed to investigate the proline accumulation and related gene expression in response to repeated deacclimation and reacclimation in peach cultivar ‘Daewol’. Proline content was analyzed using the ninhydrin method and related gene expressions were examined using quantitative real-time RT-PCR. Proline contents of ‘Daewol’ increased during the repeated deacclimation treatments. Interestingly, during the twice deacclimation, expressions of *P5CS* ( $\Delta^1$ -pyrroline-5-carboxylatesynthase) constantly decreased, whereas expressions of *P5CR* ( $\Delta^1$ -pyrroline-5-carboxylatereductase) increased. Expressions of *OAT* (ornithine- $\delta$ -aminotransferase) indicated up- and down- pattern in response to repeated deacclimation and reacclimation. Our results indicated that proline responds positively to higher temperature in the shoots of peach cultivar ‘Daewol’ and expressions of both *P5CS* and *P5CR* genes could show contrasting patterns during the deacclimation. Moreover, our results suggest that ornithine pathway could serve as an alternative pathway in proline synthesis process during deacclimation in peach.

\*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

**PC-82****Identification of single-nucleotide polymorphisms in *Sw-5b* resistance gene and development of a SNP marker to *Tomato spotted wilt virus* in tomato**

Hyung Jin Lee, Bo-Young Kim, Chang-Sik Oh\*

Department of Horticultural Biotechnology and Institute of Life Science & Resources, College of Life Sciences, Kyung Hee University, Yongin 446–701, Korea

*Tomato spotted wilt virus* (TSWV) causes one of the most destructive viral diseases that threaten tomato (*Solanum lycopersicum*) worldwide. So far, eight TSWV resistance genes, *Sw1a*, *Sw1b*, *sw2*, *sw3*, *sw4*, *Sw-5b*, *Sw-6*, and *Sw-7* have been identified and *Sw-5b* has been incorporated into tomato for prevention of TSWV. The objectives of this research are first to discover single nucleotide polymorphisms (SNPs) in *Sw-5* alleles and then to develop SNP markers to distinguish resistant genotypes against TSWV for marker-assisted breeding in tomato. First, DNA sequences of *Sw-5b* alleles from both resistant and susceptible cultivars amplified using known *Sw-5* gene-based marker was analyzed. The single functional SNP (G→A) was detected as non-synonymous substitution because this SNP causes change of arginine (Arg<sup>599</sup>) to glutamine (Gln<sup>599</sup>). Next, the primer pair for high resolution melting analysis (HRM) was designed around this SNP. To determine accuracy of this SNP marker to distinguish resistant *Sw-5b* genotypes against TSWV, genotypes of 32 commercial tomato cultivars were checked. The newly developed SNP marker could select six cultivars carrying resistant *Sw-5b* genotype, which was 100% correlated with genotypes based on the gene-based marker. These results indicate that the SNP maker developed in this study could be useful for better tracking resistance to TSWV in tomato breeding.

\*Corresponding Author: Tel. 031-201-2678, E-mail: co35@khu.ac.kr

---

**PC-83****Development of the single-nucleotide polymorphism marker in *Cf-9* gene conferring resistance to a leaf mold pathogen *Cladosporium fulvum* in tomato**

Bo-Young Kim, Hyung Jin Lee, Chang-Sik Oh\*

Department of Horticultural Biotechnology, College of Life Sciences, Kyung Hee University, Yongin 446–701, Korea.

Leaf mold disease in tomato (*Solanum lycopersicum*) is caused by *Cladosporium fulvum*, a fungal leaf pathogen. One of effective ways to control leaf mold is to breed disease-resistant tomato cultivars. *Cf-4* and *Cf-9* resistance (R) genes encode proteins that carry a leucine rich repeat domain and are located in plasma membrane. They trigger hypersensitive response following recognition of corresponding Avr4 and Avr9 proteins of *C. fulvum*, respectively. *Cf-4* and *Cf-9* genes are originated from wild tomato species *S. habrochaites* and *S. pimpinellifolium* and have been introgressed into commercial tomato cultivars. These two highly homologous orthologs exist as a cluster with four highly homologous paralogs. Due to this reason, development of genetic markers to distinguish these two functional R genes from their orthologs and paralogs is difficult. In this study, we tried to develop single-nucleotide polymorphism (SNP) markers to select tomato cultivars carrying resistant *Cf-9* genotype. The genomic sequences of resistant *Cf-4* and *Cf-9* alleles, susceptible *cf-9* alleles, and their paralogs were obtained from the GenBank database, and two functional SNPs causing non-synonymous substitution were found among them. Based on two SNPs, the *Cf-9\_2*-SNP-F/R primer set for high resolution melting (HRM) analysis was developed. HRM analysis with this primer set could successfully distinguish tomato cultivars carrying resistant *Cf-9* allele among 30 commercial tomato cultivars, which were characterized with the gene-based marker. These indicate that the SNP marker developed in this study is useful to trace *Cf-9* genotype efficiently in marker-assisted selection in tomato.

\*Corresponding Author: Tel. 031-201-2156, E-mail: co35@khu.ac.kr

**PC-84****Molecular characterization of transgenic plants using Next Generation Sequencing and Junction Sequence Analysis**

Ji Hye Ohn<sup>1\*</sup>, Andre Silvanovich<sup>2</sup>, Carl Garnaat<sup>2</sup>, Colton Kessenich<sup>2</sup>, Qing Tian<sup>2</sup>

<sup>1</sup>Monsanto Korea, Ltd, Seoul, Korea

<sup>2</sup>Monsanto Company, St. Louis, Missouri, U.S.A.

Molecular characterization of crops improved through biotechnology has traditionally been conducted using Southern blot analysis which has been used to determine T-DNA copy number, the presence or absence of backbone (sequence outside of the T-DNA) and to demonstrate generational stability of the T-DNA insert. The advancement of high-throughput DNA sequencing (HTS) technology allows efficient characterization of the transgene incorporated into the genome of the plant by rapidly sequencing the entire plant genome. By combining NGS (Next Generation Sequencing) technologies with bioinformatic methods that identify the T-DNA insert derived from the plasmid vector and genome-T-DNA junction sequences, it has been shown that conclusions equivalent to those of a Southern blot are readily obtained. NGS is done at sufficient coverage depth (>75x) across the entire genome. By mapping the sequence reads to the plasmid vector, and identifying the number of unique junctions, we can confirm insert number, copy number, absence of backbone, across multiple generations. With the widespread availability of NGS and steadily decreasing costs it is likely that academia and industry will fully transition to NGS-based molecular characterizations in the near future.

\*Corresponding Author: Tel. 02-3393-3765, E-mail: ji.hye.ohn@monsanto.com

## QTL analysis for Agronomic Traits of Rice Recombinant Inbred Lines under Different Environments

Mi-Ok Woo, Xing Huang, Eunbyeol Koh, Hee-Jong Koh\*

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

Understanding how crops interact with their environments is increasingly important in breeding program, especially in light of highly anticipated climate changes. A total of 150 recombinant inbred lines (RILs) of F<sub>12</sub> generation derived from Dasanbyeo (Indica) x TR22183 (Japonica) were evaluated at Suwon 2010, Shanghai 2010, IRRI 2010 wet season, Suwon 2011, Shanghai 2011, IRRI 2011 dry season, and IRRI 2011 wet season as a total of seven diverse environments. Traits evaluation included eight important agronomical traits such as days to heading (DTH), culm length (CL), panicle length (PL), panicle number per plant (PN), spikelet number per panicle (SN), spikelet fertility (SF), 100-grain weight (GW), and grain yield (GY). As a result of genotyping using 384-plex GoldenGate oligo pool assay (OPA) set (RiceOPA3.1), the linkage map for 235 SNP markers covering a total of 926.53 cM with an average interval of 4.01 cM was constructed and a total of 44 main-effect quantitative trait loci (QTL)s and 35 QTLs by environment interaction (QEI) were detected for all eight traits using single environment and multi-environments analysis, respectively. Of these, fourteen putative QTLs for DTH, CL, PN, SN, GW and GY found in single environment analysis had the similar position to QEI for those traits, suggesting that these same QTLs from both single-and multi-environments are major and stable for certain traits. To the best of our knowledge, 12 QTLs consisted of four QTLs for CL (*qCL2*, *qCL8.1*, *qCL8.2*, and *qCL8.3*), six QTLs for GW (*qGW3.1*, *qGW3.2*, *qGW7*, *qGW8*, *qGW10.1*, and *qGW10.2*), one QTL for GY (*qGY3*) and one for SF (*qSF4*) out of 44 QTLs obtained from single environment analysis were considered to be novel since no overlapping QTL was reported from previous studies. In addition, 12 out of 35 QTLs obtained from multi-environments analysis were also novel. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

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

## **Proteome alterations towards understanding molecular mechanism upon copper stress in Sorghum**

Swapan Kumar Roy<sup>1</sup>, Soo Jeong Kwon<sup>1</sup>, Won-Ju Lee<sup>1</sup>, Jong-Ho Yang<sup>1</sup>, Sang-Woo Kim<sup>1</sup>, Tae-Wook Jung<sup>2</sup>, Jung-In Kim<sup>2</sup>, Tae-Seok Ko<sup>3</sup>, Sun-Hee Woo<sup>1\*</sup>

<sup>1</sup>Dept. of Crop Science, Chungbuk National University, Cheong–ju 361–763, Korea

<sup>2</sup>Department of Functional Crop, NICS, RDA, Miryang 627–803, Korea

<sup>3</sup>Institute of Ecological Phytochemistry, School of Plant and Environmental Science, Hankyong National Univ., 167 Jungang–ro, Kyonggi–do, 456–749, Korea

Copper (Cu) is an essential micronutrient required for growth and development of plants. But, at a high concentration in soil, copper acts as a major toxic element to plant cells due to its potential inhibitory effects against many physiological and biochemical processes. In this study, the morphological and physiological changes were observed in the leaf of sorghum plants treated with different concentrations (0, 100, and 150  $\mu$ M) of Copper (Cu). The results linked to morphological changes that plants treated with Cu suffered reduction in growth and morphological changes. In the ion concentration investigation, the concentrations of  $\text{Cu}^{2+}$  increased, the concentration of others interacting ions ( $\text{Zn}^{2+}$ ,  $\text{Ca}^{2+}$ ,  $\text{Mn}^{2+}$ ,  $\text{Fe}^{2+}$ ) were changed dramatically. For proteome analysis, 2-D combined with MALDI-TOF-TOF mass spectrometry was performed. Two dimensional gels stained with silver staining, a total of 422 differential expressed proteins ( $\geq 2$ -fold) were identified using Progenesis SameSpot software. A total of 24 spots from Cu-induced sorghum leaf and 21 spots from Cu-induced sorghum root were analyzed by mass spectrometry. Out of 24 protein spots from Cu-stressed leaf, of which 16 protein spots were up-regulated and 8 protein spots were down-regulated whereas out of 21 protein spots, a total of 9 protein spots were up-regulated and 12 spots were down-regulated from Cu-stressed root. Taken together, these studies revealed the effects of heavy metal, Cu on the growth and physiological characteristics in sorghum seedlings and proteome investigation, hoping to provide references on the mechanism of heavy metal damaging plants.

Acknowledgements: This work was supported by grant from the Bio-Green 21 project (No. PJ009101012014) of the Rural Development Administration, Republic of Korea.

\***Corresponding Author:** Tel. 043-261-2515, E-mail: shwoo@chungbuk.ac.kr

## **Proteome analysis unravelling cadmium toxicity and tolerance in Sorghum leaves**

Swapan Kumar Roy<sup>1</sup>, Sang-Woo Kim<sup>1</sup>, Jong-Ho Yang<sup>1</sup>, Seong-Woo Cho<sup>2</sup>, Tae-Wook Jung<sup>3</sup>, Jung-In Kim<sup>3</sup>, Tae-Seok Ko<sup>4</sup>, Sun-Hee Woo<sup>1\*</sup>

<sup>1</sup>Dept. of Crop Science, Chungbuk National University, Cheong–ju 361–763, Korea

<sup>2</sup>Crop Breeding Research Division, NICS, RDA, Wanju–gun 565–851, Korea

<sup>3</sup>Department of Functional Crop, NICS, RDA, Miryang 627–803, Korea

<sup>4</sup>Institute of Ecological Phytochemistry, School of Plant and Environmental Science, Hankyong National Univ., 167 Jungang–ro, Kyonggi–do, 456–749, Korea

Cadmium (Cd) pollution is thought to be one of the leading threat to the environment due to its high toxicity. However, the molecular responses induced by Cd have so far been grossly overlooked. This study examines the morpho-physiological alterations combined with proteome changes in leaves of *Sorghum bicolor* when exposed to Cd. Ten days old sorghum seedlings were exposed to different concentrations (0, 100, and 150  $\mu$ M) of CdCl<sub>2</sub> and a significant accumulation of Cd in the leaves was recorded by ICP analysis. Furthermore, the effects of Cd exposure on protein expression patterns in *S. bicolor* was investigated by two-dimensional gel electrophoresis (2-DE) and the 2-DE profile of leaf proteins from both control and Cd-treated seedlings were compared quantitatively using Progenesis SameSpot software. Results lined to morphological changes that plants treated with Cd suffered reduction of growth. The concentration of Cd was markedly reversed by the Cd treatments, whereas the absorption degree of Cd was increased by the higher concentration of Cd by confocal microscopy. Using 2-DE method, a total of 33 differentially expressed protein spots were identified by MALDI-TOF-TOF mass spectrometry. Of those, 13 protein spots were significantly enhanced/reduced while 20 reduced under Cd treatment. The most of the up-regulated proteins are involved in oxidative response, glutathione and sulfur metabolism as well as the secondary metabolite biosynthesis. Collectively, our study provides insights into the integrated molecular mechanisms of early responses to Cd and growth and physiological characteristics of sorghum seedlings hoping to provide references on the mechanism of heavy metal damaging plants.

**Acknowledgements:** This work was supported by grant from the Bio-Green 21 project (No. PJ009101012014) of the Rural Development Administration, Republic of Korea.

**\*Corresponding Author:** Tel. 043-261-2515, E-mail: shwoo@chungbuk.ac.kr

## **Protein profile changes induced by hormones in diploid and tetraploid roots of *Platycodon grandiflorum***

Soo-Jeong Kwon<sup>2</sup>, Swapan Kumar Roy<sup>1</sup>, Won-Ju Lee<sup>1</sup>, Hae-Ryong Jeong<sup>1</sup>, Hag-Hyun Kim<sup>2</sup>, Yong-Gu Cho<sup>1</sup>, Hee-Ock Boo<sup>3</sup>, Sun-Hee Woo<sup>1\*</sup>

<sup>1</sup>Dept. of Crop Science, Chungbuk National University, Cheongju 361-763, Korea

<sup>2</sup>Dept. of Food Nutrition and Cookery, Woosong College, Daejeon 300-715, Korea

<sup>3</sup>WellPhyto Co. Ltd., BI Center, GIST, Gwangju 500-712, Korea

The roots of *Platycodon grandiflorum* are known as traditional medicine, has been extensively used since ancient times as a therapeutic to treat cold, cough and asthma in Korean traditional medications. This study was conducted in order to profile proteins from the hormone induced diploid and tetraploid roots using high throughput proteome approach. Two dimensional gels stained with CBB, a total of 64 differential expressed proteins were identified from the diploid root using image analysis by Progenesis SameSpot software. Out of total differential expressed spots, 20 differential expressed protein spots ( $\geq 2$ -fold) were analyzed using MALDI-TOF-TOF mass spectrometry whereas a total of 13 protein spots were up regulated and 7 protein spots were down-regulated. However, in the case of tetraploid root, a total of 78 differential expressed proteins were identified from tetraploid root of which a total of 28 differential expressed protein spots ( $\geq 2$ -fold) were analyzed by mass spectrometry whereas a total of 16 protein spots were up regulated and a total of 12 protein spots were down-regulated. However, proteins identified using iProClass databases revealed that the identified proteins from the explants were mainly associated with the nucleic acid binding, oxidoreductase activity, transporter activity and isomers activity. The exclusive protein profile may provide insight clues for better understanding the characteristics of proteins and metabolic activity in various explants of the economically important medicinal plant *Platycodon grandiflorum*.

Acknowledgements: This research was supported by High Value-added Food Technology Development Program (112076-03-1-SB010) of iPET (Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, Forestry and Fisheries), Ministry of Agriculture, Food and Rural Affairs, Republic of Korea.

\***Corresponding Author:** Tel. 043-261-2515, E-mail: shwoo@chungbuk.ac.kr

## Proteome responses of diploid and tetraploid root: Towards understanding functional characterization in *Platycodon grandiflorum*

Soo-Jeong Kwon<sup>2</sup>, Swapan Kumar Roy<sup>1</sup>, Min-Heon Yun<sup>1</sup>, Je-Hyeok Yu<sup>1</sup>, Hag-Hyun Kim<sup>2</sup>, Hee-Ock Boo<sup>3</sup>, Moon-Soon Lee<sup>4</sup>, Sun-Hee Woo<sup>1\*</sup>

<sup>1</sup>Dept. of Crop Science, Chungbuk National University, Cheong–ju 361–763, Korea

<sup>2</sup>Dept. of Food Nutrition and Cookery, Woosong College, Daejeon 300–715, Korea

<sup>3</sup>WellPhyto Co. Ltd., BI Center, GIST, Gwangju 500–712, Korea

<sup>4</sup>Dept. of Industrial Plant Science & Technology, Chungbuk National University, Cheong–ju 361–763, Korea

The roots of *Platycodon grandiflorum* are massively used in traditional herbal medicine as a remedy for pulmonary disease and respiratory disorders. However, in spite of its potential medicinal significance, the molecular mechanism of its roots is still unknown. In the present study, high throughput proteome approach was conducted to profile proteins from 3, 4 and 5 months aged diploid and tetraploid roots of *Platycodon grandiflorum*. Two dimensional gels stained with CBB, a total of 68 differential expressed proteins were identified from diploid root out of 767 protein spots using image analysis by Progenesis SameSpot software. Out of total differential expressed spots, 29 differential expressed protein spots ( $\geq 2$ -fold) were analyzed using LTQ-FTICR MS whereas a total of 24 protein spots were up regulated and 5 protein spots were down-regulated. On the contrary, in the case of tetraploid root, a total of 86 differential expressed proteins were identified from tetraploid root out of 1033 protein spots of which a total of 39 differential expressed protein spots ( $\geq 2$ -fold) were analyzed using LTQ-FTICR MS whereas a total of 21 protein spots were up regulated and a total of 18 protein spots were down-regulated. It was revealed that the identified proteins from the explants were mainly associated with the nucleotide binding, oxidoreductase activity, transferase activity. In that way, the exclusive protein profile may provide insight clues for better understanding the characteristics of proteins and metabolic activity in various explants of the economically important medicinal plant *Platycodon grandiflorum*.

Acknowledgements: This research was supported by High Value-added Food Technology Development Program (112076-03-1-SB010) of iPET (Korea Institute of Planning and Evaluation for Technology in Food, Agriculture, Forestry and Fisheries), Ministry of Agriculture, Food and Rural Affairs, Republic of Korea.

\*Corresponding Author: Tel. 043-261-2515, E-mail: shwoo@chungbuk.ac.kr

## Development of a PCR marker for monitoring of transgene introgression in resveratrol-enriched transgenic rice plant

Yang Qin<sup>1</sup>, So-Hyeon Baek<sup>2</sup>, Soon-Jong Kweon<sup>2</sup>, Taek-Ryoun Kwon<sup>1</sup>, Myung-Ho Lim<sup>1</sup>, Kong-Sik Shin<sup>1</sup>, Hyun-Suk Cho<sup>1</sup>, Hee-Jong Woo<sup>1\*</sup>

<sup>1</sup>National Academy of Agricultural Science, Rural Development Administration, Jeonju, Korea

<sup>2</sup>National Institute of Crop Science, Rural Development Administration, Wanju, Korea

A variety of genetically modified (GM) crops have been developed in Korea. In these crops, the resveratrol-enriched transgenic rice plant has moved ahead to generate the dossier for regulatory review process required for commercialization of GM crop. The resveratrol-enriched transgenic rice plant could be released to farmers for cultivation after national regulators have determined that it is safe for the environment and human health. Here we developed a PCR-based DNA marker based on flanking sequences of transgene for the discrimination of zygosity in resveratrol-enriched transgenic rice plant. This DNA marker will be useful for identifying of resveratrol-enriched transgenic rice plant, and can also be use to estimate transgene movement occurred by pollen transfer or seed distribution.

\*Corresponding Author: Tel. 063-238-4706, E-mail: woo001@korea.kr

## Selection of $\beta$ -carotene enhanced transgenic soybean containing single-copy transgene and analysis of integration sites

Yang Qin<sup>1</sup>, Soon-Jong Kweon<sup>2</sup>, Young-Soo Chung<sup>3</sup>, Sun-Hwa Ha<sup>4</sup>, Kong-Sik Shin<sup>1</sup>, Myung-Ho Lim<sup>1</sup>, Taek-Ryoun Kwon<sup>1</sup>, Soon Ki Park<sup>5</sup>, Hyun-Suk Cho<sup>1</sup>, Hee-Jong Woo<sup>1\*</sup>

<sup>1</sup>National Academy of Agricultural Science, Rural Development Administration, Jeonju, 560–500, Korea

<sup>2</sup>National Institute of Crop Science, Rural Development Administration, Suwon, 441–707, Korea

<sup>3</sup>Department of Genetic Engineering, Dong-A University, Busan, 604–714, Korea

<sup>4</sup>Department of Genetic Engineering, KyungHee University, Yongin, 446–701, Korea

<sup>5</sup>School of Applied Biosciences, Kyungpook National University, Daegu, 702–701, Korea

The  $\beta$ -carotene biofortified transgenic soybean was developed recently through *Agrobacterium* -mediated transformation using the recombinant *PAC* (*Phytoene synthase-2A-Carotene desaturase*) gene in Korean soybean (*Glycine max* L. cv. Kwangan). GM crops prior to use as food or release into the environment required risk assessments to environment and human health in Korea. Generally, transgenic plants containing a copy of T-DNA were used for stable expression of desirable trait gene in risk assessments. Also, information about integration site of T-DNA can be used to test the hypothesis that the inserted DNA does not trigger production of unintended transgenic proteins, or disrupt plant genes, which may cause the transgenic crop to be harmful. As these reasons, we selected four transgenic soybean lines expressing carotenoid biosynthesis genes with a copy of T-DNA by using Southern blot analysis, and analyzed the integration sites of their T-DNA by using flanking sequence analysis. The results showed that, T-DNA of three transgenic soybean lines (7-1-1-1, 9-1-2, 10-10-1) was inserted within intergenic region of the soybean chromosome, while T-DNA of a transgenic soybean line (10-19-1) located exon region of chromosome 13. This data of integration site and flanking sequences is useful for the biosafety assessment and for the identification of the  $\beta$ -carotene biofortified transgenic soybean.

\*Corresponding Author: Tel. 063-238-4706, E-mail: woo001@korea.kr

---

PC-92

## Comparative nutritional analysis for marker-free transgenic *Bt* rice and non-transgenic counterparts

Hee-Jong Woo<sup>1\*</sup>, Kong-Sik Shin<sup>1</sup>, Myung-Ho Lim<sup>1</sup>, Jin-Hyoung Lee<sup>1</sup>, Yang Qin<sup>1</sup>, Soon Ki Park<sup>2</sup>, Hyun-Suk Cho<sup>1</sup>

<sup>1</sup>National Academy of Agricultural Science, Rural Development Administration, Jeonju, 560–500, Korea

<sup>2</sup>School of Applied Biosciences, Kyungpook National University, Daegu, 702–701, Korea

The selectable marker-free rice plants containing *mcry1Ac* insecticidal gene isolated from *Bacillus thuringiensis* (*Bt*) were generated using a non-selection approach by *Agrobacterium tumefaciens*-mediated transformation. The nutritional composition of two lines of transgenic rice plants (RTB5 and RTB11) was compared with that of its non-transgenic counterpart. The results showed that, except for small differences in dietary fiber and some minerals, there was no significant difference between transgenic rice and conventional counterpart variety with respect to their nutrient composition. Most of measured levels of nutrients were within the range of values reported for other commercial cultivars, showing substantial equivalency. Therefore, the insertion of transgenes did not affect the nutritional composition of transgenic RTB5 and RTB11 rice grains.

\*Corresponding Author: Tel. 063-238-4706, E-mail: woo001@korea.kr

PC-93

## Characterization of chrysanthemum genome by NGS

So Youn Won<sup>1\*</sup>, Seulki Lee<sup>1</sup>, Jae-A Jung<sup>2</sup>, Jung Sun Kim<sup>1</sup>, Sangho Kang<sup>1</sup>, Seong-Han Sohn<sup>1</sup>

<sup>1</sup>National Academy of Agricultural Science, RDA, Jeonju, 560–500, South Korea

<sup>2</sup>National Institute of Horticultural and Herbal Science, RDA, Wanju, 565–852, South Korea

The Asteraceae/Compositae family is one of the biggest families in flowering plants and has more than 23000 species including the economically important lettuce, sunflower, and chicory as well as the agronomic weeds. With its significance and the progress in sequencing technology, its species have been subjected to the genome sequencing project worldwide. Although chrysanthemum is an important plant in the floricultural industry, however, it has been less studied at the level of genomics, compared with other species in the Asteraceae. There were only several reports on comparative analysis of transcriptome for chrysanthemum. Actually, the genome of *Chrysanthemum* species is known to be gigantic and complex with diverse status ranging from diploid to decaploid. Since the cultivated and commercial chrysanthemum exhibits hexaploid genome, we decided to select the diploid species with smaller genome as a material for reference genome sequencing. Thus, we launched a genome sequencing project with *C. boreale* which was previously reported to be diploid by cytogenetic analysis. We constructed sequencing libraries with insert size 300bp and 500bp and sequenced them from the paired end in 100bp read length with Illumina's HiSeq platform. After quality checking, we preprocessed raw reads by removing duplicated reads and trimming reads with low quality value. Kmer frequency analysis with the cleaned reads showed that the genome is heterozygous, highly repetitive and gigantic, ranging from 2.9Gb to 5.8Gb. The cleaned reads were further subjected to error correction and primary assembly with SOAPdenovo2. Here, we'll report the result of Kmer frequency analysis and genome assembly.

\*Corresponding Author: Tel. +82-63-238-4561, E-mail: soyounwon@korea.kr

## 미성숙화기를 이용한 ‘우람’ 억새 식물체 재분화

유경단\*, 장윤희, 안중웅, 최인후, 문윤호, 차영록, 이지은, 안기홍, 이경보

전남 무안군 청계면 무안로 199, 국립식량과학원 바이오에너지작물연구소

억새(*Miscanthus* spp.)는 화본과 중 광합성 효율이 높은 C<sub>4</sub> 식물군에 속하는 식물로 한국, 일본, 중국 등 동아시아가 원산지인 대표적인 바이오에너지 원료작물이다. 억새는 주로 지하경을 이용하여 번식하여 왔으나 지하경을 이용한 번식은 유전형은 유지할 수 있으나 우량 품종 개발에 불리하다는 문제점이 있다. 조직배양기술은 유용 자원을 이용한 돌연변이 육종과 형질전환 기술을 이용한 신품종 육종을 위한 기반기술로 활용 될 수 있어 바이오매스의 확보 측면에서 유용하다. 국내 유망 바이오매스 자원인 억새의 신품종 육성을 위해서는 캘러스 유도 및 식물체 재분화에 효율적인 조직배양 기술을 확립하는 것이 중요하다. 본 연구에서는 농촌진흥청에서 선발한 ‘우람’ 억새(*Miscanthus sacchariflorus* cv. Wooram)의 미성숙 화기를 이용한 안정적인 캘러스 유도 및 식물체 재분화 조건을 확립하여 신품종 육종을 위한 기초자료를 확보하고자 하였다. 식물재료는 국립식량과학원 바이오에너지작물연구소 내의 억새 재배 포장에서 미성숙 화기가 5 mm 이하로 분화한 개체만 채취하여 사용하였으며, 수집한 재료는 70% EtOH로 2분, 0.45% NaOCl로 20분간 표면 살균하여 배지에 치상하였다. 미성숙화기로부터 캘러스 유도율을 조사한 결과, MS배지에 성장조절제인 3 mg L<sup>-1</sup> 2,4-D를 첨가한 처리가 캘러스 유도율 93.3 %로 가장 높게 나타났고 3 mg L<sup>-1</sup> 2,4-D + 0.1 mg L<sup>-1</sup> BA를 혼합 처리한 배지에서도 86.6 %의 캘러스 유도율을 나타냈다. 이후 캘러스로부터 식물체 재생 실험에서 3 mg L<sup>-1</sup> 2,4-D에 0.1 mg L<sup>-1</sup> BA를 혼합 처리한 배지에서 유도된 캘러스가 3 mg L<sup>-1</sup> 2,4-D 처리 배지에서 유도된 캘러스보다 식물체 재분화율이 높게 나타났다. 캘러스 유도에는 최종적으로 3 mg L<sup>-1</sup> 2,4-D + 0.1 mg L<sup>-1</sup> BA 처리 배지가 가장 효과적인 것으로 나타났다. 식물체 재분화를 위한 최적 성장조절제 농도에 대한 실험에서는 5 mg L<sup>-1</sup> BA + 0.1 mg L<sup>-1</sup> NAA 배지에서 재분화율 86.6 %로 가장 효과적이었다.

\*주저자: Tel. 061-450-0138, E-mail: gyeongdan@korea.kr

---

**PC-95****Rice FLAVIN-BINDING, KELCH REPEAT, F-BOX 1 (OsFKF1) promotes flowering independent of photoperiod.**Su-Hyun Han<sup>1\*</sup>, Soo-Cheul Yoo<sup>2\*</sup>, Nam-Chon Paek<sup>1</sup><sup>1</sup>Department of Plant Science, Plant Genomics and Breeding Institute, Research Institute of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea<sup>2</sup>Department of Plant Life and Environmental Science, Hankyong National University, Ansong 456-749, Korea,

In the facultative long-day (LD) plant *Arabidopsis thaliana*, FLAVIN-BINDING, KELCH REPEAT, F-BOX1 (FKF1) is activated by blue light and promotes flowering through the transcriptional and post-transcriptional regulation of CONSTANS under inductive LD conditions. By contrast, the facultative short day (SD) plant rice (*Oryza sativa*) flowers early under inductive SD and late under non-inductive LD conditions; the regulatory function of OsFKF1 remains elusive. Here we show that *osfkf1* mutants flower late under SD, LD, and natural LD conditions. Transcriptional analysis revealed that OsFKF1 up-regulates expression of the floral activator Ehd2 and down-regulates expression of the floral repressor Ghd7; these regulators up- and down-regulate Ehd1 expression, respectively. Moreover, OsFKF1 can upregulate Ehd1 expression under blue light treatment, without affecting the expression of Ehd2 and Ghd7. In contrast to the LD-specific floral activator *Arabidopsis* FKF1, OsFKF1 likely acts as an autonomous floral activator because it promotes flowering independent of photoperiod, probably via its distinct roles in controlling expression of rice-specific genes including Ehd2, Ghd7, and Ehd1. Like *Arabidopsis* FKF1, which interacts with GI and CDF1, OsFKF1 also interacts with OsGI and OsCDF1 (also termed OsDOF12). Thus, we have identified similar and distinct roles of FKF1 in *Arabidopsis* and rice.

\*Equal contributors to this work.

**PC-96****Investigation of Saponin Biosynthesis Related Uridine Diphosphate Glycosyltransferase(UGT) Genes in *Platycodon grandiflorum* Using RNA-seq**Jemin Yoo<sup>1</sup>, Yurry Um<sup>2</sup>, Yi Lee<sup>1\*</sup><sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University<sup>2</sup>Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369-873, Korea

*Platycodon grandiflorum* is a species of herbaceous flowering perennial plant of the family Campanulaceae. The major ingredients are platycosides, terpenoid saponins. It contains 1-4 % of the dry weight and there are about 20 types of platycosides. Among them, platycodin D have various pharmacological effects on cough and cold. Platycosides are synthesized from oleanane by mevalonic acid pathway and cytochrome P450s and UGTs are important enzymes in the saponin biosynthesis. UGT is glucose transfer enzyme and act on the final step of the secondary metabolite biosynthesis. In this study, we tried to identify UGT genes involved in saponin biosynthetic pathway from the various tissues of *P. grandiflorum* and non germinated seeds using RNA-seq analysis. The sequencing was performed using Illumina Hi-Seq platform after cDNA library preparation. The produced reads were assembled using CLC Genomics Workbench software (CLC Bio, Inc.). We obtained 122,663 contigs and found 137 putative UGT genes. The phylogenetic relationship was analyzed and putative genes related to platycoside biosynthesis were selected and cloned for further analysis.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01035104)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

## **Analysis of Phylogenetic Relationship in *Platycodon grandiflorum* using RAPD Molecular Marker**

Jemin Yoo<sup>1</sup>, So Hyeon Park<sup>1</sup>, Yurry Um<sup>2</sup>, Yi Lee<sup>1\*</sup>

<sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University

<sup>2</sup>Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369–873, KOREA

*Platycodon grandiflorum* is a perennial herbal plant belongs to Campanulaceae family. It has very important genetic value as a major plant in Asterids order. The major ingredients are platycosides, terpenoid saponins. In Korean industrial plants market, it was produced 5,633 tons in 2013, and the total amount of production was less than only five species, omija, ginger, raspberry, yam and deodeok. *P. grandiflorum* is called ‘Gilgyung’ and is used as a fresh vegetable and an ornamental plant. Nowadays, various components of *P. grandiflorum* were already published. But, genetic research is in the starting stage. In this study, 11 cultivars; 1. Maries II, 2. Hakone double white, 3. Hakone double blue, 4. Fuji white, 5. Fuji pink, 6. Fuji blue, 7. Astra white, 8. Astra pink, 9. Astra blue, 10. Astrasemi double blue, 11. Jangback, were analyzed using 60 Operon Universal RAPD primers. The results were phylogenetically analyzed and related to the morphological characteristics of the cultivars.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01035104)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

## **Investigation of Cytochrome P450 Genes Related to Saponin Biosynthesis in *Platycodon grandiflorum* Using RNA-Seq Analysis**

Jemin Yoo<sup>1</sup>, Yurry Um<sup>2</sup>, Yi Lee<sup>1\*</sup>

<sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University

<sup>2</sup>Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369–873, KOREA

*Platycodon grandiflorum* is a herbal flowering perennial plant belongs to Campanulaceae family. The saponins derived from *P. grandiflorum* were termed platycosides and platycodin D, which is the most abundant saponin in the plant and pharmacologically active component, was intensively studied. Platycodin D is synthesized from triterpenoids by several enzymes including cytochrome P450. Cytochrome P450 is known to exist in superfamily in plant kingdom and essential roles in saponin biosynthetic pathway by hydroxylation or oxidation of triterpene skeletons. However, the key genes of P450 involved in biosynthesis of saponin was not identified because of its low conservation rate in amino acid sequence level among plant species and gene superfamilies. Recently, next generation sequencing (NGS) technology is rapidly developed as a method to discover target genes. In this study, we tried to identify P450 genes involved in saponin biosynthetic pathway from the various tissues of *P. grandiflorum* using RNA-seq analysis. The sequencing was performed using Illumina Hi-Seq platform after cDNA library preparation. The produced reads were assembled using CLC Genomics Workbench software (CLC Bio, Inc.). We obtained 122,663 contigs and found out 191 putative P450 genes. The phylogenetic relationship was analyzed and putative genes related to platycoside biosynthesis were selected and cloned for further analysis.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01035104)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

## Genome-wide identification of Receptor-like Protein in *Capsicum annuum*

DongKue Yun<sup>1</sup>, BoSeu Park<sup>2</sup>, JuneSung Lee<sup>2</sup>, Won-Hee Kang<sup>3</sup>, Seungill Kim<sup>4</sup>, Myung-Shin Kim<sup>4</sup>, Doil Choi<sup>4</sup>, Seon-In Yeom<sup>2,3\*</sup>

<sup>1</sup>Division of Applied Life Science, Gyeongsang National University, Jinju 660–701, Korea

<sup>2</sup>Department of Agricultural Plant Science, Gyeongsang National University, Jinju 660–701, Korea

<sup>3</sup>Institute of Agriculture & Life Sciences, Gyeongsang National University, Jinju 660–701, Korea

<sup>4</sup>Department of Plant Science, Seoul National University, Seoul 151–742, Korea

Sessile organism, plants constitutively challenged with pathogens have been developed various strategies for protection, such as preformed and inducible defense mechanisms. Receptor-like Proteins(RLPs) play critical roles in defense response as well as in plant development and growth. The domain structure of RLPs consists of extracellular leucine-rich repeats, a transmembrane domain, and a short cytoplasmic tail. Here, we identified putative 170 RLP genes from pepper genome using *in-house* bioinformatics pipeline. The distribution of RLPs on pepper pseudomolecule showed uneven spread and a number of RLPs were physically clustered by tandem array in the specific chromosome. Motifs analysis of pepper RLPs showed conserved LRR sequences (LxxLxxLDLxxNxxxGxIP). To understand further functional and evolutionary characteristics, evolutionary relationship and gene profiling analysis are on progress.

\*Corresponding Author: E-mail: sunin78@gnu.ac.kr

## The *Citrus unshiu* carotenoid isomerase gene, *CuCRTISO*, has a activity of the carotenoid isomerase in the tomato *CRTISO* mutant *Tangerine*.

Chang-Ho Eun<sup>1\*</sup>, In-Jung Kim<sup>1,2</sup>

<sup>1</sup>Subtropical Horticulture Research Institute, Jeju National University, Jeju 690–756, Republic of Korea

<sup>2</sup>Faculty of Biotechnology, College of Applied Life Sciences & Research Institute for Subtropical Agriculture and Biotechnology, SARI, Jeju National University, Jeju 690–756, Republic of Korea

Carotenoid isomerase (CRTISO) catalyzes the isomerization of polyycopene to all-trans-lycopene in the carotenoid biosynthetic pathway. We isolated two full-length cDNA gene, *CuCRTISO* and *CuCRTISO-like*, from *Citrus unshiu*. To confirm whether these two genes have the function of the carotenoid isomerase, The full-length cDNA of *CuCRTISO* and *CuCRTISO-like* gene, respectively, were fused with 35S promoter and NOS terminal region and then transformed into tomato *CRTISO* mutant, *Tangerine*, which shows orange fruit due to lack of carotenoid isomerase activity. The mature fruit color of the transgenic line expressing *CuCRTISO* gene changed from orange to red, which was similar to the fruit color of the tomato “Money Maker”. We also carried out HPLC analysis to detect all-trans lycopene, which is produced from polyycopene by carotenoid isomerase. In the transgenic line expressing *CuCRTISO* the all trans lycopene was detected from mature fruit but in the tangerine mutant several polyycopenes were detected from it. On the other hand, the transgenic line expression of *CuCRTISO* gene retained the orange-color fruit at the mature stage as *Tangerine* mutant. These studies indicate that the *CuCRTISO* gene has a function of carotenoid isomerase and also plays a role of it in other plant species, and that the *CuCRTISO-like* gene might be not enough to produce the all trans lycopene or has a another unknown function(s).

\*Corresponding Author: Tel. 064-754-3357, E-mail: mong6908@gmail.com

---

**PC-101****Phylogenomic analysis and a systematic view of MLO family in rice**

Van Ngoc Tuyet Nguyen, Ki-Hong Jung

Department of Plant Molecular Systems Biotechnology &amp; Graduate School of Biotechnology, Kyung Hee University, Yongin 446–701, Republic of Korea

MLO is a unique gene family which is identified in plant and carries out abiotic and biotic stress responses in various plants. The understanding on the roles and functional diversity of this family is quite limited in rice, a model crop plant. Rice genome has 12 potential MLO family members. To do systematic functional assignment of *MLO* family in rice, we performed phylogenomic analysis of integrating meta-expression data based on public sources of microarray data or RT-PCR data into the phylogenetic tree. As a result, we identified 12 *MLO* genes carrying various tissue-preferred expression patterns such as leaf, root, pollen, and ubiquitous expression, suggesting functional diversity in terms of anatomy or development. RT-PCR analysis confirmed, integrated transcriptome data were used to estimate the functional redundancy or specificity among MLO family: MLO12 showed mature pollen preferred expression; MLO4, root tip; MLO10, overall root except root tip; MLO8, leaf; MLO2 and MLO9 showed redundant expression in overall tissues except root. Also, abiotic stress meta-expression data and RT-PCR performance suggested the functional association of 5 MLO and 6 MLO genes with heat and cold stress, respectively. Our analysis will provide basic information to study diverse developmental or physiological phenomena mediated by MLO family in rice, a major model crop plant.

**PC-102****Functional characterization of soybean *FT* homologs in photoperiod-dependent flowering time control**

Kyung-Hee Lee, Cheol Woo Choi, Wook-Hun Jung, Min-Chul Kim\*

Division of Applied Life Science (BK21 Plus), Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 660–701, Korea.

*FT* is one of the major floral activator in photoperiod-dependent flowering pathway. To understand the role of *FT* homologs in flowering time control of short-day plant soybean, we identified ten soybean *FT* genes and named *GmFTs*. Phylogenetic analysis revealed that ten *GmFT* genes were further categorized into three subclades. Gene expression analysis showed that the most *GmFT* genes are mainly expressed in leaves. The expression of *GmFT2a*, *GmFT2b*, *GmFT5a*, and *GmFT6* was strongly induced under the floral inductive short-day condition, but *GmFT4* exhibited opposite expression pattern compared to those of *GmFT2a*, *GmFT2b*, *GmFT5a*, and *GmFT6*. To understand roles of *GmFT* genes in flowering, we generated *Arabidopsis* transgenic plant overexpressing *GmFT* genes. Both 35S:*GmFT2a* and 35S:*GmFT5a* transgenic plants showed extremely early flowering. In contrast, overexpression of *GmFT4* delayed flowering of transgenic plants compared to wild type *Arabidopsis*. The results indicated that *GmFT2a* and *GmFT5a* might function as floral activators, while *GmFT4* has an opposite function in soybean flowering. Moreover, domain swapping approaches between *GmFT2a* and *GmFT4* revealed that the substitution of the segment B region alone, which is located in 4<sup>th</sup> exon, was sufficient to change the function of *GmFT2a* to floral repressor and *GmFT4* to floral activator. The results suggested that soybean *FT* homologs have been functionally diversified during evolution and might play different roles in photoperiod-dependent flowering of soybean.

\*Corresponding Author: Tel. 055-772-5428, E-mail: mckim@gnu.ac.kr

---

**PC-103****Transgenic Forage Plants Overexpressing a alfalfa *Hsp23* Gene Exhibit Enhanced Tolerance to Abiotic Stresses**

Ki-Won Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang, Sang-Hoon Lee\*

Grassland and Forages Division, National Institute of Animal Science, Rural Development Administration, Cheonan, 330-801, Korea

To develop transgenic forage crops with enhanced tolerance to abiotic stress, we introduced an alfalfa *Hsp23* gene expression vector construct through *Agrobacterium*-mediated transformation. Integration and expression of the transgene were confirmed by PCR, northern blot, and western blot analyses. Under normal growth conditions, there was no significant difference in the growth of the transgenic plants and the non-transgenic controls. However, when exposed to various stresses such as salt or arsenic, transgenic plants showed a significantly lower accumulation of hydrogen peroxide and thiobarbituric acid reactive substances than control plants. The reduced accumulation of thiobarbituric acid reactive substances indicates that the transgenic plants possessed a more efficient reactive oxygen species-scavenging system. We speculate that the high levels of *MsHsp23* proteins in the transgenic plants protect leaves from oxidative damage through chaperon and antioxidant activities. These results suggest that *MsHsp23* confers abiotic stress tolerance in transgenic forage crops and may be useful in developing stress tolerance in other crops. (This work was carried out with the support of Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ008599042015))

\*Corresponding Author: Tel. 041-580-6754, E-mail: sanghoon@korea.kr.

**PC-104****음나무(*Kalopanax septemlobus*) 종자유래 식물체 재생과 재생 식물체의 ISSR에 기초한 유전적 다양성 분석**이나년<sup>1,2\*</sup>, 김지아<sup>1</sup>, 김용욱<sup>1</sup>, 최용익<sup>2</sup>, 문홍규<sup>1</sup><sup>1</sup>경기도 수원시 권선구 온정로 39 국립산림과학원 산림유전자원부 산림생명공학과<sup>2</sup>강원도 춘천시 강원대학길1 강원대학교 산림자원학과

청원 소재 음나무(*Kalopanax septemlobus*)의 미숙종자에서 캘러스를 유도하여 15개의 배발생 캘러스를 얻었다. 증식된 배발생 캘러스를 재료로 체세포배를 유도하여 15개체의 기내 식물체를 얻었다. 체세포배 유도는 1/2 MS배지에 0.1 mg/L abscisic acid (ABA), 7% polyethylene glycol (PEG), 0.02% activated charcoal, 3% sucrose를 첨가하고, 0.5% gelrite로 경화하여 사용하였다. 식물 재생용 배지는 배지는 1/2MS배지에 2% sucrose, 0.3% gelrite로 하였고, 발아 촉진을 위해 GA<sub>3</sub> 1.0 mg/L 처리 혹은 기본배지를 사용하였다. 15개체의 체세포배 발생 빈도는 다르게 나타났고, 재생된 식물체의 GA<sub>3</sub> 효과는 크지 않았다. 유전적 다양성을 조사하기 위하여 ISSR (Inter-Simple Sequence Repeats) 표지자 분석을 실시하였다. 5개의 ISSR 프라이머에서 증폭산물을 관찰하였고, 유전적 다양성을 나타내는 P (Percentage of polymorphic loci)값과 S.I. (Shannon's information index)를 조사하였다. ISSR 마커를 이용하여 재분화 식물체의 유전적 안정성을 분석한 결과, 체세포 유래 재분화된 식물체의 개체간에 유전적 구조가 균일하며, 유전적 변이는 관찰되지 않았다.

\*주저자: Tel. 031-290-1165, E-mail: nanda49@epost.go.kr

## 식물성 오일의 혈중 지질 수치 감소 효과

최정란<sup>1</sup>, 김형욱<sup>3</sup>, 장인건<sup>3</sup>, 이상협<sup>1,2\*</sup>

<sup>1</sup>서울특별시 광진구 군자동 세종대학교 생명과학대학 식물생명공학전공

<sup>2</sup>서울특별시 광진구 군자동 세종대학교 식물생명공학연구소

<sup>3</sup>서울특별시 광진구 군자동 세종대학교 생명과학대학 바이오융합전공

어유에서 추출한 Omega-3 long-chain polyunsaturated fatty acids (LC-PUFA), 특히, EPA (20:5)와 DHA (22:6)는 심혈관계 질환을 예방하는데 중요한 역할과 함께 대사성 증후군 또는 비만 발병과 관련있다고 알려져 있다. 동물 모델을 이용해 고지방식이 섭취 후 어유 추출 오일과 식물성 오일 투여로 혈중 지질 농도 감소 효과를 비교하고 작용 기전을 확인함으로써 고지혈증을 포함한 심혈관계 질환의 예후인자를 알아보고자 한다. 42마리의 C57BL6J 마우스를 이용해 정상식이군 (18마리)과 고지방식이군 (24마리)으로 나눈 후 정상식이군 3개 그룹 (대조군, 어유 오일, 식물성 오일)으로 설정하고 고지방식이군도 3개 그룹 (대조군, 어유 오일, 식물성 오일) 각각으로 나누어 실험을 진행했다. 고지방식이군은 4주 단위 투여로 비만을 유도한 후 체중 20g 당 100 $\mu$ l의 식물성 오일과 어유 추출 오일을 각각 투여하여 각 그룹 별로 매일 1회 씩 털 색깔, 몸 전체 모양, 털 빠짐 등 일반증상을 관찰하고 사망동물이나 빈사 상태를 확인했다. 오일 투여 직전과 투여 후 1, 3, 7일에 체중변화를 측정하고 10주 후 마취시켜 부검 후 외관검사 실시와 육안 소견을 관찰하고 장기를 적출하여 효소항체검사법 (enzyme-linked immunosorbent assay test, ELISA)를 통해 지방 활성화에 관련된 혈중 지질 농도를 측정했다. 고지방식이 섭취 4주 후 정상식이군 ( $p=0.56$ )에 비해 고지방식이군 ( $p=0.04$ )에서 체중변화가 나타났고 고지방식이군에서 어유 오일군 (41.27 $\pm$ 7.0)에 비해 식물성 오일군 (45.37 $\pm$ 6.45)에서 체중감소가 적었지만 물만 먹인 대조군 (48.87 $\pm$ 1.0)에 비해 두 그룹 모두 체중이 감소하는 효과가 있었고 ( $p=0.04$ ), 10주 투여 기간동안 오일 투여군에서 체중 감소가 나타났다. 부검 후 적출한 장기에서 관찰된 혈중 지질 농도 수치 역시 정상식이군에 비해 고지방식이군에서 감소하는 것으로 보였지만, 고지방식이군 중 어유 오일 그룹과 식물성 오일 그룹에서 혈중 지질 농도 수치 감소가 거의 비슷한 수준으로 나타나는 것을 알 수 있었고 추후 동물모델을 추가 시험함으로써 확인하는 것이 필요할 것으로 보인다. 식물성 오일 섭취로 혈중 지질 수치가 감소함을 관찰함으로써 향후 혈관질환의 진단 및 예후인자로 이용할 수 있을 것으로 여겨진다.

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

## **Characterization of Siberian wild rye grass *EsHsp16.9* Gene and Their Expression under Various Environmental Conditions**

Sang-Hoon Lee, Ki-Yong Kim, Hee Chung Ji, Tae Young Hwang, Ki-Won Lee\*

Grassland and Forages Division, National Institute of Animal Science, Rural Development Administration, Cheonan, 330-801, Korea

Small heat shock proteins (Hsps) are one of most conserved molecular chaperones that protect stress-inducible denaturation of substrates in living organisms. Small Hsps consist of a large subfamily categorized by subcellular localization ranging in size from 12 to 40 kDa. Here, we identified and characterized a small Hsp 16.9 gene (*EsHsp16.9*) from Siberian wild rye (*Elymus sibiricus* L.). *EsHsp16.9* is a 456-bp cDNA with an open reading frame predicted to encode a 151-amino acid protein. It possesses a conserved  $\alpha$ -crystallin domain, which is a unique domain for small Hsps; shares high sequence similarity with cytosolic class I small Hsps among the small Hsp subfamily in Arabidopsis; and is close (96% similarity) to small Hsp in wheat. Northern blot analysis showed that *EsHsp16.9* transcripts were enhanced by heat, drought, arsenate, methyl viologen, and H<sub>2</sub>O<sub>2</sub> treatments. Moreover, we expressed and purified recombinant *EsHsp16.9* proteins in *Escherichia coli* to confirm its activity as a molecular chaperone. We found that recombinant *EsHsp16.9* exhibits effective molecular chaperone activity, as determined by inhibition of thermal aggregation of malate dehydrogenase (MDH), which is broadly used as a model substrate.

This work was carried out with the support of Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ008599042015)

\*주저자: Tel. 041-580-6757, E-mail: kiwon@korea.kr

---

**PC-107****벼 줄무늬 잎마름병의 주요 유전자 *Stv-b* 관련 QTL 탐색**

이섫별<sup>1</sup>, 허연재<sup>1</sup>, 김태현<sup>1</sup>, 신동진<sup>1</sup>, 한상익<sup>1</sup>, 조준현<sup>1</sup>, 이지윤<sup>1</sup>, 손영보<sup>1</sup>, 남민희<sup>1</sup>, 송유천<sup>1</sup>, 이종희<sup>3</sup>, 김정민<sup>2</sup>, 권영업<sup>1</sup>, 박동수<sup>1\*</sup>

<sup>1</sup>경남 밀양시 내이동 점필재로 20국립 식량과학원 남부작물부 논이용작물과

<sup>2</sup>대구광역시 북구 대학로 80 경북대학교 농업생명과학대학

<sup>3</sup>전북 전주시 완산구 농생명로 300 농촌진흥청 연구정책국 연구운영과

아열대 및 온대지역에서 주로 발생하는 애멸구는 5월~8월 사이 편서풍을 타고 우리나라에 비례하며 벼 바이러스 병인 줄무늬잎마름병을 매개한다. 줄무늬잎마름병은 벼의 수량감소와 미질을 떨어뜨리는 주요 병해 중 하나이다. 애멸구와 같은 멸구류는 대부분 살충제에 의해 방제를 하고 있으나 이러한 약제의 계속된 사용은 환경오염과 약제 저항성 개체의 발생을 유발시킬 수 있는 큰 단점이 있다. 이와 같이 벼에 심각한 피해를 입히는 병해충에 대한 저항성 품종 육성은 병해충을 방제하는 가장 경제적이고 효과적인 방법으로 알려져 있다. 줄무늬잎마름병의 저항성 관련 유전자는 'Modan'에서 유래한 *Stv-b'*, 일본 발벼 또는 열대 자포니카 품종에서 유래한 *Stv-a*, *Stv-b*가 알려져 있으며, 국내에서는 주로 *Stv-b'*가 도입된 저항성 품종들이 육성되고 있다. 단일 유전자를 이용한 저항성 품종육성은 새로운 바이러스의 등장에 취약하므로 저항성 유전자원의 다양화와 새로운 유전자의 탐색이 필요하다. 본 실험에서는 *Stv-a*와 *Stv-b*가 보고된 USA 품종인 Zenith의 형질을 일품에 도입하여 180계통의 F<sub>2</sub> 집단을 육성하여 생물검정과 함께 QTL분석에 이용하였다. 줄무늬 잎마름병에 대한 Zenith에 대한 QTL을 탐색한 결과, 11번 염색체에서 LOD 11.9, 설명가능한 표현형 변이 27%인 QTL이 확인되었다. 줄무늬 잎마름병 연관 QTL 및 이와 관련된 marker는 향후 줄무늬잎마름병에 대한 새로운 저항성 유전자인 *Stv-b*를 보유하는 품종육성을 위한 MAS 체계 확립에 이용할 것이다.

\*주저자: Tel. 055-350-8114, E-mail: qyftpro@gmail.com

**PC-108****Characterization and Genetic Mapping of Narrow and Adaxially Rolled Leaf Mutant in Rice**

Yoon Kyung Lee, Yunjoo Lee, Hee-Jong Koh\*

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

To understand the molecular mechanism of leaf morphogenesis in rice, ethylmethane sulfonate (EMS) treated Ilpoom mutant line with semi-narrow and adaxially rolled leaf phenotype was identified. The leaf rolling character is said to be more advantageous under high temperature and heat stress, and play as one of the defensive mechanisms. The F<sub>1</sub> plants, generated from a cross of Ilpoom and mutant, showed normal phenotype. Genetic analysis of its F<sub>2</sub> population suggested that the mutation was controlled by a single recessive gene with segregation ratio of 3:1. Using F<sub>2</sub> mapping population derived from a cross of Ilpoom mutant and Milyang23, each chromosomes were screened with STS markers by the bulked segregant analysis (BSA) method. The candidate region was detected to a long arm of chromosome 1 near the centromeric region. Fine mapping of the locus is currently conducted. Moreover, other morphological characterizations of the mutant plants were identified. Cytological analysis of the leaf suggested that deformation of the bulliform cells led to the smaller size and less number of the bulliform cells, and caused leaf rolling trait. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

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

---

**PC-109****Production of soybean transgenic plants to improve agronomic traits**

Yoon Jeong Lee<sup>1</sup>, Jin Ho Yang<sup>1</sup>, Jin Sol Park<sup>1</sup>, Hye Jeong Kim<sup>1</sup>, Hyun Suk Cho<sup>1</sup>, Jae Seong Kim<sup>1</sup>, Hyun Hee Im<sup>1</sup>, Ki Jung Lee<sup>1</sup>, Jeong Il Kim<sup>2</sup>, Soon Chun Jeong<sup>3</sup>, Dong Hee Lee<sup>4</sup>, Yung Soo Chung<sup>1\*</sup>

<sup>1</sup>Dept. of Genetic Engineering, Dong-A University, Busan, Korea

<sup>2</sup>Department of Biotechnology and Kumho Life Science Laboratory, Chonnam National University, Kwangju 500-757, Korea

<sup>3</sup>BioEvaluation Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Korea.

<sup>4</sup>Venture Bldg 306 Pohang Techno Park Pohang, Kyungbuk;790-824, Korea

Soybean is a crop of importance economically and nutritionally in many parts of the world. Thanks to many new genes brought from genomic research, it is possible to introduce various candidate genes through genetic transformation to see the performance of the genes in field. In our lab, soybean transformations have been tried for last 10 years to probe the possibility of traits improvement by transformation of new gene into soybean. For this purpose, three different genes were transformed into Korean soybean variety, Kwangan. First, the gene that controls early flowering of plant was transformed into Kwangan. Second, a candidate gene for soybean mosaic virus (SMV) resistance was transformed to produce transgenic plants. Third, another candidate gene for drought tolerance was transformed. All the transgenic plants from three genes transformation were produced for their gene insertion and their expression using PCR, qRT-PCR. Further analysis including harvesting seeds is currently undertaken.

**PC-110****Proteomic Analysis of High and Low- Molecular Weight Subunits in Korean Common Wheat Cultivars**

Jong-Yeol Lee\*, Hye-Rang Beom, Sun-Hyung Lim, Young-Mi Kim

National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea

Although it is known that the composition of HMW-GSs and LMW-GSs are important factor for end-product quality as bread, noodle and cookie, it is still not clear which HMW-GSs and LMW-GSs confer specific processing properties. In this study, to investigate distinctive glutenin proteins and expression level for characteristic processing properties, we carried out qualitative and quantitative analysis of glutenin protein in noodle and bread wheat cultivars by two-dimensional electrophoresis. Unexpectedly, five LMW-GS spots were found to be expressed at a common position in all cultivars and these spots may play something in glutenin biosynthesis. Also we found LMS-GS spots to distinguish Korean wheat cultivars mostly used as noodle and western bread wheat cultivars. These spots may contribute to characteristic processing properties. The 2DE results for each cultivar will be used as reference map or protein marker discriminating wheat cultivars, wheat and rice, imported and Korean flour. For quantitative analysis of glutenin, we calculated relative expression level of the HMW-GS, LMW-GS and HMW-GS/ LMW-GS ratio in each cultivar by 2DE. The results presented in this study provide new insight into relation of specific glutenin proteins and end-use quality and will be useful to choose elite breeding line for improvement of wheat flour quality.

\*Corresponding Author: E-mail: jy0820@korea.kr

## **Comprehensive Identification of Low-Molecular-Weight Glutein Subunit Genes and Their Protein Products in a Korean Common Wheat Variety “Keumkang”**

Hye-Rang Beom\*, Sun-Hyung Lim, Young-Mi Kim, Jong-Yeol Lee

National Academy of Agricultural Science, RDA, Suwon, 441–707, Korea

Although it is well known that low-molecular-weight glutenin subunits (LMW-GS) affects bread and noodle processing quality, the function of specific LMW-GS proteins mostly remain unclear. It is important to find a corresponding gene for a specific LMW-GS protein in order to understand the function of the specific LMW-GS protein. The objective of this study was to identify LMW-GS genes and haplotypes using well known *Glu-A3*, *Glu-B3* and *Glu-D3* gene specific primers and to interlink their protein products by proteomic approaches in a wheat variety. A total of 36 LMW-GS genes and pseudo-genes were amplified including 11 *Glu-3* gene haplotypes, designated as *GluA3-13K* and *GluA3-22K* (pseudogene) at *Glu-A3* loci, *GluB3-33K* and *GluB3-43K* at *Glu-B3* loci and *GluD3-11K*, *GluD3-21K*, *GluD3-31K*, *GluD3-42K*, *GluD3-5K*, *GluD3-6K* and *GluD3-393K* (pseudogene) at *Glu-D3* loci. To determine the relationship between gene haplotypes and their protein products (to identify the corresponding LMW-GS proteins), we conducted N-terminal amino acid sequencing and tandem mass spectrometry (MS/MS) analysis of the 17 LMW-GS spots separated by 2-DGE. Successfully, LMW-GS proteins of the *Glu-3* gene haplotypes except pseudo-genes mentioned above were identified. This is the first report on comprehensive characterization of LMW-GS genes and their corresponding proteins and establishment of specific correspondence between each other in a single wheat cultivar. Our approach will be useful to understand the molecular basis of the LMW-GS and to study their contribution to the end-use quality of flour.

\***Corresponding Author:** E-mail: [gpfkd0629@jbnu.ac.kr](mailto:gpfkd0629@jbnu.ac.kr)

## Activation of Anthocyanin Biosynthesis by Expression of the Radish R2R3 MYB Transcription Factor gene *RsMYB1*

Sun-Hyung Lim<sup>1\*</sup>, Sun-Hwa Ha<sup>2</sup>, MinJi Choi<sup>1</sup>, Da-Hye Kim<sup>1</sup>, SangKyu Park<sup>1</sup>, Jong-Yeol Lee<sup>1</sup>, Young-Mi Kim<sup>1</sup>

<sup>1</sup>National Academy of Agricultural Science, Rural Development Administration, JeonJu, 560–500, Korea

<sup>2</sup>Graduate School of Biotechnology, Kyung Hee University, Yongin, 446–701, Korea

Anthocyanins, providing the bright red-orange to blue-violet colors, flavonoid-derived pigments with strong antioxidant activity that have benefits for human health. We isolated *RsMYB1*, which encodes an R2R3 MYB transcription factor (TF), from red radish plants (*Raphanus sativus* L.) that accumulate high levels of anthocyanins. *RsMYB1* shows higher expression in red radish than in common white radish, in both leaves and roots, at different growth stages. regulatory genes. Transient expression of *RsMYB1* in tobacco showed that *RsMYB1* is a positive regulator of anthocyanin production. Also, the synergistic effect of *RsMYB1* with *B-Peru* was larger than the effect of *Arabidopsis* plants stably expressing *RsMYB1* produced red pigmentation throughout the plant, accompanied by up-regulation of the six structural and two regulatory genes for anthocyanin production. This broad transcriptional activation of anthocyanin biosynthetic machinery in *Arabidopsis* included up-regulation of *TRANSPARENT TESTA 8*, which encodes a bHLH-type TF. These results suggest that overexpression of *RsMYB1* promotes anthocyanin production by triggering the expression of endogenous bHLH genes as potential binding partners for *RsMYB1*. In addition, *RsMYB1*-overexpressing *Arabidopsis* plants had a higher antioxidant capacity than did non-transgenic control plants. Taken together, *RsMYB1* is an actively positive regulator for anthocyanins biosynthesis in radish plants and it might be one of the best targets for anthocyanin production by single gene manipulation being applicable in diverse plant species.

\*Corresponding Author: Tel. 063-238-4615, E-mail: limsh2@korea.kr

---

**PC-113****Comparative Whole-Genome Analysis of Tall Transgenic Bt Line and wild-type Line**

Jin-Hyoung Lee<sup>1</sup>, Kong-Sik Shin<sup>1\*</sup>, Seok-Cheol Suh<sup>1</sup>, Hee-Jong Woo<sup>1</sup>, Myung-Ho Lim<sup>1</sup>, Yang Qin<sup>1</sup>, Taek-Ryoun Kwon<sup>1</sup>, Soon-Ki Park<sup>2</sup>, Hyun-Suk Cho<sup>1</sup>

<sup>1</sup>Biosafety Division, National Academy of Agricultural Science, RDA, JeonJu 560–500, Korea

<sup>2</sup>School of Applied Biosciences, Kyungpook National University, Daegu, 702–701, Korea

Natural and artificially induced mutants have provided valuable resources for plant genetic studies and crop improvement. Some variations induced in the process of plant transformation have often been observed in regenerated plants. In this study, we investigated the insertion number of transgene and the flanking sequences of T-DNA in tall-induced line BP23, which was unexpectedly gained in the process of transformation of insect-resistant rice with *cryBPI* gene, and also analyzed the whole-genome sequencing by using the NGS technologies to gain a better understanding of the sequence and structural changes between tall line or natural cultivar and rice reference. than others, was confirmed with two copies of foreign gene insertion, which was inserted in one genomic site facing each other between the position 2,430,152~2,430,151 of rice chromosome 12 without any deletion of genomic sequences. Sequencing analysis also revealed that 18bp-unknown sequences were added in the 5' insertion site of T-DNA. This position in rice genome was confirmed with none of expressed gene sites. By the NGS analysis, we detected 86560 SNPs and 1091/1472 large insertion/deletion (indel) sites (100bp) between BP23 and rice reference, and 84743 SNPs and 1094/1451 large indels between natural cultivar Nagdong and rice reference. The possible mechanisms for the gene mutation, the developmental and tissue expression of the taller height in BP23 line may need to be scrutinized a few more.

\*Corresponding Author: Tel. 063-238-4707, E-mail: koreabreed@hotmail.com

**PC-114****Predicting consensus sequence of pre-mRNA splicing signals in legume family**

Chaeyoung Lee<sup>1</sup>, Jin-Hyun Kim<sup>1</sup>, Joo-Seok Park<sup>2</sup>, Hong-kyu Choi<sup>3\*</sup>

<sup>1</sup>Department of Medical Bioscience, Dong-A University, Busan, Republic of Korea

<sup>2</sup>Department of Applied Bioscience, Dong-A University, Busan Republic of Korea

<sup>3</sup>Department of Genetic Engineering, Dong-A University, Busan, Republic of Korea

For purposes of studying intron structures and predicting consensus splice motifs, a total of 102 legume species were used to isolate introns across the family. Of 196 gene-targeted PCR primer pairs, we successfully amplified 118 intron-containing genes (60.2%) and obtained a total of 1,870 introns with an average size of 143 nucleotides. Species-based compilation of 5'- and 3'-splicing motifs showed lineage-specific conservation in each splicing motif. Compilation of the entire intron set permitted prediction of the consensus sequences of splicing signal motifs in legumes, A<sup>Y</sup>G<sup>W</sup>GTA<sup>B</sup>A<sup>B</sup>G<sup>H</sup> and T<sup>V</sup>NC/TAGG<sup>H</sup>T<sup>V</sup> for the 5'- and 3'-splicing motifs, respectively. Interestingly, these consensus motifs are very similar to the corresponding splicing signals of two model systems, *Arabidopsis* and rice. This result is suggestive of conservation of pre-mRNA splicing mechanisms in higher plants. Multiple alignments of CALTL introns demonstrated that the region from the branch point to 3' splice site was relatively more conserved than the region from 5' splice site to the branch point. Phylogenetic analysis demonstrated that each of three splicing motifs, 5'-splice sites, 3'-splice sites, and branch site, was relevant to evolutionary divergence of species and phylogenetically informative, suggesting that splice signal sequences would be useful as a potential tool for the molecular phylogenetic analysis.

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

## **Analysis of Genetic Diversity and Evaluation of Phenotypic Traits in Chrysanthemums**

Byung-Chun In, Sung-Chur Sim, Hyung-Won Choi, Sukyoung Jung, Yealim Yi, Bo-Kyung Choi, Yong-Seok Oh, Chang-Kyu Lee, Jin Hee Lim\*

Department of Bioresources Engineering, Sejong University, 98 Gunja-dong, Gwangjin-gu, Seoul 143-747, Korea

*Chrysanthemum* (*Chrysanthemum morifolium*) is one of the most popular ornamental species in the world due to the great diversity of inflorescence form and color. There has been increasing demands for various types of chrysanthemums, such as cut flowers, potted plants and bedding plants. However, the genomic studies of this species have been not extensively conducted relative to other ornamental species due to high levels of polyploidy ( $2n = 4x = 36$  or  $2n = 6x = 54$ ) and heterozygosity as well as large genome size. In this work, we developed a molecular tool for cultivar identification using simple sequence repeats (SSRs) and investigated genetic diversity in 127 chrysanthemum cultivars. Of the 150 SSR primer pairs tested in this study, 62 primers were obtained from previous studies, while 88 primers were designed using the unigene sequences of *C. nankingense* and the Expressed Sequence Tag (EST) sequences of *C. morifolium* in the NCBI database. Thirty SSR primers were selected based on polymorphism and banding patterns in a subset of 8 cultivars and used to amplify the DNA of 127 chrysanthemum cultivars. The UPGMA dendrogram based on these 30 SSR markers showed that most of chrysanthemum cultivars were divided into five clusters. These results will benefit chrysanthemum research community to develop elite cultivars.

\***Corresponding Author:** Tel. +82234084374, E-mail: jinheelim@sejong.ac.kr

## Development of SNP markers associated with citrus canker

Sanghyun Lim<sup>1</sup>, Seunghee Ko<sup>1</sup>, Young Chul Park<sup>2</sup>, Yoon Kyung Uhm<sup>1</sup>, Jae Joon Kim<sup>1</sup>, Kwan Jeong Song<sup>3</sup>, Ho Bang Kim<sup>1\*</sup>

<sup>1</sup>Life Sciences Research Institute, Biomedic Co., Ltd., Bucheon 420–852, Republic of Korea

<sup>2</sup>Agricultural Research and Extension Services, Jeju Special Self-governing Province, Jeju 697–828, Republic of Korea

<sup>3</sup>Faculty of Bioscience and Industry, Jeju National University, Jeju 690–756, Republic of Korea

Citrus canker caused by *Xanthomonas citri* is a notorious disease affecting a decrease in fruit productivity and quality. Citrus export to USA is also prohibited by the disease. Therefore, development of citrus canker resistant variety is essential and exploitation of markers for molecular breeding is urgent. To develop DNA molecular markers, we performed whole genome resequencing for 8 varieties: 4 citrus canker resistant varieties including *C. hybrid* ‘Kioymi’ and 4 citrus canker susceptible varieties including *C. iyo* ‘Miyachiiyokan’. In total, 642 polymorphic SNPs were detected between resistant and susceptible varieties. Of the 642 SNPs, 50 SNPs were preferably selected based on integrative genomics viewer. To apply the markers in a broad range of citrus variety, we performed genotyping with 6 other varieties very well known as citrus canker resistant and susceptible varieties in addition to previous mentioned 8 varieties. Three of the 50 SNPs were identified as a marker to distinguish citrus canker resistant varieties from susceptible varieties. Secondly, we developed molecular markers to apply for F1 lines crossed by ‘Kiyomi’ and ‘Miyachiiyokan’. Of the 50 SNPs, we identified 2 SNP markers to distinguish between F1 resistant and susceptible lines. One of them is a resistance gene that plays a role in plant defense mechanism. In this study, we developed 5 molecular marker candidates possible to apply for molecular breeding to develop citrus canker resistant variety. We are working on development of candidate markers related to citrus canker.

Acknowledgments: This research was supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-3-SBS30 to H.B. Kim, Biomedic Co., Ltd.), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS).

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

---

**PC-117**

## **TE-TRAP : New Marker System for Gamma Irradiated Sorghum (*Sorghum bicolor* L.)**

Seung Bin Im, Jaihyunk Ryu, Sang-Wook Jeong, Soon-Jae Kwon, Joon-Woo Ahn, Dong Sub Kim, Hee-bong Lee, Si-Yong Kang\*

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongup, Jeonbuk 580–185, Korea, 1Chungnam National University Dept. of Applied Botany

The transposable element is a DNA sequence that can be changed its position within the genome, sometimes it can create or reverse mutations and altering the cell's genome size. Target region amplification polymorphism (TRAP) is a rapid and efficient PCR-based marker technique, which uses bioinformatics tools and expressed sequence tag (EST) database information to generate polymorphic markers around targeted candidate gene sequences. TE-TRAP is a new marker system which used terminal inverted repeat (TIR) instead of targeted candidate gene sequences. Sorghum holds a good potential plant organism for transposon tagging due to its small genome size, low amount of repetitive DNA and co-linearity with other cereal genomes, which allows the use of information derived from sorghum in other cereal grasses. IS2868 of sorghum accession was treated Gamma irradiation on seed. To define availability and utilization of TE-TRAP, twenty-one accessions were used to evaluate the genetic diversity and underlying relationships. One-thousand thirty-three TE-TRAP markers were amplified by thirty-one primer combination. Altogether, 712 (62.8%) markers were observed polymorphic segregation, whereas 421 (37.2%) showed monomorphic patterns. To estimate genetic differentiation of population by various gamma radiation doses, the analysis of molecular variance (AMOVA) was performed using 4 to 5 different radiation doses population of M1 sorghum individuals. This study and marker system will provide valuable information to assist radiation mutation breeding.

**PC-118**

## **Functional Characterization of *PaLEAFY*, a *FLORICAULA/LEAFY* orthologue in *Phalaenopsis aphrodite***

Seonghoe Jang<sup>1,2</sup>

<sup>1</sup>Biotechnology Center in Southern Taiwan/Agricultural Biotechnology Research Center, Academia Sinica, Taiwan

<sup>2</sup>Institute of Tropical Plant Science, National Cheng Kung University, Tainan, Taiwan

The plant-specific transcription factor, *LEAFY* (*LFY*) is considered to be a master regulator of flower development in the model plant, *Arabidopsis*. This protein plays a dual role in plant growth, integrating signals from the floral inductive pathways and acting as a floral meristem identity gene by activating genes for floral organ development. Although *LFY* occupies an important position in flower development, the functional divergence of *LFY* homologues has been demonstrated in several plants including monocots and gymnosperms. In particular, the functional roles of *LFY* genes from orchid species such as *Phalaenopsis* that contain unique floral morphologies with distinct expression patterns of floral organ identity genes remain elusive. Here, *PaLFY*, a orthologue of *Arabidopsis LFY* from *Phalaenopsis aphrodite* subsp. *formosana*, a Taiwanese native monopodial orchid was isolated and characterized through analyses of expression and protein activity. *PaLFY* transcripts accumulated in the floral primordia of developing inflorescences and the *PaLFY* protein had transcriptional autoactivation activity forming as a homodimer. Furthermore, *PaLFY* rescues the aberrant floral phenotypes of *Arabidopsis lfy* mutants. Over-expression of *PaLFY* alone or together with *PaFT1*, a *P. aphrodite* subsp. *formosana* homologue of *Arabidopsis FLOWERING LOCUS T (FT)* in rice caused precocious heading. Consistently, higher chlorophyll content in the sepals and morphological changes in epidermal cells were observed in the floral organs of *PaLFY* knock-down orchids generated by virus-induced gene silencing. Taken together, these results suggest that *PaLFY* is functionally distinct from *RICE FLORICAULA/LEAFY (RFL)* but similar to *Arabidopsis LFY* based on phenotypes of our transgenic *Arabidopsis* and rice plants.

---

**PC-119****Analysis of Candidate Genes for Grain Weight Traits Using NILs from An Interspecific Cross in Rice**Yun-A Jeon<sup>1</sup>, Dong-Min Kim<sup>2</sup>, Hyun-Sook Lee<sup>1</sup>, Ju-Won Kang<sup>1</sup>, Yun-Joo Kang<sup>1</sup>, Sang-Nag Ahn<sup>1\*</sup><sup>1</sup>Department of Agronomy, College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305–764, Republic of Korea<sup>2</sup>Seed Testing and Research Center, Korea Seed and Variety Service, Gimcheon 740–220, Republic of Korea

Grain weight is the most important target not only as a major component of grain yield, but also of the cooking qualities in rice breeding program. In a previous study, a high-resolution physical map targeting a cluster of yield-related QTLs for grain weight, spikelets per panicle has been constructed using series of BC<sub>3</sub>F<sub>4</sub> nearly isogenic lines (NILs) derived from a cross between the Korean *japonica* cultivar Hwaseong and *O. rufipogon*. The QTLs including grain weight trait have been mapped in a 25.5kb region containing three genes. Based on GenBank database, these genes include male sterility 5 (*OsMs5*, LOC\_Os09g36740), similar ascorbate peroxidase (*OsApx*, LOC\_Os09g36750) and glutelin family protein (*OsGlu*, LOC\_Os09g36760). Their endogenous expression patterns were analyzed in various rice tissues (2-week seedling, flag leaf, root and panicle) from the parental lines, Hwaseong and NIL-*gw9*. Semi-quantitative RT-PCR and qRT-PCR were performed using gene specific primer sets. The cDNAs of the similar *OsApx* gene of Hwaseong and NIL-*gw9* were cloned. Over-expression and RNAi knock-down transgenic plants using three genes are under construction for the functional characterization of the genes. The results will be discussed.

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

**PC-120****Delaying the tomato fruit ripening by sound wave treatment**Mi-Jeong Jeong<sup>1\*</sup>, Joo-Yeol Kim<sup>1</sup>, Jin Su Lee<sup>2</sup>, Soo In Lee<sup>1</sup>, Jin-A Kim<sup>1</sup><sup>1</sup>Department of Agricultural Biotechnology, National Academy of Agricultural Science (NAAS), 370 Nongsaengmyeong-ro, Wansan-gu, Jeonju, Jeollabuk-do, 560–500, Korea<sup>2</sup>Postharvest Research Team, National Institute of Horticultural and Herbal Science (NIHHS), 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, 565–852, Korea

Regulation of fruit ripening may help extend fruit shelf life and prevent losses due to spoilage. Here, we investigated whether sound treatment could delay tomato fruit ripening. We treated harvested tomato fruits with low-frequency sound waves (1 kHz) for 6 h, and then monitored various characteristics of the fruits over 14-day period at 23±1°C. Seven days after the treatment, 85% of the treated fruits were green, versus fewer than 50% of the non-treated fruits. Most of the tomato fruits had switched to the red ripening stage by 14 days after treatment. Ethylene production and respiration rate were lower in the treated than non-treated tomatoes. Furthermore, changes in surface color and flesh firmness were delayed in the treated fruits. To investigate how sound wave treatment affects fruit ripening, we analyzed the expression of ethylene-related genes by quantitative real-time RT-PCR analysis. We found that the expression level of several ethylene biosynthetic and ethylene signaling pathway-related genes was influenced by sound wave treatment. These results demonstrate that sound wave treatment delays tomato fruit ripening by altering the expression of important genes in the ethylene biosynthesis and ethylene signaling pathways.

\*Corresponding Author: Tel. 063-238-4617, E-mail: center1097@korea.kr

---

**PC-121****Enhanced post-germinative growth of encapsulated somatic embryos of Siberian ginseng (*Eleutherococcus senticosus*) by carbohydrate addition to the encapsulation matrix.**

Su-Jin Jung<sup>1\*</sup>, Ui-Soo Yoon<sup>2</sup>, Yong-Eui Choi<sup>3</sup>

<sup>1</sup>Div. of Biotechnology, Korea Forest Research Institute, Suwon, Republic of Korea

<sup>2</sup>Dept. of Biology, Kongju Nat'l Univ., Kongju, Republic of Korea

<sup>3</sup>Dept. of Forestry, Kangwon Nat'l Univ., Chuncheon, Republic of Korea

This experiment was carried out to enhance plantlet conversion and *ex vitro* survival of encapsulated somatic embryos of Siberian ginseng. Cotyledonary somatic embryos were encapsulated with 3.0% sodium alginate and 96% of conversion rate in terms of plantlet with well-developed epicotyl marked when the encapsulated embryos were placed on perlite soils wetted with sucrose solution as for carbon source. However, post-germinative growth of encapsulated embryos was suppressed in case of sucrose did not added. Instead of sucrose alone, the addition of both sucrose and starch to the sodium alginate enhanced the post-germinative growth of the embryos. In sodium alginate matrix with 2% sucrose, the survival rate of the encapsulated embryos was more than twice (23.5%) that of ones without sucrose (10.0%). Embryos encapsulated with both 2% sucrose and 1% starch showed the highest percentage (42.1%) of survival rate was shown. In analysis of Iodine staining and starch content in the sodium alginate matrix, the starch component was decomposed when the embryos started to germinate. This result indicated that the carbohydrate treatments (starch and sucrose) in the encapsulation matrix enhanced the survival rate of post-germinative growth of encapsulated embryos in Siberian ginseng.

\*Corresponding Author: Tel. 010-4412-2038, E-mail: windy7942@hanmail.net

**PC-122****Characterization of roles of soybean *GIGANTEA* genes in day-length dependent flowering**

Wook-Hun Jung, Cheol Woo Choi, Kyung Hee Lee, Hyun Min Cho, Min Chul Kim\*

Division of Applied Life Science (BK21 Plus program), The Research Institute of Natural Science, Gyeongsang National University, Jinju 660-701, Korea

Major loci controlling flowering time and maturity of short-day plant soybean, *E1*, *E2*, *E3*, *E4*, *E5*, *E6*, *E7* and *E8*, have been identified in soybean. The gene corresponding to *E2* locus is a homolog of *Arabidopsis GIGANTEA (AtGI)*. We identified three *GI* homologs in soybean and are verifying their roles in day-length dependent flowering. Expression analysis indicated that *GmGIs* are ubiquitously expressed at all developmental stages of soybean plants. Diurnal expression of *GmGIs* fluctuates within light/dark cycles of long-day (LD) and short-day (SD). *GmGI2* and *GmGI3* have identical expression patterns under both day length conditions with the highest peak at zeitgeber time 8 h (ZT8) under LD and at ZT4 under SD. *GmGI1* shows the peak at ZT12 under LD and at ZT8 under SD. All of *GmGIs* exhibit the earlier peak and the shorter phase under SD than LD. The results indicated that day length affects expressions of *GmGIs*. Subcellular localization analysis showed that *GmGIs* are mainly targeted to nucleus, similar to the localization of *AtGI*. Overexpression of *GmGIs* in *Arabidopsis* transgenic plants showed no significant effect on flowering time nor rescue of *gi-2* mutant phenotype. The results suggested that *GmGIs* have different molecular functions in flowering time regulation of short-day plant soybean compared to long-day plant *Arabidopsis*. To investigate the molecular mechanisms of *GmGIs*' functions in soybean flowering time control, we intend to identify target gene of *GmGIs* and interacting proteins by using yeast two-hybrid assay.

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

---

**PC-123****Characterization of *OsJAC1* which is responding to different types of ionizing radiation**

In jung Jung\*, Jung Eun Hwang, Sung Min Han, Hong-Il Choi, Soon-Jae Kwon, Jin-Baek Kim, Si-Yong Kang, Dong Sub Kim

Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongseup 580–185, Republic Korea

Ionizing radiation affects gene expression from plant genomes. To monitor the genome-wide transcriptional changes induced by three types of ionizing radiation, we used the rice RNA sequencing to identify genes that are up- or down-regulated by gamma rays (GAs), proton (PRs) and ion beams (IBs). The *Oryza sativa* jacalin-like lectin domain containing proteins (*OsJAC1*) gene was highly induced by GAs, PRs and IBs. *OsJAC1* was selected based on the expression patterns of a genome-wide dataset of RNA sequencing. Many jacalin-related lectin genes have been shown to be associated with disease resistance, biotic and abiotic stress signaling. Therefore, we studied its expression pattern in response to different abiotic stress and phytohormone treatments. The expression patterns of *OsJAC1* under two different abiotic stress conditions (salt and heat stress) and phytohormones (salicylic acid and methyl jasmonate) were examined. The transcripts of *OsJAC1* were significantly induced in response to abiotic stress conditions, including salt and heat treatments. In addition, it was induced in response to the salicylic acid and methyl jasmonate treatments, respectively. To investigate the sub-cellular localization of *OsJAC1*, the gene was expressed as a fusion protein tagged with GFP, in tobacco leaf epidermis and examined under confocal microscope. The *OsJAC1* was clearly localized at the nucleus. These results provide critical insights into the molecular functions of the rice jacalin-like lectin domain containing proteins as receptors of external signals.

\*Corresponding Author: Tel. 063-570-3311, E-mail: bioplant@kaeri.re.kr

**PC-124*****De novo* transcriptome assembly of *Perilla citriodora* and expression profile study**

Junkyoung Choe<sup>1</sup>, Woo Kyung Lee<sup>1</sup>, Ji-Eun Kim<sup>1</sup>, Myoung Hee Lee<sup>2</sup>, Tae-ho Kim<sup>3</sup>, Sung-Hwan Jo<sup>1</sup>, Jeong-Hee Lee<sup>1\*</sup>

<sup>1</sup>SEEDERS Inc., 11–3, 1 Techno-ro, Yuseong-gu, Daejeon 305–509, Korea

<sup>2</sup>National Institute of Crop Science, RDA, Miryang 627–803, Korea

<sup>3</sup>Genomics Division, National Academy of Agricultural Science, RDA, Jeonju 560–500, Korea

The high quality of gene set is necessary to study the functional research of genes. Although perilla is cultivated as an oil crop and as a vegetable crop in Asian countries such as Korea, Japan, northeast China and Nepal, the reference genome is absent. To assembly perilla gene set, we sequenced the various tissues of perilla (*Perilla citriodora*) RNA-seq with Illumina HiSeq platform, generating 548,549,314 short reads. When *de novo* transcriptome assembly was performed with five samples, 86,396 and 38,413 transcripts were assembled as total and representative transcripts, respectively. Using 1,917,424 proteins at Phytozome ver. 9.1, we annotated the perilla assembled transcripts, and 66,139(76.55%) and 24,030(62.55%) transcripts showed the similarity with known plant proteins (E-value < 1e-10) as total and representative transcripts, respectively. Among the diverse molecular functions, we were interested in the regulatory components, such as transcription factor and transcription regulator. Using this data, we identified 499 transcripts annotated the putative transcription factor differentially expressed transcripts. 165 putative transcription factors were significantly expressed in perilla flower and 121 putative transcription factors in both leaf and flower. This study provides the perilla reference gene set and the understanding of the molecular regulation of transcription factor dependent on the tissue.

\*Corresponding Author: Tel. 042-710-4035, E-mail: jhlee@seeders.co.kr

## **Investigation of morphological characteristics and pollen germination in *Senna tora***

Jin-Tae Jeong<sup>1\*</sup>, Seon-Woo Cha<sup>1</sup>, Bo-Keun Ha<sup>2</sup>

<sup>1</sup>Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, RDA, Eumseong 369–871, Republic of Korea

<sup>2</sup>Chonnam National University, Gwangju 500–757, Republic of Korea

*Senna tora* (L.) Roxb. belongs to Leguminosae and its seeds are usually roasted and boiled in water to produce tea in Korea. Also the plants are well known for the treatment of Hypertension, Hepatitis, Constipation and Conjunctivitis. This study was conducted to investigate the morphological characteristics and pollen germination rates of *Senna tora* with the aim of genetic mapping of this species. First, we investigated morphological characteristics of domestic and international genotypes containing 51 lines in Korea and 2 lines in China. No significant differences in growth characteristics were observed among 53 genotypes. However, ST-9 line which was collected in Pyung-chang showed high growth rate at the early stage. The flower of *Senna tora* consists of 5 petals, 10 surgeries (7 main surgeries, 3 small surgeries), 1 pistil, and 5 sepals. After bud emergence, each petal was white in 1-2 days, turn into ivory in a week, then yellow in 8-9 days and finally bloomed in 9-10 days. Although the average flowering times of the plants were July 24, ST9 flowered in July 12. In addition, the flowers of ST9 differed from the flowers of the other genotypes. Flower of ST9 joined together with one another. Therefore, ST9 showing high growth rate at the early stage and unique flowering characteristics was selected to as the paternal line for genetic mapping study. Second, we investigated pollen germination rates for each stage of flower development. Pollen started to germinate at the yellow bud stage and pollen germination rate was highest in the bloomed flower stage. This results show that self-fertilization hardly occurs when the flower is ivory bud stage, and there is no need to use young bud flowers for artificial crossing. This work is intended to serve as the basis for the breeding of new varieties in *Senna tora*.

\*주저자: Tel. 043-871-5576, E-mail: powjtt@korea.kr

## **Molecular Breeding of Pepper Varieties (*Capsicum annuum*) Containing High Levels of Capsinoids**

Hyeon-Seok Jeong, Hee-Bum Yang, Siyoung Jang, Yeong Deuk Jo, Byoung-Cheorl Kang\*

Department of Plant Science, Seoul National University, Seoul 151–921, The Republic of Korea

Capsinoids, low-pungent compounds, have the same biological effects as capsaicinoids such as anticancer and anti-obesity. A precursor of capsinoids, vanillyl alcohol, is known to be produced by mutations in the *putative-aminotransferase (pAMT)* gene. In the previous study, ‘SNU11-001’ (*Capsicum chinense*) containing high levels of capsinoids was identified in germplasm collections of *Capsicum*. This collection has a unique mutation in the *pAMT* gene that can cause dysfunction of this gene. In order to develop pepper varieties containing high capsinoids contents, marker-assisted foreground and background selections were performed during backcross breeding. Compared to the conventional backcrossing, marker-assisted backcrossing (MABC) is extremely useful for recovery of a recurrent parent’s genetic background. For foreground selection, plants carrying the *pAMT/pamt* genotype were selected from a BC<sub>1</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>1</sub> populations using SCAR markers derived from the unique *pAMT* mutation of ‘SNU11-001’. To obtain background selection markers, a total of 412 single nucleotide polymorphism (SNP) markers was screened on ‘Shinghong’ parental lines and ‘SNU11-001’ to obtain polymorphic SNP markers. Of the 412 SNP markers, 144 and 204 polymorphic SNP markers evenly distributed in pepper genome were finally selected. BC<sub>1</sub>F<sub>1</sub> and BC<sub>2</sub>F<sub>1</sub> plants carrying the *pAMT/pamt* genotype were subjected to background selection using the selected marker sets. Multiple genotype analysis was done using a high-throughput genotyping system (EP1™, Fluidigm®, USA). As a result, one BC<sub>1</sub>F<sub>1</sub> plant 84% similar to the recurrent parent and several BC<sub>2</sub>F<sub>1</sub> plants more than 96% recovery rate of the recurrent parent were selected. Genetic backgrounds of the selected BC<sub>2</sub>F<sub>1</sub> plants were evaluated by the genotype-by-sequencing (GBS) method in order to confirm the background selection results using the SNP marker set. GBS results showed that recovery rate and positions of introgressed segments were well matched between two methods demonstrating MABC can be successfully done with a couple hundred SNP markers.

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

## Genome Cloud 서버 연결 NCBI-SRA 데이터를 이용한 SNP 마커 발굴용 컨베이어 QUEUE 시스템 개발

최준경, 이봉우, 김지은, 오재은, 이보미, 이정희, 조성환\*

대전광역시 유성구 테크노1로 11-3 N218, (주)씨더스

주요 작물들의 표준유전체, 핵심집단 재분석, 전사체 등의 다양한 NGS 정보가 NCBI와 같은 공개 데이터베이스에 빠르게 축적되고 있다. 현재 NCBI의 SRA(Sequence Read Archive) DB에 등록되어 있는 토마토 유전체(genome) 시퀀싱 데이터만 800건 이상, 파일 크기는 23.5 Tb에 달한다. 그러나 이러한 NGS 데이터로부터 원하는 정보를 추출하기 위해 사용할 수 있는 분석용 대용량 서버 자원 및 빅데이터(big data) 처리 기술이 접목된 생물정보분석 프로그램은 매우 제한적이다. 이에 따라 대용량 서버를 갖추고 있지 않아도 대규모 유전체 데이터를 분석할 수 있도록 Genome Cloud 서버에서 작동하는 웹 기반의 SNP 분석 프로그램을 개발하고, 분석 자동화 컨베이어 QUEUE 시스템을 적용하였다.

이 프로그램은 사용자가 분석하고자 하는 SRA accession을 수집하여 프로그램에 입력하면, 자동으로 NCBI-SRA DB에 접속하여 SRA 파일을 서버로 다운로드하면서 SRA 포맷에서 FASTQ 포맷으로 전환한다. 전환된 FASTQ 파일은 자동으로 SNP 분석 파이프라인에 입력되어 SNP가 추출되고, 결과물은 데이터베이스화 된다. 또한 이 프로그램에는 컨베이어 QUEUE 시스템이 접목되어 IO 버퍼와 같은 시스템 과부하를 막아 효율적으로 분석 파이프라인이 진행된다. 1개 FASTQ 파일이 분석되는 동안, 다음 분석이 진행될 1개 SRA 파일의 다운로드 및 포맷 전환이 자동 진행된다. 위 시스템을 적용하였을 때, 1개 SRA(서열 길이 14Gbp)를 Cloud 서버(16 core CPU, RAM 64Gb 사양)로 다운로드하고 포맷을 전환하는데 약 30분~1시간이 소요되었으며, SNP 분석에는 약 6시간이 소요되었다. Cloud의 장점인 확장성을 적용하여 서버 5대를 병렬로 연결하여 사용할 경우, 500개의 샘플을 한 달 이내에 처리할 수 있을 것으로 예상된다. 현재 약 200여개의 토마토 SRA resequencing 데이터에서 표준유전체 대비 수백만 개의 SNP genotype을 확보하였다. 분석 결과물은 토마토 계통 및 집단 정보를 이용하여 향후 Haplotype, LD 분석 등의 주요 응용 분석을 진행하고, TGSol(<http://tgsol.seeders.co.kr>)에 데이터베이스로 구축하여 제공하고자 한다.

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

---

**PC-128**

## **Developing Marker and Fine Mapping of the Powdery Mildew Resistance Gene in *Capsicum annuum***

Jinkwan Jo<sup>1</sup>, Gyung Ja Choi<sup>2</sup>, Jin-Kyung Kwon<sup>1</sup>, Byoung-Cheorl Kang<sup>1\*</sup>

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

<sup>2</sup>Research Center for Biobased Chemistry, Korea Research Institute of Chemical Technology, Daejeon 305-600, Republic of Korea

Powdery mildew disease caused by *Leveillula taurica* is a serious fungal threat to greenhouse pepper production. In contrast to most epiphytic powdery mildew species, *L. taurica* is an endophytic fungus which colonizes in the mesophyll tissues of the leaf. In the genus *Capsicum*, several studies have been conducted to identify resistance sources to *L. taurica*. In previous studies, five quantitative trait loci (QTLs) for powdery mildew resistance have been identified. An F<sub>2</sub> population derived from self-pollination of the commercial cultivar *Capsicum annuum* 'PM Singang' was used for genetic analysis of powdery mildew resistance. Resistance of the F<sub>2</sub> plants was tested under the natural environmental conditions. Sporulation intensity on infected leaves was used as a disease scale to assign resistance levels to plants, where 0-5% is Resistant, 6-15% Moderate resistant and 16-100% Susceptible. A total of 83 F<sub>2</sub> plants were evaluated for resistance. The results showed that 59 plants were resistant, 10 susceptible and 14 moderately resistant. If we consider MR as S, segregation ratio fitted to a single dominant resistance gene model. In the future study, closely linked molecular marker will be developed and tested to locate this gene. The developed marker will be used to identify the powdery mildew resistance gene.

**PC-129**

## **Transformation of soybean with AT-hook binding protein genes to delay senescence**

Hyun Suk Cho<sup>1</sup>, Jin Ho Yang<sup>1</sup>, Jin Sol Park<sup>1</sup>, Hye Jeong Kim<sup>1</sup>, Yoon Jeong Lee<sup>1</sup>, Jae Seong Kim<sup>1</sup>, Hyun Hee Im<sup>1</sup>, Ki Jung Lee<sup>1</sup>, Dong Hee Lee<sup>1,2</sup>, Young Soo Chung<sup>1\*</sup>

<sup>1</sup>Dept. of Genetic Engineering, Dong-A University, Busan, Korea

<sup>2</sup>Venture Bldg 306 Pohang Techno Park Pohang, Kyungbuk;790-824, Korea

High yield is the most important trait in various agricultural characteristics. Many approaches to improve yield have been tried in conventional agricultural practice and recently biotechnological tools employed for same goal. Genetic transformation of key genes to increase yield is one way to overcome current limitation in the field. We are producing transgenic soybean plants through high efficient transformation method by introducing all gene member with AT-hook binding domain, hoping to obtain manageable delay of senescence. Many transgenic soybean plants are growing in greenhouse and GMO field, and will be evaluated their senescence and any association with yield increase.

---

**PC-130**

## **Development of novel strategy for antifungal crop using trans-kingdom small RNA movement**

Byung-Jun Jin, Hyun Jin Chun, Min Chul Kim\*

Division of Applied Life Science (BK21 Plus Program), The Research Institute of Natural Science, Gyeongsang National University, Jinju 660-701, Republic of Korea.

Small RNAs, such as microRNAs (miRNAs) and small interfering RNAs (siRNAs), play crucial roles in post-transcriptional gene silencing (PTGS) in eukaryotes. Small RNAs function cell-autonomously as well as non-cell-autonomously. It has been well characterized that pathogenic fungi secrete some effector molecules facilitating their infection into plants. However, it is unclear whether molecules produced in plant cells are able to move into fungal cells during infection. To test if small RNAs generated from plant cells can move to fungal cells during infection, we generated transgenic *Arabidopsis* and rice plants expressing siRNAs targeting *GFP* gene generated from double-stranded RNA interference (dsRNAi) constructs for *GFP* gene. And then these transgenic plants were inoculated with transgenic rice blast fungus, *Magnaporthe oryzae*, expressing *GFP* transgene. Here, we showed that ectopic expression of siRNAs targeting *GFP* gene in transgenic plants significantly suppressed *GFP* expression in rice blast fungi inoculated, indicating that small RNA molecules generated in plant cells can move into infected fungal cells and efficiently degrade fungal *GFP* transcripts. Our results would provide a new small RNA-based strategy for the development of resistant crops against fungal pathogens.

\*Corresponding Author: Tel. 055-772-5428, E-mail: mckim@gnu.ac.kr

**PC-131**

## **Caffeic acid *O*-methyltransferase (COMT) is involved in the melatonin synthesis in rice (*Oryza sativa*) plants**

Geun-hee Choi, Yeong Byeon, Hyoung Yool Lee, Kyoungwhan Back\*

Department of Biotechnology, Bioenergy Research Center, Chonnam National University, Gwangju, Republic of Korea

Caffeic acid *O*-methyltransferase (COMT) methylates *N*-acetylserotonin into melatonin; that is, it has *N*-acetylserotonin *O*-methyltransferase (ASMT) activity. The ASMT activity of COMT was first detected in *Arabidopsis thaliana* COMT (AtCOMT). To confirm the ASMT activity of COMT in other plant species, we evaluated the ASMT activity of a COMT from rice (*Oryza sativa*) (OsCOMT). Purified recombinant OsCOMT protein from *Escherichia coli* was used to validate the high ASMT activity of OsCOMT, similar to that of AtCOMT. The  $K_m$  and  $V_{max}$  values for the ASMT activity of OsCOMT were 243  $\mu$ M and 2,400 pmol/min/mg protein, which were similar to those of AtCOMT. Similar to AtCOMT, OsCOMT was localized in the cytoplasm. *In vitro* ASMT activity was significantly inhibited by either caffeic acid or quercetin in a dose-dependent manner. Analogously, *in vivo* production of melatonin was significantly inhibited by quercetin in 4-week-old detached rice leaves, suggestive of a positive role of COMT in melatonin biosynthesis in plants.

\*Corresponding Author: Tel. 062-530-0441, E-mail: kback@chonnam.ac.kr

## **Development of *Oryza sativa* Alternative Spliced Transcripts Detecting Microarray.**

Songhwa Chae<sup>1</sup>, Kyong-Mi Jun<sup>2</sup>, Joung Sug Kim<sup>1</sup>, Baek-Hie Nahm<sup>1,2</sup>, Yeon-Ki Kim<sup>1\*</sup>

<sup>1</sup>Division of Bioscience and Bioinformatics, Myongji University, Yongin, Korea,

<sup>2</sup>Plant molecular genetics Institute, GreenGene Biotech Inc., Yongin, Korea

Expression profiling was conducted with the *Oryza sativa* alternative splicing detecting microarray v.4 (OsASDM). Probe features are designed based on rice genome IRGSP\_1.0 (<http://rapdb.dna.affrc.go.jp/>). The genome contains 37,868 genes. Among these 5,254 genes have alternative spliced sites, 11,938 transcripts. In the microarray, a total of 41,953 transcripts are covered from all the loci and 9112 alternative spliced transcripts. Four 60-nt long probes were designed from each transcript starting 60 bp ahead the end of stop codon and with shifting 30 bp so 4 probes cover 150 bp in the 3' region of the gene. Genes from chloroplast (123) and mitochondria (74) and selection markers such as *gfp*, *gus*, *hyg*, *bar*, and *kan* are included. In total, 125,956 probes were designed.

To find organ specific transcripts RNA was prepared from leaf, root, panicle at 1 cm (P1cm). The signal intensity files were analyzed with limma package. Background correction and normalization were performed with libraries in the package. 13,486 genes are organ specific and 1,856 transcripts are alternatively spliced. Transcripts that specifically alternatively spliced in leaf are Os02t0197600-02\_UE; Chlorophyll a-b binding protein 8, Os11t0707000-01\_UE; Ribulose biphosphate carboxylase/oxygenase, Os12t0291100-01\_UE; ribulose 1,5-biphosphate carboxylase small subunit. Transcripts that specifically alternatively spliced in root are Os03t0669100-02\_UE; Deoxyuridine 5'-triphosphate nucleotidohydrolase, Transcripts that specifically alternatively spliced in tissues at P1cm are Os11t0210300-02\_UE; Alcohol dehydrogenase 1, Os04t0631200-02\_UE; Xyloglucan endotransglycosylase. Os03t0669100-02\_UE ; Deoxyuridine 5'-triphosphate nucleotidohydrolase, Os11t0210300-02\_UE ; Alcohol dehydrogenase 1, Os04t0631200-02\_UE; Xyloglucan endotransglycosylase. These results show that OsASDM could be used to find alternatively spliced gene at ease.

**\*Corresponding Author:** E-mail: kim750a11@gmail.com

---

**PC-133****Season-related variations of growth and metabolic profiles in *Pinus densiflora***Mi Na Choi<sup>1,2\*</sup>, Hyo-Ryeon Lee<sup>1</sup>, Eung-Jun Park<sup>1</sup><sup>1</sup>Department of Forest Genetic Resources, Korea Forest Research Institute, Suwon 441–847, Korea<sup>2</sup>Department of Forest resources, Kangwon National University, Chuncheon 200–701, Korea

The effect of seasonality is one of the most significant external sources of variation affecting cambial activity and the development of newly divided cells, and therefore influencing stem growth of trees. Here, we investigated changes in the seasonal concentrations of metabolites of current-year stem tissues in 6-year-old *Pinus densiflora* at June, August, and October. 76, 75, and 78 metabolites were assigned at June, August, and October by GC/MS. Among these compounds, 55 metabolites were commonly found in all three times, and they were divided into six groups according to the variation of concentrations in each times. Among 56 metabolites, the concentrations of three inositol-methylated derivatives, myo-inositol, ononitol, and pinitol in current-year stem tissues at August were significantly correlated with the heights of nursery-grown trees. Furthermore, we found that such metabolites were significantly correlated with stem diameter at 27 years for two consecutive years. Therefore we suggest that seasonal differences in the contents of inositol derivatives may explain much of the natural variation seen for tree stem size in even-aged pine forests. And these have the potential as metabolic markers of inherently rapidly growing trees in the early selection of those conifer families.

\*Corresponding Author: Tel. 031-290-1164, E-mail: mnchoi1022@korea.kr

**PC-134****Systemic analyses of expression patterns and structural variation of soybean flowering genes in natural accessions**

Cheol-Woo Choi, Wook-Hun Jung, Kyung-Hee Lee, Min-Chul Kim\*

Division of Applied Life Science (BK21 Plus), Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju 660–701, Korea.

Soybean is a short-day plant, which means short day length promotes flowering. So far nine major loci, *E1* to *E8* and *J*, affecting the timing of flowering and maturity have been genetically identified in soybean. To understand the roles of soybean flowering genes in photoperiod-dependent flowering time control in soybean, we analyzed not only expression patterns of *E1*, *E2*, *E3* and *E4* genes as well as soybean *FT* homologs, including *GmFT2a*, *GmFT5a* and *GmFT4*, but also structural variation of *E1*, *E2*, *E3*, and *E4* genes in various soybean accessions exhibiting a broad range of flowering time. The mRNA level of *GmFT2a* and *GmFT5a* was low in late flowering accessions, but high in late flowering accessions. In contrast, *GmFT4* exhibited opposite expression pattern to those of *GmFT2a* and *GmFT5a*. Structural variation of *E1*, *E2*, *E3* and *E4* gene in these accessions revealed that early and moderate flowering accessions contained non-functional alleles of *E1*, *E2*, *E3* and *E4* genes in their genome. These results suggested that expression patterns of *GmFT2a*, *GmFT5a* and *GmFT4* would be important factor determining flowering time in soybean and allelic variation and genetic combination of upstream *E1*, *E2*, *E3*, and *E4* genes would be more important in soybean flowering time control than their gene expression patterns.

\*Corresponding Author: Tel. 055-772-5428, E-mail: mckim@gnu.ac.kr

## Characterization of the aquaporin family genes and stress responsive expression profiling in *Brassica rapa*

Md. Abdul Kayum, Jong-In Park, Nasar Uddin Ahmed, Gopal Saha, Ill-Sup Nou\*

Department of Horticulture, Sunchon National University, Suncheon 540–742, Korea

Efficient infiltration of water through cell membranes is arbitrated by a family of transmembrane water channels called aquaporins (AQPs). Aquaporin belongs to a highly conserved group of membrane proteins called major intrinsic proteins that facilitate the transport of water and a variety of low molecular weight solutes across biological membranes, which is essential for plants to survive in stress conditions. This study identified 59 *BrAQP* genes from *B. rapa* database and Br135K microarray dataset, which was formed by applying low-temperature stresses to contrasting Chinese cabbage two inbred lines, Chiifu and Kenshin. Based on phylogenetic analyses of BrAQPs revealed four distinct subfamilies, such as plasma membrane intrinsic proteins (PIP), tonoplast intrinsic proteins (TIP), NOD26-like intrinsic proteins (NIP), small basic intrinsic proteins (SIP) with aquaporin of Tomato and *Arabidopsis thaliana*. All *BrAQP* genes were firstly examined through homology study with existing biotic and abiotic stress resistance-related *aquaporin* genes of other plant species and found a high degree of homology. We selected PIP subfamily genes for expression analysis based on microarray data with high and differential transcript abundance levels and homology study with stress related aquaporin genes of other plant species. In our study, we characterized all *B. rapa* aquaporin genes and understanding the BrPIP subfamily gene function in plants under various environmental stimuli, the expressions of *BrPIP* genes under various abiotic stress conditions including cold, drought, salinity, water logging, ABA treatment and *Fusarium oxysporum* f. sp. *Conglutinans* infection were investigated by a quantitative real-time reverse transcription-PCR analysis. In our expression analysis, 4 *BrPIP* genes showed responsive expression against *F. oxysporum* f. sp. *Conglutinans* infection. The selected genes showed an organ-specific expression, and 12 out of 22 *BrPIP* genes were differentially expressed in Chiifu compared to Kenshin under cold stresses. Only 7 genes showed up regulation under drought stress and in case of salt stress 17 *BrPIP* genes were more responsiveness. Additionally, 18 *BrPIP* genes were up regulated by ABA treatment and all *BrPIP* genes showed down regulation under water logging stress. Together with expression and bioinformatic analyses, our results provides novel basis to allocate the stress-related biological function to each *PIP* gene.

\*Corresponding Author: Tel. +82-61-750-3249, E-mail: nis@sunchon.ac.kr

---

**PC-136****Carotenoids Synthesis Gene Analysis in pepper**

Ayoung Jung<sup>1</sup>, Hyeon-Seok Jeong<sup>1</sup>, Dong Kyu Lim<sup>2</sup>, Yeaseong Ha<sup>1</sup>, Arti Rai<sup>1</sup>, Jin-Kyung Kwon<sup>1</sup>, Sung Won Kwon<sup>2</sup>, Byoung-Cheorl Kang<sup>1\*</sup>

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

<sup>2</sup>College of Pharmacy, Seoul National University, Seoul, 151–921, Republic of Korea

Carotenoids are vital pigments responsible for yellow, orange and red color in plants. In *Capsicum*, capsanthin-capsorubin synthase (*CCS*), phytoene synthase (*PSY*),  $\beta$ -Carotene hydroxylase (*CRTZ-2*) and lycopene  $\beta$ -cyclase (*LCYB*) were identified to be involved in the carotenoids synthesis pathway. Previously molecular markers based on the *CCS* and *PSY* genes have been developed to distinguish fruit colors in pepper. However these markers can distinguish fruit colors of limited pepper genotypes. Therefore, there is need of developing additional markers for accurate prediction of fruit colors using molecular markers. In this study carotenoids contents of 16 pepper accessions were analyzed and the *CCS*, *PSY*, *CRTZ-2*, *LCYB* genes were sequenced to identify the genes affecting the fruit color. Among all the analyzed carotenoids, capsanthin was accumulated in much higher amount in red and orange fruits (1100-2500 mAU·min and 30-500 mAU·min respectively) while violaxanthin (20-1200 mAU·min) was accumulated more in yellow fruits. Sequence analysis revealed that deletions and two frame shift mutations in *CCS* gene for yellow accessions. Frame shift mutations of the *PSY* gene were detected in two orange accessions. These results show that mutations in *CCS* and *PSY* genes affect the fruit colors of pepper, and markers can be developed using mutations of these genes.

**PC-137****Isolation and Characterization of Pepper Genes Interacting with CMV-P1 Helicase Domain**

Yeaseong Ha, Joung-Ho Lee, Yoomi Choi, Min-Young Kang, JeeNa Hwang, Won-Hee Kang, Byoung-Cheorl Kang\*

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

*Capsicum annuum* ‘Bukang’ is a resistant variety to *Cucumber mosaic virus* isolate-P0 (CMV-P0), CMV-P1 can overcome the CMV resistance of ‘Bukang’ due to mutations in Helicase (Hel) domain of CMV RNA1. To identify host factors involved in CMV-P1 infection, a yeast two-hybrid system derived from *C. annuum* ‘Bukang’ cDNA library was used. A total of 156 potential clones interacting with the CMV-P1 RNA helicase domain were isolated. These clones were confirmed by  $\beta$ -galactosidase filter lift assay, PCR screening and sequence analysis. Then, we narrowed the ten candidate host genes which are related to virus infection, replication or virus movement. To elucidate functions of these candidate genes, each gene was silenced by virus induced gene silencing in *Nicotiana benthamiana*. The silenced plants were then inoculated with green fluorescent protein (GFP) tagged CMV-P1. Virus accumulations in silenced plants were assessed by monitoring GFP fluorescence and enzyme-linked immunosorbent assay (ELISA). Among ten genes, silencing of *formate dehydrogenase* (FDH) or *calreticulin-3* (CRT3) resulted in weak GFP signals of CMV-P1 in the inoculated or upper leaves. These results suggested that FDH and CRT3 are essential for CMV infection in plants. The importance of FDH and CRT3 in CMV-P1 accumulation was also validated by the accumulation level of CMV coat protein confirmed by ELISA. Altogether, these results demonstrate that FDH and CRT3 are required for CMV-P1 infection in plants.

---

**PC-138**

## **Genotyping-by-sequencing (GBS) for assessment of genetic diversity in pepper germplasm**

Koeun Han, Heayoung Lee, Jin-Kyung Kwon, Byoung-Cheorl Kang\*

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

Pepper (*Capsicum* spp.) germplasm shows diverse phenotypic variations including fruit size, color, pungency, and many other horticultural traits. Traditional markers including SSR, AFLP, and RFLP have been used to construct genetic maps using biparental populations. However to assess the genetic diversity of large number of germplasm, a robust and rapid marker development and genotyping approach is needed. We used six pepper accessions including *C. annuum*, *C. chinense*, *C. baccatum* and *C. frutescens* and performed genotyping-by-sequencing (GBS). To select the most appropriate condition, eight different 2 bp selective nucleotides were used to make GBS libraries. Selective nucleotide 'OO' showed the largest number of reads in all samples, and 11,026 to 47,957 high-quality SNPs were called in six accessions. When *C. annuum* 'CM334' genome sequence was used as a reference, *C. annuum* showed the smallest number of SNPs, while *C. baccatum* which was known to be a different *Capsicum* clade showed the largest number of SNPs. Pepper core collection chosen to represent the genetic diversity of whole germplasm will be genotyped by high-density SNPs developed from GBS. We will perform genome-wide association study (GWAS) using genetic and phenotypic variation to identify the functional genetic loci controlling horticultural traits.

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

**PC-139**

## **Effects of ionizing irradiation on mutation induction and nuclear DNA content in *Oryza Sativa* L.**

Sung Min Han\*, Jung Eun Hwang, In jung Jung, Hong-Il Choi, Soon-Jae Kwon, Jin-Baek Kim, Si-Young Kang, Dong Sub Kim

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

Ionizing radiation directly and indirectly affects gene expression within the plant genome. To access the physiological response of rice to different types of ionizing radiation, rice seeds were exposed to gamma-ray and ion beam radiation. Exposure to ionizing radiation dramatically decreased the shoot length compared with non-irradiated plants. Fluorescence-activated-cell-sorting (FACs) was used to measure DNA contents. There were significant correlations of dose-dependent between irradiated plant and non-irradiated plant. The radicals induced by the ionizing radiation in the plant could be observed by electron spin resonance (ESR). It was confirmed that the number of free radicals in cell was greatly increased all irradiated plants than non-irradiated plant. A significant positive correlation was shown between ionizing radiation dose and signal intensity. In order to determine the Genetic diversity, AFLP analysis was conducted with the irradiated plant and non-irradiated plant. Based on band patterns, the cluster analysis was conducted to evaluate the genetic variation by using the UPGMA (Unweighted Pair Grouping Method of Averages). Genetic diversity of irradiated plants by low dose ion beam was the closest non-irradiated plant and irradiated by high dose gamma-ray was the furthest from non-irradiated. We describe the detailed methods of ionizing irradiation and discuss its applications in genetic research as well as plant breeding.

\*Corresponding Author: Tel. 063-570-3310, E-mail: bioplant@kaeri.re.kr

## **Classification of Asian pears (*Pyrus* spp.) using the 12 standard set of microsatellite reference alleles**

Hyeondae Han<sup>1,2</sup>, Youngjae Oh<sup>1,2</sup>, Hyunsuk Shin<sup>1,2</sup>, Sewon Oh<sup>1,2</sup>, Jungyeon Won<sup>1,2</sup>, Seolah Kim<sup>1,2</sup>, Junhyeong Park<sup>1</sup>, Yoon-kyeong Kim<sup>3</sup>, Gidong Hwang<sup>1</sup>, Daeil Kim<sup>1,2\*</sup>

<sup>1</sup>Department of Horticulture Science, Chungbuk National University, Cheongju 362–763, Korea

<sup>2</sup>Brain Korea 21 Center for Bio–Resource Chungbuk National University, Cheongju 362–763, Korea

<sup>3</sup>Pear Research Station, National Institute of Horticultural & Herbal Science, Rural Development Administration, Naju 520–821, Korea

The objective of the study was to identify 52 Asian pear accessions, two primary pear species, and one reference pear Asian pear with 12 microsatellite markers to maintain pear germplasm collection. The number of alleles of 12 microsatellites detected ranged from eight at CH03d12 to 18 at CH01f07. Gene diversity ranged from 0.7053 at CH01d08 to 0.9224 at CH01f07. The lowest value of PIC was 0.6600 at CH01d08 and the highest was 0.9171 at CH01f07. A group consisting of ‘Ooharabeni,’ ‘Bartlett,’ and *P. calleryana* was out-grouped and served as a reference to determine the relationship among Asian pear accessions. Except for the out-group, 50 Asian pears were segregated into two groups. Group I was divided in two small groups. Each small group was characterized by *P. bretschneideri* and *P. ussuriensis*, respectively. Group II was characterized as *P. pyrifolia*, and the group was divided in four small groups. The eigenvalue, difference, proportion, and cumulative of six principal components based on PCA to 12 microsatellite. The eigenvalue of the first principal components was 5.5850. The proportion of the first principal component was 0.9308. The cumulative value of the first two principal components was 0.9801. Consequently, nearly all of the results were elucidated by the two principal components. The results from analysis of the standard set of microsatellites in this study may be used as basic materials for the management of Asian pear germplasm collections, and the data might be useful in the development of a core collection.

\*Corresponding Author: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

---

**PC-141****Analysis of transcriptional regulation of Arabidopsis *PIF* family genes in response to abiotic stresses**

Jin-Seok Moon<sup>1,3\*</sup>, Satoshi Kidokoro<sup>1</sup>, Daisuke Todaka<sup>1</sup>, Sayuri Igusa<sup>1</sup>, Junya Mizoi<sup>1</sup>, Kazuo Shinozaki<sup>2</sup>, Kazuko Yamaguchi-Shinozaki<sup>1</sup>

<sup>1</sup>Grad. Sch. Agr. Life Sci., Univ. Tokyo

<sup>2</sup>Center for Sustainable Resource Science, RIKEN

<sup>3</sup>Fruit Research Division, National Institute of Horticultural and Herbal Science, RDA, Wanju 565–850, Korea

As one of the most severe stress conditions, drought strongly affects the plant growth and productivity. *OsPIL1*, a gene encoding a rice Phytochrome Interacting Factor (PIF)-Like transcription factor, was found to be down-regulated under drought stress condition. *OsPIL1* shows a diurnal expression pattern and known to be involved in regulation of plant height. However, the mechanisms of down-regulation of *OsPIL1* expression under stress conditions are remained unclear. In this study, the expression of *PIF4* and *PIF5*, the most homologous genes of *OsPIL1* in Arabidopsis, was analyzed and the expression of these genes were found to be oscillated in circadian manner and down-regulated in response to drought and low temperature similar to that of *OsPIL1*. To identify the regions involved in the responses to drought, low temperature and diurnal cycle, the promoter analysis of *PIF4* was performed using transgenic Arabidopsis. Further promoter analysis is ongoing to specify regulatory regions in more detail.

\*Corresponding Author: Tel. 063-238-6743, E-mail: gsmoon@chol.com

**PC-142****Development of molecular markers for evaluation of low temperature germinability in rice germplasm**

Do Yoon Hyun<sup>1\*</sup>, Sukyeung Lee<sup>1</sup>, Yu-Mi Choi<sup>1</sup>, Myung-Chul Lee<sup>1</sup>, Se Jong Oh<sup>1</sup>, Thomas H. Tai<sup>2</sup>

<sup>1</sup>National Agrobiodiversity Center, NAAS, RDA, Jeonju, Korea

<sup>2</sup>USDA–ARS, Crops Pathology and Genetics Research Unit, Davis, CA, USA

Low temperature germinability (LTG) is an important trait for breeding of varieties for use in direct-seeding rice production systems. Although rice (*Oryza sativa* L.) is generally sensitive to low temperatures, genetic variation for LTG exists and several quantitative trait loci (QTLs) have been reported. The objective of this study was to develop and employ high-efficiency molecular markers for evaluation of LTG in rice germplasm. A panel of *japonica* rice accessions (n=180) from temperate regions in Asia was evaluated for LTG and genotyped with markers from regions previously reported to harbor other LTG QTLs. ANOVA revealed that four markers on chromosome 2, 4, and 11 from previously reported QTLs showed highly significant value ( $p < 1.0e-04$ ) and their  $R^2$  ranged 0.083 (qLTG11-1) to 0.190 (qLTG4b-1). An association analysis was conducted using SNP data generated by sequencing of the panel. Eight SNP markers were found to be significantly associated with LTG using general and mixed linear models. Three SNP-based CAPS and dCAPS markers from these results were developed and showed higher accuracy in predicting sensitive LTG germplasm. These new LTG markers will be useful for molecular evaluation of germplasm, particularly to identify sensitive or weak LTG accessions.

\*Corresponding Author: Tel. 063-238-4912, E-mail: dyhyun@korea.kr

## Expression of anthocyanin biosynthesis-related genes in wheat grain development

Min Jeong Hong<sup>1</sup>, Young Ha Yoon<sup>1</sup>, Dong Sub Kim<sup>1</sup>, Sang Hoon Kim<sup>1</sup>, Joon-Woo Ahn<sup>1</sup>, Si-Yong Kang<sup>1</sup>, Yong Weon Seo<sup>2</sup>, Jin-Beak Kim<sup>1\*</sup>

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

<sup>2</sup>Division of Biotechnology, Korea University, Seongbuk-Gu, Seoul 136-713, Republic of Korea

Seed color is an important factor affecting physiological and developmental process in wheat. One of the plant pigments, anthocyanins are a group of flavonoid compounds well known as pigments responsible for blue, purple, red, or yellow coloration of plant tissues. In this study, we investigated the pigmentation of purple and yellow color seed according to wheat grain developmental stages. The contents of anthocyanin and chlorophyll in the purple and yellow seeds were measured. Chlorophyll contents were changed similarly in both purple and yellow color seed, and no significant difference was observed between them. In purple color seed, the content of anthocyanin was significantly induced compared with yellow color seed. The individual anthocyanin components were investigated by ultra performance liquid chromatography (UPLC). Cyanidine-3-glucoside (C3G) and peonidine-3-glucoside (P3G) were detected as predominant anthocyanin in purple color wheat. To investigate whether structural genes in anthocyanin biosynthesis were involved in the trait differences between purple and yellow color seed, we examined the expression of anthocyanin biosynthesis-related genes (*CHS*, *CHI*, *F3H*, *DFR*, *ANS*, *UGT*) and MYB transcription factor in developing wheat grains by using qRT-PCR. This study indicates that the expression of anthocyanin biosynthesis-related genes and MYB transcription factors correlate with anthocyanin levels of grain.

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

## DNA 바코드 분석을 통한 국내 자생 난지형 잔디의 분류

양대화<sup>2+</sup>, 홍민지<sup>1+</sup>, 정옥철<sup>2+</sup>, 진일두<sup>2</sup>, 박미영<sup>2</sup>, 김양지<sup>1</sup>, 이효연<sup>1,2\*</sup>

<sup>1</sup>제주대학교 생명공학부

<sup>2</sup>제주대학교 아열대원예산업연구소

+공동1저자

잔디는 공원과 정원, 학교운동장, 묘지, 골프장, 스포츠경기장, 도로변과 같이 다양한 장소에 식재되고 있는 주요 작물이다. 이러한 잔디는 생육적온에 따라 크게 난지형 잔디와 한지형 잔디로 구분된다. 그 중 한국잔디(*Zoysiagrass*)는 대표적인 난지형 잔디로, 들잔디(*Zoysia japonica*)와 금잔디(*Zoysia matrella*), 갯잔디(*Zoysia sinica*), 왕잔디(*Zoysia macrostachya*) 등이 있지만, 국내 자생 잔디의 품종 구분이 명확하지 않아 체계적인 보존과 관리가 어려운 실정이다. 최근 특정 염기서열 구간을 이용해 종을 식별하는 DNA 바코드 분석법이 개발되어, 다양한 생물종을 빠르고 정확하게 구별하는 것이 가능해졌다. 따라서, 본 연구에서는 자생 잔디의 분류를 위한 DNA 바코드 시스템 구축하고 이것을 바탕으로 체계적인 잔디 관리를 수행하고자 국내의 자생 한국잔디(들잔디, 금잔디, 갯잔디) 약 500점 이상 수집하고, 지역별로 들잔디와 금잔디, 갯잔디의 DNA 바코드 분석을 수행 중에 있다.

사사: 본 연구는 산림청 국립품종관리센터 산림유전자원개발사업과 2009년도 정부(교육부)의 재원으로 한국연구재단의 지원을 받아 수행된 기초연구사업임(No.2009-0094059)

\*주저자: Tel. 064-754-3347, E-mail: hyoyeon@jejunu.ac.kr

## 국내 자생 난지형 잔디의 FTIR을 이용한 대사체 분석 및 구별

홍민지<sup>1+</sup>, 양대화<sup>2+</sup>, 안명숙<sup>3+</sup>, 정옥철<sup>2</sup>, 진일두<sup>2</sup>, 김석원<sup>4\*</sup>, 이효연<sup>1,2\*</sup>

<sup>1</sup>제주대학교 생명공학부

<sup>2</sup>제주대학교 아열대원예산업연구소

<sup>3</sup>한국생명공학연구원 식물시스템공학연구센터

<sup>4</sup>한국생명공학연구원 생물자원센터

\*공동1저자

잔디는 운동장과 골프장, 공원, 묘지 등의 다양한 장소에 식재되는 주요 원예작물이다. 국내에 자생하는 한국잔디(*Zoysiagrass*)로는 들잔디(*Zoysia japonica*)와 금잔디(*Zoysia matrella*), 갯잔디(*Zoysia sinica*) 등이 있다. 주요 원예작물에 대한 대사체 분석은 다양하게 연구가 이루어지고 있지만 아직 잔디의 대사체 성분 분석은 거의 이루어진 바 없다. FTIR(Fourier Transform Infrared Spectroscopy)은 적외선을 통해 얻어지는 sample의 흡광도를 이용하여, 해당 시료의 성분 및 양을 측정할 수 있는 기법으로써, HPLC와 같은 기존의 대사체 분석 방법 보다 쉽고 빠르게 결과를 알 수 있어 최근 다양한 분야에서 사용되고 있다. 따라서 본 연구에서는 다년간 수집된 국내 자생 잔디(들잔디, 금잔디, 갯잔디) 약 240점의 FTIR분석을 통해 대사체 수준에서 자생 잔디의 식별체계를 확립하고자 하였다. PCA(principal component analysis)와 PLS-DA(Partial least square discriminant analysis)분석 결과, 갯잔디는 들잔디와 금잔디 라인들과 뚜렷하게 식별되었으며 PCA dendrogram에서도 같은 결과를 얻을 수 있었다. 이를 통해 갯잔디의 대사체 성분들이 들잔디와 금잔디와 비교하여 매우 다른 특징을 가지고 있음을 알 수 있었다. 수집지별로 들잔디 라인들의 PCA 분석 결과에서는 산악지대와 해안지대에 서식하는 잔디가 식별되는 경향을 보였으며, PLS-DA와 PLS-DA dendrogram 분석결과에서는 두 그룹이 더욱 뚜렷하게 구분되어 서식지에 따른 들잔디의 대사산물의 패턴 차이가 크게 나타남을 확인할 수 있었다.

사사: 이 연구는 2014년도 정부(교육부)의 재원으로 한국연구재단의 지원을 받아 수행된 기초연구사업(No.2009-0094059)과 2015년도 농림수산식품부(111161-5)의 지원을 받아 수행된 농생명산업기술개발사업에 의해 수행되었음.

\*주저자: Tel. 064-754-3347, E-mail: hyoyeon@jejunu.ac.kr

Tel. 042-860-4647, E-mail: kimsw@kribb.re.kr

**들잔디(*Zoysia japonica* Steud.)의 상동재조합 효율 분석**홍민지<sup>1</sup>, 김재훈<sup>1,2</sup>, 이효연<sup>1,2</sup>, 권용익<sup>2\*</sup><sup>1</sup>제주대학교 생명공학부<sup>2</sup>제주대학교 아열대원예산업연구소

Gene targeting (GT)은 식물체 내로 삽입하려는 donor DNA와 식물체 내의 endogenous DNA 간의 상동재조합 (Homologous recombination)의 원리를 이용하여, plant genome내의 목표 유전자를 특수한 목적으로 만들어진 modified donor DNA로 교체하는 기술이다. 식물에서는 비상동재조합 (Non-Homologous End Joining)이 homologous recombination보다 높은 비율로 일어나기 때문에 GT의 효율이 동물에 비해 현저하게 낮다. 이를 해결할 수 있는 방안으로 1) 형질전환 효율을 향상시키거나 2) 상동재조합의 효율을 높이는 것 또는 3) 선별 체계의 정확도를 높이는 것이 있는데, 그 중 상동재조합의 효율을 증가시키는 방법에 double strand breaks (DSB)가 큰 영향을 주는 것으로 보고된 바 있다.

따라서 본 연구에서는 *Agrobacterium* 형질전환을 이용해 한국 잔디인 들잔디 (*Zoysia japonica* Steud.) 캘러스에 상동재조합이 일어났음을 확인할 수 있는 marker인 pGU.C.USB를 삽입하고, southern blot과 GUS assay를 통해 자연 상태에서 일어나는 들잔디 본래의 상동재조합 효율을 측정하였다. 추후 DSB를 유도하여 향상된 상동재조합의 효율을 측정할 것이다.

사사: 농촌진흥청 차세대 바이오그린21사업(PJ011280012015)의 지원에 의해 수행되었음

이 논문은 2015년도 정부(교육부)의 재원으로 한국연구재단의 지원을 받아 수행된 기초연구사업임(No. 한국연구재단에서 부여한 과제번호 : 2009-0094059)

\*주저자: Tel. 064-754-3987, E-mail: yongikk@jejunu.ac.kr

## **Development of Novel SSR Markers using NGS sequencing and Genetic Relationship Analysis in Blueberry (*Vaccinium* spp.)**

Jee-Hwa Hong<sup>1\*</sup>, Eun-Jo Shim<sup>1</sup>, Moo-Kyoung Yoon<sup>2</sup>, Eun-Hee Soh<sup>1</sup>

<sup>1</sup>Seed Testing & Research Center, Korea Seed & Variety Service, Ministry of Agriculture, Food and Rural Affairs, Gimcheon 740–220, Republic of Korea

<sup>2</sup>Plant Variety Protection Division, Korea Seed & Variety Service, Ministry of Agriculture, Food and Rural Affairs, Gimcheon 740–220, Republic of Korea

Blueberry (*Vaccinium* spp.) is a member of the Ericaceae and eleven varieties have been registered at the Korea Seed & Variety Service for Plant Variety Protection (PVP). This study was to develop simple sequence repeat (SSR) markers next generation sequencing (NGS) analysis and to analysis genetic relationship of blueberry 31 varieties. Highbush blueberry ‘Camellia’ and rabbiteye blueberry ‘Alapaha’ varieties were used as sequencing materials. Out of total 987 SSR primers detected between ‘Camellia’ and ‘Alapaha’, 148 SSR primers were initially applied to select SSR markers for identification of blueberry varieties. Fourteen SSR markers showed polymorphism between 8 varieties. Seven SSR markers showed reproducibility and clear peak among 14 SSR markers. Genetic relationships of 31 blueberry varieties were analyzed and identified using 7 SSR markers. A total of 30 polymorphic SSR alleles were obtained and two to seven alleles were detected for each locus with an average of 4.3 alleles per locus. Average polymorphism information content was 0.556, ranging from 0.374 to 0.714. Genetic distance of clusters ranged from 0.38 to 0.93 by unweighted pair-group method with arithmetical average based on Jaccard’s distance coefficients. These newly developed SSR markers indicate usefulness for variety identification related to seed dispute and distinctness, uniformity and stability (DUS) test for blueberry.

\***Corresponding Author:** Tel. 054-912-0230, E-mail: hongjh19@korea.kr

## **C<sub>0</sub>t Analysis of *Chrysanthemum boreale*: the Realization of its Genome Characteristics**

Abigail Rubiato Cuyacot<sup>1</sup>, So Youn Won<sup>2</sup>, Sang Kun Park<sup>3</sup>, Seong-Han Sohn<sup>2</sup>, Ki-Byung Lim<sup>4</sup>, Hyun Hee Kim<sup>1</sup>, Franklin Hinosa Mancia<sup>1</sup>, Yoon-Jung Hwang<sup>1\*</sup>

<sup>1</sup>Department of Life Science, Sahmyook University, Seoul 139–742, Republic of Korea

<sup>2</sup>National Academy of Agricultural Science, Rural Development Administration, Jeollabuk–do 565–851, Republic of Korea

<sup>3</sup>National Institute of Horticultural & Herbal Science, Rural Development Administration, Jeollabuk–do 565–852, Republic of Korea

<sup>4</sup>Department of Horticultural Science, Kyungpook National University, Daegu 702–701, Republic of Korea

In the genus *Chrysanthemum*, repetitive DNA sequences, the dominant part of a genome, are still to be elucidated. To explore the matter, the present study applied fluorescent *in situ* hybridization (FISH) to the mitotic metaphase chromosome of *Chrysanthemum boreale* with C<sub>0</sub>t DNA as probes. Based on DNA re-association kinetics, three kinds of C<sub>0</sub>t DNA exhibiting different degrees of repetitive nature were fractionated and used as FISH probes to map the repetitive sequences. Signals from all C<sub>0</sub>t DNAs were successfully observed but their coverage on the chromosomes was different among C<sub>0</sub>t-1, C<sub>0</sub>t-10, and C<sub>0</sub>t-100. C<sub>0</sub>t-1 FISH signals resulted to have its intensity on the telomeric region and were also dispersed on both chromosome arms except for some distal regions. In C<sub>0</sub>t-10, signals were observed in all parts of the chromosome with greater intensity around pericentromeric regions. FISH with C<sub>0</sub>t-100 DNA was observed in bright signals all over the chromosome. Signals of C<sub>0</sub>t FISH found in this study covered the regions where ribosomal DNAs and telomeric repeats of *C. boreale* have been distributed (previous report), thus signifying their repetitive attributes. The present results could enhance the efficiency of studying genomes, chromosomes and repetitive sequences of *C. boreale* and subsequently hasten the realization of the genetic scheme of *Chrysanthemum*.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ010448)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 02-3399-1718, E-mail: [hyj@syu.ac.kr](mailto:hyj@syu.ac.kr)

## Overexpression of the RNA binding gene from *Medicago truncatula* regulates flowering time

Hyun-Ju Hwang<sup>1,2\*</sup>, Hyemin Lim<sup>2</sup>, A-Ram Kim<sup>2</sup>, Dae-Woo Lee<sup>3</sup>, Jong-Seong Jeon<sup>3</sup>, Jong Won Han<sup>1</sup>, Gang-Seob Lee<sup>2</sup>

<sup>1</sup>LMO Technology Development Team, Converging Research Division, National Marine Biodiversity Institute of Korea, 325–902, Korea

<sup>2</sup>Biosafety Division, Department of Agricultural Biotechnology, National Academy of Agricultural Science, Rural Development Administration, Suwon 441–853, Korea

<sup>3</sup>Crop Biotech Institute & Graduate School of Biotechnology, Kyung Hee University, Yongin 446–701, Korea

FLOWERING TIME CONTROL PROTEIN, *FPA* gene encode RNA Recognition Motif (RRM) domain protein and plays important roles in flowering time control in Arabidopsis. Floral transition is significant for reproductive products in all flowering plants. However, little is known about the functions of *Medicago* autonomous pathway gene. We had cloned the *FPA* gene on *Medicago* based on the sequence similarity of Arabidopsis *FPA* sequence. The RT-qPCR analysis of *MtFPA* expression patterns showed that the *MtFPA* transcripts accumulated ubiquitously in roots, leaves, stems, flowers, and pods. When fused to the green fluorescence protein, MtPFA-GFP was localized in the nucleus as speckle pattern of protoplast from Arabidopsis. To examine the function of *MtFPA*, 35S::*MtFPA* transgenic plants were generated in Arabidopsis late flowering mutant background, *fpa-2*. Overexpression of *MtFPA* specifically caused early flowering under long day conditions compared with non-transgenic plants. In *MtFPA* transgenic lines, *AtFLC* expression were down-regulated whereas the floral integrators, *AtFT* and *AtSOCl* were up-regulated as compare with control plant. As these results, *MtFPA* suggest that is a functional ortholog of the Arabidopsis and may play an important role in the regulation of flowering transition in *Medicago*.

\*Corresponding Author: Tel. 041-950-0761, E-mail: hjhwang@mabik.re.kr

---

**PC-150**

## **Seed color effect on germination rate and antioxidant activity under salt stress in wheat**

Paulina Calderón Flores, Dae Yeon Kim, Yong Weon Seo\*

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

Grain color distinguishes between the pigmentation of the outer layer of the kernel. It is known that environmental factors affects the production of anthocyanins and abiotic stresses like high light intensity, low temperature, high salinity and/or drought stress, and others increase their amounts. After 7 days the germination rate between yellow and dark-purple seeds were almost the same with and without stress (100% yellow seeds under stress and without stress germinated, 93.3% under stress and 96.6% without stress of purple seeds germinated), even though at the final stage the germination was almost the same, we can conclude base on our observations that the germination takes place at a different rate. We think that this might be related to the seed color, since the germination of purple seeds under salt stress started earlier than the yellow ones, until both reached the same point. The antioxidant activity was higher in seedlings from dark-purple seeds than the yellow ones, and they were higher under salt stress than without it, supporting our hypothesis that the purple color in wheat seeds works as a protection under salt stress. Furthermore, the qRT-pCR showed that some genes related to the flavonoid pathway were expressed or had more expression in the seedlings from dark-purple seeds than yellow ones.

Acknowledgements: This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ0110212015)” Rural Development Administration. Republic of Korea.

\*Corresponding Author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

**PC-151**

## **Intronic long noncoding RNA and sumoylation of histone methyltransferase contribute to control of flowering time in rice**

Ye Jin Kwon<sup>1\*</sup>, Do Youn Kim<sup>1</sup>, Sung-il kim<sup>1</sup>, Jun Soo Kwak<sup>1</sup>, Jong Tae Song<sup>3</sup>, Hak Soo Seo<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

<sup>2</sup>Bio-MAX Institute, Seoul National University, Seoul 151-818, Korea

<sup>3</sup>School of Applied Biosciences, Kyungpook National University, Daegu 702-701, Korea

Flowering time is a important agronomic trait for grain production in rice. So the control of flowering time is a critical step. In Arabidopsis, expression of certain key flowering gene such as FLOWERING LOCUS C (FLC) is known to be epigenetically regulated by chromatin modification through Enhancer of Zeste[E(z)], a histone methyltransferase, that core component of repressive complex, polycomb repressive complex2(PRC2). However, the chromatin mechanism involved in the regulation of rice flowering genes is presently not well known. Here we show that predict coding region of a intronic LncRNA[termed rice COLDAIR(OsCOLDAIR)], which is expected to associate with a component of PRC2, is predicted at rice FLC gene. And additionally we suggest interaction of histone methyltransferase and E3 SUMO ligase that indicate possibility of interaction with rice E(z) gene and rice E3 SUMO ligase. Our study contribute to control of rice flowering time by observing two factor that can regulate expression of related of rice FLC gene.

\*Corresponding Author: Hak Soo Seo, E-mail: seohs@snu.ac.kr, Ye Jin Kwon, E-mail: yejin0719@snu.ac.kr

---

**PC-152****Flowering time is repressed by sumoylation of FLC**

Jun Soo Kwak<sup>1</sup>, Sung-Il Kim<sup>1</sup>, Do Youn Kim<sup>1</sup>, Ye Jin Gyeon<sup>1</sup>, Hak Soo Seo<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151–921, Korea

<sup>2</sup>Bio-MAX Institute, Seoul National University, Seoul 151–818, Korea

The transition from vegetative growth to flowering is a major developmental switch in the plant cycle and the timing of flowering is very critical for reproduction of plant species. In transition to flowering in plants, Flowering locus C (FLC) is one of the crucial factors. Here, we showed how the stability and activity of FLC are regulated by sumoylation mechanism. By pull-down assay, we showed that FLC interact with E3 SUMO ligase *in vitro* and *in vivo*. And we showed that FLC is sumoylated *in vitro* condition with AtSUMO1 protein. In transgenic plants with overexpression of FLC and inducible expression of AtSIZ1, sumo E3 ligase led to increase of FLC protein level and delayed the post-translation degradation of FLC indicating that Arabidopsis E3 sumo ligase AtSIZ1 stabilizes FLC. Also, the plants with overexpression of mutant FLC (K154R, a mutation of the sumoylation site on FLC) flowered considerably earlier than plants with overexpression of FLC but comparable with wild type indicating that sumoylation is an important part for function of FLC. Our data indicate that the sumoylation of FLC is critical for its role in the control of flowering time.

This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center no. PJ01108701), Rural Development Administration, Republic of Korea.

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

**PC-153****Analysis of Phylogenetic Relationship of *Codonopsis lanceolata* Cultivated in Korea using RAPD Makers**

Jinsu Gil<sup>1</sup>, Serim Kim<sup>1</sup>, Yurry Um<sup>2</sup>, Seon-Woo Cha<sup>2</sup>, Yi Lee<sup>1\*</sup>

<sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University

<sup>2</sup>Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369–873, KOREA

*Codonopsis lanceolata* is used as a natural medicine or vegetables. It originates in East Asia such as Korea, Japan and China. Similar to *Panax ginseng*, *C. lanceolata* contains saponins as effective components. *C. lanceolata* is cultivated in many regions of South Korea. But, no variety was developed yet and the origin discrimination in the distribution market of *C. lanceolata* became a problem. In this study, we collected 20 *C. lanceolata* regional groups; Hoengseong, Wonju, Samcheok, Chuncheon, Pyeongchang, Hongcheon, Yongin, Yangpyeong, Danyang, Chungju, Bonghwa, Ulleung, Yeongju, Sancheong, Muju, Gwangyang, Sinan, Hwasun, Jeju-si and Seogwipo-si, and tested the genetic relationship using RAPD molecular markers. The genomic DNA was extracted using CTAB and the RAPD analysis was performed using 32 primers of Operon Technologies. NTsys-PC program was used for the phylogenetic analysis of the data.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

## **RNA seq Transcriptional Analysis of Pre-harvest Sprouting Korean Wheat**

Dae Yeon Kim, Jae Yoon Kim, Yong Weon Seo \*

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

Pre-harvest sprouting (PHS) is the precocious germination condition of grains while the spike is still in the mother plant. 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. In this study, we evaluated PHS and germination index (GI) in 33 Korean wheat cultivars, and performed transcriptome analysis between Keumkang (susceptible) and Woori (tolerance). A total of 33 Korean wheat cultivars were used for PHS (28 cultivars) and GI assessment in greenhouse. The DAF (Day After Fertilization) 35 of Keumkang and Woori spikes were harvested to perform transcriptome analysis using RNA-sequencing. Each transcriptome was compared with PHS or ABA treated DAF 35 Keumkang and Woori spikes. The PHS in 28 Korean cultivars and GI in 33 cultivars were ranged from 1.33% to 87.44% and from 0.01% to 2.41%, respectively. Woori was demonstrated the second lowest PHS and the lowest GI, however, Keumkang was 23th of 28 cultivars in PHS and 13th of 33 cultivars in GI analysis.

Six cDNA library from the DAF 35 of Keumkang and Woori wheat grain, PHS treated DAF 35 of Keumkang and Woori, and ABA treated DAF 35 of Keumkang and Woori were constructed and sequenced. A total of 53.37 Gb of high-quality reads were obtained using HiSeq 2500. The average mapping rate of assembled transcripts were 88.98%. The differentially expressed genes (DEG) revealed total 332 DEG (105 annotated) were upregulated in DAF 35 Woori library, total 5694 DEG (4623 annotated) were upregulated in PHS treated DAF 35 Keumkang library in comparison with DAF 35 Keumkang library. A total of 86 DEG (51 annotated) were upregulated in PHS treated DAF 35 Woori library in comparison with PHS treated DAF 35 Keumkang library. The Gene ontology and further analysis will be discussed.

Acknowledgements: This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01103501)” Rural Development Administration, Republic of Korea.

**\*Corresponding Author:** Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

## **Genome-wide transcription profiling of inflorescence development in wheat**

Dae Yeon Kim<sup>1</sup>, Min Jeong Hong<sup>2</sup>, Yong Weon Seo<sup>1\*</sup>

<sup>1</sup>Department of Biotechnology, Korea University, Seoul 136–713, Republic of Korea

<sup>2</sup>Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, 29 Geumgu, Jeongeup 580–185, Republic of Korea

The control of flowering, transition from vegetative to reproductive stage, is crucial for significant success during plant development. Multiple environmental and developmental signals are transmitted to the shoot apical meristem and converted to local cue to process developmental phase. These crucial process are delicately controlled and regulated by expression of tissue specifically expressed genes involved in inflorescence development. Therefore, it is necessary that molecular mechanism associated with inflorescence development is revealed to understand control of flowering by genome-wide expression pattern of inflorescence specific genes. In this study we used Affymetrix GeneChip Wheat Genome Array for genome-wide analysis of the expressed genes of inflorescence development including apical meristem and developing spikelet to understand the mechanism of floral development in early stage of wheat inflorescence. Moreover, meta-analysis of 1479 microarray dataset of GPL 3802 provided by Gene Expression Omnibus (GEO) was conducted to determine expression pattern of each probe throughout whole life cycle. Based on meta-analysis, we demonstrate inflorescence specific expressed genes in wheat inflorescence including apical meristem, spikelet meristem to understand the mechanism of floral development of wheat inflorescence.

Acknowledgements: This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01103501)” Rural Development Administration, Republic of Korea.

\***Corresponding Author:** Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

**Genome wide DNA methylation analysis of chromo methylase CMT3 and E3 sumo ligase AtSIZ1 mutants.**

Do Youn Kim<sup>1\*</sup>, Ye-Jin Kwon<sup>1</sup>, Sung-il Kim<sup>1</sup>, Jun Soo Kwak<sup>1</sup>, Min Kim<sup>1</sup>, Jong Tae Song<sup>2</sup>, Hak Soo Seo<sup>1\*</sup>

<sup>1</sup>Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

<sup>2</sup>School of Applied Biosciences, Kyungpook National University, Daegu 702-701, Korea

Gene expression is regulated by DNA and histone methylation by DNA and histone methyltransferases, respectively. In animal system, DNA methyltransferase with CG methylation activity is modified by SUMO conjugation and then its activity was increased, which means that the activity of DNA methyltransferase is modulated by posttranslational modification. so Chromatin remodeling is a new concept for expression of controlling of gene function. We thus analyzed the effect of E3 SUMO ligase AtSIZ1 in CMT3 (chromomethylase 3)-mediated genome methylation by next-generation sequencing (NGS), methyl binding domain MeDIP-sequencing and gene analysis using *siz1-2* and *cmt3* mutants. we carried out CG-enrich analysis by MeDIP sequencing revealed that the methylation level of the genome including transposons was significantly low in *siz1-2* mutants compared to wild-type. Result showed the genes regulated by methylation, that genes related of embryo and root development, cellulose metabolism, and post-translational modifications. All of our data indicate that the methyltransferase activity of CMT3 may be able to be regulated by AtSIZ1 and thereby CMT3-mediated gene expression and plant development also can be controlled by E3 SUMO ligase activity. Besides, our data also suggest that ammonium (NH<sub>4</sub><sup>+</sup>) can stimulate AtSIZ1- and CMT3- mediated DNA methylation.

\***Corresponding Author:** Hak Soo Seo, Tel. 010-7378-5036, E-mail: seohs@snu.ac.kr

Do Youn Kim, Tel. 010-4786-1991, E-mail: kimdy0202@snu.ac.kr

**Analysis of genetic diversity of *Codonopsis lanceolata* cultivated in Korea using SSR makers**

Serim Kim<sup>1</sup>, Ji Hee Jeong<sup>2</sup>, Jinsu Gil<sup>1</sup>, Tae Dong Kim<sup>2</sup>, Yurry Um<sup>3</sup>, Ok Tae Kim<sup>3</sup>, Ho Bang Kim<sup>4</sup>, Hee Chung<sup>1</sup>, Yi Lee<sup>1\*</sup>

<sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University, Korea

<sup>2</sup>Seed & Seedling Management Division, Korea Forest Seed and Variety Center, Korea

<sup>3</sup>National Institute of Horticultural and Herbal Science, Rural Development Administration, Korea

<sup>4</sup>Life Sciences Research Institute, Biomedic Co.,Ltd., Bucheon(420–852), Korea

*Codonopsis lanceolata* is a perennial climber. The roots are used as medicinal materials or vegetables. Recently, demand for *C. lanceolata* is increasing as a healthy food. *C. lanceolata* is distributed in India and East Asia such as China, Japan as well as Korea. In South Korea, this plant is widely cultivated in Gangwon-do province. No *C. lanceolata* varieties were developed in Korea. The objective of this study is to analyze genetic diversity of *C. lanceolata* cultivated in Korea using SSR makers. *C. lanceolata* roots were collected in each region were cultivated in Chungbuk National University greenhouse. Samples were obtained from fresh leaves of 5 plants from each collection region. The genomic DNA was extracted using CTAB. Genetic diversity was analysed using 4 sets of *C. lanceolata* SSR makers. PCR was performed in total 20 µL reaction volume containing 20 ng of DNA template, 5 pmole of primers. The genotypes of the analyzed samples were very similar. That means that the genetic diversity of *C. lanceolata* cultivated in Korea is very low.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

## The Effects of ehanolic superjami bran extract on glucose and lipid metabolism in ovariectomized rats

Su-Jin Nam\*, Mi-Young Kang

Department of Food Science and Nutrition, Kyungpook National University, Daegu 702–701, Republic of Korea

The ovariectomized Sprague-Dawley female rats were randomly assigned to Sham-Control, OVX-Control, OVX-Superjami (extract) groups. The results showed that the activity of glucokinase to keep the blood sugar constant is increased by increasing insulin secretion from pancreatic  $\beta$ - cells and the homeostatic regulation of glucose. Meanwhile the glycogenesis which is involved in the actions of the enzymes glucose-6-phosphatase and phosphoenolpyruvate carboxykinase showed that the glucose level is decreased. It was confirmed that these enzymes regulate the carbohydrate metabolism. On the other hand, results of the measurement of the lipid metabolism in the fat tissue and liver tissue, effect of  $\beta$ -oxidation enzymes and carnitine palmitoyl transferase which is involved in fatty acid oxidation for energy generation is increased. Moreover, the activity of fatty acid synthase, glucose-6-phosphate dehydrogenase and malic enzyme have been reduced, therefore, it was confirmed that these enzymes regulate the lipid metabolism.

\*Corresponding Author: Tel. 053-950-6235, E-mail: say1004625@naver.com

## Repression of *DFRI* expression by *w3* mutation in Soybean

Gyu Tae Park<sup>1</sup>, Jagadeesh Sundaramoorthy<sup>1</sup>, Jeong-Dong Lee<sup>1</sup>, Hak Soo Seo<sup>2,3</sup>, Jong Tae Song<sup>1\*</sup>

<sup>1</sup>School of Applied Biosciences, Kyungpook National University, Daegu 702–701, Korea

<sup>2</sup>Department of Plant Bioscience, Seoul National University, Seoul 151–742, Korea

<sup>3</sup>Bio-MAX Institute, Seoul National University, Seoul 151–818, Korea

Soybean [*Glycine max* (L.) Merr.] have a variety of flower colors which are controlled by six different genes (*W1*, *W2*, *W3*, *W4*, *Wm*, and *Wp*). Among these genes, mutation in *W3* gene causes near white flowers in the background of *w4* genotype whereas the genotype *W3w4* does purple throat flowers. Earlier studies showed that dihydroflavonol 4-reductase 1 (*DFRI*) gene was closely linked to the flower color variants for *W3* locus. In order to find out the *W3* gene responsible for *w3* phenotype, we first, studied the candidate gene *Glyma14g07940* (*DFRI*) which is having 100% similarity with DFR probe sequence. Sequence analysis of *DFRI* between *W3* and *w3* soybeans showed one base substitution in exon 6 of *w3* mutant soybean resulting in one amino acid change in the amino acid sequence. However, comparison of amino acid sequences of DFR proteins from various crop plants showed that there is no functional change in the protein. Besides, the promoter analysis showed that, 311 bp of *indel* was traced in 5'-upstream promoter region of *DFRI* gene in the *w3* mutant. Here, we show that the near white or purple throat phenotypes in *G. max* is associated with existence or nonexistence of *indel* at 5'-upstream promoter region and low or high expression of *DFRI*, respectively. These results suggest that *w3* phenotype may be caused by certain regulator of *DFRI* gene located near or distant from *DFRI* in *G. max*. In further study, we need to check the correlation between promoter *indel* with *W3* expression level through GUS analysis.

This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01108702), Rural Development Administration, Republic of Korea.

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

---

**PC-160**

## **Phylogenetic Relationship Analysis of *Adenophora triphylla* var. *japonica* HARA Local Collections using RAPD Markers**

Ki-Chan Park<sup>1</sup>, Jinsu Gil<sup>2</sup>, Serim Kim<sup>2</sup>, Young-Guk Kim<sup>1</sup>, Seon-Woo Cha<sup>1</sup>, Yi Lee<sup>2\*</sup>

<sup>1</sup>Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369–873, KOREA

<sup>2</sup>Department of Industrial Plant Science & Technology, Chungbuk National University

*Adenophora triphylla* var. *japonica* HARA is a herbaceous plant belongs to Campanulaceae. *Adenophora* root is mainly used for medicinal purpose. It is effective for lung cleaning, sputum remove, viscera strengthening, cough stopping and cancer treatments. *Adenophora* has about 70 species in the world and 17 of the species are distributed in Korea. Genetic resources of *A. triphylla* var. *japonica* HARA are valuable as the habitat is concentrated in East Asia. The intraspecies variation is very high according to the environmental conditions. A new *A. triphylla* var. *japonica* HARA variety, ‘Harang’, was developed through polyploid breeding in 2011. But, low domestic production and passive studies caused our country to rely on imports for almost all amount of the *A. triphylla* var. *japonica* HARA demands. In this experiment, genetic diversity between the collections were analyzed using 32 RAPD primers. Through this study, limit of morphologic classification could be solved and genetic diversity of this plant could be assured.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

**PC-161**

## **The Arabidopsis abscisic acid receptors RCAR4 and RCAR5 promote disease resistance through regulation of stomatal aperture**

Woonhee Baek, Chanmi Park, Hyunhee Joo, Sung Chul Lee\*

Department of Life Science, Chung-Ang University, Seoul 156–756, Republic of Korea

Stomata are natural pores of plants and constitute the entry points for water during transpiration. However, they also facilitate the ingress of potentially harmful bacterial pathogens. The phytohormone abscisic acid (ABA) plays a pivotal role in protecting plants against biotic stress, by regulating stomatal closure. In the present study, we investigated the mechanism whereby ABA influences plant defense responses to *Pseudomonas syringae* pv. *tomato* (*Pst*) DC3000, which is a virulent bacterial pathogen of Arabidopsis, at the pre-invasive stage. We found that overexpression of two ABA receptors, namely, *RCAR4/PYL10-OX* and *RCAR5/PYL11-OX* (hereafter referred to as RCARs), resulted in ABA-hypersensitive phenotypes being exhibited during the seed germination and seedling growth stages. Sensitivity to ABA enhanced the resistance of *RCAR4-OX* and *RCAR5-OX* plants to *Pst* DC3000, through promoting stomatal closure leading to the development of resistance to this bacterial pathogen. Protein phosphatase *HAB1* is an important component that is responsible for ABA signaling and which interacts with ABA receptors. We found that *hab1* mutants exhibited enhanced resistance to *Pst* DC3000; moreover, similar to *RCAR4-OX* and *RCAR5-OX* plants, this enhanced resistance was correlated with stomatal closure. Taken together, our findings demonstrate that alteration of RCAR4- or RCAR5-HAB1 mediated ABA signaling influences resistance to bacterial pathogens via stomatal regulation.

\*Corresponding Author: Tel. 02-820-5207, E-mail: sclee1972@cau.ac.kr

## Identification of Expansin Genes in *Platycodon grandiflorum* A. Using RNA-seq Analysis

Sang Ik Park<sup>1</sup>, Jemin Yoo<sup>1</sup>, Yurry Um<sup>2</sup>, Yi Lee<sup>1\*</sup>

<sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University

<sup>2</sup>Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369–873, KOREA

*Platycodon grandiflorum* A. is a perennial plant belongs to Campanulaceae family. This plant has been used herbal medicine ingredient in East Asia. Because of the high saponin content, it is an economically important medicinal plant in Korea. It has been reported that saponins of *P. grandiflorum* were mainly synthesized in root tissues. The studies about root growth of the plant were few. Expansin is an important protein playing a role in root growth of plants, and is known as a nonenzymatic protein. Expansins are novel plant cell wall loosening proteins leading to turgor-driven cell extension. Expansin encoding genes exist in multigene family, and there are more than 30 genes in *Arabidopsis thaliana*. and more than 50 genes in *Oryza sativa*. Therefore, identification of the genes was difficult in *P. grandiflorum* because of the lack of genome sequence. Recently, the development of next generation sequencing (NGS) technologies make it possible to obtain the target genes sequences rapidly and precisely. In this study, to identify the expansin encoding genes in *P. grandiflorum*, we used RNA-seq analysis with Illumina HiSeq platform. We analyzed whole transcriptome of *P. grandiflorum* through the RNA-seq analysis based on next generation sequencing. CLC Genomics Workbench software (Clc Bio inc.) was used for assembly. We assembled 122,663 contigs and search 123 contigs were identified from the search using 61 expansin gene

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

## Functional roles of the pepper lipoxygenase, *CaLOX1*, in osmotic, drought, and high salinity tolerance

Woonhee Baek, Chanmi Park, Hyunhee Joo, Sung Chul Lee\*

Department of Life Science, Chung-Ang University, Seoul 156-756, Republic of Korea

In plants, lipoxygenases (LOXs) are involved in various physiological processes, including defense responses to biotic and abiotic stresses. Our previous study has shown that pepper 9-LOX gene, *CaLOX1*, plays a crucial role in cell death due to pathogen infection. Here, the function of *CaLOX1* in response to osmotic, drought, and high salinity was examined using *CaLOX1*-overexpressing (*CaLOX1*-OX) Arabidopsis plants. Changes in the temporal expression pattern of the *CaLOX1* gene were observed when pepper leaves were treated with drought and high salinity, but not with abscisic acid (ABA), the primary hormone in response to drought stress. During seed germination and seedling development, *CaLOX1*-OX plants were more tolerant to ABA, mannitol, and high salinity than wild-type plants. In contrast, expression of the ABA-responsive marker genes *RAB18* and *RD29B* was higher in *CaLOX1*-OX Arabidopsis plants than in wild-type plants. In response to high salinity, *CaLOX1*-OX plants exhibited enhanced tolerance, compared with wild-type, which is accompanied by decreased accumulation of H<sub>2</sub>O<sub>2</sub> and high levels of *RD20*, *RD29A*, *RD29B*, and *P5CS* gene expressions. Similarly, *CaLOX1*-OX plants were also more tolerant than wild-type plants to severe drought stress. H<sub>2</sub>O<sub>2</sub> production and relative increase of lipid peroxidation were lower, and the expression of *COR15A*, *DREB2A*, *RD20*, *RD29A*, and *RD29B* was higher in *CaLOX1*-OX plants, relative to those of wild-type plants. Taken together, our results indicate that *CaLOX1* plays a crucial role in plant stress responses by modulating the expression of ABA- and stress-responsive marker genes, lipid peroxidation, and H<sub>2</sub>O<sub>2</sub> production.

\*Corresponding Author: Tel. 02-820-5207, E-mail: sclee1972@cau.ac.kr

## **Agronomic traits evaluation of wheat germplasms**

Jin Seok Yoon, Yong Weon Seo\*

Department of Biosystems and Biotechnology, Korea University, Seoul 136–713, Republic of Korea.

Wheat is a major food source for a large proportion of the worldwide population. Wheat production is hampered by drought, cold and various diseases. Wheat germplasms contain various characteristics such as high yield, low plant height, resistance to diverse diseases and good seed quality. In this study, we evaluated agronomic traits of wheat germplasms collected from the National Plant Germplasm System (NPGS) for application of the breeding program. Total 221 wheat lines contain cultivars and landraces were provided by NPGS and USDA-ARS. The germplasms were evaluated quantitative and qualitative agronomic properties in Korea university research farm. The agronomic traits of the germplasms in each region were analysed using statistical analysis. The most of germplasms were geographically originated from America continent. The germplasms average heading date showed on May 10. The average heading date of Africa germplasms was 6 days earlier than Europe germplasms. The germplasms average plant height and spike length showed 81.7 cm and 8.6 cm, respectively. The germplasms of Europe showed 21.7 cm taller than average plant height of America continent and the germplasms of Africa showed the smallest plant height comparing with other continents. The germplasms of Asia showed taller spike length than that of other continents. Seed color in germplasm comprises white, red and purple seed color, 24%, 75%, 1%, respectively. In addition, about 39% of the germplasms indicated lodging resistant. These results could be useful for improvement of wheat breeding program.

Acknowledgements: This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01103501)” Rural Development Administration, Republic of Korea.

\***Corresponding Author:** Tel. +82-2-3290-3005, E-mail. seoag@korea.ac.kr

***Capsicum baccatum* 종내 교잡에서 SNP 분자표지를 이용한 유전자 지도 작성**

이예린, 정규미, 김해인, 은민호, 이준대\*

전라북도 전주시 전북대학교 원예학과

고추 탄저병은 국내에서 큰 피해를 일으키는 병 중의 하나이다. 최근에는 우리나라 주요 재배종인 *Capsicum annuum*에 *C. baccatum*의 탄저병 저항성을 중간교잡을 통하여 도입한 탄저병 저항성 품종이 보고되고 있다. 고추 탄저병 저항성 품종 육성에 사용된 유전자원은 *C. baccatum* 'PBC81'인데, 최근에는 이보다 더 다양한 탄저병 균주범위에 저항성을 보이는 *C. baccatum* 'PI594137'을 이용하려고 한다. 따라서 고추의 탄저병 유전자원인 *C. baccatum* 'PI594137'의 저항성에 대한 QTL 분석을 수행할 필요가 있는데, *C. baccatum*과 *C. annuum*의 중간 후대에서는 중간잡종 불화합성으로 인해 유전자 지도를 그리기가 힘들어 *C. baccatum* 종내 교잡을 통하여 유전자 지도를 작성하였다. 탄저병에 이병성인 *C. baccatum* 'Golden aji'와 탄저병에 저항성인 *C. baccatum* 'PI594137'을 교잡하여 얻은 F<sub>1</sub>을 자가 수정하여 F<sub>2</sub> 분리집단 93개체를 유전자 지도 작성에 사용하였으며, 양친의 대량 염기서열 분석(NGS)을 통해 찾은 SNP를 바탕으로 HRM 분자표지를 개발하였다. 총 555개의 HRM 분자표지 용 프라이머를 디자인하였으며, 그 중 45.3%인 275개만이 실제로 다형성이 존재하였고, 이를 이용하여 유전자 연관 지도를 작성할 수 있었다. 총 연관거리는 1,057cM이며, 20개의 연관군이 나타났다. Chr. 1, 5 및 6번의 경우 하나의 연관군으로 연결되지 않았으며 나머지 염색체는 모두 하나의 연관군으로 연결되었다. 그리고 reference genome으로 사용된 *C. annuum*의 physical map과 *C. baccatum*의 genetic map을 서로 비교하여 보았는데, Chr. 2, 4, 5, 6, 7, 10, 11 및 12의 경우는 약간의 inversion이 있었지만 전반적으로 synteny를 잘 유지하고 있었다. 특히 2개의 translocation을 발견할 수 있었는데, Chr. 1과 8의 translocation 경우는 본 연구 이전에 wild *C. annuum*, *C. frutescens* 그리고 *C. chinense* 등에서도 보고된 것이고, Chr. 3과 9번의 translocation의 경우는 본 실험에서 처음 발견하여 보고하는 것이다. 이 Chr. 3과 9번의 translocation으로 인해 *C. annuum*과 *C. baccatum* 사이에 중간불화합이 일어나는 것으로 생각된다. 본 연구 결과는 *C. baccatum* 종내에서의 최초의 유전자 지도 작성이라는 큰 의미가 있으며, 이를 이용하여 탄저병 저항성 QTL 탐색에 활용될 수 있을 것이며, 또한 *C. baccatum*의 *de novo* sequencing 작성에 기초 자료로도 활용이 가능할 것이다.

\*주저자: Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

## **Classification of Celiac disease epitopes of $\omega$ -gliadin through data mining and compared with Chinese spring genome sequence**

Cheol Won Lee, Yong Weon Seo\*

Department of Biosystems and Biotechnology, Korea University, Seoul 136–713, Republic of Korea

Celiac disease (CD) is classified as an autoimmune disease of small intestine and occurred with people with the human leucocyte antigen (HLA) DQ2(8) cells. The gluten commonly called for the gliadins and glutenins from wheat and related proteins from barley and rye is significant cause of celiac disease. There are many sequences that recognized by T-cell according to species and different types of gliadins. In  $\omega$ -gliadin, two sort of epitopes were figured out that consisting of some proline(P) and glutamine(Q) scattered in gliadin sequence.

All registered  $\omega$ -gliadin sequences deposited in NCBI database were downloaded and collected. In order to classify groups depending on sequence difference, sequence similarity and their closeness were analyzed by phylogenetic trees using by MEGA (ver.6.06). Chinese spring genome sequence database offered by URGI (Unité de Recherche Génomique Info) is used for sequence assembly. Primers to validate presence of epitopes were designed by two different type from conserved and specific region. Primer pair from consensus region were designed in conserved domain of  $\omega$ -gliadin sequences from public database by sequence alignment. And, sequence-specific primers of  $\omega$ -gliadin were designed from the unique region of each  $\omega$ -gliadin sequence comparing  $\omega$ -gliadin sequences from NCBI database with draft sequence of Chinese spring in URGI. The two known epitopes of  $\omega$ -gliadin were located on same site, approximately from the 315<sup>th</sup> nucleotide to the 348<sup>th</sup> nucleotide in CDS. Candidate epitopes present in  $\omega$ -gliadin were divided into three categories based on analysis of sequence similarity. This categorization shows similar pattern with groups that were previously reported by sequence motifs such as SRTL, AREL, ARQL and KELQ. However, sequence which has AREL motif and sequence ARQL motif were not distinguished obviously in  $\omega$ -gliadin based on sequence alignment.

Acknowledgement: This work was supported by a grant from “Next-Generation BioGreen 21 Program for Agriculture & Technology Development (Project No. PJ01103501)” Rural Development Administration. Republic of Korea.

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

## The E3 Ubiquitin Ligase COP1 Regulates Thermosensory Flowering by Triggering GI Degradation in Arabidopsis

Kiyoung Jang<sup>1</sup>, Su-Jin Jung<sup>2</sup>, Hong Gil Lee<sup>1</sup>, Nam-Chon Paek<sup>3</sup>, Pil Joon Seo<sup>1,2\*</sup>

<sup>1</sup>Department of Bioactive Material Sciences and Research Center of Bioactive Materials, Chonbuk National University, Jeonju 561–756, Republic of Korea

<sup>2</sup>Department of Chemistry and Research Institute of Physics and Chemistry, Chonbuk National University, Jeonju 561–756, Republic of Korea

<sup>3</sup>Department of Plant Science, Seoul National University, Seoul 151–921, Republic of Korea Correspondence and requests for materials should be addressed to P.J.S

Floral transition is influenced by environmental factors such as light and temperature. Plants are capable of integrating photoperiod and ambient temperature signaling into their developmental program. Despite extensive investigations on individual genetic pathways, little is known about the molecular components that integrate both pathways. Here, we demonstrate that the RING finger-containing E3 ubiquitin ligase CONSTITUTIVE PHOTOMORPHOGENIC1 (COP1) acts as an integrator of photoperiod and ambient temperature signaling. In addition to the role in photoperiodic destabilization of CONSTANS (CO), COP1 also regulates temperature sensitivity by controlling the degradation of GIGANTEA (GI). COP1-impaired mutants showed reduced sensitivity to low ambient temperature. Notably, COP1 is more stabilized at low temperature and accelerates GI turnover in a 26S proteasome-dependent manner. The direct association of GI with the promoter of FLOWERING LOCUS T (FT) depends on ambient temperature, and thus COP1-triggered GI turnover delays flowering at low temperatures via a CO-independent pathway. Taken together, our findings indicate that environmental conditions regulate the stability of COP1, and conditional specificity of its target selection stimulates proper developmental responses and ensures reproductive success.

\***Corresponding Author:** Tel. +82-63-270-3407, E-mail: pjseo1@jbnu.ac.kr

---

**PC-168**

## **The pepper RING finger protein CaRING1 plays a role in abscisic acid signaling and drought tolerance**

Hyunhee Joo, Woonhee Baek, Chanmi Park, Sung Chul Lee\*

Department of Life Science, Chung–Ang University, Seoul 156–756, Republic of Korea

Plants are constantly exposed to a variety of biotic and abiotic stresses, which include pathogens and conditions of high salinity, low temperature, and drought. Abscisic acid (ABA) is a major plant hormone involved in signal transduction pathways that mediate the defense response of plants to abiotic stress. Previously, we isolated Ring finger protein gene (*CaRING1*) from pepper (*Capsicum annuum*), which is associated with resistance to bacterial pathogens, accompanied by hypersensitive cell death. Here, we report a new function of the *CaRING1* gene product in the ABA-mediated defense responses of plants to drought stress. The expression of the *CaRING1* gene was induced in pepper leaves treated with ABA or exposed to drought or NaCl. *CaRING1*-overexpressing (OX) transgenic plants showed enhanced sensitivity to ABA during the seedling growth and establishment. Furthermore, these plants were more tolerant to drought stress than the wild-type plants because of enhanced stomatal closure and increased expression of stress-responsive genes. Together, these results suggest that the *CaRING1* acts as positive factor for drought tolerance in Arabidopsis by modulating ABA-mediated stomatal closing and gene expression.

\*Corresponding Author: Tel. 02-820-5207, E-mail: sclee1972@cau.ac.kr

**PC-169**

## **The CabZIP2 pepper pathogen-induced bzip transcription factor positive regulator of disease resistance by promoting PR protein induction**

Hyunhee Joo, Woonhee Baek, Chanmi Park, Sung Chul Lee\*

Department of Life Science, Chung–Ang University, Seoul 156–756, Republic of Korea

A pepper bZIP transcription factor gene, *CabZIP2*, was isolated from pepper leaves infected with an a virulent strain of *Xanthomonas campestris* pv. *vesicatoria* (*Xcv*). Transient expression analysis of the CabZIP2-GFP fusion protein in *Nicotiana benthamiana* revealed that the CabZIP2 protein is localized in the cytoplasm as well as the nucleus. The acidic domain in the N-terminal region of *CabZIP2* that is fused to the GAL4 DNA-binding domain is required to activate the transcription of reporter genes in yeast. Transcription of *CabZIP2* is induced in pepper plants inoculated with virulent or avirulent strains of *Xcv*. The *CabZIP2* gene is also induced by defense-related hormones such as salicylic acid, methyl jasmonate, and ethylene. To elucidate the *in vivo* function of the *CabZIP2* gene in plant defense, virus-induced gene silencing (VIGS) in pepper and overexpression in Arabidopsis were used. *CabZIP2*-silenced pepper plants were susceptible to infection by the virulent strain of *Xcv*, which was accompanied by reduced expression of defense-related genes such as *CaBPR1* and *CaAMP1*. *CabZIP2* overexpression (OX) in transgenic Arabidopsis plants conferred enhanced resistance to *Pseudomonas syringae* pv. *tomato* DC3000. Together, these results suggest that *CabZIP2* is involved in bacterial disease resistance.

\*Corresponding Author: Tel. 02-820-5207, E-mail: sclee1972@cau.ac.kr

## PC-170

### 갈색 기능성쌀 신품종 슈퍼홍미의 작물학적 특성과 성분 특성

함태호<sup>1\*</sup>, 권순욱<sup>2</sup>, 류수노<sup>1</sup>

<sup>1</sup>서울 종로구 대학로 86 한국방송통신대학교 농학과

<sup>2</sup>경남 밀양 삼량진읍 부산대학교 생명자원과학대학 식물생명과학과

벼 품종의 다양화와 기능성 특수용도의 쌀 품종 육성의 일환으로 개발한 슈퍼홍미의 작물학적 특성과 성분특성을 규명하고자 수행하였다. 슈퍼홍미는 흑진주벼와 수원 425호 교잡 후대 계통에서 선발된 C3GHi 계통과 종실이 큰 대립벼1호를 인공교배하여 초형이 양호하고 현미색이 붉은 계통을 선발하여 육성하였다. 출수기는 9월 5일로 슈퍼자미보다 10일 늦은 만생종이며, 간장은 94.7 cm로 슈퍼자미보다 13 cm 큰 장간이다. 포기당 이삭수는 5.4개로 적지만 이삭당 벼알수는 154.0 개로 슈퍼자미보다 28% 많다. 현미의 천립중은 26.8g으로 슈퍼자미와 비슷하다. 슈퍼자미의 길이는 9.05 cm이고 폭은 3.79 cm로 슈퍼자미보다 큰 대립이며 정현비율은 81.7%이다. MCF-7 세포주를 24시간 배양한 후 세포 내에 에스트로젠 활성과 관련된 단백질을 확인하였다. 에스트로젠에 의해 PR 합성이 유도되고 ER-α는 억제되는 결과가 나왔고, 슈퍼홍미 70% 에탄올 추출물로 처리하였을 때 이와 유사한 결과가 나타났다. 슈퍼홍미 추출물 농도에 따른 MCF-7 증식효과를 살펴보면, 50ppm, 100ppm 농도에서 48시간 배양이후 증식효과가 나타났으며 72시간 이후에는 모든 농도에서 14% 이상의 증식효과가 나타났다. 슈퍼홍미는 에스트로젠과 유사한 기능성을 갖고 있는 것으로 여겨지며 이에 대한 추가적인 연구가 필요하며 새로운 기능성 품종으로의 가능성이 높다.

\*주저자: Tel. 02-3668-4630, E-mail: lion78@daum.net

## PC-171

### 조생 기능성쌀 빠른슈퍼자미와 만생 기능성쌀 늦은슈퍼자미 품종의 작물학적 특성

함태호<sup>1\*</sup>, 권순욱<sup>2</sup>, 류수노<sup>1</sup>

<sup>1</sup>서울 종로구 대학로 86 한국방송통신대학교 농학과

<sup>2</sup>경남 밀양시 삼량진읍 부산대학교 생명자원과학대학 식물생명과학과

기후변화와 다양한 작부체계 적응 고기능성 조생품종 빠른슈퍼자미와 만생품종 늦은슈퍼자미의 작물학적 특성과 품질 특성을 규명하고자 수행하였다.

빠른슈퍼자미는 흑진주벼와 수원425호를 인공교배 하여 C3G함량이 높은 개통을 육성하고, 출수기가 빠른 계통을 선발하여 매년 계통재배하면서 포장선발을 실시하여 육성하였다. 늦은슈퍼자미는 검정벼와 화선찰을 인공교배 하여 C3G함량이 높은 개통을 육성하고, 출수기가 늦은 계통을 선발하여 매년 계통재배하면서 포장선발을 실시하여 육성하였다.

빠른슈퍼자미의 출수기는 흑진주보다 5일 늦은 조생종이며, 늦은슈퍼자미는 흑진주보다 30일 늦은 만생종이다. 종피색은 모두 흑자색이고 메벼이다. 빠른슈퍼자미의 잎은 색은 약간 짙은 녹색이며 길이가 다소 짧은 편이나 너비는 대조품종인 흑진주와 비슷하고, 늦은슈퍼자미의 잎은 중간길이다.

빠른슈퍼자미 종자크기는 흑진주와 비슷하지만 현미 천립중은 19.0g으로 가벼운 편이며, 늦은슈퍼자미는 19.9g으로 흑진주보다 약간 무겁다. 빠른슈퍼자미의 수장은 20.8cm으로 흑진주와 비슷하나 간장은 62.6cm로 단간종이고, 늦은슈퍼자미는 수장은 흑진주와 비슷하나 간장은 91cm로 중장간이다. 빠른슈퍼자미는 천연색소 안토시아닌의 주성분인 C3G의 함량이 흑진주보다 10배 정도로 높으며, 늦은슈퍼자미의 C3G는 흑진주벼보다 2.5배 정도 높다.

\*주저자: Tel. 02-3668-4630, E-mail: lion78@daum.net

## 천연색소 C3G 고함유 만생, 대립 “슈퍼자미2호” 벼 품종

함태호<sup>1\*</sup>, 권순욱<sup>2</sup>, 류수노<sup>1</sup>

<sup>1</sup>서울 종로구 대학로 86 한국방송통신대학교 농학과

<sup>2</sup>부산대학교 생명자원과학대학 식물생명과학과

다양한 기후 및 지역 적응을 위해 만생이면서 천립종이 무겁고, 종피의 C3G(Cyanidin-3-glucoside) 함량을 극대화시킨 슈퍼자미2호(국립종자원 품종등록: 제5131호, 2014. 8. 26) 벼 품종의 작물학적 특성과 품질 특성을 규명하고, 이를 활용하여 기능성 소재 및 건강 기능성 식품을 위한 기초자료로 활용코자 수행하였다.

본 시험은 계통명 ‘KNOU 6호’를 2009 ~ 2011년까지 3년간 중부평야 2개 지역에서 보통기 보비재배를 하여 대조품종 흑진주, 슈퍼자미의 주요 농업형질과 종피색소 특성을 비교 검토하였다. 각 지역에서 공시 품종을 5월 2일에 파종하여 6월 4일에 이앙하였으며, 재식거리는 30 × 15cm로 주당 3본으로 하였다. 시비량 및 질소분시방법은 농촌진흥청 표준재배법에 준하였다.

전통적인 교배육종을 통하여 천연색소(C3G) 함량을 높인 ‘슈퍼자미2호’(흑진주벼/수원425호//대립벼1호) 품종의 작물학적 특성과 품질특성을 조사 분석한 결과를 요약하면 다음과 같다.

1. 중부평야지 평균출수기는 8월 30일로 만생종이며, 간장은 106cm 정도이며 임실률은 82.0%였다. 또한 현미천립중은 30.1g 정도로 슈퍼자미(26.2g)보다 무거운 품종이다.
2. ‘슈퍼자미2호’ 품종의 현미 장폭비는 2.08의 장원형으로 흑진주에 비해 길이와 폭이 12%, 26%로 증가되었다. 미량원소 중 K, Ca 함량은 흑진주에 비해 낮았고, 단백질 · 회분함량은 낮게, 열량 · 지방 · 탄수화물 함량은 비슷한 수준으로 나타났다.
3. ‘슈퍼자미2호’ 품종의 C3G 색소함량은 2013년에는 1,782mg(100g 종자), 2014년에는 1,980mg(100g 종자)으로서 슈퍼자미 보다는 다소 낮았으나 흑진주 보다는 9배 이상 높았다.

\*주저자: Tel. 010-5530-9323, E-mail: lion78@daum.net

**대립, 천연색소 C3G 고함유 “대립자미” 기능성 신품종 쌀의 이화학적 특성**함태호<sup>1\*</sup>, 류수노<sup>1</sup>, 강미영<sup>2</sup><sup>1</sup>서울 종로구 대학로 86 한국방송통신대학교 농학과<sup>2</sup>대구시 북구 산격동 경북대학교 식품영양학과

흑진주벼에 비해 천연색소 C3G(Cyanidin-3-glucoside)가 3.8배 이상 높으며 종실의 크기가 1.7배 큰 대립자미(국립종자원 품종등록 : 제4150호, 2012. 10. 17)의 이화학적 특성을 밝혀 기능성 쌀 이용의 기초자료를 확립하고, 기존의 쌀과의 차이점을 밝히고자 수행하였다.

일반성분 분석은 AOAC법, 쌀 배유의 단백질 함량은 Foss Tecator로 측정하였다. 유색미 70% 에탄올 추출물의 기능성 물질 분석은 Singleton(1965)의 방법, Jia 등(1999)의 방법을 수정하여 실험하였다.

일반성분의 경우 수분함량은 일품벼가 가장 높았고, 흑진주, 대립자미, 슈퍼자미 순이었고, 식미와 관계가 있는 조단백질과 조지방함량은 흑진주벼보다 낮아 대립자미의 취반특성이 우수한 것으로 평가되었다. 아밀로스 함량은 밥의 부피와 끈기, 노화지연에 관계가 있는데, 대립자미가 낮아 기존의 유색미보다 취반특성이 좋은 것으로 확인되었다. 대립자미의 1,000립중은 28.1g으로 흑진주벼보다 1.7배, 천연색소 C3G 함량은 3.8배 높은 특징을 가진 품종으로 항산화 생리활성을 가지는 총 폴리페놀 함량과 전자공여능을 측정한 결과 대립자미는 높은 생리기능성을 가진 품종으로 확인되었다.

슈퍼자미의 총 항산화력이 375.34 AEAC로 가장 높은 값을 나타내었으며 대립자미가 355.92, 흑진주가 274.58의 값을 나타내었다. Hydroxy radical 소거능과 SOD 유사활성 역시 다른 항산화 측정 결과와 유사하게 대립자미와 슈퍼자미에서 일반현미와 흑진주보다 유의적으로 높은 활성을 나타낸다. 유기 용매의 극성에 따른 슈퍼자미와 대립자미의 분획추출물의 DPPH 라디칼소거능은 비슷한 경향을 나타냈다.

\*주저자: Tel. 010-5530-9323, E-mail: lion78@daum.net

## 눈이 크고 C3G색소 고함유 품종 “큰눈자미” 기능성 쌀의 이화학적 특성

함태호<sup>1\*</sup>, 류수노<sup>1</sup>, 권순욱<sup>2</sup>

<sup>1</sup>서울 종로구 대학로 86 한국방송통신대학교 농학과

<sup>2</sup>경상남도 밀양시 삼랑진읍 부산대학교 식물생명과학과

흑자색 현미의 기능성 천연색소 C3G 함량을 증대시키고 영양가치가 우수한 거대배 특성을 결합한 큰눈자미(국립종자원 품종등록: 제4152호, 2012. 10. 17)의 이화학적 특성을 밝혀 기능성 식품소재로서의 활용 가치를 확대하기 위해 수행하였다.

종피의 C3G 함량은 C3G 간이검량법으로 분석하였다(Ryu et al., 1998). 열량 및 탄수화물 함량은 식품공전 계산법으로 분석하였고, 지방 함량은 식품공전 에테르추출법, 회분함량은 식품공전 회분시험법으로 분석하였다(Food code, 2000). 단백질은 Kjeldahl법으로, 양이온 함량은 ICP-AES 측정법으로 측정하였다. 조사한 결과를 요약하면 다음과 같다.

현미천립중은 18.9g 정도이고, 장폭비는 2.14로 중원형이며, 현미에서 쌀눈의 비율이 8.2% 수준으로 흑진주벼의 2.5배 정도이며, 현미 1립 기준 쌀눈의 무게가 흑진주벼의 2.8배 수준인 거대배아미 품종이다. 현미의 지방함량과 Lysine 함량이 흑진주벼 보다 높고, 종피의 안토시아닌 주색소인 C3G 함량이 흑진주벼에 비해 2배 정도 높은 품종으로 건강기능성 소재로서 활용가치가 높을 것으로 기대된다.

\*주저자: Tel. 010-5530-9323, E-mail: lion78@daum.net

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

## 차세대BG21사업단

OD. 농생물게놈활용연구사업단

OE. GM작물개발사업단

OF. 식물분자유종사업단

PD. 식물분자유종사업단





2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# 농생물게놈활용연구사업단





## **Achievements and Perspectives of GWAS Case Study in Rice Core Set**

Yong-Jin Park<sup>1</sup>, Tae-Sung Kim<sup>1</sup>, Kyu-won Kim<sup>1</sup>, Chang-Yong Lee<sup>2</sup>, Ju-Hyun Lee<sup>3</sup>, Yong-Soo Choi<sup>4</sup>, Il-Pyung Ahn<sup>5</sup>, Won-Il Kim<sup>5</sup>, Boem Seok Park<sup>5</sup>

<sup>1</sup>Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan, Republic of Korea

<sup>2</sup>Department of Industrial and Systems Engineering, Kongju National University, Kongju, Republic of Korea

<sup>3</sup>Department of Applied Bioscience, Konkuk University, Seoul, Republic of Korea

<sup>4</sup>Natural Products Research Center, Korea Institute of Science and Technology, Gangneung, Republic of Korea

<sup>5</sup>National Academy of Agricultural Science (NAAS), Rural Development Administration (RDA), Jeonju, Republic of Korea

In order to breakthrough upcoming challenges for the food production, the efficient use of rice germplasm would be a indispensable. These rice germplasm, adapted from diverse eco-systems, are undiscovered treasures for rice breeders/researchers, potentially providing a broad array of useful alleles that enrich gene pools of current cultivated rice varieties. Although growing *ex-situ* conservation efforts are an important for preserving diverse rice genetic resources, the activity on finding the novel and favorable genetic variants from the vast genebank collection is greatly challenging, requiring extensive screening processes. Therefore, rice core collection is a powerful solution to accelerate utilizations of the exotic germplasm of the entire population. In addition, The application of whole genome re-sequencing technology would establish a potent platform for fast forward genetic study, such as genome wide association study (GWAS). The GWAS has been implemented to efficiently identify candidate genes related to various useful agricultural traits in many crop species including rice. Given the significant associations between genetic variations and phenotypic diversity does not require prior knowledge, GWAS using high genome coverage of SNP markers provides a genomics platform to dissect previously unknown adaptive or other useful genetic variation accumulated in plant germplasm resources over the times. Once pinpointing candidate genes, GWAS allows informed choice of parents for QTL analysis based on the haplotype information, along with suggesting targets for following mutagenesis and transgenics. Here, we are to report our current achievements and perspectives from GWAS and post-GWAS undertaken to dissect and exploit useful alleles underlying many agricultural traits from Rice core set, including PHS (Pre-Harvest Sprouting), salt tolerance and disease resistance and so forth. Also, we will introduce the integrated Omics based GWAS case study using transcriptomes, proteomes, metabolomes and ionomes of our rice core set.

Keywords: Rice, Core-set, GWAS, Genomics, Transcriptome, Proteome, Metabolome, Ionome.

---

**OD-02****고밀도 콩 SNP array 이용 유전분석 집단 및 유전체 육종 토대 구축**

문중경<sup>1</sup>, 강성택<sup>2</sup>, 정순찬<sup>3</sup>, 김남산<sup>3</sup>, 전태환<sup>4</sup>

<sup>1</sup>국립식량과학원

<sup>2</sup>단국대학교

<sup>3</sup>한국생명공학연구원

<sup>4</sup>부산대학교

2010년에 Nature에 발표된 콩 표준유전체 공개 이후 재배종 및 야생종 콩 유전자원의 전장유전체 재분석 연구는 필연적으로 유전체 정보의 폭발적인 증가와 이들 정보를 이용한 유전체 육종의 시대를 조만간 열 것으로 기대되고 있다. 이에 본 연구에서는 유전체 육종의 시대를 선도하기 위해서 국내 콩 연구진이 수년간 수행한 유전체 육종 연구에서 필수적인 초고밀도 분자표지 genotyping, 표현형 변이의 정밀 카다로그 및 유전체 육종을 이끌 통계 유전학적 분석이 종합적으로 가능하게 하는 방법 즉, 각종 정보, 유전체 정보, 표현형 정보, 유전자원 정보, 핵심집단 정보 등의 DB를 통합분석을 단일 인터페이스하에서 가능하게 하여 육종가, 유전연구자 등의 모든 콩 연구자가 손쉽게 빅데이터를 단순하게 시각화하여 종합분석이 가능한 인터페이스 개발을 통해서 미래를 이끌 유전체 육종 연구의 현재까지의 결과와 향후 조만간 달성을 목표로 하는 유전체 육종의 새로운 모습에 대한 내용을 제시한다.

\*Corresponding Author: E-mail: moonjk2@korea.kr

**OD-03****Genome-wide association study (GWAS) in pepper using a core collection**

Hea-Young Lee<sup>1\*</sup>, Ho-Cheol Go<sup>2</sup>, On-Suk Heo<sup>2</sup>, Jin-Kyung Kwon<sup>1</sup>, Byoung-Cheorl Kang<sup>1\*</sup>

<sup>1</sup>Department of Plant Science and Vegetable Breeding Research Center CALS, Seoul National University, Seoul 151-921, Korea

<sup>2</sup>National Academy of Agricultural Science, Rural Development Administration, Jeonju 560-500, Korea

GWAS (Genome-wide association study) provides a useful to associate phenotypic variation to genetic variation. It has emerged as a powerful approach for identifying genes underlying complex diseases or morphological traits at an unprecedented rate. Despite benefits, there are only a few examples applied in crop plants due to lack of effective genotyping techniques and well prepared resources for developing high density haplotype maps. In this study, 350 core accessions selected from almost 5,000 *Capsicum* accessions were used for GWAS. We are planning to construct a high-density haplotype map using GBS platform and perform GWAS for various agronomic traits including fruit traits and metabolites related to pungency to identify genes controlling the traits. These results will not only provide a list of candidate loci but also a powerful tools for finding genetic variants that can be directly used for crop improvement and deciphering the genetic architecture of complex traits.

\*Corresponding Author: Tel. +82-2-880-4573, E-mail: sweettin@snu.ac.kr, bk54@snu.ac.kr

## **Multiple reference genome of Cucurbits (melon and Korean melon) for Genome Wide Association Study (GWAS)**

Ah-Young Shin<sup>1</sup>, HyeRan Kim<sup>1</sup>, Jongmoon Ahn<sup>2</sup>, Seokhyeon Nahm<sup>2</sup>, Jeong Mee Park<sup>1</sup>, Suk-Yoon Kwon<sup>1</sup>

<sup>1</sup>Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 305–806, Korea

<sup>2</sup>Nongwoo Bio Co., LTD., Yeosu, Jeonnam-do 595–885, Korea

The Cucurbitaceae (Cucurbits) family has 825 species in 118 genera, predominantly distributed in tropical and subtropical regions. Major cucurbit crops including cucumber (*Cucumis sativa*), melon (*Cucumis melo*), watermelon (*Citrullus lanatus*), and squash/pumpkin (*Cucumis pepo*) are important in the human diet and the rural economy. In recent years, large amount of genome information has been analyzed and reported in major cucurbit crops, such as cucumber, melon, and watermelon. To construct high quality reference genome sequence of Korean melon (Chamoe), genomic and transcriptomic sequence data were generated from Korean native (Gotgam) and elite (SW3) Chamoe inbred line using Illumina HiSeq2000 platform. In case of genome analysis, 4,773 scaffolds covering 98% of Gotgam Chamoe were assembled through *de novo* genome assembly and reference-based assembly. Large number of simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs) were detected between two inbred lines and these markers were used for construction of genetic maps and discrimination of cultivars or species. In addition, genome sequence of other Chamoe and melon including Chang Bougi, Sakata's Sweet, Prescott Fond Blanc and Banana melon will be constructed by *de novo* genome analysis. Genetic markers of these will also be detected and used for marker-assisted breeding and further analysis to investigate major traits of Chamoe, fruit color and flesh color. In conclusion, the newly constructed reference genome will provide genome information for comparative genomics and breeding of other cucurbit crops.

## 과수 분야 핵심집단 및 계놈전체연관분석을 통한 유전체 육종 기반구축

김대일<sup>1\*</sup>, 허운영<sup>2</sup>, 최철<sup>3</sup>, 김정희<sup>2</sup>, 김윤경<sup>2</sup>, 오상근<sup>4</sup>, 박범석<sup>5</sup>

<sup>1</sup>충북대학교 원예과학과

<sup>2</sup>농촌진흥청 국립원예특작과학원

<sup>3</sup>경북대학교 원예과학과

<sup>4</sup>충남대학교 응용생물학과

<sup>5</sup>차세대바이오그린21사업단 농생물활용유전체사업단

과수작물은 국내 농업총생산액의 8.3%정도를 차지하는 주요 작목으로 목본성, 영년생 식물에 해당하며 열매가 재배의 최종산물이다. 영년생 식물의 특성 상 종자의 발아에서부터 개화까지 길게는 10년 이상의 기간이 소요되어 세대진전이 늦기 때문에 교배 후 후대의 전개와 조사가 어렵다. 또한 많은 경우 자가불화성과 교배불친화성이 존재하기 때문에 유전형이 이형접합상태이므로 유전특성을 분석하고 이해하는데 어려움이 크다. 따라서 유전현상에 대한 이해도가 낮아 효율적이고 정밀한 품종육성에 큰 제한이 되고 있다. 최근 NGS 기반의 대량 유전정보의 활용기술은 과수작물에서도 유전현상 이해의 어려움을 극복할 수 있는 새로운 기술로 각광 받고 있다. 대규모 과수작물의 유전체 육종 연구가 미국, 유럽 등 선진국을 중심으로 추진 중이지만 아직까지 초본성 작물에 비해 시작단계에 불과하므로 아직까지 기술적 수준 차가 크지 않아 연구와 기술개발의 경쟁력이 있다고 할 수 있다. 국내에서는 농생물계놈활용연구사업단에서 교목성 자가불화합성 장미과 과수인 사과와 배, 덩굴성 자가화합성 과수인 포도를 대표작물로 선정하고 1단계에서 핵심집단을 구축한 바 있으며, 현재 자원을 이용한 계놈전체연관분석이 추진 중이다. GWAS기술을 이용한 유용유전자의 동정과 분자표지의 개발은 과수작물이 가진 유전분석의 어려움을 극복하고 유전자원을 이용하여 농업적으로 중요한 형질과 관련된 유전자를 탐색과 이용에 대한 효율을 높일 수 있는 장점이 있다. 따라서 그 연구결과는 해당 작물뿐 아니라 과수 전체의 유전현상에 이해를 높이고 고효율, 정밀 육종을 통해 국내 과수육종의 경쟁력을 크게 증진할 수 있을 것이다.

\*주저자: Tel. 043-261-2527, E-mail: dkpomo@cbnu.ac.kr

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# GM작물개발사업단





## 피노믹스 연구개발 동향 : 혁신 플랫폼

권택윤, 김경환, 윤혜진, 이성곤

농촌진흥청 국립농업과학원 농업생명자원부

농업에 있어서 기술혁신이 필요한 시기이다. 전 세계적으로 자유무역경쟁체제가 심화되고 있다. 양질의 농산물을 저렴하게 생산 공급하는 국가와 기업이 경쟁력을 더 가지게 된다. 또한 농업 생산에 도전적인 요소로 가뭄 등 심각한 기후변화 상황에 직면하고 있다. 미래 농업은 ‘고생산력’, ‘고품질’ 그리고 ‘고경쟁력’을 마련하여 줄 수 있는 있는 기술혁신을 필요로 한다. 그 기술혁신은 식량 작물을 정밀하게 이해하는 것에서 시작한다. 『피노믹스』는 작물의 표현이나 기능을 로봇+영상+정보 기술을 농업에 융합하여 정밀하게 측정하는 시스템이다. 식물 표현 및 기능 관찰에 있어서 기존의 아날로그식 육안 관찰 방식으로부터 디지털 통합 융합기술시스템으로 진화를 한 것이다. 피노믹스는 기존 아날로그 방식에서 얻는 단순 정보보다 수십 배에서 수백 배에 상당한 생산성 및 품질 관련 정보를 획득 가능하게 하여 준다. 이는 농업 전 분야에 있어서 새로운 성장 동력이면서 경쟁력 향상에 큰 도움이 된다. 유럽의 여러 국가는 이런 점에서 피노믹스 관련 기술개발과 세계 시장 확보에 전력을 다하고 있다. 특히, 현재는 종자산업 분야와 농업 생산물의 품질 관리에 적극 적용하고 있다.

피노믹스는 또한 우리나라 스마트 자동 팜의 기초기반기술이다. 피노믹스는 수천가지 작물 표현 및 기능 특성을 담은 빅데이터 생산이 가능하게 하여 준다. 작물 성장 반응 빅데이터는 최고의 생산성 획득을 위한 스마트 팜 환경 조절에 활용 가능하다. 피노믹스에서 얻은 식물 생산 능력 정보에다 생산물의 유통정보를 더하면 소비자 맞춤형 농업생산 공급이 가능하도록 하여줄 수 있다.

농촌진흥청은 2017년까지 80억을 피노믹스 인프라 구축에 투자 예정이다. 현재 농업 관련 연구개발 규모를 고려하면 더욱 큰 규모의 확실한 투자가 필요하다고 본다. 튼튼한 미래 혁신농업 구현을 위해서는 신속한 피노믹스 인프라의 구축 및 활용이 필요한 때이다.

\*주저자: Tel. 063-238-4715, E-mail: trkwon@korea.kr

## 식물표현체 기술을 이용한 작물육종효율 증진

김도순\*, 이태영, 김진원

서울대학교 농업생명과학대학 식물생산과학부

최근 작물유전체 기술이 비약적으로 발전하고 있어서 이러한 기술과 얻어진 유전체정보를 활용할 경우 작물 육종이 새롭게 도약하는 계기가 될 것이라 기대하고 있다. 그러나 실상 작물유전체 정보가 작물분자육종에 효과적으로 활용되고 있지 못하고 있다. 작물육종의 궁극적인 목표는 원하는 표현형질을 갖는 품종을 개발하는 것이나 작물유전체정보나 개별 오믹스 정보만으로는 전통적인 표현형지표와 연결시켜 작물육종에 활용하기 어렵다. 다양한 생명공학적, 분자육종적 기술을 활용해 보다 다양한 계통창출이 가능해 졌으나 전통적인 표현형평가방식으로는 효과적으로 우량계통을 선발하기 어렵고, 비용도 많이 소요된다. 따라서 새로운 개념의 식물표현체 정보(열영상, 형광영상, RGB영상 등)를 작물유전체 정보와 연계시키고, 작물의 주요형질에 식물표현체정보를 연계시킨다면 작물육종의 효율성제고에 활용 가능할 것으로 기대하고 있다. 따라서 이번 발표에서는 식물표현체 기술을 활용하여 주요 환경스트레스에 대한 벼와 콩의 생리적 반응을 대용량으로 조기진단하고 이러한 진단방법과 결과를 환경스트레스 내성 계통이나 품종선발에 얼마나 효율적으로 활용할 수 있는지 평가한 결과를 보고하고자 한다. 아울러 그동안의 연구결과와 경험을 바탕으로 식물표현체 기술을 활용한 작물분자육종 효율증진 방안과 작물유전체 연구에의 활용가능성 등을 제시하고자 한다.

\*주저자: Tel. 02-880-4542, E-mail: dosoonkim@snu.ac.kr

## **Sound waves delay tomato fruit ripening by negatively regulating ethylene biosynthesis and signaling genes**

Mi-Jeong Jeong<sup>1\*</sup>, Joo-Yeol Kim<sup>1</sup>, Jin Su Lee<sup>2</sup>, Soo In Lee<sup>1</sup>, Jin-A Kim<sup>1</sup>

<sup>1</sup>Department of Agricultural Biotechnology, National Academy of Agricultural Science (NAAS), 370 Nongsaengmyeong-ro, Wansan-gu, Jeonju, Jeollabuk-do, 560-500, Korea

<sup>2</sup>Postharvest Research Team, National Institute of Horticultural and Herbal Science (NIHHS), 100, Nongsaengmyeong-ro, Iseo-myeon, Wanju-gun, Jeollabuk-do, 565-852, Korea

Regulation of fruit ripening may help extend fruit shelf life and prevent losses due to spoilage. Here, we investigated whether sound treatment could delay tomato fruit ripening. We treated harvested tomato fruits with low-frequency sound waves (1 kHz) for 6 h, and then monitored various characteristics of the fruits over 14-day period at 23±1°C. Seven days after the treatment, 85% of the treated fruits were green, versus fewer than 50% of the non-treated fruits. Most of the tomato fruits had switched to the red ripening stage by 14 days after treatment. Ethylene production and respiration rate were lower in the treated than non-treated tomatoes. Furthermore, changes in surface color and flesh firmness were delayed in the treated fruits. To investigate how sound wave treatment affects fruit ripening, we analyzed the expression of ethylene-related genes by quantitative real-time RT-PCR analysis. We found that the expression level of several ethylene biosynthetic and ethylene signaling pathway-related genes was influenced by sound wave treatment. These results demonstrate that sound wave treatment delays tomato fruit ripening by altering the expression of important genes in the ethylene biosynthesis and ethylene signaling pathways.

\***Corresponding Author:** Tel. 063-238-4617, E-mail: center1097@korea.kr

**국립농업과학원 농업생명자원부 GM격리포장 소개 및 운영계획**

이강섭

국립농업과학원 농업생명자원부 생물안전성과

국립농업과학원은 2012년 6월 농업생명연구단지 착공식을 하고 2014년 8월 수원에서 전주로 이전하였다. 더불어 농업생명자원부 GM격리포장도 2013년 12월 농업용 LMO격리포장 신고확인서를 발급 받아 포장을 사용할수 있게 되었다. 농업생명자원부는 포장 이용의 최적화를 위하여 준공전 2012년부터 2014년까지 3년간 녹비작물을 재배하여 포장 숙진화 작업을 하였고, 2014년에는 용역재배를 통하여 포장상태를 점검하였다. 그 결과 2015년 하계작물부터 실험용 작물을 재배하기 시작하였고 차년도에는 이를 전국의 연구자들에 공개 하여 전문적인 GM작물 시험재배를 할수 있도록 준비하고 있다.

**\*주저자:** Tel. 063-238-4714, E-mail: kangslee@korea.kr

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# 식물분자유종사업단





---

## OF-01

### 유전체기반 분자유종을 위한 생물정보분석 파이프라인

유익수

파이젠 유전체연구소, (주)파이젠

최근 들어 다양한 신규 유전체 정보의 집적이 기하급수적으로 증가하고 있으며, transcriptome, non-coding RNAs, methylome 등의 데이터 생산 또한 급속하게 증가하고 있다. 이는 차세대 DNA 분석장비의 혁신적 진보에 기인한 현상으로 다양한 omics기반의 데이터를 활용하여 유전체 및 유전자 발현, 조절 등에 대한 통합적 이해를 돕고 있다. 또한 주요 농업작물의 표준유전체 완성과 resequencing 또는 Genotype-by-Sequencing 등의 NGS 기술을 이용한 genotyping의 접목은 다양한 유전자원대상의 NGS 데이터 생산을 가속화 시키고, 이들 정보를 이용하여 중요 농업 형질 연관 유전적 변이를 발견하고 이를 작물개량에 활용할 수 있는 환경을 제공하고 있다.

유전체기반 분자유종시스템은 분자유종의 현장에서 효율적이고, 실용적으로 사용될 수 있는 시스템을 개발하기 위해 3가지의 목표를 가지고 수행한다. 1) 각기 산재되어있는 다양한 유전체정보 (유전체, 전사체, SNP정보, 분자마커 정보, 표현형 정보 등)를 수집하여 통합 유전체 데이터베이스화 하여 시스템 내에서 유전체, 전사체 정보를 정보를 비교, 분석이 가능한 형태로 운영하며 상호 연결된 정보를 제공하도록 구축한다. 2) 또한 최근 들어 농업에 적극 활용되는 NGS기반의 SNP genotyping에 필요한 효율적 파이프라인을 제공하여, GBS 또는 resequencing 기반의 데이터를 효율적으로 분석하고 그 결과를 토대로 genetic map구축, QTL동정, association mapping, 분자마커 개발 등에 효율성을 주는 시스템을 개발하고 3) 유전체정보와 변이정보를 연동하여 visualization 할 수 있는 브라우저와 분자마커 개발에 필요한 도구의 개발이다.

통합유전체 데이터베이스, 효율적 genotyping 시스템, 통합브라우저 등의 구축은 데이터의 생산과 분석에 표준화된 지표, 용이성을 제공하여 고도화된 유전체 정보를 분자마커 개발, QTL 탐지, 후보 유전자 동정 등 분자유종에 효율적으로 활용할 수 있게 하며, 이를 통해서 분자유종의 선진화와 종자산업의 활성화에 기여하고자 한다.

## OF-02

### DNA-free Genome Editing in Plants

Soon-Il Kwon<sup>1</sup>, Je Wook Woo<sup>1</sup>, Jungeun Kim<sup>2,3</sup>, Jin-Soo Kim<sup>2,3</sup>, Sunghwa Choe<sup>1,4</sup>

<sup>1</sup>Convergence Research Center for Functional Plant Products, Advanced Institutes of Convergence Technology, Suwon 443-270, Korea

<sup>2</sup>Department of Chemistry, Seoul National University, Gwanak-gu, Seoul 151-747, South Korea

<sup>3</sup>Center for Genome Engineering, Institute for Basic Science, Gwanak-gu, Seoul 151-747, South Korea

<sup>4</sup>School of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea

CRISPR/Cas9-based genome editing technology fast replaces the previous methods that require protein engineering such as Zinc Finger Nucleases (ZFNs) and TALE nucleases (TALENs). Conventional genome editing of plant cells using CRISPR/Cas9 technology largely depends on Agrobacterium-mediated transformation of the plant cells and subsequent regeneration of whole plants from the edited cells. During this process, unwanted foreign DNAs including the antibiotics gene and fragments of the T-DNA can be introduced into plant genome. Insertion of these unwanted DNA causes lots of regulatory restrictions when commercializing the LMO products. To step aside these issues, we designed DNA-free ribonucleoprotein-based method and regenerated whole plants from the successfully engineered cells. We will share our discovery on the successful implement of this technology in lettuce protoplasts.

## **Soybean germplasm, a rich genetic resource to be explored for the identification of salt tolerance genes and their mechanism of action**

Sajeesh Kappachery<sup>1</sup>, Jagadeesh Sundaramoorthy<sup>1</sup>, Gyu Tae Park<sup>1</sup>, Jeong-Dong Lee<sup>1</sup>, Hak Soo Seo<sup>2,3</sup>, Jong Tae Song<sup>1\*</sup>

<sup>1</sup>School of Applied Biosciences, Kyungpook National University, Daegu 702–701, Korea

<sup>2</sup>Department of Plant Bioscience, Seoul National University, Seoul 151–742, Korea

<sup>3</sup>Bio-MAX Institute, Seoul National University, Seoul 151–818, Korea

Soybean germplasm have diverse accessions with great variation in their ability to survive and reproduce under salt stress conditions. In general, cultivated soybeans are more sensitive to salt stress than their wild relatives, however exceptions are found in both the groups. These variations in response to salt stress makes soybean germplasm an interesting collection of genetic resources to be explored for the identification of salt-tolerance genes, and their mechanism of action. Here, in this report we presented a data showing differential response of selected accessions of both cultivated and wild soybeans to salt stress. Two modes of salt treatment; gradual salt stress (GS) as well as salt shock (SS) were used in this study. The GS was found more effective in finding the difference in response of soybean accessions to salt stress. Various genetic marker based methods are in use to identify and isolate the potential genes contributing to the salt tolerance in soybean. Even then there is a paucity of knowledge on the key genes contributing to the salt tolerance in soybean. We expect that a recently developed functional screen based method, like yeast based functional screen, using cDNA library generated from different salt tolerant accessions of soybean could lead to identification of novel genes responsible for salt tolerance in soybean. Also, we propose for the use of RNA isolated from different stages of GS and SS for making cDNA library to be used for functional screening. This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01109202), Rural Development Administration, Republic of Korea.

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

**Isolation of rice T-DNA tagged mutants being resistant to brassinosteroid (BR) biosynthetic inhibitor Propiconazole (Pcz)**

Claudia Corvalán<sup>1</sup>, Soon Il Kwon<sup>2,3</sup>, Haerim Kim<sup>3</sup>, Doyeon Kim<sup>3</sup>, Jewook Woo<sup>2,3</sup>, Sunghwa Choe<sup>1,2,3</sup>

<sup>1</sup>School of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea

<sup>2</sup>Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

<sup>3</sup>Convergence Research Center for Functional Plant Products, Advanced Institutes of Convergence Technology, 864-1 Iui-dong, Yeongtong-gu, Suwon-si, Gyeonggi-do 443-270, Korea

Hormones play a crucial role in controlling physiological processes, and thus plants grow and develop in response to environmental cues through the interlocked actions of the hormones. Brassinosteroids (BRs) were found as growth-promoting steroid hormones. Rice, as a monocotyledonous model plants and the major staple crop, has been used to study BR action mechanisms. However, many components of BR pathways and the mechanisms of their molecular interactions have yet to be fully understood. Because the use of the BR biosynthetic inhibitor, Brassinazole (Brz), allowed us to identify important components of BR signaling such as the transcription factor BZR1, we decided to employ a similar strategy to identify novel signaling factors using propiconazole (Pcz), a new potent BR inhibitor. We screened a rice T-DNA mutant population which belongs to Dongjin variety and were developed by the Gene An's group using pGA2715 T-DNA vector. Using Pcz treatments we searched for resistant plants, which were reflected on their lengths of roots and/or leaves. We isolated a total of 17 mutant lines, which are being analyzed phenotypically and at molecular level. So far, we have been able to found various lines presenting high or low yield compared to their wild type counterparts. We have found differences in panicle organization of these mutants. Our current experiments include the confirmation of Pcz resistance of these lines and molecular studies involving BR marker genes to understand the relation among yield and BR action in rice.

## Identification and characterization of the novel gene encoding a protein responsible for biosynthesis of DDMP saponin in soybean

Jagadeesh Sundaramoorthy<sup>1</sup>, Gyu Tae Park<sup>1</sup>, Sajeesh Kappachery<sup>1</sup>, Jeong-Dong Lee<sup>1</sup>, Hak Soo Seo<sup>2,3</sup>, Jong Tae Song<sup>1\*</sup>

<sup>1</sup>School of Applied Biosciences, Kyungpook National University, Daegu 702–701, Korea

<sup>2</sup>Department of Plant Bioscience, Seoul National University, Seoul 151–742, Korea

<sup>3</sup>Bio-MAX Institute, Seoul National University, Seoul 151–818, Korea

Soybean [*Glycine max* (L.) Merr.] seeds are abundant in high-quality proteins and fats. In addition, soybean seeds are also rich in secondary metabolites, such as isoflavones, lecithin, and saponins. Triterpene saponins are major components of these physiologically active metabolites in soybean seeds. Soybean saponins are classified as group A and DDMP saponins. Among them group A saponins are undesirable component of food products due to bitterness and astringency and also cause foaming in tofu production. Whereas, DDMP saponins and their derivatives are less bitter and astringent and beneficial to human health when consumed as regular diet. Therefore, reducing the group A saponins or increasing the DDMP saponins are required to improve the food quality. The present study focused to identify and characterize the gene which is encoding a protein responsible for biosynthesis of DDMP saponins. EMS mutant lines (*sg-7-1* & *sg-7-2*) which lack DDMP saponins were developed. The breeding cross has been made with these two mutants with two cultivars, Pungsannamul and Wooram to study the segregation and genetic linkage analysis, respectively. The segregation analysis showed that the mutant phenotype is controlled by single recessive gene. TLC analysis for phenotyping F<sub>2</sub> population of Wooram X *sg-7-1* showed mutant, wild and heterozygous types. To surprise two more patterns were detected and they were named as strange type1 (ST1) and strange type2 (ST2). Further, SSR marker analysis will be carried out to locate the gene which encoding a protein responsible for biosynthesis of DDMP saponins.

Acknowledgements: This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01109202), Rural Development Administration, Republic of Korea.

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

## **Small RNA and degradome profiling reveals a role for miRNAs and their targets in the regulation of NB-LRR disease resistance genes**

June Hyun Park<sup>1</sup>, Igojo Kang<sup>1</sup>, Chanseok Shin<sup>1,2\*</sup>

<sup>1</sup>Department of Agricultural Biotechnology, Seoul National University, Seoul, 151–921, Republic of Korea

<sup>2</sup>Plant Genomics and Breeding Institute, Seoul National University, Seoul, 151–921, Republic of Korea

MicroRNAs (miRNAs) are a class of non-coding RNAs approximately 21-nt in length which play important roles in regulating gene expression in plants. Although many miRNA studies have focused on a few model plants, miRNAs and their target genes remain largely unknown in hot pepper (*Capsicum annuum*), one of the most important crops cultivated worldwide. We here employed high-throughput small-RNA and degradome sequencing to comprehensively identify small-RNAs and their targets in pepper. From these, we identified several novel targets of miRNAs, including the major de novo methylation enzyme involved in RNA-directed DNA methylation in plants. Furthermore, we identified several highly abundant 22-nt miRNA families that target conserved domains in NB-LRRs and trigger the production of phased secondary siRNAs. We showed that transient co-expression of can-miR482 with *Rpi-blb1*, one of the potato NB-LRRs, resulted in the attenuation of the hypersensitive responses in *Nicotiana benthamiana*, suggesting that interaction between miR-482 family and disease resistance proteins is likely to serve as a conserved trigger for defense mechanism in Solanaceae. This work provides the first reliable draft of the pepper small RNA transcriptome that offers an expanded picture of miRNAs in relation to NB-LRR regulation, providing a basis for understanding the functional roles of miRNAs in disease resistance pepper.

This work is supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ01115601), Rural Development Administration, Republic of Korea.

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

---

**PD-05****Molecular breeding and commercialization of high yielding rice through the modification of plant type and introduction of new alleles.**

Hee-Jong Koh\*

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

The goals of this research project are to identify the genes controlling plant architecture through the establishment of foundation for molecular breeding and to develop new rice varieties with useful characters associated with high yield leading to its commercialization. The research subjects of this project are as follows: improvement of plant architecture including tiller angle and number associated to harvest-index, construction of genetic and QTL map related to plant architecture and isolation of target genes, development of molecular markers with high efficiency, and further study for the mechanisms of recombination event and reproductive barrier occurring from cross between subspecies, development of new elite rice varieties with high yield and its commercialization. The isolated genes and products of this research project will be patented and molecular markers for those genes will be applied to breeding procedure. The breeding materials produced as outcomes will be provided to other breeders for further breeding programs. The developed varieties will be patented and registered to the national list of varieties, and will be distributed to our agricultural industries for the increase of its competitiveness and farmer's income. The patents for genes, molecular markers, and varieties will be licensed out to uphold the agricultural biotechnology industries.

This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ011024012015), Rural Development Administration, Republic of Korea.

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

**PD-06****Detection of a new genetic locus for the high amylose content in rice mutant.**

Heng Wang<sup>1</sup>, SeongGyu Jang<sup>1</sup>, DaEun Lim<sup>1</sup>, Ji-Ung Jeung<sup>2</sup>, Soon-Wook Kwon<sup>1\*</sup>

<sup>1</sup>Department of Plant Bioscience, Pusan University, Miryang 627-706, Republic of Korea

<sup>2</sup>National Institute of Crop Science, Rural Development Administration, Wanju 565-851, Republic of Korea

Goami 2 is now well known as its extinguishing endosperm characteristics - it is far from the wild type, Ilpum, a premium taste Korean japonica cultivar. The endosperm of Goami 2 is high in fat, protein, and indigestible carbohydrate contents. One of the most extraordinary endosperm characteristic of Goami 2 is high level of amylose content, even though the hulled rice (brown rice) is totally opaque. There have been many studies to address the unique physico-chemical properties and possible usages as a healthy and functional food ingredient, especially, the high-amylose rice had a positive effect on lowering the blood glucose response in obesity and type 2 diabetes. Genetic analysis by using 44 SSR markers, crude linkage map (3~5 anchor markers per chromosome) was then constructed based on the genotypes detected among 112 F<sub>2</sub> progenies derived from Goami 2 / Milyang 23 showed that major chromosomal regions on Chromosome 2 responsible for the variation of amylose contents. M2-53 on Chromosome 2 explains the highest variation and this region has not been reported as a putative QTL for amylose contents yet. More closely markers for application to breeding program can be developed using MutMap or Re-sequence methods.

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

## 염생식물 나문재의 종자구조 및 염농도에 따른 유묘생장 특성

권혁균<sup>1</sup>, 전효진<sup>1</sup>, 백정선<sup>1</sup>, 신소희<sup>1</sup>, 정재혁<sup>2</sup>, 이승재<sup>3</sup>, 정남진<sup>\*</sup>

<sup>1</sup>전라북도 전주시 덕진구 덕진동 전북대학교 농업생명과학대학 농학과

<sup>2</sup>전라북도 전주시 완산구 농생명로 300 농촌진흥청 작물재배생리과

<sup>3</sup>전라북도 전주시 덕진구 덕진동 전북대학교 화학과

새만금 간척지를 포함하여 우리나라는 넓은 간척지를 보유하고 있으나 제염되지 않은 간척지에서 재배할 수 있는 농작물은 매우 한정적이다. 따라서 높은 염농도에서도 재배 가능한 염생식물인 나문재의 작물로서의 이용을 위하여 본 연구에서는 나문재의 종자구조와 염농도에 따른 유묘생육 특성을 조사하였다. 나문재는 쌍떡잎 식물로서 종자 내에 배유층이 존재하지 않으며, 종자를 화피가 감싸고 있고 결실기에 화피가 바깥쪽으로 신장되어 오각형의 별모양의 형태를 보였다. 종자 크기는 길이가  $0.44 \pm 0.10\text{cm}$ , 너비가  $0.47 \pm 0.09\text{cm}$ , 폭이  $0.31 \pm 0.06\text{cm}$ 이었으며 천립중은  $1.58 \pm 0.07\text{g}$ 이었다. 화피를 제거하면 길이  $0.31 \pm 0.05\text{cm}$ , 너비  $0.31 \pm 0.06\text{cm}$ , 폭은  $0.12 \pm 0.04\text{cm}$ 였으며 천립중은  $0.74 \pm 0.06\text{g}$ 이었다. 종피가 감싸고 있는 종자의 내부는 shoot apex를 중심으로 배축이 나선형으로 두 번 반정 감겨져서 종자 바깥쪽으로 radicle이 향하고 있는 구조를 가지고 있다. 종자 침종 후 발아하는 데는  $30^\circ\text{C}$ 에서 평균 3일 정도가 소요되었으며, 발아 시 radicle이 종피를 뚫고 신장하였으며, 이 때 나선형의 배축이 풀리고 황색의 떡잎은 길은 초록색으로 변하면서 갈라져 신장하였다. 염조건에 따른 유묘의 생장 특성을 조사하기 위하여 초장 10cm 내외의 유묘를 상토에 이식하고 염농도를 0, 20, 50, 100, 200mM로 처리하고 5주 간 생육조사를 실시하였다. 그 결과, 나문재의 초기 생장량은 염농도 50mM에서 초장이  $55.95 \pm 6.30\text{cm}$ , 분지가 56개로 가장 많았으며, 100mM에서는 50mM의 생장량보다 약간 적었으나 유의한 차이를 보이지는 않았다. 반면, 생육이 가장 부진하였던 200mM에서는 50mM에 비하여 초장은 19.05cm, 분지는 13개 감소하였다. 이와 같은 결과로 볼 때, 나문재는 적정 생육 염농도는 50~100mM 정도로 판단되었다.

\*주저자: Tel. 063-270-2512, E-mail: njchung@jbnu.ac.kr

---

PD-08

## Analysis of Phylogenetic Relationship from *Angelica gigas* collected in Korea using RAPD Markers

Jinsu Gil<sup>1</sup>, Serim Kim<sup>1</sup>, Yurry Um<sup>2</sup>, Ok Tae Kim<sup>2</sup>, Hee Chung<sup>1</sup>, Seon-Woo Cha<sup>2</sup>, Yi Lee<sup>1\*</sup>

<sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University

<sup>2</sup>Department of Herbal Crop Research, NIHHS, RDA, Eumseong 369–873, KOREA

*Angelica gigas*, also called Dang Gui or Korean Angelica, is a major medicinal herb used in Asian countries such as Korea, Japan and China. In Korea, we are using the roots of *A. gigas*., but, they are using *Angelica sinensis* in China and using *Angelica acutiloba*. in Japan to obtain many active constituents such as decursin, decursinol angelate, nodakenetin, nodakenin, umbelliferone,  $\beta$ -sisterol, or  $\alpha$ -pinene. The plants of the Angelica family are used to improve gynecological health. The biggest problem in the cultivation of *A. gigas* is bolting. If the bolting occurs, *A. gigas* can not be used as a medicinal component because the roots are lignified. In this study, 11 *A. gigas* genetic resources in Korea; 1. Hwangje variety, 2. Sungwoo Jongmyo company, 3. Bonghwa No. 1, 4. Bonghwa No. 2, 5. Bonghwa No. 3, 6. Bonghwa No. 4, 7. Jechun local variety, 8. Jirisan local variety, 9. Manchu variety in Eumseong, 10. Manchu variety in Bonghwa, 11. Jinbu local variety, were collected and performed phylogenetic analysis using RAPD molecular markers.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

PD-09

## Protein phosphatase 2C induced by abscisic acid positively regulates *Rsv3*-mediated extreme resistance

Jang-Kyun Seo<sup>1,2</sup>, Sun-Jung Kwon<sup>3</sup>, Won Kyong Cho<sup>1</sup>, Hong-Soo Choi<sup>2</sup>, Kook-Hyung Kim<sup>1</sup>

<sup>1</sup>Department of Agricultural Biotechnology and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151–921, Republic of Korea

<sup>2</sup>Crop Protection Division, National Academy of Agricultural Science, Rural Development Administration, Suwon 441–707, Republic of Korea

<sup>3</sup>Horticultural and Crop Herbal Environment Division, National Institute of Horticultural and Herbal Science, Rural Development Administration, Suwon 440–310, Republic of Korea

Effector-triggered immunity (ETI) is an active immune response triggered by interactions between host resistance proteins and their cognate effectors. Although ETI is often associated with the hypersensitive response (HR), various R genes mediate an HR-independent process known as extreme resistance (ER). In the soybean-*Soybean mosaic virus* (SMV) pathosystem, the strain-specific CI protein of SMV functions as an effector of *Rsv3*-mediated ER. In this study, we used the soybean (*Rsv3*)-SMV (CI) pathosystem to gain insight into the molecular signaling pathway involved in ER. We used genome-wide transcriptome analysis to identify a subset of the type 2C protein phosphatase (PP2C) genes that are specifically up-regulated in *Rsv3*-mediated ER. Gain-of-function analysis of the most significantly expressed soybean PP2C gene, *GmPP2C3a*, showed that ABA-induced GmPP2C3a functions as a key regulator of *Rsv3*-mediated ER. Our results further suggest that the primary mechanism of ER against viruses is the inhibition of viral cell-to-cell movement by callose deposition in an ABA signaling-dependent manner.

---

PD-10

## Evaluation of sprouting rate of mature and developing seeds in red grain wheat (*Triticum aestivum* L.)

Dae Yeon Kim, Oonha Shin, Yong Weon Seo\*

Department of Biotechnology, Korea University, Seoul 136–713, Republic of Korea

Nutritious and functional foods from crop have received great attention in recent years. Colored-grain wheat contains high phenolic compound and a large number of flavonoid. One of plant pigments, wheat anthocyanin is increasingly emerging as natural compounds for consumer's health and condition. Red grains and white grains with different antioxidant activity was used to conduct germination assay. Antioxidant enzyme assay of POD, APX, CAT, GST, GR and GPx was conducted during the imbibitional phase of mature seeds. Malondialdehyde (MDA) content was analyzed to assess the activity of ROS during imbibition phase of mature seeds and alpha-amylase contents were quantified for 3 days during dark imbibition. Additionally, sprouting rates of developing seeds in spikelet after anthesis with damp condition were measured in each red grain groups for two weeks to evaluate sprout ability affected by phytochemical of red grain wheat. In summary, we identified that red grain wheat showed higher antioxidant enzyme activity involved in ROS scavenging during imbibition. Sprouting rate during dark imbibition in developmental spikelet of four groups classified by color suggest that phytochemicals in dark red grain wheat caused negative effects to sprouting.

Acknowledgements: This work was carried out with the support of "Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ0110212015)" Rural Development Administration. Republic of Korea.

\*Corresponding Author: Tel. +82-2-3290-3005, E-mail: seoag@korea.ac.kr

PD-11

## Potential hybrids of *Miscanthus sinensis* x *M. sacchariflorus* revealed by morphological traits analysis

Soo-Hyun Lim<sup>1</sup>, Hae-Rim Park<sup>1</sup>, Dong-Gil Kim<sup>1</sup>, DoKyoung Lee<sup>1,2</sup>, Gyoungju Nah<sup>1</sup>, Do-Soon Kim<sup>1\*</sup>

<sup>1</sup>Department of Plant Science, Seoul National University, Seoul 151–921, Republic of Korea

<sup>2</sup>Department of Crop Sciences, University of Illinois at Urbana Champaign, IL 61801, USA

More than 300 *Miscanthus* accessions as a potential bioenergy crop were collected in Korea and their morphological traits were investigated at various growth stages. Among morphological traits, stem growth habit, the presence of awn in spikelet, and autumn new shoot are the most important key traits enabling to cluster *Miscanthus* accessions into *M. sinensis* and *M. sacchariflorus* groups. *Miscanthus sinensis* has bunch stem growth habit and awn in spikelet, and produces autumn new shoot, while *M. sacchariflorus* has scattering stem growth habit with no awn in spikelet and does not produce autumn new shoot. Interestingly, we found several *Miscanthus* accessions showing intermediate morphological traits. 7 *M. sinensis* accessions showed morphological traits similar to *M. sacchariflorus* and 17 *M. sacchariflorus* accessions showed morphological traits similar to *M. sinensis*. Flow cytometry and chromosome counting finally revealed 5 *Miscanthus* hybrids, suggesting that they are resulted from natural hybridization between *M. sinensis* and *M. sacchariflorus*. Therefore, these *Miscanthus* hybrids can be used to understand genetic recombination between these two *Miscanthus* species and our understanding may support future efforts for breeding new *Miscanthus* variety with high biomass productivity and environmental adaptability.

\*Corresponding Author: Tel. 02-880-4542, E-mail: dosoonkim@snu.ac.kr

---

**PD-12**

## **Complete chloroplast genomes of two *Miscanthus* species**

Gyoungju Nah\*, Ji-Hoon Im, Soo-Hyun Lim, Kyunghee Kim, Do-Soon Kim\*

Department of Plant Science, Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul 151–921, Korea

The complete chloroplast (cp) genomes of two *Miscanthus* species, *M. sinensis* and *M. sacchariflorus*, were sequenced and investigated for genes, genome size variation, and polymorphisms. There are 154 genes in both cp genomes, consisting of 122 coding genes, 40 tRNA genes, and 8 rRNA genes. The cp genome contains two inverted repeat (IR) regions, separated by large single copy (LSC) region and small single copy (SSC) region. 112bp indels in *M. sinensis* and 152bp in *M. sacchariflorus* were found mainly in LSC and SSC, which are responsible for 40 bp-difference in cp genome size in two species. Likewise, out of 94bp of SNPs, 88bp were found in LSC and SSC regions. Although gene number and sequence structure were quite well conserved, indel distribution and size were different in these two *Miscanthus* species.

\*Corresponding Author: Tel. 02-880-4542, E-mail: dosoonkim@snu.ac.kr

**PD-13**

## **Quantitative shotgun proteomic analysis of rice anther under the cold stress**

Joohyun Lee\*, Mijeong Kim, Yoonjung Lee

Department of Applied Bioscience, Konkuk, University, Seoul 143–701, Republic of Korea

In rice, the stage of the meiosis in the pollen is sensitive stage resulted in the pollen sterility to reduce yield. Dianxi4 is a cold tolerant line. To monitoring the proteome expression patterns in the pollen of Dianxi4 under the cold stress, shotgun proteomic analysis was conducted to the anther of Dianxi4. The rice plant was grown in the peedy rice field then in the 10 DBH(days before heading), one individual rice plant was moved in the growth chamber under the condition of 12°C/RH70%(12h day/12h night). Also the plant used as control was moved in the growth chamber under the condition of 28°C/RH70%(12h day/12h night). after 4 days treatment, the plant were moved in a greenhouse. The treated rice anther were collected in the one day before heading. From the shotgun proteomic analysis, total of 3,855 non-redundant proteins were identified. Among them, 2,360 proteins were reproducibly identified through the treatment and replications. By the T-test, 1,181 differentially expressed proteins were detected. Through the GO analysis, proteins related in gene expression, cellular process, cellular biosynthetic process were enriched.

\*Corresponding Author: Tel. 02-450-3769, E-mail: joohyun00@gmail.com

## 무(radish)에서 자가불화합(self-incompatibility)을 결정하는 *S* locus core region에 위치한 *SLL2* 유전자 변이를 이용한 *S* haplotyping 시스템 구축

김대현, 김성길\*

광주광역시 북구 용봉동 전남대학교 농업생명과학대학 식물생명공학부

십자화과 작물에서 *SRK*와 *SP11* 유전자는 자가불화합 반응을 매개하는 주요 유전자이다. 무(radish)에서 *S*-locus haplotype을 분류 및 확인하기 위한 첫 단계로, *SRK*와 *SP11* 유전자의 온전한 서열확보를 위해 기존 연구를 통해 밝혀진 *Brassica rapa*의 *SRK* 유전자 서열을 활용해 local blast를 수행했다. 이를 통해 무 draft genome sequence에서 *SRK* 유전자와 높은 상동성이 있는 15개의 후보유전자들을 찾았다. 이후 *B. rapa* genome data를 활용한 synteny analysis를 통해 무 draft genome sequence에서 *B. rapa*의 *S*-locus region과 synteny를 가지는 scaffold를 R7 연관그룹에서 확인했다. 해당 scaffold에서 *SRK*와 *SLG* 유전자의 서열을 확보할 수 있었다. 이렇게 확보한 *SRK* 유전자서열의 정보를 통해 NCBI database에서 동일한 유전자서열을 찾을 수 있었고, 해당 논문에서 연구된 같은 haplotype의 *SP11* 유전자서열을 local blast의 query로 사용해서 무 draft genome sequence에서 *SP11* 유전자정보가 포함된 scaffold를 찾을 수 있었다. 이로써, *SRK*, *SLG*, *SP11/SCR* 유전자를 포함하는 53,785bp, 42,804bp, 10,165bp 크기의 온전한 genomic 서열을 확보하게 되었다. 무 *S* locus haplotype을 분류하기 위한 체계를 만들기 위해 *S*-locus core region에 있는 *SLL2* 유전자를 활용했다. *SRK* 유전자의 경우, 무 genome내에 상동성이 높은 homologous gene을 가지고 있고, *SP11* 유전자의 경우는 exon지역의 다형성이 너무 높아 PCR기반의 marker 개발이 어렵기 때문에 *SLL2* 유전자를 활용했다. 가지고 있는 다양한 무 육종계통에서 *SLL2* 유전자에 특이적인 primer set을 사용해 *SLL2* 유전자를 증폭시킨 뒤, sequencing하여 *SLL2* 유전자에 대한 다양한 대립유전자들의 서열을 확보할 수 있었다. 확보한 *SLL2* 대립유전자 서열을 비교함으로써 *S* locus haplotype 분류체계를 만드는 데 활용 가능한 conserved region을 exon2와 exon6에서 확인할 수 있었고, 해당 부분에 design된 primer를 통해 다양한 무 육종계통에서 단일한 PCR band를 확인할 수 있었다. 이는 직접적인 sequencing을 통해 *S* locus haplotype을 식별하는데 충분한 정보를 제공함으로써 무 육종에 큰 도움이 될 것이라 생각된다.

\*주저자: Tel. 062-530-2061, E-mail: dronion@jnu.ac.kr

---

**PD-15**

### **E3 SUMO ligase AtSIZ1 regulates the amounts of nutrient reservoir cruciferins in *Arabidopsis thaliana* seed.**

Sung-Il Kim<sup>1</sup>, Joo Yong Kim<sup>1</sup>, Do youn Kim<sup>1</sup>, Ye Jin Gyeon<sup>1</sup>, Jun Soo Kwak<sup>1</sup>, Hak Soo Seo<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Science, Research Institute for Agriculture and Life Sciences, and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

<sup>2</sup>Bio-MAX Institute, Seoul National University, Seoul 151-818, Korea

*Arabidopsis* E3 SUMO ligase SIZ1 (AtSIZ1) controls vegetative growth and development including responses to nutrient deficiency and environment stresses. Here, we analyzed the effect of AtSIZ1 on the stability and amount of seed proteins. Proteomic analysis showed that the amount of three major nutrient reservoir proteins, CRUCIFERIN (CRU) 1, 2 and 3, were decreased in *siz1-2* mutants. However, quantitative real-time RT-PCR showed that transcript levels of *CRU1*, 2 and 3 genes were rather significantly higher in *siz1-2* mutants than wild-type plants. Yeast two hybrid analysis revealed that AtSIZ1 interacts with CRU1, CRU2 and CRU3, strongly suggesting that CRU1, 2 and 3 proteins are sumoylated by AtSIZ1. In addition, the analysis of amino acid composition by HPLC showed that the contents of amino acids were a bit high in *siz1-2* mutants. Our data indicate that AtSIZ1 plays an important function for accumulation of seed storage proteins through its ligase activity.

This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center no. PJ01108701), Rural Development Administration, Republic of Korea.

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

**PD-16**

### **Genetic diversity analysis of wild *Codonopsis lanceolata* in Korea using SSR makers**

Serim Kim<sup>1</sup>, Ji Hee Jeong<sup>2</sup>, Jinsu Gil<sup>1</sup>, Tae Dong Kim<sup>2</sup>, Yurry Um<sup>3</sup>, Ok Tae Kim<sup>3</sup>, Ho Bang Kim<sup>4</sup>, Yi Lee<sup>1\*</sup>

<sup>1</sup>Department of Industrial Plant Science & Technology, Chungbuk National University, Korea

<sup>2</sup>Seed & Seedling Management Division, Korea Forest Seed and Variety Center, Korea

<sup>3</sup>National Institute of Horticultural and Herbal Science, Rural Development Administration, Korea

<sup>4</sup>Life Sciences Research Institute, Biomedic Co.,Ltd., Bucheon(420-852), Korea

In this study, genetic diversity of wild *Codonopsis lanceolata* collected in Korea were analysed using SSR makers. Wild *C. lanceolata* roots were collected in Jeollanam-do Jangheung-gun Choentae Mountain as in roots. The wild *C. lanceolata* plants were cultivated in Chungbuk National University greenhouse and the leaves were sampled from 36 plants. The genomic DNA of *C. lanceolata* was extracted using CTAB. PCR was performed using a program of 35 cycles at 94°C for 30 sec, 60°C for 30 sec, and 72°C for 30 sec with an pre-denaturation of 94°C for 5 min and a final extension of 72°C for 30 min. The PCR reaction mixture contains 5 pmole of primers and 20 ng of DNA template in a 20 µL reaction volume. The genotype of the analyzed samples were very different. Therefore, the wild *C. lanceolata* collected in Korea look genetically diverse.

This work was carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project No. PJ01102202)” Rural Development Administration, Republic of Korea.

\*Corresponding Author: Tel. 043-261-3373, E-mail: leeyi22@cbnu.ac.kr

## **Soybean molecular breeding platform based on variation blocks**

Yul-Ho Kim<sup>1\*</sup>, Hyang-Mi Park<sup>2</sup>, Sunghoon Lee<sup>3</sup>, Yu-Young Lee<sup>4</sup>, Su Jeong Kim<sup>1</sup>, Whang-Bae Sohn<sup>1</sup>, Su-Young Hong<sup>1</sup>, Jeong-Hwan Nam<sup>1</sup>, Kibum Kweon<sup>1</sup>, Jin-Cheol Jeong<sup>1</sup>

<sup>1</sup>Highland Agriculture Research Center, NICS, RDA, Pyeongchang, Gangwondo 232–955, Republic of Korea

<sup>2</sup>National Institute of Crop Science, RDA, Wanju-gun, Jeollabuk-do, 565–851, Republic of Korea

<sup>3</sup>Theragen Bio Institute, TheragenEtex, Suwon 443–270, Republic of Korea

<sup>4</sup>Department of Central Area, NICS, RDA, Suwon 441–707, Republic of Korea

Much effort has been expended to find agronomically important QTLs for improving soybean yield. However, the complexity of genome, such as genome duplication, limits the utility of genome-wide association studies and linkage analyses to identify genes controlling yield traits. We propose the variation block method, a three-step process for recombination block detection and comparison. The first step is to detect variations by comparing short-read DNA sequences of the cultivar to a reference genome of the target crop. Next, sequence blocks with variation patterns are examined and defined. The boundaries between the variation-containing sequence blocks are regarded as recombination sites. All the assumed recombination sites in the cultivar set are used to split the genomes, and the resulting sequence regions are named as variation blocks. The practicality of this approach was demonstrated by the identification of a putative locus determining soybean hilum color and known genes such as flower color gene. We suggest that the variation block method is an efficient genomics method for recombination block-level comparison of crop genomes. We expect that this method holds the prospect of developing crop genomics by bringing genomics technology to the field of crop breeding.

**\*Corresponding Author:** Tel. 033-330-1840, E-mail: kimyuh77@korea.kr

## Overexpression of the *Arabidopsis* vacuolar H<sup>+</sup>-pyrophosphatase *AVP1* gene in rice plants improves grain yield under paddy field conditions

Il-Sup Kim<sup>1\*</sup>, Young-Saeng Kim<sup>2</sup>, Yul-Ho Kim<sup>3</sup>, Hyang-Mi Park<sup>3</sup>, Ho-Sung Yoon<sup>1</sup>

<sup>1</sup>Department of Biology, Kyungpook National University, Daegu 702-701, Republic of Korea

<sup>2</sup>Division of Biological Sciences, University of California San Diego, La Jolla, California 92093-0116, USA

<sup>3</sup>National Institute of Crop Science, Rural Development Administration, Suwon 441-857, Republic of Korea

The *Arabidopsis* gene *AVP1* encodes a vacuolar H<sup>+</sup>-translocating inorganic pyrophosphatase (EC3.6.1.1) that functions as an electronic proton pump in the vacuolar membrane and affects growth development and stress responses in plants. This study was conducted to evaluate the molecular properties of the *A. thaliana* vacuolar H<sup>+</sup>-pyrophosphatase (*AVP1*) gene in rice. Incorporation and expression of the transgene was confirmed by PCR and quantitative real-time PCR, respectively. Expression of the *AVP1* gene in transgenic rice plants (TRP1 and TRP2) resulted in significantly enhanced tolerance to 100 mM NaCl under greenhouse conditions when compared to control wild-type (WT) rice plants. Augmented *AVP1* expression in the transgenic rice plants also affected total biomass and improved ion homeostasis through increased accumulation of Na<sup>+</sup> ions in whole tissues when compared to control WT rice plants under high salinity conditions. The *Fv/Fm* values of transgenic rice plants were higher than those of WT rice plants, even though the values decreased over time in both WT and transgenic (TRP1 to TRP8) rice plants. Furthermore, rice grain yield and biomass of the transgenic rice plants were at least 15% higher based on the culm and root weights and panicle and spikelet numbers when compared to those of the WT rice plants during the farming season in Korea. Thus, these results suggest that ectopic *AVP1* expression conferred tolerance and stress resistance to genetically modified transgenic crop plants by improving cellular ion homeostasis against salt conditions, which enhanced the rice yield and biomass under natural conditions in paddy fields.

\*Corresponding Author: Tel. 053-950-5348, E-mail: 92kis@hanmail.net

## SNP 마커를 이용한 고추의 적색소 함량 연관 QTL mapping

김정호\*, 안울균, 이해은, 김진희, 김도선, 조명철, Sandeep Karna

전라북도 완주군 이서면 농생명로 100 국립원예특작과학원 채소과

고추의 적색소는 고추의 상품성을 가늠하는 중요한 척도이면서 식재료 뿐 아니라 상업적으로도 다양하게 활용되고 있다. 본 연구는 적색소 성분의 함량과 관계하는 QTL 마커를 개발하기 위하여 적색소 성분 분석을 위한 mapping 집단을 육성하였고, 적색소 성분에 대한 QTL mapping을 수행하였다. 적색소 분석을 위한 mapping 집단인 ‘만다린’과 ‘블랙클러스터’를 양친으로 하는 F<sub>7</sub> RIL 집단에서의 색도(ASTA value) 분포는 1.64에서 117.26의 범주에 있으며 그 분포 양상은 정규분포를 보여 QTL분석에 적합한 것으로 확인되었다. Mapping 집단의 양친들에 대해서 454 GS-FLX pyrosequencing을 이용한 NGS를 수행하였고, 그 결과 ‘만다린’과 ‘블랙클러스터’ 각각 120.44Mb와 142.54Mb의 염기 서열 데이터를 확보할 수 있었으며, ‘만다린’에서 1,025개, ‘블랙클러스터’에서 1,059개의 SNP들을 확보하게 되었다. 이 SNP들을 HRM 분석에 용이하도록 프라이머를 제작하여 유전자 지도 작성을 수행한 결과 총 246개의 SNP 마커를 이용하여 약 512cM을 설명할 수 있는 21개 연관군의 유전자 지도가 작성되었다. 분석 집단 93계통들에서 측정된 ASTA 값을 이용하여 수행한 QTL 분석 결과 총 6개의 QTL을 확인하였다. 이들 QTL과 근접한 마커들은 향후 고추의 적색소 함량 연구에 매우 유용한 정보로 활용될 것이며, 아직까지 개발된 바 없는 적색소 함량 연관 마커 개발에 가능성을 열어줄 것으로 기대한다.

\*주저자: Tel. 063-238-6673, E-mail: gogh1221@gmail.com

## Identification of modulatory elements in xylem development for biomass production

Jinu Kim<sup>1</sup>, Hwi Seong Jeon<sup>1</sup>, Hong Joo Cho<sup>1</sup>, Soon Il Kwon<sup>1</sup>, Young Hoon Jung<sup>1</sup>, Jae-Soon Lee<sup>2</sup>, Eun Woon Noh<sup>2</sup>, Kyoung Heon Kim<sup>1</sup>, Ohkmae K. Park<sup>1</sup>

<sup>1</sup>Korea University

<sup>2</sup>Korea Forest Research Institute

The vascular system of plants consists of two conducting tissues, xylem and phloem, which differentiate from procambium cells. Xylem serves as a transporting system for water and signaling molecules and is formed by sequential developmental processes, including cell division/expansion, secondary cell wall deposition, vacuole collapse, and programmed cell death (PCD). PCD during xylem differentiation is accomplished by degradation of cytoplasmic constituents, and it is required for the formation of hollow vessels, known as tracheary elements (TEs). Our recent study revealed that the small GTPase RabG3b acts as a regulator of TE differentiation through its autophagic activation. By using an *Arabidopsis in vitro* cell culture system, we showed that autophagy is activated during TE differentiation. Overexpression of a constitutively active *RabG3b* (*RabG3bCA*) significantly enhances both autophagy and TE differentiation, which are consistently suppressed in transgenic plants overexpressing a dominant negative form (*RabG3bDN*) or *RabG3bRNAi* (*RabG3bRNAi*), a brassinosteroid-insensitive mutant *br1-301*, and an autophagy mutant *atg5-1*. Wood (called secondary xylem) is the most abundant biomass produced by land plants including *Populus* and *Eucalyptus*, and therefore is considered to be one of the most cost-effective and renewable bioenergy resources. In an attempt to enhance xylem differentiation and thus to improve biomass traits in poplars, we generated transgenic poplars overexpressing the *RabG3bCA* form. As notable phenotypes, both stem height and diameter were increased and xylem area in vascular bundles was significantly expanded in *RabG3bCA* transgenic poplars compared to control plants. Taken together, these results demonstrate that *RabG3b* regulates xylem differentiation in both *Arabidopsis* and *Populus*. This study enhances our understanding of biological mechanisms underlying wood formation and serve as a framework to engineer the quality and quantity of wood as useful biomass.

## The Effects of Superjami bran on in vitro and in vivo antioxidative and bone mineral density activities in ovariectomized rats

Su-Jin Nam\*, Mi-Young Kang

Department of Food Science and Nutrition, Kyungpook National University, Daegu 702–701, Republic of Korea

Superjami is a new rice breed resulted from crossing ‘C3GHi (has high amount of Cyanidin 3-glucoside, and was developed from a cross between ‘Heugjinjubyeo’ and ‘Suweon 425’) and ‘Daeribbyeo 1’. Superjami has 10.9 times higher C3G content compared with ‘Heugjinjubyeo’. It also contains the highest essential amino acids of all kinds (except tryptophan content). This study was done to investigate the effects of extracts from superjami bran on the in-vitro antioxidant metabolism, in-vivo antioxidant metabolism and bone metabolism on menopause-induced condition in experimental rats. Overall, extract from superjami bran was confirmed of improving antioxidant and bone metabolism which can be considered as a good dietary supplement.

\*Corresponding Author: Tel. 053-950-6235, E-mail: say1004625@naver.com

---

PD-22

## Cloning and functional characterization of an acyl-ACP thioesterase (CvFatB) from *Cuphea viscosissima* in *Arabidopsis*

Kyung Hee Roh<sup>\*</sup>, Han-chul Kang, Jong-Bum Kim, Hyun Uk Kim, Kyeong-Ryeol Lee

Department of Agricultural Biotechnology, National Academy of Agricultural Science, RDA, Jeonju 560–500, Republic of Korea

Acyl-acyl carrier protein (ACP) thioesterase (TE) catalyze the hydrolysis of the thioester bond that links the acyl chain to the sulfhydryl group of the phosphopantetheine prosthetic group of ACP. This reaction terminates acyl chain elongation of fatty acid biosynthesis, and in plant seeds it is the biochemical determinant of the fatty acid compositions of storage lipids. A full-length cDNA of an acyl-ACP thioesterase, named CvFatB, was isolated from oil plant *Cuphea viscosissima* accumulating up to 90% caprylate (8:0) and caprate (10:0) in its seed oil. This cDNA contains a 1,245-bp open reading frame that encodes a protein of 415 amino acids. The deduced sequence also contains two essential residues (H<sup>317</sup> and C<sup>352</sup>) for TE catalytic activity and a putative chloroplast transit peptide at the N-terminal. Overexpression of the CvFatB cDNA in *Arabidopsis* resulted in increased levels of saturated fatty acid, especially palmitate, and reduced levels of unsaturated fatty acids. The findings suggest that CvFatB from oil plant *C. viscosissima* can function as a saturated acyl-ACP TE and can potentially be used to diversify the fatty acid biosynthesis pathway to produce novel fatty acids.

**\*Corresponding Author:** Tel. 063-238-4606, Email: rohkh@korea.kr

PD-23

## The influence of silver thiosulfate and thidiazuron on shoot regeneration from cotyledon explants of *Brassica napus*

Kyung Hee Roh<sup>\*</sup>, Han-chul Kang, Jong-Bum Kim, Hyun Uk Kim, Kyeong-Ryeol Lee

Department of Agricultural Biotechnology, National Academy of Agricultural Science, RDA, Jeonju 560–500, Republic of Korea

The influences of ethylene inhibitors (AgNO<sub>3</sub> and silver thiosulfate) and cytokinins (BAP and TDZ) on shoot regeneration from cotyledon and hypocotyl explants of *B. napus* cv. Youngsan were investigated. The presence of 50 μM Silver thiosulfate (STS) in shoot regeneration medium formed shoots at 60–68% after 3–4 weeks of culture, which was enhanced by 2-fold compared to that of Silver nitrate (AgNO<sub>3</sub>). Moreover, cotyledon explants were more regenerative than hypocotyls; shoots from cotyledon explants began to occur 4–5 days earlier than that of hypocotyl explants. TDZ at a concentration of 8–10 μM was effective for shoot regeneration, compared with BAP. Consequently, the optimal shoot regeneration response was observed in medium supplemented with 50 μM STS + 8 μM TDZ. In transmission electron microscopy (TEM) analysis, higher density of silver nanoparticles was shown to be accumulated widely inside the cell wall and plasmodesmata of regenerating leaf cultured in medium supplemented with AgNO<sub>3</sub>. By contrast, in the cell cultured in medium with STS, fine-grained deposits were partly observed in the surroundings of the cell wall.

**\*Corresponding Author:** Tel. 063-238-4606, Email: rohkh@korea.kr

**A review on change in plant proteome following biotic stress.**

R. Krishna, Ravi Gupta, Chul Woo Min, So Wun Kim, Sun Tae Kim

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

Different biotic agents such as bacteria, fungi, nematode and virus interact with plants, and causes significant annual crop loss. The plants interact with these pathogen and undergo various changes at physiological, biochemical and molecular levels. The omics technique is a powerful way which provides important information related to molecular changes occurring during plant-pathogen interaction. Several studies have been conducted and revealed either up or down-regulation of many genes involved in metabolism, energy, photosynthesis, signaling, defense and ROS upon pathogen interaction. In this review, we highlight recent progress in proteomic studies of plant-pathogen interaction, which could be useful for controlling disease and development of molecular markers for early detection of different diseases.

**천연색소 C3G 고함유 “슈퍼자미” 기능성 신품종 쌀의 이화학적 특성**류수노<sup>1\*</sup>, 함태호<sup>1</sup>, 강미영<sup>2</sup><sup>1</sup>서울 종로구 대학로 86 한국방송통신대학교 농학과<sup>2</sup>서울 동대문구 경희대로 26 경희대학교 식품영양학과

흑진주벼 보다 C3G(Cyanidin-3-glucoside) 함량이 높고 아토피억제효과 및 항당뇨 효과가 있는 슈퍼자미(국립종자원 품종등록 : 제4151호, 2012. 10. 17)에 대한 이화학적 특성을 밝혀 기능성 쌀 이용 기초자료를 확립하고, 기존의 쌀과의 차이점을 밝히고자 수행하였다.

슈퍼자미 품종의 조단백질 · 조지방은 AOAC방법, 아밀로오스 함량은 Juliano법, 쌀가루의 물결합능력은 Medcalf & Gilles 법, 총 폴리페놀 함량은 Folin-Denis 방법, 전자공여능은 DPPH의 환원성을 이용하여 UV/Visible spectrophotometer로 측정하였다.

슈퍼자미의 단백질 함량은 기존의 유색미보다 낮아서 취반을 하였을 때 식미를 크게 저하하지 않을 것이라 사료된다. 아밀로오스 함량이 낮아 일반미와 혼합하여 밥을 지었을 때보다 부피 증가가 작고, 끈기가 많으며, 식미가 좋을 것이라고 생각된다. 물결합능력은 흑진주 > 슈퍼자미 > 일품 순이다. 일반계 쌀인 일품에 비해 흑진주와 슈퍼자미의 총 폴리페놀 함량이 1.2배 높은 것으로 나타났고 흑진주보다 슈퍼자미의 함량이 유의적으로 높았다. 흑진주보다 슈퍼자미의 DPPH 라디칼소거능이 높은 것으로 나타나 슈퍼자미가 강한 항산화 활성 능력을 가진 것으로 평가되었다.

\*주저자: Tel. 010-4229-2161, E-mail: ryusn@knou.ac.kr

---

PD-26

## Searching For Transcription Factors Involved In Ammonium Assimilation and Root Growth in Rice Plants

Ryza A. Priatama, Vikranth Kumar, Jin-hee Jeong, Chang-deok Han

Division of Applied Life Science, Plant Molecular Biology & Biotechnology Research Center (PMBBRC), Gyeongsang National University, Jinju 660–701, Korea

Nitrogen in rice paddy soils and utilized as the major source for N-assimilation in rice crops. In roots, transcriptional activities of ammonium uptake and assimilation genes are highly sensitive to the availability of exogenous ammonium. However, little is known about the transcription factor genes that regulated by ammonium supply and its role to roots and plant developments. To study the transcription factor genes that involved in Ammonium response, two weeks old rice seedlings treated using Ammonium from 0 to 3 hours. Total RNA collected from each sample and samples were prepared for Agilent 8x60K microarray system. Based on the microarray data, we select transcription factor genes that highly affected by ammonium and selected knock out mutant candidates that used for phenotype screening.

PD-27

## MSP1 triggers cell death and defense response in rice

Qingfeng Meng<sup>1</sup>, Yiming Wang<sup>2</sup>, Kyu Young Kang<sup>3</sup>, Ravi Gupta<sup>1</sup>, Sun Tae Kim<sup>1</sup>

<sup>1</sup>Department of Plant Bioscience, Pusan National University, Miryang, Korea

<sup>2</sup>Department of Plant Microbe Interactions, Max Planck Institute for Plant Breeding Research, Carl-von-Linne Weg 10, Cologne, 50829, Germany

<sup>3</sup>Plant Molecular Biology and Biotechnology Research Center, Gyeongsang National University, Jinju, Korea

When the rice blast fungus attacks rice, fungal proteins are secreted into the plant apoplast to facilitate infection. The rice plant recognizes such secreted proteins, which result in the induction of defense responses. However, the molecular mechanisms of how rice plant recognizes secreted proteins remain elusive. Here, we report that a small, secreted protein, *Magnaporthe oryzae* snodprot1 homolog (MSP1), is recognized by rice plants and triggers host cell death and defense responses. Furthermore, pre-treatment of rice with Domain II, elicitor-active epitope of MSP1, induces resistance to the pathogen KJ301. We demonstrated that secretion of MSP1 into the apoplast is prerequisite for triggering cell death and activating defense-related gene expression, suggesting that it is recognized by a receptor in the host plasma membrane. Through comprehensively analysis of transcriptional profile in rice leaves and suspension cultured cells (SCCs) in response to exogenous MSP1 and Domain II treatment using 60K Agilent microarray chip, we found that 27 signaling genes, such as F-box(6), MAPK(4), protein kinase(11), transcription factor(6), were up-regulated in leaves and SCCs and six protein kinases were targeted into plasma membrane. Thus, we suggest that some of these genes may act as receptor of MSP1 in response to exogenous MSP1 treatment. Expression pattern of candidate genes was further checked in response to different environment cues using open rice data. These results demonstrate that these genes may be also involved in the signaling in response to cold stress, root-JA treatment and brown plant hopper (BPH) attack.

## **Overexpression of a novel E3 ubiquitin ligase causes coiled branches phenotype in *Arabidopsis***

Gyu Tae Park<sup>1</sup>, Jagadeesh Sundaramoorthy<sup>1</sup>, Jeong-Dong Lee<sup>1</sup>, Hak Soo Seo<sup>2,3</sup>, Jong Tae Song<sup>1\*</sup>

<sup>1</sup>School of Applied Biosciences, Kyungpook National University, Daegu 702-701, Korea

<sup>2</sup>Department of Plant Bioscience, Seoul National University, Seoul 151-742, Korea

<sup>3</sup>Bio-MAX Institute, Seoul National University, Seoul 151-818, Korea

The wild relatives of soybean [*Glycine soja* Sieb. and Zucc.] have curly/wavy nature whereas cultivated varieties are upright. Such morphological characteristics have agronomic importance too. To investigate the molecular mechanism of development contributing to coiled morphology, screening was carried out to look for *Arabidopsis* mutants in activation tagging lines obtained by activation T-DNA treatment that have curly/wavy morphology. A mutant named Coiled Branch 1 (*cbr1*), is found to have a wavy and curly morphology with coiling branches. 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 sites, and showed the activation of an E3 ubiquitin ligase gene. Database search showed that the gene with the RING domain belongs to a family of E3 ubiquitin ligases. Complementation test by overexpression and RNA interference of the gene was also carried out. The complementation test results showed that the novel gene activation tagging affected the *cbr1* mutant phenotypes. Ubiquitylation has been linked virtually to every cellular process including plant development. E3 ubiquitin ligase has been reported to recognize target proteins that are to be ubiquitinated for further degradation by the proteasome complex. Further, more detailed studies are needed to identify the specific substrate(s) of the novel E3 ubiquitin ligase gene.

This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01108702), Rural Development Administration, Republic of Korea.

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

---

**PD-29**

## **Self-directed control of the diurnal *CONSTANS* dynamics in *Arabidopsis* photoperiodic flowering**

Mi-Jeong Park<sup>1</sup>, Young-Ju Kwon<sup>1</sup>, Kyung-Eun Gil<sup>1</sup>, Pil Joon Seo<sup>2</sup>, Jae-Hoon Jung<sup>3</sup>, Chung-Mo Park<sup>1,4\*</sup>

<sup>1</sup>Department of Chemistry, Seoul National University, Seoul 151-742, Korea

<sup>2</sup>Department of Bioactive Material Sciences and Research Center of Bioactive Materials, Chonbuk National University, Jeonju 561-756, Korea

<sup>3</sup>Sainsbury Laboratory, University of Cambridge, Cambridge CB2 1LR, UK

<sup>4</sup>Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-742, Korea

The circadian clock control of *CONSTANS* (*CO*) transcription and the light regulation of *CO* stability coordinately regulate photoperiodic flowering by triggering rhythmic expression of the floral integrator *FLOWERING LOCUS T* (*FT*). The diurnal pattern of *CO* accumulation is modulated sequentially by distinct E3 ubiquitin ligases, such as HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 1 (*HOS1*) in the morning, FLAVIN-BINDING, KELCH REPEAT, F-BOX 1 (*FKF1*) in late afternoon, and CONSTITUTIVE PHOTOMORPHOGENIC 1 (*COP1*) at night. In particular, *CO* is stabilized by *FKF1* in late afternoon only under long days. Here, we show that *CO* abundance is not simply regulated by the E3 enzymes in a passive manner but also self-regulated actively through dynamic interactions between two *CO* isoforms. *CO* alternative splicing produces two protein variants, the full-size *COa* and the C-terminally truncated *COb*. Notably, *COb*, which is resistant to the E3 enzymes, induces the interactions of *COa* with *CO*-destabilizing *HOS1* and *COP1* but inhibits the association of *COa* with *CO*-stabilizing *FKF1*. These observations demonstrate that *CO* plays an active role in sustaining its diurnal accumulation dynamics in *Arabidopsis* photoperiodic flowering.

\*Corresponding Author: Tel. 02-880-6640, E-mail: cmpark@snu.ac.kr

**PD-30**

## **CaLEA1 is a late embryogenesis abundant protein in pepper that positively regulates abscisic acid signaling, drought and salt stress response**

Chanmi Park, Hyunhee Joo, Woonhee Baek, Sung Chul Lee \*

Department of Life Science, Chung-Ang University, Seoul 156-756, Republic of Korea

Drought and high salinity are the most important abiotic factors limiting plant development, growth, and crop productivity in agriculture (Munns and Tester 2008, Sengupta and Majumder 2009, Zhu 2002). As sessile organisms, plants are frequently exposed to drought and high salinity conditions, which alter water potential and cause osmotic stress, leading to serious damage to plant tissues (Bartels and Sunkar 2005, Boudsocq and Lauriere 2005). During exposure to water stress, plants display many physiological changes, such as reduction of water content, closure of stomata, and decreased cell enlargement and growth. In addition, severe and continuous water stress in plants causes the cessation of photosynthesis and disturbance of metabolism, and finally results in death (Nath et al. 2005, Shao et al. 2008). To adapt to these abiotic stress conditions, plants show a variety of responses, including the accumulation of abscisic acid (ABA) and expression of a large number of stress-related proteins (Krasensky and Jonak 2012, Lee and Luan 2012, Skriver and Mundy 1990, Stewart and Lee 1974). Although the cellular and molecular responses to environmental stress are well studied (Hasegawa et al. 2000, Thomashow 1999), the mechanisms underlying the functional modifications caused by osmotic stress are yet to be clarified, because of the complexity at the cellular level as well as at the whole plant level (Ashraf and Harris 2004, Flowers 2004, Foolad et al. 2003a, 2003b, Xiong et al. 2002).

\*Corresponding Author: Tel. 02-820-5207, E-mail: sclee1972@cau.ac.kr

---

**PD-31**

## **The putative E3 ubiquitin ligase CaAIR1 in pepper regulates abscisic acid signaling and drought stress response**

Chanmi Park, Hyunhee Joo, Woonhee Baek, Sung Chul Lee\*

Department of Life Science, Chung-Ang University, Seoul 156-756, Republic of Korea

Several E3 ubiquitin ligases have been associated with the response to abiotic and biotic stresses in higher plants. Here, we report that the hot pepper (*Capsicum annuum*) abscisic acid (ABA)-insensitive RING protein 1 gene (*CaAIR1*) is essential for a hypersensitive response to drought stress. *CaAIR1* contains a C3HC4-type RING finger motif, which plays a role for attachment of ubiquitins to the target protein, and a putative transmembrane domain. The expression levels of *CaAIR1* are upregulated in pepper leaves by ABA treatments, drought, and NaCl, suggesting its role in the response to abiotic stress. Our analysis showed that CaAIR1 displays self-ubiquitination and localized in the nucleus. We generated *CaAIR1*-silenced peppers via virus-induced gene silencing (VIGS) and *CaAIR1*-overexpressing (OX) transgenic Arabidopsis plants to evaluate their responses to ABA and drought. VIGS of *CaAIR1* in pepper plants conferred an enhanced tolerance to drought stress, which was accompanied by low levels of transpirational water loss in the drought-treated leaves. *CaAIR1*-OX plants displayed an impaired sensitivity to ABA during seed germination, seedling, and adult stages. Moreover, these plants showed enhanced sensitivity to drought stress because of reduced stomatal closure and decreased expression of stress-responsive genes. Thus, our data indicate that *CaAIR1* is a negative regulator of the ABA-mediated drought-stress tolerance mechanism.

\*Corresponding Author: Tel. 02-820-5207, E-mail: sclee1972@cau.ac.kr

**PD-32**

## **Comparative transcriptome analysis of tolerant rice mutant and its wild type in response to arsenate stress**

Hyeon Mi Park, Sun-Goo Hwang, Cheol Seong Jang\*

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

Arsenic (As) is accumulated in rice grain due to environmental reasons such as polluted ground water and soil, and As toxicity constitutes a serious threat to human health. However, the accurate information required for understanding As-responsive mechanisms remain mostly unknown in rice. Here, we performed the comparative genome-wide transcriptome analysis between As tolerance type (ATT) rice mutant induced by  $\gamma$ -irradiation and its wild type (WT). As compared to WT after As treatment of 150 ppm, ATT exhibited the phenotypic differences such as vigorous growth in shoots and root hairs, and low accumulation of H<sub>2</sub>O<sub>2</sub> in rice roots. In transcriptome analysis, we found between WT and ATT that As toxicity commonly affected to inhibit gene regulations involved in photosynthesis, mitochondrial electron transport and lipid biosynthesis metabolism. While, many genes associated with cysteine synthesis metabolism considerably up regulated in both As-treated plants. Additionally, we found the potential As tolerance-related genes involved in abiotic stress-responsive mechanism and RNA-protein synthesis for protein degradation and modification. To further analyzes the genetic variations of As-responsive genes, the DNA polymorphic DEGs associated with oxidoreductase significantly distributed in ATT more than in WT.

\*Corresponding Author: Tel. 033-250-6416, E-mail: sjang@kangwon.ac.kr

---

PD-33

## Mutation of *SPOTTED LEAF3 (SPL3)* impairs abscisic acid-responsive signaling and delays leaf senescence in rice

Seung-Hyun Wang, Jung-Hyun Lim, Yasuhito Sakuraba, Nam-Chon Paek\*

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

Lesion mimic mutants commonly display spontaneous cell death in pre-senescent green leaves under normal conditions, without pathogen attack. Despite molecular and phenotypic characterization of several lesion mimic mutants, the mechanisms of the spontaneous formation of cell death lesions remain largely unknown. Here, we examined the rice lesion mimic mutant *spotted leaf3 (spl3)*. In mutants grown under a light/dark cycle, *spl3* mutants appeared similar to wild type at early developmental stages, but lesions gradually appeared in the mature leaves close to heading stage. By contrast, in mutants grown under continuous light, severe cell death lesions formed in developing leaves, even at the seedling stage. Histochemical analysis showed that hydrogen peroxide accumulated in the mutants, likely causing the cell death phenotype. By map-based cloning and complementation, we showed that a 1-bp deletion in the first exon of *Oryza sativa Mitogen-Activated Protein Kinase Kinase Kinase1 (OsMAPKKK1)/OsEDR1/ OsACDR1* causes the *spl3* mutant phenotype. We found that the *spl3* mutants were insensitive to abscisic acid (ABA), showing normal root growth in ABA-containing media and delayed leaf yellowing during dark-induced and natural senescence. Expression of ABA signaling-associated genes was also less responsive to ABA treatment in the mutants. Furthermore, the *spl3* mutants had lower transcript levels and activities of catalases, which scavenge hydrogen peroxide, probably due to impairment of ABA-responsive signaling. Finally we discuss a possible molecular mechanism of lesion formation in the mature leaves of *spl3* mutants. This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01106301)”, Rural Development Administration, Republic of Korea.

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

PD-34

## Study on Phenotypes and Agronomical utility of a Rice *GT1 (grassy tillers 1, OsGT1)* Homologue

Vikranth Kumar, Yuan Hu Xuan, Byoung Il Je, Soon Ju Park, Jin Huang, Jing Miao Liu, Ryza A. Priatama, Vimal Raj K, Sung Hoon Kim, Jin-hee Jeong, Chang-deok Han

Division of Applied Life Science, Plant Molecular Biology & Biotechnology Research Center (PMBBRC), Gyeongsang National University, Jinju 660–701, Korea

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 induced by shading and 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 showed that *OsGT1* overexpressors reduced tillers and panicles while RNAi lines increased them, compared to wild type. Shade signal is an important factor in determining lateral branching. To understand the relationship between *OsGT1* and shade avoidance, plants have been grown under 50% shading in the field. Also, double genetic combinations with phytochrome mutants (*phyA, B, and C*) are being examining for tillering phenotype. These ongoing researches will provide insights in determining the action of *OsGT1* on branching and shade avoidance in rice.

## **Genome-specific transcripts analysis in a 2BS.2RL wheat-rye translocation using custom array**

Yong-Jin Lee<sup>1</sup>, Tong-Geon Lee<sup>1,2</sup>, Yong-Weon Seo<sup>1\*</sup>

<sup>1</sup>Division of Biotechnology, Korea University, Seoul 136–701, Republic of Korea

<sup>2</sup>Department of Crop Sciences, University of Illinois, Urbana, IL61801, USA

Common wheat has complex genome composition of homoeologous hexaploid (AABBDD,  $2n = 6x = 42$ ) and each homoeologous genome has high similarity. Due to these complexity, wheat genome study is a large challenge to researchers for genomic and genetic study. We analyzed expressions of individual wheat genome and rye genome specific transcripts using custom array with 2BS.2RL wheat-rye translocation. Genomic probes were synthesized within each diploid progenitors (AA, BB, DD,  $2n = 14$ , respectively) of wheat, common wheat, and rye (RR,  $2n = 14$ ). Total RNA isolated from seedlings of *T. urartu*, *Ae. speltooides*, *Ae. squarrosa*, ‘Chinese Spring’, ‘Chaupon’, and 2BS.2RL were hybridized on arrays. Each homoeologous gene differentially expressed in hexaploid wheat and rye were identified on the custom array and the transcripts were clustered based on hybridization values. qRT-PCR was performed to verify the custom array result with a set of five genes by highly replicated experiments (three biological and three technical replications). The qRT-PCR results demonstrated genome specific expression of five genes in sympathy with array results. Here we provide information of each individual genome specific transcripts and it will be a useful data to study complex wheat genome compositions.

Acknowledgement: This work was carried out with support of ‘Next-Generation BioGreen 21 Program for Agriculture & Technology Development (Project No. PJ01103501)’, Rural Development Administration, Republic of Korea

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

## **Global investigation of small RNA expression on nutrient stress responses provides information on nutrient-responsive microRNAs involved in crop productivity**

Sang-Yoon Shin<sup>2</sup>, Dooyoung Lee<sup>1</sup>, Ju-Kon Kim<sup>3</sup>, Chanseok Shin<sup>1,2\*</sup>

<sup>1</sup>Department of Agricultural Biotechnology, Seoul National University, Seoul 151–921, Republic of Korea

<sup>2</sup>Interdisciplinary Program in Agricultural Genomics, Seoul National University, Seoul 151–921, Republic of Korea

<sup>3</sup>Seed Biotechnology Institute, Green Bio Science and Technology, Seoul National University, Pyeongchang-gun, Kangwon-do, Republic of Korea

Nitrogen is a key component in the growth of crop plant. To increase the yield of crops, an enormous amount of nitrogen fertilizer is currently being used, which increases the total production cost and leads to environmental pollution by the residual nitrogen sources. For these reasons, researchers have tried to improve the crop's nitrogen use efficiency (NUE) as a solution for reducing the amount of nitrogen fertilizer used.

MicroRNAs are a class of small non-coding RNAs regulating the expression of target genes. Recent studies suggested that the expression pool of microRNAs changes in response to a variety of nutrient deficiencies and that such changes play important roles in adapting to or resisting the consequential nutritional stresses. Here, we aim to identify and characterize rice microRNAs whose expression changes upon nitrogen starvation and re-supplementation. By applying RNA-Seq, we observed that the expression of a set of genes involved in nitrogen assimilation was altered in response to nitrogen deprivation. We also found that a considerable number of microRNAs exhibited dynamic expression changes in a nitrogen supply state-dependent manner and that the expression of genes targeted by those differentially regulated microRNAs was altered reciprocally. Our study suggests that microRNAs may have roles in regulating the response of rice to nitrogen supply state and subsequently modulating NUE.

This work is supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ01115601), Rural Development Administration, Republic of Korea.

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

***OsVIL* genes, which encode PRC2 chromatin remodeling factors, may be used for improving grain yield by increasing biomass in rice.**Jung-Il Yang, Hee Joong Jeong, Lae-Hyeon Cho, Jinmi Yoon, Gynheung An\*

Graduate School of Biotechnology &amp; Crop Biotech Institute, Kyung Hee University, Yongin, 446–701, Republic of Korea

Post-translational modifications of nucleosomal core histones play important roles in biological processes via altering chromatin structure and creating target sites for proteins acting on chromatin. Molecular genetic studies with *Arabidopsis* have verified several epigenetic factors that regulate flowering time. However, the roles of chromatin remodeling factors have not been well explored in rice. Here, we identified chromatin remodeling factors, *OsVIL1*, 2, and 4 (*Oryza sativa* *VIN3-LIKE*) genes, that regulate grain yield. *OsVIL* proteins contain a plant homeodomain (PHD) finger, which is a conserved motif of histone binding proteins. We showed that plant height and number of spikelets per panicle were increased in the *OsVIL2*-overexpression (*OsVIL2-OX*) and *osvil4* plants, respectively. Each mutants (*OsVIL2-OX* and *osvil4*) exhibited longer internodes and thicker stems than wild type controls. Histochemical analysis revealed that cells are smaller in *OsVIL2-OX* and *osvil4* plants. We performed an RNA-seq using 1st internodes of WT and *OsVIL2-OX* stems and got the suppressed target genes in the *OsVIL2-OX*. *OsCKX2*, which encodes cytokinin oxidase/dehydrogenase is one of the suppressed genes in the OX plants and we verified decrease of that gene using qRT-PCR and closed chromatins of *OsCKX2* were enriched in the OX plants by using ChIP. As results of these, cytokinins were enriched in the OX plants. These demonstrate that *OsVIL2* and *OsVIL4* antagonistically regulate plant height and number of spikelets by controlling cytokinin contents. Like *OsVIL2-OX* and *osvil4* plants, besides, *OsVIL1-OX* plants were also shown increased plant height and biomass. We propose that *OsVILs* may be used for improving grain yield by increasing biomass.

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

## Structural and Functional Insights into Enzymes in Nitrogen Remobilization Pathway

Inchul Shin, Kitae Han, Sangkee Rhee\*

Department of Agricultural Biotechnology, Seoul National University, Seoul 151-741, Republic of Korea

Nitrogen is an essential nutrient in plants including many crops. The storage and remobilization of nitrogen constitutes the main metabolic process for growth and development of plants. Ureide pathway is the lately characterized metabolic route for purine degradation and is conserved in plants, as well as some bacteria and fungi. The catabolic pathway catalyzes in a stepwise manner a conversion of N-rich uric acid into glyoxylate, with the release of ammonia, and plays a pivotal role in the storage and recovery of nitrogen from metabolites. In Next Generation BioGreen21 project, we aim to understand structural and functional features of enzymes involved in this nitrogen recycling pathway, by using genes from *Arabidopsis thaliana*. In this study, we report our current progress on this project including two different enzymes; ureidoglycine aminohydrolase (UGlyAH), and ureidoglycolate amidohydrolase (UAH). In UGlyAH, the metal-binding site plays a crucial role in catalysis, with a release of ammonia. We were able to characterize catalytic residues in the active site and provides a detailed view of a metal-dependent enzyme mechanism. Recently, we were able to characterize structural properties of UAH. Based on our analysis, we are performing enzymatic analysis to identify functional aspects of the enzyme. Taken together, these studies would provide a novel functional feature of the enzymes involved in the nitrogen recycling pathway and could serve as a framework to develop crops with an enhanced N-efficiency.

\*Corresponding Author: Tel. 02-880-4647, E-mail: srheesu@snu.ac.kr

## 고추 탄저병 및 CMV 저항성 마커 개발과 복합내병성 품종 육성과제 진도 보고

박석진, 도재왕, 한정현, 윤재복

(주)고추와 육종

본 과제는 “고추 육종가 맞춤형 고효율 분자육종시스템 실용화” 과제의 주관과제인, 고추 탄저병 및 CMV 저항성 마커 개발과 복합내병성 품종 육성(고추와 육종, 윤재복)으로, 세부과제인 고추 유용 분자표지의 foreground selection 용 multiplexing 기술 개발(전북대학교, 이준대)과 협업을 통해 2015~2017 년까지 탄저병과 오이모자이크바이러스 (cucumber mosaic virus, CMV)에 대한 복합내병성 품종 개발을 목표로 하고 있다. 탄저병과 CMV는 국내외에서 심각한 문제를 일으키고 있는 병원체로, 저항성 품종 육성 효율을 높이기 위해서는, 탄저병 저항성 연관 신규 분자표지와 CMV 강병원성 계통(기존 저항성 Cmr1 극복 CMV, CMV-P1)에 대한 저항성 연관 분자표지 개발이 필요하다. 본 과제의 성공적인 수행을 위해 현재까지 진행된 연구결과는 다음과 같다. 탄저병 저항성 연관 신규 분자표지 개발의 경우, 탄저병 및 CMV복합 CMS모계(B)와 부계(C) 계통, GMS 모계는 각각 BC<sub>1</sub>F<sub>3</sub>와 F<sub>4</sub>, F<sub>5</sub>, BC<sub>1</sub>F<sub>6</sub> 까지 세대 진전하였다. 탄저병과 바이러스에 단독 혹은 복합 내병성을 지닌 CMS와 GMS 모계, 탄저병저항성 C계통 간에 156개 교배조합을 작성하였고, 시교 사업은 경북, 경남, 충북, 충남, 전남, 전북, 강원, 인천, 제주지역을 포함하는 138개 지역에 수행하고 있다. CMV-P1 저항성 연관 분자표지 개발의 경우, 국내에서 분리된 18개 CMV 분리의 저항성 정도를 평가하여 4가지 유형으로 분류하였고, 이들을 이용해 고추유전자원의 CMV 저항성을 조사한 다음 CMV 병원형 판별 품종 후보를 선발하였다. 한편, 고추 포장에서 CMV에 강 저항을 보인 개체의 후대를 대상으로 CMV-P1대한 저항성 유전 분석을 수행하였고, 분자표지 검정을 통해 저항성과 연관된 후보 마커를 선발하였다. 금년 하반기에는 새로운 탄저병 저항성 마커 개발을 위한 저항성 유전분석 및 분리집단을 선발할 예정이며, 차년도에는 탄저병 및 CMV복합 계통의 세대진전과 신규교배 조합을 작성할 예정이다. 또한 새로운 탄저병 저항성 분자표지 개발 및 CMV-P1 저항성 연관 후보 분자표지를 이용해 CMV 병원형 판별 계통을 최종적으로 선발하고자 한다.

## 유전체기반 분자유종시스템 구축

유익수, 최범순, 이승욱, 김경희, 진행운, 이현오, 신지언, 박미소, 강경대

파이젠 유전체연구소, (주)파이젠

차세대 DNA 염기서열 분석장비 (NGS)의 발달은 유전체 대상의 DNA 정보 생산에 필요한 가격과 시간을 획기적으로 단축시켰고, 그 결과로 많은 식물들의 신규 유전체 정보가 생산 되고 있다. 또한 transcriptome, non-coding RNAs, methylome 등의 NGS기반의 데이터들은 유전체 sequence내에 유전자의 위치탐색과 유전자간 또는 유전자와 regulatory element 간의 관계를 규명하여 유전체에 대한 통합적 이해를 돕고 있다. 벼, 콩, 옥수수, 토마토, 고추, 배추 등 주요 농업작물 표준유전체 정보의 완성은 유전체 정보를 분자유종 이용할 수 있는 기반을 제공하였으며, NGS기술 (resequencing 또는 Genotype-by-Sequencing)을 통한 다양한 유전자원대상의 유전변이 정보의 생산은 유전체 정보를 육종에 적극 활용하여 중요 농업 형질과 연관된 유전적 변이를 발견하고 이를 작물개량에 활용할 수 있는 환경을 제공하고 있다.

유전체기반 분자유종시스템은 분자유종의 현장에서 효율적이고, 실용적으로 사용될 수 있는 시스템을 개발하기 위해 3가지의 목표를 가지고 수행한다. 1) 각기 산재되어있는 다양한 유전체정보 (유전체, 전사체, SNP정보, 분자마커 정보, 표현형 정보 등)를 수집하여 통합 유전체 데이터베이스화 하여 시스템 내에서 유전체, 전사체 정보를 정보를 비교, 분석이 가능한 형태로 운영하며 상호 연결된 정보를 제공하도록 구축한다. 2) 또한 최근 들어 농업에 적극 활용되는 NGS기반의 SNP genotyping에 필요한 효율적 파이프라인을 제공하여, GBS 또는 resequencing 기반의 데이터를 효율적으로 분석하고 그 결과를 토대로 genetic map구축, QTL동정, association mapping, 분자마커 개발 등에 효율성을 주는 시스템을 개발하고 3) 유전체정보와 변이정보를 연동하여 visualization 할 수 있는 브라우저와 분자마커 개발에 필요한 도구의 개발이다.

통합유전체 데이터베이스, 효율적 genotyping 시스템, 통합브라우저 등의 구축은 데이터의 생산과 분석에 표준화된 지표, 용이성을 제공하여 고도화된 유전체 정보를 분자마커 개발, QTL 탐지, 후보 유전자 동정 등 분자유종에 효율적으로 활용할 수 있게 하며, 이를 통해서 분자유종의 선진화와 종자산업의 활성화에 기여하고자 한다.

---

## The *Arabidopsis* MYB96 Transcription Factor Is a Positive Regulator of *ABI4* in the Control of Seed Germination

Kyounghee Lee<sup>1\*</sup>, Hong Gil Lee<sup>1\*</sup>, Seongmun Yoon<sup>2</sup>, Hyun Uk Kim<sup>2</sup>, Pil Joon Seo<sup>1,3</sup>

<sup>1</sup>Department of Bioactive Material Sciences and Research Center of Bioactive Materials, Chonbuk National University, Jeonju 561-756, Korea

<sup>2</sup>Department of Agricultural Biotechnology, National Academy of Agricultural Science, Rural Development Administration, Suwon 441-707, Korea

<sup>3</sup>Department of Chemistry and Research Institute of Physics and Chemistry, Chonbuk National University, Jeonju 561-756, Korea

Seed germination is a key developmental transition that initiates the plant life cycle. The timing of germination is determined by coordinated action of two phytohormones, gibberellin (GA) and abscisic acid (ABA). In particular, ABA plays a key role in integrating environmental information and inhibiting the germination process. Utilization of embryonic lipid reserves contributes to seed germination by acting as an energy source, and ABA suppresses lipid degradation to modulate the germination process. Here, we report that the ABA-responsive R2R3-type MYB transcription factor MYB96, which is highly expressed in embryo, regulates seed germination by controlling the expression of *ABA-INSENSITIVE 4* (*ABI4*). In the presence of ABA, germination was accelerated in *MYB96*-deficient *myb96-1* seeds, whereas the process was significantly delayed in *MYB96*-overexpressing activation-tagging *myb96-ox* seeds. Consistently, *myb96-1* seeds degraded a larger extent of lipid reserves even in the presence of ABA, while reduced lipid mobilization was observed in *myb96-ox* seeds. MYB96 directly regulates *ABI4*, which acts as a repressor of lipid breakdown, to define its spatial and temporal expression. Genetic analysis further demonstrated that *ABI4* is epistatic to *MYB96* in the control of seed germination. Taken together, the MYB96-ABI4 module regulates lipid mobilization specifically in the embryo to ensure proper seed germination under suboptimal conditions.

\*Corresponding Author: Tel. 010-8948-0992, E-mail: kyounghee@jbnu.ac.kr

---

PD-42

## 페튜니아 원형질체 배양을 통한 CRISPR/Cas9 기반 타겟형질 교정

이종숙<sup>1</sup>, 최서희<sup>1</sup>, 박누리<sup>1</sup>, 하혜정<sup>1</sup>, 배상수<sup>2</sup>, 이궁주<sup>1\*</sup>

<sup>1</sup>충남대학교

<sup>2</sup>한양대학교

유전자 가위(Engineered nuclease)는 최근 유전자의 특정염기서열을 인식하여 목적 유전자 부위만을 정확히 편집하여 형질 교정을 유도하는 획기적인 기술이다. 본 연구에서는 세포벽으로 인해 형질교정율이 동물 시스템에 비하여 상대적으로 낮은 식물세포에 적용시켜 효율을 높이기 위한 조건을 확립하고자 함을 연구목적으로 하였다. 타겟 유전자인 질소환원효소(Nitrate reductase)에 맞춤형 제작된 3세대 유전자가위 RGEN (RNA-guided Engineered nuclease)을 이용하여 페튜니아의 원형질체 수준에서 고효율의 형질교정을 유도시키는 조건을 조사하였다. 종자로부터 기내에서 자란 페튜니아의 어린 잎을 사용하여 cellulose, viscozyme, pectinEX이 포함된 혼합 효소액을 처리한 후 원형질체의 분리를 유도하였다. 예비 실험으로 PEG와 형질전환에 사용된 플라스미드 DNA인 pBI1221-GFP의 농도를 조절하여 원형질체에 도입한 결과, PEG의 농도가 40%이고 Plasmid DNA의 농도를 50ug을 이용하였을 때, 30% 이상의 가장 높은 유전자 도입 효율을 보이는 것을 확인하였다. 동일한 조건으로 페튜니아 NR 유전자에 맞춤형 제작된 CRISPR/Cas9을 원형질체에 도입하여 세포배양을 실시한 후 배양세포로부터 DNA를 추출하여 mid-seq을 통한 변이체 발생 비율을 확인한 결과 최대 12%까지 타겟 유전자의 교정이 유도됨을 확인할 수 있었다. 본 연구에서 확립한 조건을 바탕으로 다른 가지과 작물의 다양한 선별 유전자에 적용시켜 목적 형질의 교정을 유도할 수 있는 새로운 작물 육종기술로 본 유전체 편집기술이 이용되도록 그 기반을 확립할 것이다.

본 연구는 농촌진흥청 차세대바이오그린 21사업의 식물분자유종사업단 지원으로 수행되었습니다.

\*주저자: Tel. 042-821-7826, E-mail: gjlee@cnu.ac.kr

---

PD-43

## InsP<sub>6</sub>-Sensitive Variants of the Gle1 mRNA Export Factor Rescue Growth and Fertility Defects of the *ipk1* Low-Phytic-Acid Mutation

Ho-Seok Lee, Du-Hwa Lee, Hyun-Sook Pai\*

Department of Systems Biology, Yonsei University, Seoul 120-749, Korea

*Myo*-inositol-1,2,3,4,5,6-hexakisphosphate (InsP<sub>6</sub>), also known as phytic acid, accumulates in large quantities in plant seeds, serving as a phosphorus reservoir, but is an animal antinutrient and an important source of water pollution. Here we report that Gle1 (GLFG lethal 1) in conjunction with InsP<sub>6</sub> functions as an activator of the ATPase/RNA helicase LOS4 (Low expression of osmotically responsive genes 4), which is involved in mRNA export in plants, supporting the Gle1-InsP<sub>6</sub>-Dbp5 (LOS4 homolog) paradigm proposed in yeast. Interestingly, plant Gle1 proteins have modifications in several key residues of the InsP<sub>6</sub>-binding pocket, which reduce the basicity of the surface charge. *Arabidopsis* Gle1 variants containing mutations that increase the basic charge of the InsP<sub>6</sub>-binding surface show increased sensitivity to InsP<sub>6</sub> concentrations for the stimulation of LOS4 ATPase activity *in vitro*. Expression of the Gle1 variants with enhanced InsP<sub>6</sub> sensitivity rescues the mRNA export defect of the *ipk1* (*inositol 1,3,4,5,6-pentakisphosphate 2-kinase*) InsP<sub>6</sub>-deficient mutant, and furthermore, significantly improves vegetative growth, seed yield, and seed performance of the mutant. These results suggest that Gle1 is an important factor responsible for mediating InsP<sub>6</sub> functions in plant growth and reproduction, and that Gle1 variants with increased InsP<sub>6</sub> sensitivity may be useful for engineering high-yielding low-phytate crops.

---

PD-44

## Development of EMS mutant populations in *Capsicum annuum* and identification of non-pungent mutants

Muhammad Irfan Siddique, Koeun Han, Doyeon Hwang, Hee-Jin Jeong, Arti Rai, Byoung-Cheorl Kang\*

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

Plant breeding requires genetic diversity of useful traits for crop improvement. EMS-induced mutation is practiced to generate mutations at loci regulating economically important traits and/or to knock out the genes to elucidate their functions. The present study was aimed to induce mutations in a Korean local land race *Capsicum annuum* ‘Yuwol-cho’. This accession is pungent and also has advantage to mature early. A total of about 1,500 M<sub>2</sub> families were screened and three non-pungent mutants were identified and crossed with wild type ‘Yuwol-cho’. After phenotyping of F<sub>2</sub> population for pungency, MutMap approach will be used to identify the genes controlling the pungency in mutants. In addition to this, another *C. annuum* accession “Micro-Pep” was used to develop a mutant population. Micro-Pep is a small, pungent pepper generally used as ornamental purpose. Having compact growth habit, and small size, it has advantage to handle and utilize easily in mutation study and molecular research. On the basis of preliminary experiment 1.3% of mutagen was used for treatment of pepper seeds and 30% less germination percentage was observed in EMS treated seeds in comparison to control seeds. A total of 4,674 M<sub>1</sub> plants are grown under greenhouse condition and M<sub>2</sub> population will be studied for characterization of phenotypic variation including fruit color and pungency. Newly constructed mutant populations will be valuable assets for identification of functional genes and molecular breeding of pepper.

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

PD-45

## Development of a New Wheat Mutant of Low-Molecular-Weight Glutenin Subunit at *Glu-B3* Locus

Jong-Yeol Lee<sup>1\*</sup>, Hye-Rang Beom<sup>1</sup>, Sun-Hyung Lim<sup>1</sup>, Young-Mi Kim<sup>1</sup>, Chul-Soo Park<sup>2</sup>

<sup>1</sup>National Academy of Agricultural Science, RDA, Jeonju, 560-500, Korea

<sup>2</sup>Department of Crop Agriculture and Life Science, Chonbuk National University, Jeonju 561-756, Korea

A wheat mutant of low-molecular-weight glutenin (LMW-GS) “Gunji-2” at *Glu-B3* locus was derived among the double haploid lines. Gunji-2 was derived from F<sub>1</sub> plants of Keumkang and Olgeuru crosses using the wheat × maize system according to the procedures of Inagaki and Mujeeb-Kazi at International Maize and Wheat Improvement Center (CIMMYT). Deletion of *Glu-B3* LMW-GS proteins was found by allele specific DNA marker, one dimensional SDS-PAGE and two dimensional gel electrophoresis (2-DGE). Tandem mass spectrometry (MS/MS) was used to obtain direct evidence of LMW-GS deletion. In addition, we examined the basic agronomic traits, protein content, dough properties of mixing and bread loaf volume of Gunji-2 and parental wheat cultivars grown for two years. This mutant will represent a valuable resource in quality test for specific allele or gene at *Glu-B3* locus.

\*Corresponding Author: E-mail: jy0820@korea.kr

## Integrated analysis of the transcriptomes and primary metabolite profiles of adventitious roots of *P. ginseng* cultivars

Yun Sun Lee<sup>1†</sup>, Hyun-Seung Park<sup>1†</sup>, Dong-Kyu Lee<sup>3†</sup>, Murukarthick Jayakodi<sup>1</sup>, Nam-Hoon Kim<sup>1</sup>, Sang-Choon Lee<sup>1</sup>, Jinkyung Kim<sup>1</sup>, Hana Lee<sup>1</sup>, Dong-Yup Lee<sup>4,5</sup>, Sung Won Kwon<sup>3\*</sup>, Tae-Jin Yang<sup>1,2\*</sup>

<sup>1</sup>Department of Plant Science, Plant Genomics and Breeding Institute, Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, 151–921, Republic of Korea

<sup>2</sup>Crop Biotechnology Institute/GreenBio Science and Technology, Seoul National University, Pyeongchang 232–916, Korea

<sup>3</sup>College of Pharmacy and Research Institute of Pharmaceutical Sciences, Seoul National University, Seoul 151–742, Republic of Korea

<sup>4</sup>Bioprocessing Technology Institute, A\*STAR (Agency for Science, Technology and Research), 20 Biopolis Way, #06–01 Centros, Singapore 138668

<sup>5</sup>Department of Chemical and Biomolecular Engineering, Synthetic Biology Research Consortium, National University of Singapore, 4 Engineering Drive 4, Singapore 117585

<sup>†</sup>YSL, H–SP & D–KL have contributed equally in this work

*Panax ginseng* C.A. Meyer (family: *Araliaceae*) is a perennial crop that has been widely used as a traditional medicine in Korea. Various *P. ginseng* cultivars exhibit a range of morphological and physiological traits as well as genetic diversity. To elucidate the differences of primary metabolism underlying such genetic diversity, we performed primary metabolite profiles in adventitious roots from five *Panax ginseng* cultivars using gas chromatography-mass spectrometry (GC-MS). The GC-MS analysis revealed eight primary metabolites as biomarkers and allowed us to classify the five cultivars into three groups. We selected three cultivars to represent each group and analyzed their transcriptomes by Illumina sequencing. We inspected 100 unigenes involved in seven primary metabolite biosynthesis pathways and found that 21 unigenes encoding 15 enzymes were differentially expressed among the three cultivars. Integrated analysis of transcriptomes and metabolomes revealed that the *ginseng* cultivars differ in primary metabolites as well as in the putative genes involved in the complex process of primary metabolic pathways. Our data derived from this integrated analysis provide insights into the underlying complexity of genes and metabolites that co-regulate flux through these pathways in *ginseng*.

\*Corresponding Author: Sung Won Kwon, E-mail: swkwon@snu.ac.kr, Tae-Jin Yang, E-mail: tjyang@snu.ac.kr

## 고추 유용 형질 연관 분자표지의 Fluidigm용 SNP 분자표지로의 전환

김해인, 이예린, 정규미, 은민호, 이준대\*

전라북도 전주시 전북대학교 원예학과

고추에서는 역병, 탄저병, 바이러스병 등이 큰 피해를 주고 있기 때문에 내병성 및 고품질계 고추 품종 육성의 중요성이 지속적으로 증가하는 상황이다. 때문에 현재 개개의 분자표지를 한번에 1개씩 분석하는 시스템에서 다수의 분자표지로 고추의 유전자형을 빠르고 정확하게 분석할 수 있는 시스템 개발이 절실히 필요하다. 본 연구에서는 Fluidigm 192.24chip을 이용하여 192개의 고추 개체에 대해 24개의 SNP 분자표지를 한 번에 분석하고자 하였다. 이 방법은 한 번의 실험을 통해 4,608개의 data points를 얻을 수 있다. 이를 위해 본 연구에서는 기 개발된 STS 또는 HRM 분자표지를 대량분석이 가능한 Fluidigm용 SNP 분자표지로 전환하고자 하였으며, 총 191개의 고추 샘플과 24개의 내병성 및 응성불임 분자표지를 이용하여 실험하였다. 실험에 이용된 분자표지는 세균반점병 저항성, 탄저병 저항성, CMV 저항성, 응성불임성, TMV 저항성, 역병 저항성, CMS 회복유전자, Potyvirus 저항성, TSWV 저항성 분자표지로서 총 24개를 Fluidigm용 SNP 분자표지로 디자인하였다. 식물재료로는 JN F<sub>5</sub> 분리집단 96점과 고추 유전자원 91점, GMS<sub>k</sub> F<sub>2</sub> 분리집단 4점 등 총 191점의 식물샘플을 이용하였고, 나머지 하나는 음성대조군으로 사용하였다. 192.24chip을 분석한 결과 24개의 분자표지 중 19개의 분자표지가 다형성이 구분되는 것으로 판단되었다. 각각의 분자표지에 대한 정확성을 판단하기 위해 기존의 STS 또는 HRM 분자표지의 분석 결과와 비교하였다. 본 연구를 통해 고추의 유용 형질과 연관된 foreground selection용 multiplexing 분자표지를 개발함으로써 신속하고 저렴하게 분자표지를 동시에 분석할 수 있는 기술을 확보할 수 있을 것으로 기대된다.

\*주저자: Tel. 063-270-2560, E-mail: ajfall@jbnu.ac.kr

## 야생벼 유전자원의 수량안정성 유전자 탐색 이용

이현숙<sup>1</sup>, 강주원<sup>1</sup>, 상세티<sup>1</sup>, 전윤아<sup>1</sup>, 레이잉핀<sup>1</sup>, 노심<sup>1</sup>, 코코명<sup>1</sup>, 강윤주<sup>1</sup>, 윤여태<sup>2</sup>, 안상낙<sup>1\*</sup>

<sup>1</sup>대전시 유성구 공동 충남대학교 농업생명과학대학

<sup>2</sup>충청남도 농업기술원

야생벼나 잡초벼와 같은 유전자원은 각 지역의 환경조건에 오랜 기간 동안 적응하며 집단을 유지하였기 때문에 여러 가지 저항성이나 불량한 환경에 대한 내성 등 유용한 특성을 갖고 있다. 본 연구는 이러한 야생 유전자원에서 고수량성 및 미량원소의 함량 조절 등에 관여하는 유용 유전자를 선별적으로 재배벼에 이전시키는 육종방법을 개발하고 우량 품종 육성을 목표로 한다. 이들 목적을 위하여 재배벼의 유전적 배경에 야생 유전자원의 염색체 단편이 이입된 근동질 계통을 육성, 이용하여 양적형질유전자의 고밀도 지도를 작성하고 관여 유전자 특성을 분석 중에 있다. 야생벼와 재배벼 (화성벼/*O. rufipogon*) 교잡 유래 이입계통을 이용하여 출수기 조절 유전자, *gw9*를 탐지하였고 이들 유전자좌에서 유력한 후보 유전자 3 종, male sterility 5 (MS5), ascorbate peroxidase(AP), glutelin 유전자를 선별하였다. 이들 유전자의 염기서열을 분석한 결과 화성벼와 *O. rufipogon* 사이에 염기서열 차이를 확인하였다.

야생벼인 *Oryza grandiglumis* 에서 유래된 종자중 관여 유전자 *qGW2* 의 근동질계통을 이용하여 벼의 아연함량 조절 유전자, *OsPCRI* (plant cadmium resistance 1)과 *qGW2* 유전자가 서로 상호관계가 있음을 보였다. *qGW2* 근동질계통의 종자 발달시 *OsPCRI* 유전자의 발현이 대조구에서 보다 증가하였고, *OsPCRI* 형질전환체에서 종자중과 아연함량의 변화를 관찰하였다. 또한 이들 *OsPCRI-1* 의 염기서열을 다양한 벼 품종들간에 비교한 결과, 자포니카형 품종들과 인디카형 또는 야생벼 (*O. rufipogon*, *O. glaberrima*, *O. grandiglumis*) 간에 염기서열 변이가 존재하여 아미노산 서열의 차이를 확인하였다. 직파재배에서 중요한 중배축 신장성에 관한 유전자 고밀도지도 작성을 위하여, 선행연구에서 탐색된 QTL (*qMel-1*, *qMel-3*) 을 잡초벼/일품벼 조합계통에서 분석한 결과, *qMel-1* 과 *qMel-3* 은 각각 염색체 1번의 RM8260과 염색체 3번 RM426 에서 탐지되었고, 중배축 신장성 관여 유전자의 분리를 위하여 Nipponbare/Kasalath 교배조합의 근동질계통을 이용하여 초고밀도 지도를 작성하였다.

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

## Development of molecular markers tightly linked to bacterial wilt resistance genes in pepper (*Capsicum annuum* L.)

Daewoong Lee<sup>1</sup>, Yul-Kyun Ahn<sup>2</sup>, Younghoon Park<sup>3</sup>, Tae-Hwan Jun<sup>1\*</sup>

<sup>1</sup>Department of Plant Bioscience, Pusan National University, Miryang, Republic of Korea

<sup>2</sup>Vegetable Research Division, National Institute of Horticultural & Herbal Science, Rural Development Administration, Wanju-gun, Republic of Korea

<sup>3</sup>Department of Horticultural Bioscience, Pusan National University, Miryang, Republic of Korea

Bacterial wilt (BW) caused by *Ralstonia solanacearum* is one of the most common soil-borne vascular diseases of many solanaceous crops such as pepper and tomato. This study aimed to develop molecular markers closely linked to bacterial wilt resistance genes using a 150 F<sub>8</sub> recombinant inbred line (RIL) population obtained from a cross of ‘YCM334’ x ‘Taeae’. For pathogen inoculations, *R. solanacearum* isolate WR-1 was cultured on NB medium at 28°C for 48 h and a bacterial suspension was adjusted to 1 x 10<sup>7</sup> to 1 X 10<sup>8</sup> CFU/mL (A 600 = 0.3 to 0.4). Each RIL and the parents were sown in a 72-cell plastic tray filled with sterilized soil, and the seedlings were inoculated at the 6 to 8 leaf stage using soil-drenching (3 to 5 ml/ plant) inoculation methods with 3 replications. After 10 days post inoculation (dpi), each line was evaluated visually for occurrence of bacterial wilt ranging from 1 (most resistant) to 5 (most susceptible). Two candidate R-response genes, AT4G14130 and AT3G23730, were selected to find SNPs between YCM334 and Taeae. In previous transcriptome analysis, these two genes were reported as significantly differentially expressed in *Capsicum annuum* L. root inoculated with *R. solanacearum*, which were up-regulated in a resistant genotype. Once the synteny of the gene locations between Arabidopsis and pepper was documented, the sequences on pepper chromosome 12 were obtained from pepper. v.1.55 (<http://solgenomics.net>). SNP markers associated with resistance to BW will be mapped using pepper RIL population.

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

## 화피를 제거한 통통마디 종자의 발아특성과 염농도에 따른 초기생육 특성

전효진<sup>1</sup>, 권혁규<sup>1</sup>, 백정선<sup>1</sup>, 신소희<sup>1</sup>, 정재혁<sup>2</sup>, 이승재<sup>3</sup>, 정남진<sup>1\*</sup>

<sup>1</sup>전라북도 전주시 덕진구 덕진동 전북대학교 농업생명과학대학 농학과

<sup>2</sup>전라북도 전주시 완산구 이서면 혁신로 181 농촌진흥청 국립식량과학원 작물재배생리과

<sup>3</sup>전라북도 전주시 덕진구 덕진동 전북대학교 농업생명과학대학 화학과

간척지에서 재배될 수 있는 염생식물은 국토의 효율적 이용과 식량의 안정적인 확보 측면에서 매우 중요한 유전자원이다. 본 연구에서는 염생식물인 통통마디의 작물로서의 이용을 위하여 종자의 발아특성과 염농도에 따른 생육특성을 규명하고자 하였다. 통통마디 종자는 화피로 둘러싸여 있는 난형으로 연한 갈색을 띠었으며, 수분흡수 후 종피가 파열되면서 유근이 출현하여 발아가 시작되었다. 통통마디 종자의 발아에서 화피의 영향을 알아보기 위하여 최적 발아온도로 알려진 25°C와 30°C에서 raw seed와 화피제거 종자의 발아율을 조사하였다. Raw seed는 25°C에서 5%, 30°C에서 7%의 발아율을 보인 반면, 화피 제거 종자는 25°C에서 53%, 30°C에서 58%의 발아율을 보여 화피 제거에 의하여 종자의 발아율이 급격히 상승하였다. 따라서 종자의 발아율을 높이기 위하여 500 $\mu$ m sieve를 이용하여 화피를 제거할 수 있는 기계적 방법을 개발하였으며 이 방법에 의하여 화피가 제거된 종자를 90% 이상 확보할 수 있었다. 화피 제거 종자의 염농도에 따른 종자의 발아율을 조사한 결과, 0mM에서 53%, 50mM에서 49%, 100mM에서 35% 그리고 200mM에서는 26%로 염농도가 낮을수록 발아율이 높은 것으로 나타났다. 한편, 유묘의 염농도에 따른 생장량 조사를 위하여, 2주된 유묘를 상토에 이식하고 0~200mM의 염처리를 하여 5주간 초장과 분지수를 조사한 결과, 통통마디의 생장량은 100mM에서 가장 많았다. 따라서 통통마디의 유묘확보율을 높이기 위해서는 종자의 화피를 제거하여 염농도 0mM인 25~30°C에서 발아를 시키고, 유묘생장단계에서는 100mM 전후의 염농도가 최적조건으로 판단되었다.

\*주저자: Tel. 063-270-2512, E-mail: njchung@jbnu.ac.kr

## **Drought stress-responsive transcript analysis of wheat-rye translocation line using cDNA-AFLP**

Woo Joo Jung, Yong Weon Seo\*

Dept. of Biosystems & Biotechnology, Korea University, Seoul 136–713, KOREA

Wheat-rye translocation lines are widely used in wheat breeding programmes by reason of biotic stress tolerances. Though there have been a number of researches regarding abiotic stress tolerance, the tolerance of the lines depends on wheat genetic background, not on rye chromosome. Here, we investigated wheat-rye translocation specific transcripts derived from cDNA-AFLP under drought stress, which may help to elucidate the reaction under the stress. ‘OK91G117’ (1BL.1RS translocation) and ‘OK91G144’ (non-translocation) were used as materials, which are near-isolines for 1RS. 25% PEG 6000 was added in culture solution to simulate drought condition and root tissues were sampled at each 0 h, 3 h, 6 h, 12 h, 24 h, and 48 h after PEG treatment for RNA extraction. As a result of cDNA-AFLP, TDFs (transcript derived fragments) that were specific to OK91G117 were sequenced. GO functions of each sequenced TDF were annotated by Blast2GO using standard parameter with cut-off level 3 and mapped to the GO term (i.e. biological process; BP, molecular function; MF, cellular component; CC). The term with “organic substance metabolic process”, “primary metabolic process”, and “cellular metabolic process” account for almost 50 % of BP. The most represented terms among probes classified to MF were “transferase activity” and most of TDF were annotated in “cell part” of CC. In addition, rye-chromatin specific markers were developed by BLAST comparing sequence of TDF with wheat and rye genome data. RT-PCR was conducted to validate expression patterns of selected TDF. Further studies will be needed to elucidate functions of the highly expressed genes under drought stress.

**Acknowledgements:** This work was carried out with the support of “Next-Generation BioGreen21 Program for Agriculture & Technology Development (Project No. PJ01103501)” Rural Development Administration, Republic of Korea.

**\*Corresponding Author:** Tel. 02-3290-3464, E-mail: seoag@korea.ac.kr

## Targeted mutagenesis of *SSS4A* gene related starch biosynthesis using gene editing technology in Dongjin rice

Yu Jin Jung<sup>1,2</sup>, Maral Tsevelkhoroloo<sup>1</sup>, Hyun Ju Lee<sup>1</sup>, Yeo Jin Jung<sup>1</sup>, Hyo Ju Lee<sup>1</sup>, Yong Gu Cho<sup>3</sup>, Kwon Kyoo Kang<sup>1,2\*</sup>

<sup>1</sup>Department of Horticulture, Hankyong National University, Ansong, 456–749, Korea

<sup>2</sup>Institute of Genetic Engineering, Hankyong National University, Ansong 456–749, Korea

<sup>3</sup>Department of Crop Science, Chungbuk National University, Cheongju, Korea

Zinc finger nucleases (ZFNs) have been used for targeted mutagenesis in eukaryotic cells. Custom-designed ZFNs can induce double-strand breaks (DSBs) at a specific locus. Our custom ZFN dimer was designed 3-finger of left and 4-finger of right with 2 kb size using 2A. A Ti-plasmid vector, pTA7002 containing the target site of *SSS4A* gene for a ZFN pair, that was shown to be active in yeast, was integrated in the rice genome. This promising technique for genome engineering was induced into 4 exon region of *SSS4A* gene in rice genome using *Agrobacterium*-mediated transformation. The *SSS4A* full-length cDNA was 5,070 bp consisting of a 318 bp 5'-untranslated region (UTR), a complete ORF of 2,928 bp encoding a polypeptide of 975 amino acids and a 3'-UTR of 1,824 bp. The vector is based on glucocorticoid receptor inducible gene expression system. Thus, *SSS4A::ZFN* expression was tightly controlled and the phenotype in low concentrations 10uM of the glucocorticoid hormone dexamethasone (DEX). In plant cells, transient ZFN expression is achieved by direct gene transfer into the target cells. For an alternative, ZFN delivery and production of mutant plants using a tobacco transient expression system for indirect transient delivery of ZFNs into a variety of tissues and cells of plants. ZFN activity was determined by PCR and sequence analysis of the target site. ZFN induced plants were obtained in up to 2% of the PCR products, consisting of deletions ranging between 1 and 100 bp and insertions ranging between 1 and 10 bp. Our results describe an alternative to direct gene transfer for ZFN delivery and for the production of mutated rice.

---

PD-53

## Toward mapping of genes conferring broad spectrum resistance to rice brown planthopper

Hyeonso Ji<sup>1\*</sup>, Eokkeun Ahn<sup>2</sup>, Seung-Bum Lee<sup>1</sup>, Seok-Chul Suh<sup>1</sup>

<sup>1</sup>Department of Agricultural Biotechnology, National Academy of Agricultural Science, Jeonju 560–500, Republic of Korea

<sup>2</sup>Department of Central Area, National Institute of Crop Science, Suwon 441–707, Republic of Korea

Brown planthopper (BPH) is a phloem sap-sucking insect pest of rice, which causes severe yield loss annually. Gayabyeo, a Tongil type rice variety, is known to have broad spectrum resistance to BPH. Before, it was estimated that Gayabyeo has at least two BPH resistance genes. We started a research for mapping resistance genes of Gayabyeo. We did a cross between Taebaekbyeo, a BPH susceptible Tongil type rice variety, and Gayabyeo. We grew F1 plants in winter season of 2014-2015, and planted F2 population in this year. About 100 DNA markers (SSR and InDel markers) showing polymorphism between Gayabyeo and Taebaekbyeo were selected. In addition, we are going to do resequencing Gayabyeo and Taebaekbyeo using Illumina Hiseq2000 to find much more DNA polymorphisms between the two varieties and develop new markers for mapping. The BPH response data will be acquired using F3 plants from the cross between Gayabyeo and Taebaekbyeo next year. In a while, crosses between Gayabyeo and high quality japonica rice varieties are being carried out to introduce BPH resistance genes of Gayabyeo into japonica high quality rice varieties. We expect to develop new DNA markers for BPH resistance genes of Gayabyeo through mapping and produce several japonica high quality rice lines harboring those genes at the end of this project.

\*Corresponding Author: Tel. 031-299-1697, E-mail: jhs77@korea.kr

PD-54

## Identification of quantitative trait loci for fusarium wilt resistance in radish (*Raphanus sativus*)

Juyeon Jung, Jaehwang Ryu, Yeonok Choi, Young-Pyo Lee\*

Dongbu Farm Hannong Co., Ltd, Anseong-si, Gyeonggi-do, 456–933, Republic of Korea

Radish, *Raphanus sativus* (2n = 18), belonging to the brassicaceae family, is herbaceous plant with 1-2 years life cycle. It is cultivated worldwide for producing leafy and root vegetables. Although an economically important crop, the genetics of yield and quality traits, disease resistance are not well-studies. The major purpose of this project is development of molecular breeding technology in radish. In this project, quantitative trait loci (QTL) for Fusarium wilt resistance of radish were analyzed. To identify QTL, genetic linkage map of radish was constructed using F2 mapping population derived from a cross between two inbred lines, “DB01” (resistant) and “DB05” (susceptible). A total 319 markers have been mapped into nine linkage groups, covering 639.3cM with an average distance of 2cM between loci. QTL mapping detected 2 loci conferring Fusarium wilt resistance. Two QTLs were located on LG3 and LG7, respectively. The QTL of LG3, flanked by EAGGMCT6 and WALK500 marker, exhibited a LOD value ranging from 2.3 to 8.7, and the R<sup>2</sup> (Phenotypic variations) ranging from 28 to 48% in four tests. This QTL was named *qYR1*. The QTL of LG7, flanked by EACCMCAC-202 and DCJ14-390 marker, exhibited a LOD value ranging from 6.2 to 10.6, and the R<sup>2</sup> ranging from 42 to 55% in four tests. This QTL was named *qYR2*. The results of the QTL analysis may be useful in marker-assisted selection (MAS) of Fusarium wilt resistant radish cultivars.

\*Corresponding Author: Tel. 031-674-6911, E-mail: youngpyo@dongbu.com

## Overexpression of the 3' half of the *PHYB* phytochrome partially suppresses dwarfism in the brassinosteroid-insensitive *bri1-5* mutant

Yu Jeong Jeong<sup>1+</sup>, Soon Il Kwon<sup>2+</sup>, Slki Park<sup>1</sup>, Su Jeoung Suh<sup>1</sup>, Richard Cha<sup>2</sup>, Yoong Eun Kim<sup>2</sup>, Sunghwa Choe<sup>1,2,3\*</sup>

<sup>1</sup>School of Biological Sciences, College of Natural Sciences, Seoul National University, Seoul 151-747, Korea

<sup>2</sup>Convergence Research Center for Functional Plant Products, Advanced Institutes of Convergence Technology, 864-1 Iui-dong, Yeongtong-gu, Suwon-si, Gyeonggi-do 443-270, Korea

<sup>3</sup>Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea

<sup>+</sup>Equal contribution

Brassinosteroids (BRs) control virtually every aspect of plant growth and development. BRs act alone or with other exogenous and endogenous signals including auxin and light. To screen for the novel player involved in BR signaling in Arabidopsis, we employed cDNA overexpression strategy. We created a cDNA library to be expressed under the 35S overexpression promoter, and introduced into a weak *brassinosteroid insensitive 1 (bri1)* mutant. The mutant dubbed *bri1-5* with long petiole (*blp*) was identified to display bigger stature especially in hypocotyl and petiole length relative to *bri1-5*. Sequence analysis of the rescued transgene revealed that *blp* consisted of a chimeric DNA consisting of a 3' half of *PHYB*, 2 bp insertion, and a part of a chloroplast ribosomal RNA. Re-introduction of chimeric DNA into *bri1-5* recapitulated *blp* phenotype. The *blp* phenotypes being similar to *phyB* mutants led us to examine both the *PHYB* transcript and protein levels in the *blp 35Spro:PHYB* doubly homozygous line. Lower levels of both transcripts and proteins of *PHYB* suggested that introduction of the chimeric gene interfered with the stability of *PHYB* transcripts. Our results highlight that overexpression mutagenesis facilitates functional genomics to decipher a function of Arabidopsis genome.

Keywords: *Brassinosteroid*, Overexpression mutagenesis, *blp*, *phyB*, Gateway-cDNA library

## Quantitative trait locus mapping and candidate gene analysis for heading date in an early maturing rice mutant induced by gamma irradiation

Sun-Goo Hwang, Cheol-Seong Jang\*

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

In recent years, the efficiency and accuracy of QTL analysis for identification of useful traits have been increased by high-throughput genotyping. In a previous study, the genome variation of significant DNA polymorphism was observed in early maturing type rice mutant (EMT) by comparing with that of wild type (WT). For detection of major QTL for flowering time, we constructed a linkage map of 36 InDel- and 6 SNP- markers. In the linkage analysis of F<sub>2</sub> plants derived from the cross "WT x EMT", we have detected one potential QTL region on chromosome 6 by M6-3 marker. Also, the *Hdl*, which contained the target fragment of M6-3 marker, exhibited the relatively high nonsynonymous substitutions in genes located on chromosomal region from M6-2 to M6-4. To evaluate the reliable allele segregation related to expected Mendelian ratio between M6-3 and its flanking markers, M6-3 marker developed in *Hdl* gene exhibited the 1:2:1 ratio as clear monogenic segregation in heterozygous F<sub>3</sub> plant. Additionally, we further analyzed the different transcript regulations of *OsGI* and *Hd3a* gene related to *Hdl* involved in photoperiodic flowering pathway. Although the mRNA levels of *Hdl* had no difference between WT and EMT, the *Hd3a* as downstream effector of *Hdl* significantly upregulated in EMT, suggesting that *Hdl* gene may become nonfunctional.

\*Corresponding Author: Tel. 033-250-6416, E-mail: csjang@kangwon.ac.kr

## 초형개량 초다수성 콩 분자육종 Molecular breeding for high-yielding soybean with improved plant type

이석하<sup>1</sup>, 정지원<sup>2</sup>

<sup>1</sup>서울대학교

<sup>2</sup>씨제이 제일제당

본 연구과제의 목적은 1) 양질 다수성 콩 기술 이전, 2) 양질 다수성 콩 품종 출원, 3) 고밀도 유전자지도 작성을 통한 다수성관련 QTL 동정 및 다수성 형질 연관 마커 개발, 4) 콩 품종 판별 마커 개발, 5) 기능성 콩 가공식품 개발이다. 이를 위해 당해연도는 양질 다수성 콩 품종 육성을 위한 생산력 검정 및 지역적응성 검정을 실시하고 초다수성 우량 계통 육성을 위해 1단계 사업에서 선발된 우량 계통들을 지속적으로 세대진 전하고자 한다. 특히 다수성관련 형질연관 QTL 동정을 위해 길육69 x SS0404-T5-76 RIL 집단(400계통)을 육성하였고 이 집단을 이용한 고밀도 유전자지도 작성하고자 한다. 먼저 모부분 염기서열 변이 탐색 및 RIL들의 다수성 형질 표현형을 조사할 것이다. 한편, 품종보호 및 종자순도 관리에 있어서 중요한 분자 마커 개발을 위해 주요품종들에 대한 SSR 마커 분석을 실시하였다. 당해연도에는 1단계 사업에서 개발된 'CJ행복한1호' 콩 품종 육성을 위한 채종포를 제주도과 괴산 등지에 조성하며 두부 장류용 우량 계통 SS408-T5-99 에 대한 제품 생산 가능성 분석하고 장류발효과정 중 아이소플라본의 성분 변화를 분석할 것이다.

## 간척지 재배 가능한 내염성 사료용 콩 선발

이정동<sup>1\*</sup>, 김정화<sup>1</sup>, 김민수<sup>1</sup>, 박철우<sup>1</sup>, 정재은<sup>1</sup>, 아세코바소베톨<sup>1</sup>, 한두호<sup>2</sup>, 송중태<sup>1</sup>

<sup>1</sup>대구광역시 북구 대학로 80, 경북대학교 응용생명과학부

<sup>2</sup>충남 서산시 부석면 천수만로, 현대서산농장

1960년대 이후 간척한 농경지 면적은 135,100 ha나 되지만 간척지는 토성이 불량하고, 염분농도가 높아 작물생육에 매우 부적합하여 작물 수량의 안정적 확보와 다양한 작물 재배를 위해서는 토양 개량과 그에 알맞은 재배기술 및 내염성 품종 개발이 시급한 실정이다. 간척지는 염분 함량이 매우 높기 때문에 다른 작물보다 내염성이 있는 벼를 재배하여 간척지 활용을 증대시킬 수 있지만 소비 감소로 인한 쌀 재고량이 급증하여 벼 대신에 밭작물 재배나 사료 작물 재배를 통하여 안정적인 농가 소득을 확보할 수 있는 시스템이 필요하다.

본 연구는 현대서산간척지에 재배 가능한 내염성 콩을 선발하기 위하여 실시하고 있다. 내염성 콩을 선발하기 위해 야생콩 PI483463(내염성) x Hutcheson(감수성) 유래 52개의 내염성 RIL, 65개의 감수성 RIL, S-100(내염성) x PI483463(내염성) 유래 106개의 RIL, Hutcheson과 우람콩(감수성)으로 여교배하여 DNA 마커로 선발된 94개의 내염성 BC1F3계통을 난괴법 2반복으로 재식하였다. 모든 계통은 무염포와 저염포(약 0.2%)에 심었다. 재식밀도는 70 x 15cm, 1주 2본으로 하였으며, 파종은 2015년 5월 8-9일간에 실시하였다. 현재까지 콩 생육을 살펴보면 무염포나 저염포에서 콩의 발아는 정상적으로 나타났으나, 저염포에서 감수성 콩 계통의 잎이 황변하고 하위엽의 경우 염해에 의해 타들어 가는 것을 관찰할 수 있었고, 내염성 계통들은 염해의 증상이 없었으나 무염포 보다는 전체적으로 생육이 저조한 것으로 나타났다. 출아 후부터 생육 전반에 걸쳐 내염성 계통과 감수성 계통이 저염 조건에서 농업적 형질이 어떻게 반응하는지에 대한 연구를 계속할 것이며 최종적으로 간척지중 저염지대에 재배 가능한 콩을 선발할 것이다.

\*주저자: Tel. 031-296-6898, E-mail: koreabreed@hotmail.com



2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# GSP 사업단

OG. GSP 식량종자사업단

OH. GSP 원예종자사업단 & GSP 채소종자사업단





2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# GSP 식량종자사업단





## 옥수수의 해외시장 진출을 위한 육종연구에 대한 제안

이명훈

동국대학교

옥수수는 벼, 밀과 더불어 세계 3대 식량작물의 하나로서 단위면적당 생산량이 매우 높으며 가축의 사료로서 중요한 작물이다. 옥수수의 주요 생산국은 미국과 중국이며 세계 생산량의 37%와 21%를 각각 차지하고 있으며, 미국과 중국의 옥수수 재배면적은 3,200만 ha 정도로 비슷하지만 미국의 단위생산량이 월등히 높아 전체 생산량이 많다. 우리나라의 옥수수 재배면적은 26,000ha 정도이고 매년 800~900만 톤의 옥수수를 수입하고 있으며 자급률은 1% 이하이다. 세계 옥수수 종자시장 규모는 76억불 정도이고 종자량으로는 800만 톤 정도이다. 몬산토, 파이오니어, 신젠타 등의 글로벌 종자회사가 세계시장의 65% 이상을 차지하고 있으며, 우리나라 종자시장 규모는 50억 원 정도로서 매우 영세한 실정이다. 해외기술 현황으로는 미국은 글로벌 종자회사 중심으로 막대한 자본과 연구인력, 최상의 기술력으로 세계시장을 석권하고 있으며, 중국도 국가의 적극적인 지원 하에 최근 육종기술이 급속히 발전하고 있다. 태국도 육종기술이 매우 발전하여 동남아 시장을 석권하고 있으며 인도는 아직은 미흡하지만 급속한 발전 가능성을 보유하고 있다. 그 밖에 필리핀, 인도네시아, 캄보디아, 베트남 등도 옥수수 품종개발 연구를 수행하고 있다.

해외시장 진출을 위한 옥수수 육종의 가장 중요한 목표는 수량성이지만 병충해 저항성이나 불량환경 저항성도 매우 중요한 형질이다. 특히 열대지방은 온대지방보다 옥수수에 발생하는 병해충이 많으며 특히 노균병(Downy mildew), 녹병(Rust), 잎마름병(Leaf blight), 바이러스 등이 많이 발생하고 있어 이에 대한 저항성 육종이 절실히 필요하다. 불량환경 저항성 육종으로는 한발저항성 품종개발이 최근에 중요한 과제로서 대두되고 있다. 세계 여러 나라에서는 한발저항성 육종연구를 활발히 수행되고 있으며 어느 정도 성과를 거두고 있는 것으로 보고되고 있다. 또한 동남아 개발도상 국가에서는 비료가격이 높아 옥수수 재배 시에 충분한 비료를 사용하지 못하고 있는 실정이기 때문에 소비재배에 적합한 품종개발 연구도 수행하고 있다. 품질개선을 위한 육종으로는 최근 미국에서 베타카로틴이 매우 높은 황색옥수수 품종을 개발하고 있다.

동남아 시장에 권장할 수 있는 옥수수 품종은 수량성이 높은 단교잡종(Single cross)과 더불어 종자가격이 낮은 3계교잡종(3-way cross)이 초기에 농가보급에 유리할 것으로 생각되며, 경제적이 이유로 신품종을 구입할 수 없는 농가에 재래종을 대체할 수 있을 품종으로 합성품종(Synthetic variety)이 가능할 것으로 생각된다. 옥수수 육종의 성패를 좌우할 수 있는 가장 중요한 요인은 우수한 육종재료의 확보이며, 가장 중요한 육종재료는 현지에서 재배되고 있는 상업용 품종과 재래종 품종이며, 또한 모집단(Population)을 육성하고 개량하는 것이 절대적으로 필요하다. 우수한 교잡종을 육성하기 위해서는 일반조합능력과 특정조합능력을 이용한 정통적인 방법도 중요하지만 단기간에 육종 성과를 높이기 위해서는 임의교배(Random mating)에 의한 많은 조합의 교잡종을 검정하는 것이 바람직하다.

육종연구에 고려해야 할 몇 가지 사항은 외국 농업기업에 대한 현지의 법적규제와 권장 사항 등을 정확히 파악해야 되며, 해당 국가가 개발한 품종이 원활하게 보급되지 못하고 있는 원인을 정확히 분석해야 한다. 병충해 저항성이나 불량환경 저항성 품종개발 시에는 자연조건에서 선발하는 것보다 적극적이고 실질적인 환경 하에서 선발하는 것이 육종효율을 높이고 육종기간을 단축할 수 있으며, 광지역 적응성 품종개발 보다는 특정 환경에 적응하는 품종개발에 중점을 두는 것이 바람직하다. 끝으로 본 프로젝트로 우리나라와 해당 국가가 공동으로 혜택을 받을 수 있는 방법을 강구하는 것이 바람직하며, 본 프로젝트의 종료 후에도 지속적으로 옥수수 육종 연구가 수행될 수 있는 기반을 조성하는 것이 절실히 요구된다.

## **Multiple Recognition of RXLR Effectors is Associated with Nonhost Resistance of Pepper Against *Phytophthora infestans***

Doil Choi

Department of Plant Science, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Republic of Korea

Nonhost resistance is a plant immune response to resist most pathogens. The molecular basis of nonhost resistance remains poorly understood but recognition of pathogen effectors by immune receptors, a response known as effector-triggered immunity, has been proposed as a component of nonhost resistance. We performed transient expression of 54 *P. infestans* RXLR effectors in pepper accessions using optimized heterologous expression methods and analyzed the inheritance of effector-induced cell death in an F2 population derived from a cross between two pepper accessions. Pepper showed a localized cell death response upon inoculation with *P. infestans*, suggesting that recognition of effectors may contribute to nonhost resistance in this system. Nonhost pepper accessions recognized from 2 to 36 effectors. Among the effectors, PexRD8 and Avrblb2 induced cell death on a broad range of pepper accessions. Segregation of effector-induced cell death in an F2 population derived from a cross between two pepper accessions fit a 15:1, 9:7 and 3:1 depending on the effector. Our genetic data suggests that single or two independent/complementary dominant genes are involved in the recognitions RXLR effectors. Our findings indicate that multiple loci recognizing a series of effectors underpin nonhost resistance of pepper to *P. infestans* and may confer resistance durability.

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# GSP 원예종자사업단 & GSP 채소종자사업단





## **Gene-specific marker development of cabbage for an efficient molecular breeding**

Yoonkang Hur<sup>1</sup>, Yong-Pyo Lim<sup>1</sup>, Ill-Sup Nou<sup>2</sup>

<sup>1</sup>Chungnam National University, Daejeon, Korea

<sup>2</sup>Sunchon National University, Jeonnam, Korea

Molecular markers, such as PCR-based and SNP-based markers, are extremely useful for plant genetics and crop breeding. Marker-assisted selection (MAS) has been widely applied in plant breeding to improve crop yield, quality, and tolerance to biotic and abiotic stresses. To develop gene-based (or -specific) molecular markers, three different approaches have been used in *Brassica* species: Known-gene-based, RNA seq/Exon-based and RNA seq/Intron-based molecular marker development for several years. Using these techniques, molecular markers have been developed to identify flowering time, anthocyanin accumulation and abiotic stresses in *B. rapa* and *B. oleracea*. Markers were distributed in exons as well as introns, and coding sequences and untranslated regions (UTRs). All markers developed have been transformed into SNP marker after HRM confirmation. I will discuss efficiency, accuracy, and potential problems and contribution of these markers for *Brassica* breeding. [This research was supported by Golden Seed Project (Center for Horticultural Seed Development, No. 213003-04-2-SB230), Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA), and Korea Forest Service (KFS).]

## **Molecular breeding strategies for pyramiding viral resistances in tomatoes**

Inhwa Yeam

Department of Horticulture and Breeding, Andong National University, Andongsi, Gyeongsangbukdo, 760-749, Republic of Korea

Marker assisted selection (MAS) for disease resistance is widely applied in practical tomato breeding program both in public and private sectors. Due to the commercial value and the importance as a model crop system, tomato has taken the lead in MAS among the other horticultural crops. A wide range of disease resistance genes were identified and the mechanism of the resistances has been explored in tomatoes. In the case of disease resistance Tomato yellow leaf curl virus (TYLCV) is one of the major threats for tomato production worldwide, and several resistance sources for TYLCV resistance have been identified among wild tomato species. Ty1/3 resistance gene has been recently identified as a DFDGD-class RNA dependent RNA polymerase (RDR). Late blight (LB) in tomato is caused by *Phytophthora infestans*, and several resistances sources have been applied in the practical breeding program. *Ph3* resistance, a LB resistance against a wide-range of *P. infestans* isolates, has been reported as a gene coding a CC-NBS-LRR gene on chromosome 9. In this study, we developed reliable and comprehensive molecular markers based on the single nucleotide polymorphisms (SNPs) or insertion/deletion (InDel) directly responsible for the resistance phenotype. These functional molecular markers are expected to enhance the effectivity and accuracy of MAS for disease resistance in tomato breeding programs.

## **High-density genetic map construction and QTL analysis for seed size of fruits and powdery mildew resistance in watermelon**

Gung Pyo Lee

Dept. of Integrative Plant Science, Chung-Ang University, 456-756, Republic of Korea

Recently, many breeders have preferred to use molecular markers for introgression backcross programs enabling foreground and background selection to cope with rapid cultivar changing of seed markets. In accumulation of target traits with marker-assisted selection, larger numbers of markers should give better resolution. For the analysis of quantitative traits, a high-density genetic map with a large number of markers is required for discovering more accurately linked markers with traits. Watermelon is a recalcitrant plant to generate a high-density genetic map with conventional molecular markers including simple sequence repeats (SSRs), since watermelon has narrow genetic diversity background and severe segregation distortions of those SSR markers. Thus, we have developed efficient and valid way to assemble genetic map and markers by next-generation sequencing coupled with genotyping by sequencing in F<sub>2</sub> generation. After crosses between *Citrus lanatus* ssp. *citroides* (PI254744 and PI189225) and *C. lanatus* ssp. *lanatus* (TS34, Korean cultigen), 163 of F<sub>2</sub> progeny were sequenced through Illumina's Hi-Seq GAI platform. From sequence information of those variant call files, the SNPs were indexed and filtered by sequencing depth with genotype converter (SNP Genotyper), and optimized by heuristic physical bin mapping to construct more reliable genetic linkage map. Reliable SNP loci were determined and compared to sequences of physical reference map. Using the genetic map, we determined QTLs in F<sub>2:3</sub> population and found major loci corresponding to seed size and powdery mildew race1 resistance in watermelon.

## **Genomics approach to develop molecular markers for targeted breeding of radish**

Ji-Young Lee, Kook Hui Ryu, Jung-Hun Lee, Khushboo Rastogi, Goh Choi

School of Biological Sciences, Seoul National University, Seoul Korea

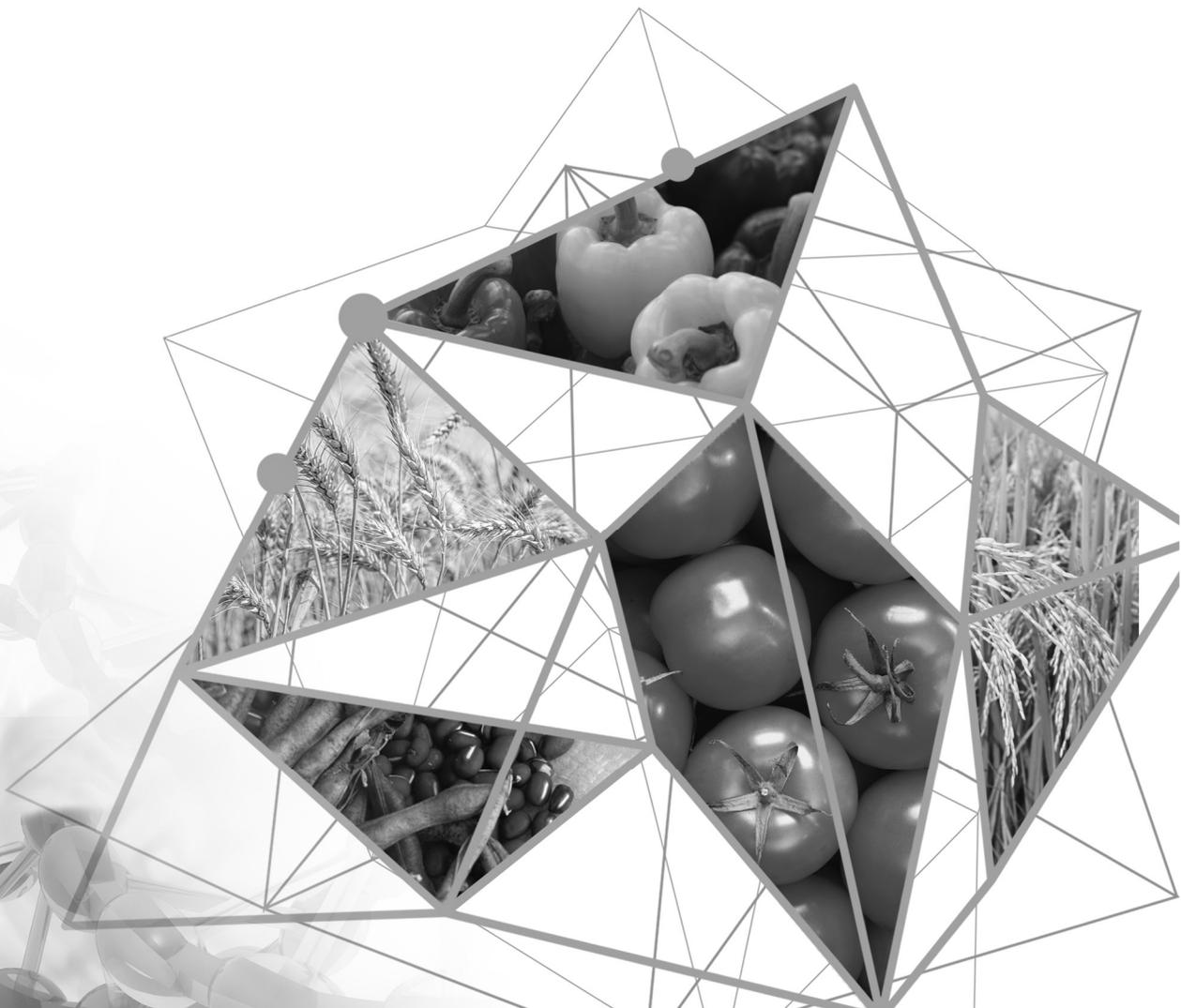
Radish is one of the most widely consumed vegetable crops in Korea. Root is the major part of radish supplied to the market, thus the size, shape, and quality of radish roots are main targets of breeding programs. Despite of the importance of this crop, the molecular breeding of radish is still in the rudimentary stage.

In Golden Seed Project, we aim to establish the molecular breeding program of radish using genome-wide approaches. To this end, we selected inbred lines that have distinctive root traits such as yield, shape, disease resistance, and texture. Single nucleotide variation (SNV) among these lines will be identified based on the low coverage genome sequencing data. These SNVs can be used for finding genomic regions associated with root traits from segregating mapping populations which are also in the middle of development.

Korean radish roots are harvested after being grown for only nine weeks. During that period, root biomass reaches to more than two kilograms. While investigating the root growth of radish inbred lines, we found that cytokinin contributes as a key growth regulator that promotes radial growth of radish roots. A difference in growth rates of two distinctive inbred lines was explained by the difference in response to cytokinin. Genes responsive to cytokinin are highly enriched in the cambium, the meristematic cell population that drives radial growth. For comprehensive understanding of genes that affect yields of radish roots, we turned to developing a tissue specific transcriptome data using laser capture microdissection. We expect that the compendium of genomics-based data will help establishing molecular breeding of radish at a fast track.

2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# 2015년 한국육종학회상





---

## 2015년 한국육종학회 학회상 시상

○ 일시 및 장소 : 2015년 7월 2일(목), 19:10

○ 시상내용

### 1. 농우육종학회상

- 수상자 : 박효근 (서울대학교 명예교수)
- 선정사유 : 채소작물의 유전자원 수집과 내병성 고추 품종 개발에 헌신하고 후학 양성에 힘써 우리나라 육종학의 학문적 발전과 종자산업 발전에 크게 공헌

### 2. 연구상(연구부문)

- 수상자명 : 강권규 (한경대학교)
- 논문제목 : Transgenic Tomato Plants Expressing *BrOAT1* gene from *Brassica rapa* var. SUN-3061 Show Enhanced Tolerance to Salt Stress
- Plant Breed. Biotech. 2013 (March) 1(1):70~79

### 3. 연구상(품종부문)

- 수상자명 : 김기영 외 20명 (농촌진흥청 국립식량과학원)
- 품종명 : 제3307호(2010. 9. 13)
- 품종명(논문제목) : 벼 증만생 고품질 내도복 신품종 ‘새누리’

### 4. 공로상

- 한국육종학회 27대 회장, 임상중 (국립식량과학원)



2015 한국육종학회 · 차세대BG21사업단 · GSP사업단 공동심포지엄

# 색 인





Name	Page	Name	Page	Name	Page
<b>■ 국 문 ■</b>					
┌					
강경대	291	김남신	254	김정주	47, 50, 55, 56, 58, 68
강경호	46, 60, 71, 74	김대영	97	김정태	102
강달순	42, 79	김대욱	76	김정호	278
강미영	247, 281	김대일	256	김정화	305
강범규	37, 38, 48, 49	김대현	275	김정희	256
강성택	254	김도선	278	김종보	145
강성환	117	김도순	260	김종윤	81
강소미	131	김만조	84	김종환	110
강위금	57, 58	김명기	44, 58, 60, 63	김지아	144, 198
강윤주	297	김명식	62	김지은	214
강주원	297	김미향	58	김지홍	32
강지남	131	김민수	305	김진영	66
강창성	66	김보경	40, 45, 46, 47, 50, 55, 56, 57, 60, 63, 68, 84	김진원	260
강천식	40, 51, 54, 55, 82	김보민	32	김진희	278
강현중	46	김상근	102	김창기	32
강혜정	51	김상민	82	김철우	84
강홍규	131, 132	김상열	52, 101	김태현	201
고갑천	75	김석만	74	김학신	51
고상욱	120, 122	김석원	225	김해인	241, 296
고석민	131	김성국	102	김현명	84
고윤희	40	김성길	275	김현순	45, 46, 47, 56, 68
고재권	45, 46, 47, 56, 68	김성업	62	김현영	37, 48, 49
고종민	37, 38, 48, 49	김성택	42, 79	김현일	119, 123
고종철	47, 56, 90	김세종	99	김현태	37, 38, 48, 49
고지연	90	김세현	84	김현호	69
곽병삼	49	김수정	81	김형욱	199
곽상철	49	김수진	120, 122	김혜자	26
구자환	76	김승유	97	김홍식	49, 84
권순옥	26, 245, 246, 248	김양길	40, 82	김효정	108, 109
권순중	76	김양지	224	김효중	50
권영업	52, 76, 102, 201	김연규	44	김희곤	50
권오덕	52	김영국	92, 118	┌	
권오창	105	김영미	110, 144	나해영	50, 88, 89
권용익	131, 132, 226	김영호	66	남민희	52, 101, 201
권택윤	259	김용욱	144, 198	남상식	72, 115
권혁규	271, 299	김용현	49	남정권	46, 47, 50, 55, 56, 57, 68
기광연	75	김우재	45, 46, 47, 50, 55, 56, 57, 68	남정환	81
김경민	76, 201	김유진	32	남종철	120, 122
김경호	40, 82	김윤경	256	노상득	51
김경환	259	김윤희	81	노심	297
김정훈	40, 76	김인혜	66	노일래	97
김정희	51, 291	김재명	72, 115	노희선	145
김광수	42, 79	김재훈	226	┌	
김기선	81	김재희	84	도재왕	290
김기영	46, 47, 50, 55, 56, 68, 90	김정석	116, 117, 182		

Name	Page	Name	Page	Name	Page
<b>ㄹ</b>		박태성	182	신운철	46, 47, 50, 56, 57, 58
레아잉핀	297	박향미	58	신유승	110
류기중	132	박현수	45, 47, 50, 55, 56, 57, 68	신은영	71
류수노	25, 26, 245, 246, 247, 248, 281	박형빈	116	신지연	291
류시환	51	박형호	76	심하식	38
<b>ㄴ</b>		배상수	293	<b>ㅇ</b>	
마경호	108, 109	배석복	62	아세코바소베틀	305
모영준	58, 63	배은지	88, 89	안경구	66
문병호	91	배정숙	82, 99	안기홍	193
문운호	193	배태웅	91	안동춘	126
문중경	48, 90, 254	배환희	102	안명숙	225
문진영	72	백남현	44, 58	안상낙	297
문초아	182	백만기	44, 47, 50, 55, 56, 68	안승현	72, 115
문흥규	144, 198	백성범	102	안억근	44, 58, 63, 74, 99
<b>ㄷ</b>		백소현	46, 47	안율균	278
박광근	76, 82	백인순	32	안종웅	193
박기진	51, 64	백인열	37, 38, 48, 49	안주희	116, 117, 182
박기훈	47, 82	백정선	271, 299	안찬훈	92
박노봉	52	변학수	71	안태진	92, 118
박누리	293	<b>ㄷ</b>		양대화	224, 225
박덕심	66	사규진	64	양운호	60, 63
박동수	52, 101, 201	상세티	297	양정옥	72, 115
박미소	291	샤 시오난	119, 123	양창인	44, 58, 60, 63
박미영	26, 132, 224	서대하	60	엄유리	118
박민영	86	서명훈	86	여운상	52, 60, 101
박민우	63	서민정	102	오기원	62
박범석	256	서영호	51	오상근	256
박석진	290	서정필	44, 58, 63	오성환	52, 101
박선경	145	서종택	81	오세관	63
박성화	116, 117, 182	선현진	131, 132	오영진	40, 82
박수권	101	성낙식	60	오은영	62
박수형	86	성열규	60, 71	오인석	62, 90
박영기	84	손동모	50	오재은	214
박영춘	69	손범영	102	오혜진	71
박유진	144	손영보	52, 101, 201	요네야마 카오리	119, 123
박은성	109	손재한	40	요네야마 코이치	119, 123
박인희	101	손황배	81	용우식	51
박장환	102	송경순	66	우관식	90
박재인	144	송석보	90	원용재	44, 58, 60, 63, 99
박종열	51, 64	송연상	72, 115	유경단	193
박종철	40, 82	송유천	52, 101, 201	유동림	81
박종호	45, 56	송종태	305	유의수	265, 291
박철수	51, 54, 55	송현진	91	유정	26
박철우	305	신동진	101, 201	육은수	32
		신성휴	102	윤건식	82
		신소희	271, 299	윤광섭	44, 60

Name	Page	Name	Page	Name	Page
윤덕상	69	이영희	37, 38, 48, 49, 52, 101	전용희	58, 99
윤무경	86	이예린	241, 296	전윤아	297
윤여태	297	이유석	50	전재범	46, 74
윤영미	54, 55	이윤지	92	전태환	254
윤영환	44	이은자	99	전효진	271, 299
윤재복	290	이장용	51	정국현	44, 58, 60, 99
윤혜진	259	이재생	90	정규미	241, 296
윤홍태	37, 38, 48, 49, 66	이재원	84	정남진	271, 299
은민호	241, 296	이점식	63	정미남	72
이가영	49	이점호	44, 47, 55, 56, 57, 58, 60, 63, 71, 76, 99, 102	정병룡	126
이강섭	262	이정동	99, 305	정성민	120, 122
이경보	42, 72, 115, 193	이정로	109	정수진	144
이경보	79	이정훈	92, 118	정순천	32, 254
이경준	108, 109	이정희	44, 58, 63, 71, 99, 214	정영근	40, 82
이규성	58, 60	이종경	66	정오영	58, 60, 63
이공주	293	이종숙	293	정옥철	224, 225
이기안	108, 109	이종희	52, 101, 201	정용모	105, 126
이나념	144, 198	이주경	64	정응기	58, 60, 63, 99
이동우	66	이준대	241, 296	정재은	305
이동진	108, 109	이준설	72, 115	정재혁	271, 299
이동희	132	이지석	84	정종민	56, 58, 63, 71, 74
이명훈	311	이지윤	52, 101, 201	정종욱	108, 109
이명희	62	이지은	193	정지웅	46, 54, 55, 58, 71, 74
이미자	82	이진구	66	정지원	304
이병실	91	이진석	102	정지희	110
이병원	37, 38, 48, 49	이태영	260	정찬식	62
이병정	105, 126	이현숙	297	정태욱	90, 102
이보미	214	이현오	291	정하나	132
이보희	69	이형운	72, 115	조명철	278
이봉우	214	이혜은	278	조상균	38
이상권	25	이호선	108, 109	조성우	46
이상대	105, 126	이효연	131, 132, 224, 225, 226	조성환	214
이상복	44, 58, 63, 71, 99	임수정	71	조수현	71, 82
이상협	63, 199	임청택	47	조아르나	110
이삿별	201	임혜리	71	조양희	109
이석기	37, 49			조영일	66
이석영	108, 109			조영찬	44, 47, 50, 55, 56, 58, 60, 63, 68
이석하	304			조용섭	66
이선이	97	장동철	81	조은진	54, 55
이성곤	259	장영석	42, 79	조준현	52, 101, 201
이성기	91	장윤희	193	조현숙	58
이승엽	46	장은규	49, 66	좌지방	132
이승욱	291	장인건	199	주정일	69
이승재	271, 299	장재기	52, 58, 60, 99	진영돈	105, 126
이영병	105	장하영	86	진일두	224, 225
이영화	42, 79	전명기	37, 38, 48, 49	진행운	291
이영훈	37, 38, 48, 49	전영아	108, 109		

**Name Page**

**ㄸ**

차선우	92, 118
차영록	193
채원병	86
최규환	42, 72, 79
최대식	101
최만수	37, 38, 48, 49
최명은	90
최범순	291
최서희	293
최용의	198
최용환	58
최유미	90
최은영	25
최인배	82
최인후	72, 193
최임수	44, 58, 60, 63
최재근	51
최재성	82
최정란	199
최준경	214
최철	256
최충원	63
최택용	69
최홍집	99

**ㅋ**

코코멍	297
키스기 타카야	119, 123

**ㅎ**

하건수	71
하기용	45, 46, 47, 50, 56, 68
하운구	58, 60, 99
하태정	38, 81
하혜정	293
한두호	305
한상익	201
한선경	72, 115
한수범	116, 117, 182
한옥규	66, 76, 82
한원영	37, 48, 49
한윤열	99
한정아	66
한정현	290
한지학	32
한태호	75, 116, 117, 182

**Name Page**

함태호	26, 245, 246, 247, 248, 281
허목	92, 118
허연재	201
허윤영	120, 122, 256
현웅조	44, 63, 71, 74
현종내	76
홍경낙	144
홍민지	224, 225, 226
홍수영	81
홍용표	144
홍하철	44, 58, 60, 63
황세구	84
황순임	89
황엄지	72
황운하	101
황종진	76
황주천	105, 126

**A**

Abdula Sailila E.	70
Ahmed Nasar Uddin	16, 18, 20, 219
Ahn Eokkeun	302
Ahn Hyo-Min	103
Ahn Il-Pyung	253
Ahn Jongmoon	255
Ahn Joon-Woo	78, 85, 104, 146, 208, 224
Ahn Kyounggu	28
Ahn Sang-Nag	24, 39, 61, 209
Ahn Su Ran	69
Ahn Yul-Kyun	147, 298
An Gynheung	289
An Jeong-Tak	130
Anil Kumar N.C	60, 127
Asekova Sovetgul	23, 64

**B**

Back Kyoungwhan	173, 174, 216
Bae Hwan Hee	81, 139
Bae Hyun-Kyung	33
Bae Jeong-Suk	41, 59
Bae Ki-Deuk	171, 172, 173
Bae Seon-Hwa	150
Bae Wonsil	85
Baek Hyung-Jin	69
Baek In-Youl	87, 88
Baek Man-Ki	67

**Name Page**

Baek Seong-Bum	81, 139
Baek So-Hyeon	156, 191
Baek Woonhee	237, 239, 244, 284, 285
Beom Hye-Rang	202, 203, 294
Boo Hee-Ock	189, 190
Boo Kyung-Hwan	103
Byeon Yeong	173, 174, 216

**C**

Cha Richard	303
Cha Seon-Woo	212, 231, 237, 272
Chae Chi-Won	94
Chae Hyun Seok	97, 113
Chae Songhwa	82, 83, 217
Chang Sungyul	103
Chang Yali	92
Changkwan Amornrat	181
Chee Hark-Harn	4, 103
Cheong Young-Keun	41, 59, 177
Cho A-Ra	137
Cho Hae Ryong	114
Cho Hong Joo	279
Cho Hye-Sun	145
Cho Hyun Min	142, 210
Cho Hyun Suk	183, 202, 215
Cho Hyun-Suk	177, 191, 192, 205
Cho Jung-Il	152, 167
Cho Jun-Hyun	149, 179
Cho Lae-Hyeon	289
Cho Mijung	21, 29, 65
Cho Seong-Woo	188
Cho Won Kyong	272
Cho Yang-Hee	87, 106, 107
Cho Yong-Gu	68, 70, 110, 111, 112, 189, 128, 301
Cho Yoo-Hyun	34, 159
Cho Young-Chan	65, 67
Choe Junkyoung	211
Choe Sunghwa	265, 267, 303
Choi Beom-Soon	28, 140
Choi Bo-Kyung	206
Choi Buung	34, 158, 162, 163
Choi Cheol Woo	197, 210
Choi Cheol-Woo	218
Choi Doil	129, 175, 196, 312
Choi Eun Hye	175
Choi Eunbi	175

Name	Page	Name	Page	Name	Page
Choi Geun-hee	216	<b>G</b>		Hwang Gidong	222
Choi Goh	318	Garnaat Carl	185	Hwang Hyun-Ju	152, 167, 229
Choi Gyung-Ja	28, 130, 181, 215	Gil Jinsu	231, 235, 237, 272, 276	Hwang JeeNa	220
Choi Hong Il	83	Gil Kyung-Eun	284	Hwang Jihyun	157
Choi Hong-II	27, 78, 125, 211, 221	Go Ho-Cheol	254	Hwang Jung Eun	27, 78, 125, 211, 221
Choi Hong-Jib	100	Goo Dae Hoe	114	Hwang Sun-Goo	27, 146, 147, 285, 304
Choi Hong-Kyu	148, 205	Guo Ge	134	Hwang Tae Young	97, 113, 198, 200
Choi Hong-Soo	272	Gupta Ravi	281, 282	Hwang Yoon-Jung	228
Choi Hyung-Won	206	Gyeon Ye Jin	231, 276	Hyun Do yoon	69, 98, 114, 223
Choi Jae-Pil	168	<b>H</b>		Hyun Do-Yoon	95
Choi Jae-Seong	59, 177	Ha Bo-Keun	21, 212	Hyun Jong-Nae	124
Choi Jin-Kyeong	41	Ha Sun-Hwa	191, 204	Hyun Ung-Jo	65
Choi Man-Soo	111	Ha Yeaseong	220		
Choi Mi Na	218	Hahn Jang-Ho	150	<b>I</b>	
Choi MinJi	204	Han Chang-deok	282, 286	Igusa Sayuri	124, 223
Choi Sang-Woo	107, 109	Han Hyeondae	138, 180, 184, 222	Im Hyun Hee	202, 215
Choi Su Ryun	15, 170	Han Ji-Woong	181	Im Ji-Hoon	274
Choi Yeonok	302	Han Jong Won	229	Im Seung Bin	85, 104, 208
Choi Yong-Eui	210	Han Kitae	290	In Byung-Chun	206
Choi Yong-Soo	253	Han Koeun	221, 294	Izzah Nur Kholilatul	28
Choi Yoomi	220	Han Mi Kyung	98	<b>J</b>	
Choi Youn Jung	114	Han Ouk-Kyu	41, 59	Jang Cheol Seong	27, 146, 155, 168, 285
Choi Yu-mi	69, 98, 114, 223	Han Sang-Ik	149, 179	Jang Cheol-Seong	147, 304
Chun Hyun Jin	141, 142, 216	Han Su-Hyun	194	Jang Kiyong	243
Chung Chong-Tae	61	Han Sung Min	27, 78, 125, 211, 221	Jang SeongGyu	270
Chung Hee	235, 272	Han Sung-Jin	107, 109	Jang Seonghoe	208
Chung Jong-II	107, 109	He Qiang	34, 159, 160, 162	Jang Siyoung	213
Chung Jong-Wook	87, 94, 95, 104, 106	Heo Eun-Beom	34, 158, 162	Jang Su	22
Chung Young-Soo	191, 202, 215	Heo On-Suk	254	Jang Woojong	140
Cook Douglas R.	148	Hong Min Jeong	83, 146, 224, 233	Jang Yun-Woo	59
Corvalán Claudia	267	Hong Gi-Heung	41, 59	Jayakodi Murukarthick	140, 169, 295
Cuyacot Abigail Rubiato	228	Hong Hyeonjun	40, 43	Je Byoung Il	286
<b>D</b>		Hong Jee-Hwa	227	Jee Moo-Geun	112
Diriba Abebe Megersa	127	Hong Su-Young	89, 277	Jeon Gyoeng-Lyong	103
<b>E</b>		Hong Young-Shick	142	Jeon Hwi Seong	279
Eun Chang-Ho	196	Hosokawa Munetaka	129	Jeon Jong-Seong	229
<b>F</b>		Huang Jin	286	Jeon Su-Kyoung	156
Farooqi Muhammad Qudrat Ullah	100	Huang Xing	186	Jeon Young-Ah	87, 94, 95, 104, 106, 107
Flores Paulina Calderón	230	Hur On-Sook	69, 98, 114	Jeon Yun-A	209
Francis David M.	57	Hur Yeon-Jae	149, 179	Jeong Eun-Ju	70, 110
		Hur Yoonkang	315		
		Hur Youn Young	121		
		Hwang Bo-Hwa	133		
		Hwang Chung-Dong	87, 88		
		Hwang Doyeon	294		



Name	Page	Name	Page	Name	Page
Kim Hyun-Tae	111	Kim Kyung Hwan	61	Kim Tae Dong	235, 276
Kim Il-Sup	278	kim Kyung-A	135	Kim Tae Heon	149
Kim In-Jung	196	Kim Kyung-Hee	178, 274	Kim Tae-Heon	179
Kim Jae Joon	207	Kim Kyung-Hun	124	Kim Tae-Ho	150, 211
Kim Jae Seong	202, 215	Kim Kyung-Min	124, 135, 136, 137	Kim Tae-Sung	34, 104, 157, 159, 161, 162, 163, 164, 165, 166, 253
Kim Jae Yoon	178, 232	Kim Kyungryun	21, 29, 65	Kim Won-Il	158, 163, 253
Kim Jae-Hee	86	Kim Kyu-Won	34, 157, 161, 162, 163, 164, 165, 166, 253	Kim Woo-Nam	133
Kim Jae-Hyun	124	Kim Mahn-Jo	86	Kim Yang-Kil	59, 177
Kim Jeong Ho	147	Kim Me-Sun	68, 110, 111, 112	Kim Yeon-Ki	82, 83, 217
Kim Jeong Hoe	33	Kim Mijeong	274	Kim Ye-Sol	102
Kim Jeong Hwa	23, 64, 73	Kim Min	234	Kim Yoong Eun	303
Kim Jeong Il	202	Kim Min Chul	141, 142, 210, 216	Kim Yoon-Kyeong	138, 222
Kim Jeong-Ju	67	Kim Min-Chul	197, 218	Kim Young-Guk	237
Kim Ji-Eun	211	Kim Minkyung	179	Kim Young-Mi	151, 202, 203, 204, 294
Kim JiHyeon	151	Kim Minsu	23, 64	Kim Young-Saeng	278
Kim Jin-A	31, 209, 261	Kim Moon S.	11	Kim Youn-Sung	145
Kim Jin-Baek	78, 83, 85, 104, 125, 146, 211, 221	Kim Myung-Shin	196	Kim Yul-Ho	89, 277, 278
Kim Jin-Beak	224	Kim Nam-Hoon	140, 295	Ko Chan-Sup	145
Kim Jinhee	147	Kim Namshin	29	Ko Ho-Cheol	69, 98, 114
Kim Jin-hyuk	147	Kim Ok Tae	235, 272, 276	Ko Jee-Yeon	124
Kim Jin-Hyun	148, 205	Kim Saet-Byul	175	Ko Seunghee	207
Kim Jinkyung	295	Kim Sang Gon	81	Ko Suk-Min	134
Kim Jin-Soo	9, 265	Kim Sang Gyu	69	Ko Tae-Seok	187, 188
Kim Jinu	279	Kim Sang Heon	45	Ko Woo Ri	100
Kim Jong-Bum	280	Kim Sang Hoon	78, 85, 102, 104, 146, 224	Koeda Sota	129
Kim Joo Yong	276	Kim Sang-Woo	187, 188	Koh Eunbyeol	186
Kim Joon Young	157	Kim Sea-Hyun	86	Koh Hee-Jong	22, 30, 53, 80, 127, 186, 201, 270
Kim Joonki	68, 110, 112	Kim Seolah	138, 222	Koh Sang-Uk	121
Kim Joo-Yeol	31, 209, 261	Kim Seong-Dong	68	Koo Sung-Cheol	111
Kim Joung Sug	82, 83, 217	Kim Seongjun	143	Krishna R.	281
Kim Ju-Hee	146, 155	Kim Seo-Woo	143	Kulkarni Krishnanand P	23, 64
Kim Ju-Kon	288	Kim Serim	231, 235, 237, 272, 276	Kumar Vikranth	282, 286
Kim Jung Sun	174, 175, 192	Kim Seungill	175, 196	Kwak Jun Soo	230, 231, 234, 276
Kim Jungeun	168, 265	Kim So Wun	281	Kweon Kibum	89, 277
Kim Jung-In	187, 188	Kim Somi	176	Kweon Soon-Jong	191
Kim Jung-Tae	81, 139	Kim Su Jeong	277	Kweon Young-Up	124
Kim Keumsun	138, 180, 184	Kim Su-Jeong	89	Kwon Hyo Joung	98
Kim Ki-Taek	130	Kim Sun Tae	281, 282	Kwon Jin-Kyung	215, 220, 221, 254
Kim Ki Yong.	113	Kim Sung Hoon	286	Kwon O Hyeon	77
Kim Kil Hyun	139	Kim Sunggil	143	Kwon Soo Jeong	187
Kim Ki-Yong	97, 198, 200	kim Sung-il	230, 231, 234, 276	Kwon Soo-Jeong	189, 190
Kim Kook-Hyung	272	Kim Sungmin	21, 29, 65	Kwon Soon Il	267, 279, 303
Kim Kyeong-Hoon	41	Kim Sung-Up	87, 88	Kwon Soon-Il	265
Kim Kyeong-Hoon	177	Kim Sun-Lim	156		
Kim Kyong-Ho	41, 59, 177				
Kim Kyoung Heon	279				

Name	Page	Name	Page	Name	Page
Kwon Soon-Jae	27, 78, 83, 85, 104, 125, 208, 211, 221	Lee Hye-Eun	147	Lee Ki-Won	97, 198, 200
Kwon Soon-Wook	270	Lee Hye-Jung	68, 70, 110, 111, 112	Lee Kwang-Won	61
Kwon Suk-Yoon	255	Lee Hyerim	30	Lee Kyeong-Ryeol	280
Kwon Sung Won	169, 220, 295	Lee Hye-young	151	Lee Kyounghee	292
Kwon Sun-Jung	272	Lee Hyo Ju	301	Lee Kyung Hee	210
Kwon Taek-Ryoun	191, 205	Lee Hyo-Jeong	102	Lee Kyung Jun	94, 95, 106
Kwon Taek-Ryun	61	Lee Hyo-Ryeon	218	Lee Kyung-gin	174
Kwon Ye Jin	230	Lee Hyoung Yool	173, 216	Lee Kyung-Hee	197, 218
Kwon Ye-Jin	234	Lee Hyo-Yeon	133, 134, 176	Lee Man Bo	96
Kwon Yeong-Up	149, 179	Lee Hyun Ju	301	Lee Marina	182
Kwon Yong-Ik	133, 134	Lee Hyun Sam	151	Lee Min-Seuk	92
Kwon Young-Ju	284	Lee Hyung Jin	184, 185	Lee Mingi	138
		Lee Hyun-Ju	150	Lee Mi-Ye	168
<b>L</b>		Lee Hyun-Sook	24, 39, 61, 209	Lee Moon-Soon	190
Laila Rawnak	16	Lee Hyun-Suk	135, 136, 137	Lee Myoung Hee	211
Lee Byung-Moo	178	Lee Jae-Chul	61	Lee Myung-Chul	95, 98, 114, 223
Lee Chaeyoung	148, 205	Lee Jae-Soon	279	Lee Myung-Hee	87, 88
Lee Chang-Kyu	206	Lee Jae-Yong	145	Lee Na-Ra	156
Lee Chang-Yong	34, 162, 163, 253	Lee Je Min	182	Lee O New	98
Lee Chan-mi	53	Lee Jeom-Ho	81, 139	Lee Saisbeul	149, 179
Lee Cheol Won	242	Lee Jeong-Dong	23, 29, 64, 65, 73, 236, 266, 268, 283	Lee Sang-Choon	28, 140, 169, 295
Lee Dae-Woo	229	Lee Jeong-Hee	211	Lee Sang-Hoon	97, 198, 200
Lee Daewoong	298	Lee Jeongyeo	168	Lee Sanghyeob	62
Lee DoKyoung	273	Lee Jin Su	31, 209, 261	Lee Sanghyun	151
Lee Dong Hee	202, 215	Lee Jin-Hyoung	192, 205	Lee Seong Ho	170
Lee Dong-Kyu	169, 295	Lee Jin-Seok	81, 139	Lee Seong Tae	113
Lee Dongryung	127	Lee Jinsoo	85	Lee Seong-Tae	41, 59
Lee Dong-Sun	133	Lee Ji-Yoon	149, 179	Lee Seulki	192
Lee Dong-Yup	295	Lee Ji-Young	318	Lee Seung-Bum	302
Lee Dooyoung	288	Lee Jong-Hee	149, 179	Lee Si-Myung	177, 183
Lee Du-Hwa	293	Lee Jong-Ho	181	Lee Sok-Young	87, 93, 94, 95, 104, 106, 107
Lee Eun-Ju	145	Lee Jonghoon	28	Lee Soo In	31, 209, 261
Lee Gang-Seob	150, 152, 167, 177, 229	Lee Jong-Ro	95	Lee Su Young	77
Lee Gi-An	87, 94, 95, 104, 106, 107	Lee Jong-Yeol	202, 203, 204, 294	Lee Sukyeung	69, 98, 114, 223
Lee Gileung	22	Lee Joohyun	175, 274	Lee Sung Chul	237, 239, 244, 284, 285
Lee Gung Pyo	317	Lee Joung-Ho	220	Lee Sunghoon	277
Lee Gyu-Ho	137	Lee Ju Kyong	100, 101	Lee Tong-Geon	287
Lee Hana	295	Lee Ju Seok	21, 29, 65	Lee Won-Ju	187, 189
Lee Hea-Young	221, 254	Lee Ju-Hyun	253	Lee Woo Kyung	211
Lee Hee-Bong	104, 208	Lee JuneSung	196	Lee Ye-Ji	150
Lee Hong Gil	243, 292	Lee Jung-Hun	318	Lee Yeong-Ju	61
Lee Ho-Seok	293	Lee Jung-Ro	87, 94, 95, 104, 106, 107	Lee Yeon-Hee	61
Lee Ho-Sun	95, 104	Lee Junki	140	Lee Yi	194, 195, 231, 235, 237, 238, 272, 276
Lee Hye Jin	77	Lee Ki Jung	202, 215	Lee Yong-Jin	287

Name	Page	Name	Page	Name	Page
Lee Yoon Jeong	202, 215	Moon Sunok	33	Ouk Sothea	68, 111
Lee Yoon Kyung	201				
Lee Yoonjung	274	<b>N</b>		<b>P</b>	
Lee Young-Hee	87, 88	Na Han-Jung	61	Pae Suk-Bok	87, 88
Lee Young-Pyo	302	Nah Gyoungju	273, 274	Paek Nam-Chon	194, 243, 286
Lee Young-Sang	159	Nahm Baek-hie	82, 83, 217	Pahk Yoon Mok	82, 83
Lee Yun Sun	140, 169, 295	Nahm Seokhyeon	255	Pai Hyun-Sook	293
Lee Yunjoo	201	Nam Jeong-Hwan	89, 277	Pang Wenxing	170
Lee Yu-Young	89, 277	Nam Jeong-Kwon	67	Park Beom-Seok	34, 158, 163, 166
Li Binbin	153	Nam Jong-Chul	121	Park Boem Seok	253
Li Feng Peng	34, 162	Nam Min-Hee	149, 179	Park BoSeu	196
Li Hong-Yu	176	Nam Su-Jin	236, 279	Park Chang-Hwan	139
Li Xiaonan	170	Nguyen Thi Hoai Thuong	128, 154	Park Chanmi	237, 239, 244, 284, 285
Lim DaEun	270	Nguyen Tien Dung	33, 128, 153, 154, 169	Park Chul-Soo	41, 294
Lim Dong Kyu	220	Nguyen Van Ngoc Tuyet	197	Park Chung-Mo	284
Lim Hyemin	152, 167, 229	Nino Marjohn	68, 70, 111	Park Dong-Soo	149, 179
Lim Jin Hee	206	Nogoy Franz	110	Park Eun Seong	87, 104
Lim Jung-Hyun	286	Nogoy Franz Marielle	111	Park Eung-Jun	218
Lim Ki-Byung	134, 228	Noh Eun Woon	279	Park Gyu Tae	236, 266, 268, 283
Lim Myung-Ho	191, 192, 205	Noh Ill Sup	128	Park Hae-Rim	273
Lim Sanghyun	207	Nou Ill-Sup	16, 17, 18, 19, 20, 28, 68, 70, 111, 157, 219, 315	Park Han Yong	98
Lim Sang-Jong	124			Park Hyang-Mi	89, 277, 278
Lim Soohwan	168	<b>O</b>		Park Hyeon Mi	285
Lim Soo-Hyun	273, 274	Oh Chang-Sik	184, 185	Park Hyo Jin	169
Lim Sun-Hyung	202, 203, 204, 294	Oh Eun-Ui	92	Park Hyo-Jin	128, 154
Lim Yong Pyo	15, 170	Oh Hyun-Jeong	103	Park Hyoung-Ho	59
Lim Yong-Pyo	315	Oh In-Seok	111	Park Hyung Soo	97
Liu Jing Miao	286	Oh Ki-Won	87, 88	Park Hyung-ho	124
Liu Li	129	Oh Sang Heon	170	Park Hyun-Seung	169, 295
		Oh Se Jong	223	Park Hyun-Su	67
<b>M</b>		Oh Sejong	98, 114	Park Inkyu	168
Ma Kyung-Ho	87, 93, 94, 95, 104, 106, 107	Oh Sewon	138, 180, 184, 222	Park Jae-Wan	87
Mancia Franklin Hinosa	228	Oh Sung Aeong	33, 128, 153, 154, 169	Park Jeong Mee	255
Manoharan Ranjith Kumar	17	Oh Sung Hwan	149, 179	Park Jiho	64
Mekapogu Manjulatha	89	Oh Sung-Dug	177, 183	Park Jin Sol	202, 215
Meng Qingfeng	282	Oh Sung-II	138	Park Jong Yeol	101
Min Chul Woo	281	Oh Yong-Seok	206	Park Jong-Chul	41, 59, 177
Min Sung Ran	157	Oh Youngjae	138, 180, 184, 222	Park Jong-Ho	59, 177
Min Sun-Kyung	162	Oh Young-Jin	59, 177	Park Jonghwa	53
Mizoi Junya	124, 223	Oh Young-Ju	177	Park Jong-In	16, 17, 18, 19, 20, 219
Moon Jin-Seok	124, 223	Ohn Ji Hye	185	Park Joo-Seok	148, 205
Moon Jun-Cheol	155, 178	Oo Moe Moe	33, 154	Park June Hyun	8, 269
Moon Jung-Kyoung	156	Oo Win Htet	34, 162, 166	Park Junhyeong	222
Moon Jung-Kyung	29, 139			Park Ki-Chan	237
Moon Mi-Sun	174				

Name	Page	Name	Page	Name	Page
Park Kwang-Geun	41, 59	Ryu Hojin	85	Sohn Hwang-Bae	89
Park Kyong-Cheul	100	Ryu Jaehwang	302	Sohn Seong-Han	174, 175, 192, 228
Park Mi Suk	141, 142	Ryu Jaihyunk	85, 104, 208	Sohn Soo-In	177, 183
Park Mi-Jeong	284	Ryu Kook Hui	318	Sohn Whang-Bae	277
Park Myoung-Ryoul	156	Ryu Kyoung Ou	5	Son Beom-Young	81, 139
Park Ohkmae K.	279	Ryu Kyoung-Yul	69	Son Eun-Ho	93
Park Sang Ik	238			Son Jae-Han	41, 177
Park Sang Kun	228	<b>S</b>		Son Youngbo	149, 179
Park Sang Kyu	204	Sa Kyu Jin	100, 101	Song Deuk-Young	87, 88
Park Silki	303	Saha Gopal	18, 219	Song In-Ja	133
Park So Hyeon	195	Sakuraba Yasuhito	286	Song Jong Tae	23, 33, 154, 230, 234, 236, 266, 268, 283
Park Soo-Chul	152, 167	Seo Eunyoung	175	Song Jong-Tae	73
Park Soo-Kwon	156	Seo Hak Soo	230, 231, 234, 236, 266, 268, 276, 283	Song Kihwan	62
Park Soon Ju	286	Seo Jang-Kyun	272	Song Kitae	178
Park Soon Ki	33, 128, 153, 154, 169, 191, 192, 205	Seo Jeonghwan	127	Song Kwan-Jeong	92, 94
Park Soo-Yun	183	Seo Joodeok	28	Song Kwan Jeong	207
Park Sumin	21, 29, 65	Seo Min Jung	81	Song Seon-Kyeong	70, 112
Park Sung Han	152	Seo Min-Jung	139	Song Sung-Jun	176
Park Tae-Il	59	Seo Mi-Suk	174, 175	Song Tae-Hwa	59, 177
Park Yong Chan	168	Seo Pil Joon	243, 284, 292	Song Won-Yong	24
Park Yong-Jin	34, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 253	Seo Yong Weon	45, 83, 96, 224, 230, 232, 233, 240, 242, 273, 287, 300	Song You-Chun	149, 179
Park Young-Chul	94	Shannon J. Grover	64	Struss Darush	130
Park Young Chul	207	Shim Donghwan	34, 106, 107, 158, 163, 166	Suh Eun-Jung	61
Park Younghoon	157, 298	Shim Eun-Jo	227	Suh Jeong-Pal	145
Park Youngki	86	Shin Ah-Young	255	Suh Jung-Pil	67
Perumal Sampath	28	Shin Chanseok	8, 269, 288	Suh Seok-Cheol	205
Priatama Ryza A.	282, 286	Shin Chanseok	8, 288	Suh Seok-Chul	302
		Shin Dongjin	149, 179	Suh Su Jeoung	303
<b>Q</b>		Shin Hyunsuk	138, 180, 184, 222	Sun Hyeon-Jin	134, 176
Qin Yang	191, 192, 205	Shin Inchul	290	Sundaramoorthy Jagadeesh	236, 266, 268, 283
		Shin In-chul	290	Sung Dan	10
<b>R</b>		Shin Kong-Sik	191, 192, 205	Sung Jung-Sook	69
Ra Won-Hee	34, 162	Shin Kyoung Soon	156		
Rai Arti	220, 294	Shin Oonha	273	<b>T</b>	
Ramekar Rahul Vasudeo	100, 101	Shin Sang-Yoon	288	Tai Thomas H.	223
Rastogi Khushboo	318	Shin Seonghyu	81	Thamilarasan Senthil Kumar	17, 19
Raveendar Sebastin	87, 95, 104, 106, 107	Shin Seungho	178	Than Vicheka	135
Rhee Sangkee	290	Shinozaki Kazuo	124, 223	Thuong Nguyen Thi Hoai	169
Ro Na-Young	69, 98, 107, 114	Siddique Muhammad Irfan	130, 294	Tian Qing	185
Robin Arif Hasan Khan	16	Sierra Sheryl N.	80	Todaka Daisuke	124, 223
Roh Kyung Hee	280	Silvanovich Andre	185	Tong Wei	34, 161, 162
Roy Swapan Kumar	187, 188, 189, 190	Sim Sung-Chur	57, 206, 179	Tsevelkhoroloo Maral	301
		Soh Eun-Hee	103, 227		
		Soh Moon-Soo	33, 154		

Name	Page	Name	Page	Name	Page
<b>U</b>					
Uhm Yoon Kyung	151, 207	Yoo Chang Soo	22		
Ulziisaikhan Javzandulam	176	Yoo Jemin	194, 195, 238		
Um Yurry	194, 195, 231, 235, 238, 272, 276	Yoo Soo-Cheul	194		
Um Yurry	195, 231, 235, 238, 272, 276	Yoo Yo-Han	60, 127		
<b>V</b>					
Vicheka Than	136	Yoon Ho-Sung	278		
<b>W</b>					
Wang Heng	270	Yoon Hye-Jin	61, 82		
Wang Seung-Hyun	286	Yoon Jin Seok	240		
Wang Xiao-Qiang	162	Yoon Jinmi	289		
Wang Yiming	282	Yoon Min-Young	34, 158, 162, 163, 164		
Win Khin Thanda	62	Yoon Moo-Kyoung	227		
Won Jungyeon	138, 180, 184, 222	Yoon Seongmun	292		
Won So Youn	174, 175, 192, 228	Yoon Sun-Yung	103		
Won Yong-Jae	67	Yoon Ui-Soo	210		
Woo Hee-Jong	191, 192, 205	Yoon Ung-Han	150		
Woo Je Wook	265, 267	Yoon Yeo-Tae	39		
Woo Jinkyu	151	Yoon Young Ha	83, 146, 224		
Woo Mi-Ok	186	Yoon Young-Hwan	61		
Woo Sun-Hee	93, 187, 188, 189, 190	You Jang-Hwan	110		
<b>X</b>					
Xuan Yuan Hu	286	Yu Dal-A	68, 70, 110, 112		
<b>Y</b>					
Yacoubi Inès	45	Yu Je-Hyeok	93, 190		
Yamaguchi-Shinozaki Kazuko	124, 223	Yu Jie	34, 159, 162, 165		
Yang Hee-Bum	213	Yu Xiaona	15		
Yang Jin Ho	202, 215	Yu Yeisoo	7, 28		
Yang Jong-Ho	187, 188	Yu Yoye	30		
Yang Jung-Il	289	Yun Boo Min	128		
Yang Seon-Mo	93	Yun Byoung-Kook	34, 162		
Yang Tae-Jin		Yun Byung-Wook	135		
Yang Tae-Jin	28, 140, 169, 295	Yun Dae-Jin	142		
Yeom Inhwa	182, 316	Yun Doh-Won	177, 183		
Yeom Seon-In	175, 196	Yun DongKue	196		
Yi Gi-Hwan	135, 136, 137	Yun Geon-Sig	59		
Yi Kyunguk	94	Yun Hong-Tai	111		
Yi Yealim	206	Yun Min-Heon	93, 190		
Yoo Bong Sik	77	Yun Sopheap	135, 136		
		Yun Yeo-Tae	61		
		Yun Young-Ho	93		
<b>Z</b>					
		Zamir Dani	6		
		Zhang Chunying	62		
		Zhang Jun-Ying	176		



## 한국육종학회

Korean Society of Breeding Science

---

---

인 쇄 2015년 6월 25일  
발 행 2015년 6월 30일  
발행자 사단법인 한국육종학회  
경기도 수원시 권선구 수인로 126 국립식량과학원 중부작물부 내  
인쇄처 도서출판 (주)씨아이알 02-2275-8603  
서울특별시 중구 필동로8길 43(예장동 1-151)

---