

2014 
한국육종학회
차세대BG21사업단
골든씨드프로젝트사업단
공동심포지엄



주제 : 생산성 향상을 위한 식물 육종 전략
Plant Breeding Strategies for Improvement of Productivity

일 시 | 2014년 7월 2(수) ~ 4일(금)

장 소 | 라마다플라자 제주호텔



주 최 | 사단법인 한국육종학회

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후 원 | 한국과학기술단체총연합회, 한국농식품생명과학협회, 농촌진흥청, 국립산림과학원

:: Program

2014 한국육종학회-차세대BG21사업단-골든씨드프로젝트사업단 공동심포지엄

2014년 7월 2(수) ~ 4(금), 라마다플라자 제주호텔

1일째 [2014. 7. 2. 수]

차세대바이오그린21 사업단		
13:00~18:00	식물분자육종사업단 워크숍 등록 및 포스터 부착 · 식물분자육종사업단 발표	(장소 : 로비) (장소 : 그랜드 볼룸 1홀)
18:00~20:00	만찬	

2일째 [2014. 7. 3. 목]

09:00~17:00	공동심포지엄 학술발표회 등록 및 포스터 부착	(장소 : 로비)
08:30~11:00	· 식물분자육종사업단 발표	(장소 : 그랜드 볼룸 1홀)
11:00~12:30	· 한국육종학회 확대이사회	(장소 : 그랜드 볼룸 4홀)
골든씨드프로젝트 발표		
09:00~11:20	· GSP 채소종자사업단	(장소 : 그랜드 볼룸 3홀)
	· GSP 원예종자사업단	
	· GSP 식량종자사업단	(장소 : 그랜드 볼룸 2홀)
학술강연 및 포스터 발표		
13:00~13:10	개 회 식 (한국육종학회장 인사)	(장소 : 그랜드 볼룸)
	좌장 : 임용표 (충남대학교)	
13:10~13:50	· Plant Breeding in the European Community: economical, societal and academic aspects Christian Jung (Germany society of plant breeding, Germany)	
13:50~14:30	· SNP genotyping to accelerate crop breeding Michael Thomson (International Rice Research Institute, Philippines)	
14:30~14:50	휴 식	
	좌장 : 노일섭 (순천대학교)	
14:50~15:30	· Plant defense mechanism after flooding Ming-Che Shih (Agricultural Biotechnology Research Center, Taiwan)	
15:30~16:10	· Wheat breeding for drought resistance in Japan Hisashi Tsujimoto (Tottori University, Japan)	
16:10~16:20	휴 식	
	좌장 : 최임수 (국립식량과학원)	
16:20~17:00	· The importance of the natural variation in the plant circadian clock to enhance crop productivity under high temperature environments 김태성 (공주대학교)	
17:00~17:40	· 맞춤형 품종 개발을 위한 유전체 기반 분자 육종 플랫폼 개발 및 활용 김을호 (국립식량과학원)	
17:40~18:10	정기총회 & 학회상, 경산육종학회상 시상	
18:10~19:00	분과별 포스터 발표	(장소 : 로비)
19:00~21:00	리셉션	

3일째 [2014. 7. 4. 금]

구두발표 & 차세대바이오그린21 사업단

분과별 구두발표	
08:30~10:30	A. 수량 및 저항성육종 좌장 : 박순기(국립농업과학원), 강병철(서울대학교) (장소 : 그랜드 볼룸 1홀)
	B. 품질육종 및 유전변이, C. 분자육종 및 유전공학 좌장 : 박광근 (국립식량과학원), 이효연 (제주대학교) (장소 : 그랜드 볼룸 3홀)
작물 유전체 육종 (차세대유전체연구사업단)	
좌장 : 박범석, 김태호 (국립농업과학원) (장소 : 그랜드 볼룸 2홀)	
08:30~09:00	· 차세대유전체연구사업단의 비교유전체 연구 · 개발 박범석 (국립농업과학원)
09:00~09:30	· Distribution of Single Nucleotide Polymorphism(SNP) in Major Domestic Rice Cultivars compared to Japonica and Indica Reference Genomes 남백희 (명지대학교)
09:30~10:00	· TGsol : 가지과 유전체 정보 실용화 연계 인터페이스 개발 및 활용 조성환 ((주) 씨더스)
10:00~10:30	· Development, Validation, and Utilization of Large Axiom [®] Soybean SNP Genotyping Array 문중경 (국립식량과학원)
한·중 벼 육종 및 육종 신기술 공동 심포지움 (GM작물실용화사업단)	
좌장 : 박수철, 이강섭 (국립농업과학원) (장소 : 그랜드 볼룸 4홀)	
08:30~09:00	· Conventional breeding strategy in China Zhong-Ze Piao (Shanghai Academy of Agricultural Science, China)
09:00~09:30	· Development and utilization of hybrid rice in China Zhi-Xiang Lu (Anhui Academy of Agricultural Science, China)
09:30~10:00	· Current status of rice breeding in Korea and action plan development against transforming environment of rice industry in terms of agronomic trait 김보경 (국립식량과학원)
10:00~10:30	· Global Seed market status and R&D scope 박희영 (신젠타 코리아)
10:30~10:40	휴 식
학술강연	
좌장 : 강규석 (서울대학교) (장소 : 그랜드 볼룸 1홀)	
10:40~11:20	· Genetic diversity, gene discovery and utilization in woody populations Bernd Degen (Thünen-Institute of Forest Genetics, Germany)
11:20~12:00	· 벼 핵심집단과 중요 자원의 유전체 재분석 및 육종 활용 박용진(공주대학교)
12:00~12:30	시상식 및 폐회

⦿ Symposium Program

Plant Breeding Strategies for Improvement of Productivity

Date and Place (2014. 7. 2 ~ 4), RAMADA PLAZA JEJU HOTEL

July 2 (Wednesday)	
13:00~18:00	Registration and Poster Mounting for PMBC
Plant Molecular Breeding Center Workshop (Next-Generation BioGreen21)	
18:00~20:00	Dinner
July 3 (Thursday)	
08:30~11:00	Plant Molecular Breeding Center Workshop (Next-Generation BioGreen21)
09:00~17:00	Registration and Poster Mounting
Golden Seed Project workshop	
09:00~12:00	<ul style="list-style-type: none"> • Vegetable seed project (chinese cabbage, radish, watermelon, pepper, paprika) Yong Pyo Lim (Chungnam National University) • Horticultural seed project (cabbage, tomato, onion, tangerine, lily, mushroom) III-Sup Nou (Sunchon National University) • Crop seed project (Rice, Potato, Corn) Im-Soo Choi (National Institute of Crop Science)
Plenary Lecture & Poster Presentation	
13:00~13:20	Opening Ceremony Chair : Yong Pyo Lim (Chungnam National University)
13:20~14:00	<ul style="list-style-type: none"> • Plant Breeding in the European Community: economical, societal and academic aspects Christian Jung (Germany society of plant breeding, Germany)
14:00~14:40	<ul style="list-style-type: none"> • SNP genotyping to accelarate crop breeding Michael Thomson (International Rice Research Institute)
14:40~14:50	Coffee Break
Chair : III-Sup Nou (Sunchon National University)	
14:50~15:30	<ul style="list-style-type: none"> • Plant defense mechanism after flooding Ming-Che Shih (Agricultural Biotechnology Research Center, Taiwan)
15:30~16:10	<ul style="list-style-type: none"> • Wheat breeding for drought resistance in Japan Hisashi Tsujimoto (Tottori University, Japan)
16:10~16:20	Coffee Break
Chair : Im-Soo Choi (National Institute of Crop Science)	
16:20~17:00	<ul style="list-style-type: none"> • The importance of the natural variation in the plant circadian clock to enhance crop productivity under high temperature environments Tae-Sung Kim (Gongju National University, Korea))
17:00~17:40	<ul style="list-style-type: none"> • Genomics-assisted breeding platform for designed cultivars Yul-Ho Kim (National Institute of Crop Science, Korea)
17:40~18:10	Regular General Meeting
18:10~19:00	• Poster Presentation
19:00~21:00	Dinner

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SYMP-01**Plant Breeding in the European Community: economical, societal and academic aspects**

Christian Jung

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For a long time, public awareness of plant breeding activities was low. Since the late 1970s, the situation has changed when activists started a campaign against large multinationals because they began to buy seed companies all over the world. They were concerned about their power to control the world seed market and distribute seeds only to the rich. A few years later, with the advent of the gene technology age and the first genetically modified plants reaching the market scale a new debate came up fueled by the green movement. Since that time, any activities with genetically modified plants are strictly regulated in all industrial countries. In Europe, a number of directives have been implemented by the European Commission which have been transferred into national legislation by the member countries. Market approval for GMO varieties needs a qualified majority by the board of ministers but unfortunately there has been no agreement since more than 15 years. This was one reason why all industry activities in this field (and most academic as well) came to an end or were relocated outside the EU. Today, only a very small area (<100,000 ha) is planted with GMO seeds in Europe while acreages have been up to >150 million ha worldwide. In Europe, plant variety release and market approval is regulated by a Community Plant Variety Protection directive which gives a breeder the exclusive right to market its variety all over Europe. To get an approval, a new variety must fulfill a number of requirements. It must be novel, distinguishable and consistent and it must have an added value to the farmer/grower. Plant Breeding in worldwide and in Europe is dominated by some multinationals, however in Germany a number of small and medium sized companies are still very successful in the seed market. Those companies have a focus on a small range of crops and their activities are mostly limited to Europe with Eastern Europe gaining more importance in the past years. Interestingly, their R&D rate is among the highest of all industry (~16%) which demonstrates a great interest to adopt new technologies. The EC has supported plant breeding research by its framework programs where researchers from academia and industry work together in a multinational project. Moreover, the German government has been increasing the budget for research and technology over the past 8 years. Breeding research has been supported by numerous initiatives such as GABI, the German national plant genome project launched in 1998. Recently, a large project to improve yield and yield stability of wheat has been started by the ministry of agriculture. The German research foundation (DFG) supports basic and applied breeding research in different ways. Every scientist working in Germany can submit a proposal to the DFG at any time. Coordinated projects such as priority programs (PP) enable the collaboration of a limited number of research groups. We have initiated a PP on flowering time research 3 years ago. Twenty groups work on different aspects of flowering time regulation in model and crop plant species (<http://www.flowercrop.uni-kiel.de/en>). At the end of my talk, I will present a selection of recent results from our PP with a direct impact on plant breeding.

SYMP-02

Applying High-Throughput SNP Genotyping and Sequencing to Accelerate Progress in Rice Breeding

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We are currently developing a high-throughput single nucleotide polymorphism (SNP) genotyping service at IRRI to accelerate progress in rice breeding by providing rapid and cost-effective marker services. SNP marker development and validation is being performed based on cloned genes and QTLs, GWAS hits, and whole genome sequence data to identify predictive SNP markers at important genes for key traits for the breeding programs. Trait-based and targeted SNPs are being deployed in sets of 24 and 96 SNPs on a Fluidigm EP1 system. At the same time, 384 SNP sets and a 6K SNP chip developed by Susan McCouch at Cornell University are being used for higher density genome scans on an Illumina system. Genotyping by sequencing (GBS) approaches with 96 and 384 barcoded samples per sequence lane are also being evaluated in comparison to SNP array technology based on the number of loci, call rates, turnaround times, and cost per sample. An efficient sample processing workflow with an integrated LIMS is also being optimized to enable high throughput genotyping with sample tracking to minimize errors. Moreover, web-based SNP data analysis tools have been deployed through the IRRI Galaxy workbench to speed up SNP data analysis. Future efforts will focus on large-scale deployment of GBS across breeding materials to enable QC genotyping, tracking of donor introgressions, and integration of genome-wide prediction into the variety development pipelines. The large-scale application of high-density markers will help transform IRRI's rice breeding programs and increase the rate of genetic gain towards developing high-yielding, stress-tolerant varieties for target environments and market segments.

SYMP-03**Transcription regulatory pathways associated with hypoxia in *Arabidopsis***

Ming-Che Shih

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Transcriptional control plays an important role in regulating submergence responses in plants. Although numerous genes are highly induced during hypoxia, their individual roles in hypoxic responses are still poorly understood. Through microarray studies, we identified a number of transcription factors (TF) that are induced in different stages of hypoxia. We have chosen two TFs, *AtHRE1*, which was specifically induced during hypoxia but not by cold, drought or dehydration, and *WRKY22*, which was rapidly and strongly induced upon submergence in *Arabidopsis*, for further studies. Our results suggest that in addition to ethylene an ethylene-independent signal is also required to mediate hypoxia induction of *HRE1*. Through a series of genetic and molecular analyses, we found that hypoxia-inducible genes could be affected by *AtHRE1*-RNAi lines in two different ways: hypoxic induction of glycolytic and fermentative genes was reduced, whereas induction of a number of peroxidase and cytochrome P450 genes was increased. Taken together, our results show that *AtERF73/HRE1* is involved in modulating ethylene responses under both normoxia and hypoxia. We found that many genes in the WRKY transcription factor (TF) family were rapidly and strongly induced upon submergence in *Arabidopsis*. Notably, a large proportion of innate immunity marker genes were co-induced with *WRKYs* under submergence and other stresses. Compared to wild-type, *WRKY22* T-DNA insertion mutants, *wrky22-ko1* and *wrky22-ko2*, have lower submergence-acclimatized disease resistance. Submergence induction of innate immunity markers, such as *FRK1* and *WRKY53*, were lower in these *WRKY22* mutants. These results provide evidence that submergence triggers *Arabidopsis* immunity through *WRKY22*, allowing plants to defend simultaneous or sequential infection upon floods.

SYMP-04**Germplasm enhancement for wheat breeding for drought tolerance**

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The global population increase causes various problems as food and energy shortage and environmental change. As for food problem, innovative agricultural system is required to double food production for 10 billion people in the mid of this century. We introduced the genome or chromosomes of related wild species to the common wheat by interspecific crosses and evaluated their characters. Some alien chromosome addition wheat lines showed better bread-making quality, kernel mineral contents, or phosphorus-use efficiency. The lines with a chromosome of *Leymus* were found to secrete a substance to inhibit nitrification, which may increase nitrogen-use efficiency. In addition, we produced multiple synthetic derivative (MSD) populations in the genetic background of several practical cultivars. The morphology of each plant in the population was similar to that of the common wheat variety and relatively regular with each other, which enabled to find QTLs to elucidate tolerance of abiotic stresses. We are cultivating these lines in the North African countries and evaluating.

SYMP-05

The importance of the natural variation in the plant circadian clock to enhance crop productivity under high temperature environments

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Most eukaryotic organisms, including plants, display specialized cellular and behavioral rhythms with a period of approximately 24 hours. The circadian clock generates this rhythm to convey daily or seasonal basis of temporal information, coordinating the proper phasing of many important cellular processes. Temperature compensation (TC) is one of the defining features of the clock mechanism. Under this function, the speed of the clock or period remains relatively constant over physiologically relevant temperatures, unlike the biochemical reactions. Thus, TC allows organisms to sustain their life ordinarily in various thermal environments by providing an accurate measure of the passage of time regardless of surrounding temperatures. Previously, Edward and his colleagues performed a quantitative trait loci (QTL) study to find TC related natural variations in the recombinant inbred line (RIL) population from two *Arabidopsis* ecotypes, which are adapted to different thermal environments; one parent is *Cvi* accession (*Cvi*) which originates from the warm climate, Cape Verde Island, and the other is *Ler* accession (*Ler*) from Northern Europe. For the two most significant QTLs, the core clock components in *Arabidopsis* clock, *GIGANTEA* (*GI*) and *ZEITLUPE* (*ZTL*) are proposed as strong candidates. Moreover, the amino acid substitution leading to GI^{Cvi} and ZTL^{Cvi} (*Ler* to *Cvi*) are suggested to be the causal factors for the TC QTLs respectively. However, precise molecular mechanisms of these natural variations on TC are still not understood well. Here, we elucidate the molecular impact of the natural variation shaping GI^{Cvi} and ZTL^{Cvi} on TC function. GI^{Cvi} and ZTL^{Cvi} post-translationally regulate *ZTL* stability in antagonistic way, resulting in the opposite period/clock effects mediated by *ZTL* protein abundance. However, if both GI^{Cvi} and ZTL^{Cvi} are present, they mutually balance their own effect on *ZTL*, which in turn supports TC capacity of *Cvi* especially at high temperatures. Considering the amino acid residues in *GI* and *ZTL*, where the natural variations arise, are highly conserved across many important crop species including rice, corn, cabbage and etc., this research will give valuable insights into the TC related thermal adaptive processes in *Arabidopsis* as well as those important crop plants.

Keywords: Circadian clock, Temperature compensation, Heat tolerance, Thermal adaptive processes, Cape Verde Island, *Arabidopsis*, Major Crop species, *GIGANTEA*, *ZEITLUPE*.

SYMP-06**Genomics-assisted breeding platform for designed cultivars**Yul-Ho Kim¹, Hyang-Mi Park¹, Tae-Young Hwang¹, Dongwoo Lee², Sunghoon Lee²¹National Institute of Crop Science, Rural Development Administration, Republic of Korea²Theragen Bio Institute, TheragenEtex, Suwon 443-270, Republic of Korea

In contrast with wild species, cultivated crop genomes consist of reshuffled recombination blocks, which occurred by crossing and selection processes. Accordingly, recombination block-based genomics analysis can be an effective approach for screening target loci with agricultural traits and for developing designed cultivars. We propose the molecular breeding platform based on the variation block (VB) method, which is a three-step process for recombination block detection and comparison. The first step is to detect variations by comparing the short-read DNA sequences of the cultivar to the 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 termed variation blocks. Finally, the genomes are compared using the variation blocks. The variation block method identified recurring recombination blocks accurately and successfully represented block-level diversities in the publicly available genomes of 31 soybeans and 23 rice accessions. The practicality of this approach was demonstrated by the identification of a putative locus determining soybean hilum color. In addition, we identified recombination hot spots of soybean genome in 614 recombinant inbred lines (RILs) using VB-specific indel markers. We expect that this platform facilitate the development of designed cultivars by introducing precise target loci into plant genomes.

SYMP-07**Genetic diversity, gene discovery and utilisation in woody populations**

Bernd Degen

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Trees are extraordinary long living, sessile organisms that are faced quite variable environmental conditions and biotic stress factors during their life. They have a high level of genetic diversity to ensure adaptation and adaptability. With the massive advance in next generation DNA-sequencing, our abilities to screen this genetic variation have increased drastically. I will give an overview on the different genomic approaches, main target tree species and examples for application in the area of population genetics. Examples will show how high throughput SNP genotyping clarifies our views on taxonomy, phylogeography and provide us with useful data for different diagnostic applications such as species identification, tracking geographic origin and screening the level of pre-disposition to abiotic and biotic stress factors. Since a few years next generation sequencing and advanced molecular marker development have also been used in genetic association studies and transcriptome sequencing (RNASeq) in order to discover genes that are coding economical and ecological important phenotypic traits of trees. I will present examples on target phenotypic traits and the use in tree breeding programs.

SYMP-08

Genome re-sequencing of rice core set for breeding: Practical comparative genomics through whole genome-wide allele mining of agronomic traits

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Genetic resources play a great role in crop breeding because of containing a broad array of useful genes. Currently, the harder are rice breeders trying to develop new rice cultivars with the improved traits, they are more often handicapped by the limited availability of germplasm resources. Thus, a desirable core or heuristic (HS) set of germplasm with maximum genetic diversity can be usefully exploited to breakthrough the present and future challenges of the rice breeding. As such we previously developed the rice HS sets of 166 diverse accessions out of a total 24,368 rice germplasms. Here, we report a large-scale analysis of the patterns of genome-wide genetic variations accumulated in the HS as well as Korean rice over the time. We characterized a total of about 11.8 millions of single nucleotide polymorphisms (SNPs) across the rice genome from resequencing a total of 295 rice genomes including 137 HS and 158 KB rice sets, with an average of approximately 10x depth and > 90% coverage. Using about 460,000 high-quality SNPs (HQSNPs), we specified the population structure, confirming our HS set covers all the rice sub-populations. We further traced the relative nucleotide variabilities of HQSNPs and found the level of the diversity was dynamically changing across the KB genome, which reveals the selection history of KB lines in the past and present. In addition, the results of our genome wide association study (GWAS) suggests that our HS can be also a good reservoir of valuable alleles, pinpointing those alleles underlying the important rice agronomical traits. Overall, the resequencing of our HS set re-illuminates the past, present of the germplasm utilization, which will support the Korean rice breeding in the future.

구두발표



1. 수량 및 저항성육종
2. 품질 육종 및 유전변이
3. 분자육종 및 유전공학



OA-01

수발아 검정 방법을 이용한 백립계 수발아 저항성 육종

김정훈¹, 강천식¹, 김학신¹, 최인덕¹, 신상현¹, 손재한¹, 유인영¹, 정영근¹, 이춘기¹, 박광근¹, 박철수²¹전라북도 익산시 평동로 국립식량과학원 벼백류부 맥류사료작물과²전라북도 전주시 전북대학교 농업생명과학 작물생명과학과

수발아는 밀의 생육 단계 중에서 등숙 기간에 잦은 강우와 낮은 온도로 수확하기 전에 이삭이 발아되는 현상으로 수발아가 발생하면 품질이 저하되고 수량도 감소하게 된다. 최근 주요 밀 생산국에서 3~4년 마다 발생하고 있으며, 국내에서도 최근 이상기상으로 인해 밀 수확시기에 강우가 발생할 확률이 높아지고 있어 대비가 필요하다. 우리나라에서 70% 이상 재배되고 있는 금강밀의 수발아율은 평균 35% 정도로 높다. 수발아가 진행되면 α -amylase에 의해 전분이 분해되기 때문에 제분하여 나오는 밀가루나 가공 제품이 고유의 특성을 잃어버리게 된다. Falling number의 기준 수치인 300sec 이상으로 측정되어야 온전한 품질을 나타내지만, 수발아된 원맥은 100sec 수치를 나타내어 부적합한 특징을 알 수 있었고, 수분, 회분, 단백질, 침전가와 같은 품질 요인들을 측정하면 정상 원맥과 다른 품질을 나타내었다. 국수 가공 적성에서 면대 밝기(L*)값은 71.99로 시중의 중력분 밀가루와 금강밀에 비하여 면대색이 어두웠으며, 면대두께는 1.67mm로 중력분과는 큰 차이가 없었지만, 금강밀 1.88mm에 비해서는 얇았다. 수발아된 원맥의 면 견고성은 중력분에 비해서 높았고, 씹힘성은 중력분에 비해 낮아 식감이 좋지 않은 결과를 나타냈다. 제빵 가공 적성에서 빵부피 688ml로 시중의 강력분 밀가루 850ml에 비하여 부피가 작았으며, 속질경도는 3.17N로 강력분 0.95N보다 높아 식미감에 좋지 않은 영향을 미칠 것으로 예상되었다. 수발아 검정 방법으로는 직접 인위적으로 물을 주는 인공강우, 모래에 이삭을 꽂아두고 발아율을 측정하는 모래묻이법과, 종자 휴면 특성을 나타내는 지표인 GI(Germination index)가 있다. 인공강우, 모래묻이법은 년차간 차이가 나타났지만, GI 평가는 년차간 차이가 나타나지 않았다. GI값은 모래묻이법이나 인공강우를 이용한 수발아율과 정의 상관을 나타내어 향후 수발아 저항성 및 계통 선발의 지표로 활용이 가능할 것이다. 염색체 4AL에 존재하며 외국 밀 품종에서 수발아 저항성 관련 유전자 여부를 확인하는데에 효과적으로 활용되고 있는 SSR 마커인 ZXQ118와 Xhbe03를 이용하여 국내 밀 품종을 평가한 결과, 국내 밀 품종의 변이 폭이 다양하지 않아 수발아 저항성 유전자를 구별하기는 어려웠다. 앞으로 국내 밀에서 수발아 저항성 계통 선발에 활용이 가능한 마커 개발에 대한 연구가 필요하다. 종합적으로, 수발아에 의해 품질이 저하되고, 수량이 감소하는 것을 예방하기 위해서는 수발아 검정 방법을 활용하여 정확한 검정을 통한 수발아에 강한 계통 육성과 함께 궁극적으로는 수발아 저항성 품종 개발이 필요하다.

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OA-02

Defining the Genome Structure of “Tongil Rice”, A Cultivar for Korean Green Revolution, Derived from *indica* × *japonica* Hybridization

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Tongil (IR667-98-1-2) rice, developed in 1972, is a high-yielding rice variety derived from a three-way cross between *indica* and *japonica*. Tongil contributed to staple food self-sufficiency of Korea, an achievement that was termed the ‘Korean Green Revolution’. In this study, we analyzed the nucleotide-level genome structure of Tongil rice and compared it to those of the parental varieties. A total of 17.3 billion Illumina Hiseq reads, 47× genome coverage, were generated from Tongil rice. Three parental accessions, two *indica* and one *japonica* types, of Tongil rice were also sequenced for approximately 30x genome coverage. A total of 2,149,991 SNPs were detected between Tongil and Nipponbare; the average SNP frequency of Tongil was 5.77 per kb. Genome composition based on the SNP data by comparing with the three parental genome sequences on sliding window of Nipponbare genome sequence revealed that 91.8% of the Tongil genome originated from the *indica* parents and 7.9% from the *japonica* parent, different from the theoretical expectation in a three-way cross, i.e., 75% *indica* and 25% *japonica* parental origins on average. Copy number of SSR motifs, ORF gene distribution throughout the whole genome, gene ontology (GO) annotation, yield-related QTLs or gene locations, and polymorphic transposon insertions were also comparatively analyzed between Tongil and parents using sequence-based tools. The results indicated that each genetic factor was transferred from parents into Tongil in proportion to the whole-genome composition. The Tongil rice is the first successful superior cultivar derived from *indica* × *japonica* hybridization in Korea. Defining of genome structure demonstrates that the Tongil genome is composed mostly of the *indica* genome with a small proportion of *japonica* genome introgression. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008125), Rural Development Administration, Republic of Korea.

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OA-03

Linkage analysis between *Pi45(t)* and *SPR3* locus, and evaluation of the effect of *SPR3* locus on yield-related traits in rice

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While a wealth of genetic diversity can be found from traditional rice varieties, wild rice species and wild relatives of rice, transfer of useful genes to modern varieties are often hampered by linkage drag. In this study, the previously identified blast resistance locus *Pi45(t)* from a cross between ‘Ilpumbyeo’ and ‘Moroberekan’ was showed to be linked with the spreading-type panicle caused by the *SPR3* locus. Using InDel4 and RM17579 linked to the *Pi45(t)* and the *SPR3*, respectively, the distance between the two loci was estimated to be 6.9cM. This suggests a tight, yet incomplete linkage and provides the opportunity to utilize *Pi45(t)* in breeding programs without including *SPR3*. Two groups based on the genotype at the *SPR3* locus were assembled; the CLosed Panicle (CLP) and SPReading panicle (SPR) groups with lines, which were homozygous for the Ilpumbyeo and Moroberekan alleles, respectively. A comparison between the traits of CLP and SPR groups revealed a decrease in 1000-grain weight and length and an increase in spikelets per panicle and secondary branches in the SPR group. This complicates selection against *SPR3* as it is not clear whether these quantitative trait loci are linked to either *SPR3* or *Pi45(t)*. Re-evaluation of these traits using lines recombinant at the two loci would be necessary to clarify this issue.

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OA-04

Identification and characterization of a quantitative trait locus, *dth9*, controlling heading date in rice.

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Using a series of BC₈F₄ nearly isogenic lines(IL-20) derived from a cross between Hwaseongbyeo, as the recurrent parent, and wild rice *Oryza minuta* (IRGC Acc. No. 101144) as the donor parent we constructed a high-resolution physical map for the days to heading (*dth9*)-QTL. *dth9* QTL was mapped to the long arm of chromosome 9 across a 34.74-kb region containing 8 predicted genes. Heading date of *Japonica* rice variety Hwaseongbyeo was one week earlier than a near-isogenic line (NILs) IL-20 under natural field (NF) conditions and 3-4 days under short-day (SD) conditions implying that the *dth9*-QTL is involved in photoperiod sensitivity in rice. Of the 8 predicted genes three were protein-coding genes in *dth9*-QTL region. According to RiceXpro published data, micro-array analysis of different leaf developmental stages of Nipponbare showed a higher level of *LOC_Os09g36700* mRNA expression during panicle initiation stage. This data further supported our prediction that *dth9* locus is responsible for delayed heading in IL-20. Previous studies showed that RNase T2 family proteins are involved in photoperiod sensitivity. Based on these findings we sequenced two candidate genes, which encoded for RNase T2 family proteins. Interestingly, we found the existence of a missense mutation in *LOC_Os09g36700* gene suggesting that *dth9*-QTL might control difference in days to heading between Hwaseongbyeo and IL-20. The QTL for days to heading had not been detected in previous QTL studies between *Oryza* cultivars, indicating the existence of potentially novel allele from *O. minuta*.

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OA-05

Evaluation of wheat type I and II resistance to Fusarium head blight in the greenhouse and field in 2013.

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Fusarium head blight (FHB), primarily caused by *Fusarium graminearum* is a major disease problem on wheat and barley around the world. The objectives of this study were to evaluate for FHB resistance under greenhouse and field condition in 2012 and 2013. We screened for Type I resistance in the field using spray inoculation and for Type II resistance in the greenhouse using single floret inoculation. Sumai 3 and Ning7840 were used the FHB resistant check. Five hundred and twelve lines were evaluated for resistance to initial infection (type I) and to spread of symptoms within spike (type II). The inoculum was *F. graminearum* (GZ3639) prepared at a concentration of 1×10^5 macroconidai/ml with Tween 20. The field screening plots were inoculated twice and mist-irrigation was applied to facilitate FHB development. FHB severity was assessed visually 21 days and determined as the percentage of symptomatic spikelets from the total of all spikelets observed in 20 spikes. Both in the greenhouse and field test, we could observe five categories of FHB severity: resistant (R: 0-20%), moderately resistant (MR: 21-40%), moderate (M: 41-60%), moderately susceptible (MS: 61-80%), and susceptible (S: 81-100%). The results showed that seventy seven lines showed the R and MR category on FHB severity. In addition, nine lines showed similar FHB severity compared to Sumai 3 (13.3%).

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OA-06

콩에서 싸리수염진딧물 저항성 유전자 탐색

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기후변화에 따른 지구온난화로 작물을 가해하는 해충의 대발생 가능성이 증가됨에 따라 안정적인 식량 공급에 필수적인 내충성 품종 개발이 필요하다. 해충에 대한 저항성 자원 탐색과 관련 저항성 유전자 확보가 우선되어야 하며, 관련 유전자에 대한 분자유종시스템 적용을 위한 DNA marker 개발 등 관련기술 확보가 필수적이다. 본 연구에서는 우리나라에서 콩을 가해하는 3대 진딧물 중 하나인 싸리수염진딧물에 대한 저항성 유전자 탐색을 실시하였다. 싸리수염진딧물에 대한 저항성 검정에는 감수성 품종인 Williams 82와 저항성 품종인 PI366121의 인공 교배를 통해 유래된 144개의 RIL 집단을 이용하였다. 완전임의배치법을 이용하여 Pot에 파종 후 3분엽이 전개되기 전에 접종을 실시하였다. 접종된 RIL 집단을 Growth Chamber로 이동 후 2주간 관찰하였다. RIL 집단에 SNP marker를 이용하여 genotyping을 실시하고 이를 이용하여 QTL분석을 하였다. 분석결과 콩 Chromosom 7번에서 BARC-0428150084와 BRAC-015945-020 marker 사이에 저항성 유전자가 위치하였고, 이때 LOD 값은 46.0으로 나타나 매우 높은 QTL 효과를 보여 향후 본 유전자를 이용한 저항성 품종육성가능성을 보여주었다.

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OA-07

A New Strawberry, 'Damhyang' with High Sugar Content and Early Harvesting

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A new strawberry (*Fragaria Xananassa Duch.*) cultivar, 'Damhyang' was developed from a cross between 'Akihime' and 'Maehyang' by selection of seedlings and lines at Agricultural Development & Technology Center, Damyang in 2012. In 2006, This cultivar was showed excellent characteristics including weak dormancy, vigorous growth, high yield and fruit quality. It was named Damyang No. 1' as line name after examining the productivity in forcing culture from 2007 to 2009. Again, after regional adaptability test between 2010 and 2011, the cultivar name, 'Damhyang', was imposed on this cultivar. The general characteristics of 'Damhyang' include high vigor and erect type in growth. The flowering and harvesting date of 'Damhyang' are similar to that of 'Akihime', but earlier than 'Seolhyang'. The fruit shape is conic, fruit color is red, and fruit quality was superior to that of 'Akihime'. The average fruit weight of 'Damhyang' is about 18.8g and the marketable yield is relatively high because of low percentage of abnormal fruit bearing. It is resistant against powdery mildew but sensitive to anthracnose and aphids. 'Damhyang' is suitable for forcing culture because it shows weak dormancy, high yield and fruit quality.

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OB-01

GBSS 유전자 특성을 이용한 국수식미 개선 및 밀 품종 개발

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최근 바이오 연료용 작물의 수요증가와 기상악화는 국제 밀 생산량 감소와 국제 밀 가격이 상승으로 이어져 식량 안보가 중요시 되고 있다. 국내 식용 밀 수입량은 연간 200만톤 가량이며, 그 중 49%는 제면용으로 이용되고 있다. 국내 밀 품종은 70년 이후 약 35 품종이 개발되었고, 전남북 지역에서 생산되는 금강밀이 전국 생산량의 70%를 차지하고 다목적용으로 활용되고 있으나 소비자가 요구하는 수입밀에 비하여 식감이 다소 떨어지는 단점이 있어 식미향상이 요구되고 있다. 국수용 밀가루는 단백질함량이 10.0~12.0% 사이의 것이 적합하며, 함유 성분 중 메성 전분인 아밀로스의 함량이 낮을수록 면발이 부드럽고 점성과 탄성이 증가하여 쫄깃쫄깃한 식감을 지니게 된다. GBSS(Granule bound starch synthase)는 전분입자에 결합하는 주요 단백질로 아밀로스 합성에 관여하고, 7AS, 4AL, 7DS에 위치하고 있다. 최근 국수식미 향상을 위하여 GBSS 변이계통을 모본으로 하고, 국내 국수용 대표 품종인 금강밀을 부분으로 하여 '호중'과 '중모2012'를 개발하였다. '호중'은 GBSSI 유전자 중 *Wx-B1*이, '중모2012'는 *Wx-A1*과 *Wx-D1*이 mutant형을 지니고 있다. 메성인 '금강'의 아밀로스 함량은 22% 이상이었으나, '호중'과 '중모2012'는 각각 20.5%와 18.9%로 '금강'보다 아밀로스 함량이 낮았다. 면대밝기(L*)에서 '호중'과 '중모2012'는 각각 80.63과 80.92로 '금강'(77.62~77.94)보다 밝았고, 국수의 식미검정 결과 '호중'과 '중모2012'의 경도는 각각 2.62N과 3.19N으로 '금강'(4.34~4.21N)보다 낮아 부드러웠다. 또한, 점성과 탄성이 높아 '금강'보다 국수 식감이 우수한 것을 확인하였다. 아밀로스함량이 낮은 '호중'과 '중모2012'의 면을 삶는 시간은 3.79정도로 '금강'보다 2분 이상 짧아 산업현장에서는 연료비를 절감할 수 있어 생산비가 절감할 수 있을 것으로 기대된다. 금후 국내 국수용 밀 품종 개발은 GBSS의 특성을 이용하여 저아밀로스 다수확 국수용 밀 품종을 목표로 추진할 계획이다.

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OB-02

Natural Variation in *OsPRR37* Regulates Heading Date and Contributes to Rice Cultivation at a Wide Range of Latitudes

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Heading date and photoperiod sensitivity are fundamental traits that determine rice adaptation to a wide range of geographic environments. By quantitative trait locus (QTL) mapping and candidate gene analysis using wholegenome re-sequencing, we found that *Oryza sativa Pseudo-Response Regulator37* (*OsPRR37*; hereafter *PRR37*) is responsible for the *Early heading7-2* (*EH7-2*)/*Heading date2* (*Hd2*) QTL which was identified from a cross of late-heading rice ‘Milyang23 (M23)’ and early-heading rice ‘H143’. H143 contains a missense mutation of an invariantly conserved amino acid in the CCT (CONSTANS, CO-like, and TOC1) domain of *PRR37* protein. In the world rice collection, different types of nonfunctional *PRR37* alleles were found in many European and Asian rice cultivars. Notably, the *japonica* varieties harboring nonfunctional alleles of both *Ghd7/Hd4* and *PRR37/Hd2* flower extremely early under natural long-day conditions, and are adapted to the northernmost regions of rice cultivation, up to 53° N latitude. Genetic analysis revealed that the effects of *PRR37* and *Ghd7* alleles on heading date are additive, and *PRR37* down-regulates *Hd3a* expression to suppress flowering under long-day conditions. Our results demonstrate that natural variations in *PRR37/Hd2* and *Ghd7/Hd4* have contributed to the expansion of rice cultivation to temperate and cooler regions.

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OB-03

Determination of forage quality by near-infrared reflectance spectroscopy in soybean

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Soybeans have been the favored livestock forage for centuries. However, little studies have been succeed in estimating forage quality of soybean by near-infrared reflectance spectroscopy (NIRS). To establish NIR equations for soybean forage quality, 353 forage soybean samples, including an 181 recombinant inbred line population derived from PI 483463 (*G. soja*) × Hutcheson (*G. max*), 104 cultivated soybeans (*G. max*) and 68 wild soybeans (*G. soja*) were used to develop NIR for four quality parameters: crude protein (CP), crude fat (CF), neutral detergent fiber (NDF), and acid detergent fiber (ADF). Two NIR spectroscopy equations developed for CP and CF (2,5,5,1; multiple scatter correction [MSC]) and for NDF and ADF (1,4,4,1; MSC) were the best prediction equations for estimating these parameters. The coefficients of determination in external validation set (r^2) were 0.934 for CF, 0.909 for CP, 0.767 for NDF, and 0.748 for ADF. The relative predictive determinant (RPD) ratios for MSC (2,5,5,1) calibration indicate that the CP (3.34) and CF (3.45) equations were acceptable for quantitative prediction of soybean forage quality, whereas the NDF (2.34) and ADF (1.97) equations were useful for screening purposes. The NIR calibration equations developed in this study will be useful in predicting the contents of forage qualities and in breeding soybean for forage.

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OC-01

Identification of a major quantitative trait locus for bakanae disease resistance in rice

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Bakanae disease incidence threat is an increasing trend in the top rice growing countries. Despite it is essential to identify the resistant genes and underlying mechanisms of bakanae disease to develop resistant varieties, there are very limited genetic studies on bakanae disease in rice. The *indica* rice variety Shingwang was selected as resistant donor to bakanae disease. One hundred sixty nine NILs, YR28297 (BC₆F₄) generated by five backcrosses of Shingwang with the genetic background of susceptible *japonica* variety, Ilpum were used for QTL analysis. Rice bakanae disease pathogen, CF283, was mainly used in this study and inoculation and evaluation of bakanae disease was performed with the method of the large-scale screening method developed by Kim et al. (2014). The proportion of healthy plants of Shingwang and Ilpum after inoculation was confirmed using bakanae disease pathogen, CF283. While inoculated Ilpum showed thin and yellowish-green phenotype which is typical symptom of Bakanae disease, Shingwang showed similar healthy phenotype with control plants. A major QTL for resistance against bakanae disease on chromosome 1 was identified using SSR marker, RM9, which explaining 65 % of the total phenotype variation. The major QTL designated as *qBK1* and mapped to a 4.4 Mbp region between RM24 (19.30 Mb) and RM11295 (23.72 Mb). The information of *qBK1* could be useful for improving rice bakanae disease resistance in marker-assisted breeding.

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OC-02

분자마커를 이용한 내병충성 유전자 복합화 계통들의 농업적 특성

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본 연구에서는 도열병저항성유전자(*Pi40*), 흰잎마름병저항성유전자(*Xa4, xa5, Xa21*), 벼멸구저항성유전자(*Bph18*)와 연관된 분자마커를 이용하여 진부벼 유전적배경에 이들 저항성 유전자를 모두 집적한 14계통을 육성하였으며, 이들 계통들은 도열병, 흰잎마름병 및 벼멸구 생물검정에서도 모두 강한 저항성 반응을 보였다. 이들 14계통 중에서 초형이 양호한 3계통(GPL1, GPL2, GPL3)을 선발하여 수량 등 농업적 특성을 평가하였다. 출수기는 3계통 모두 진부벼보다 4~5일정도 늦었으며, 간장은 비슷하거나, 다소 작았고, 수장은 길어졌고, 수수는 1~4개정도 적어졌다. 수당립수는 진부벼보다 29~34개 많아졌으나, 등숙율이 66~73%로 상당히 낮아졌다. GPL1계통은 진부벼보다 수량성이 7.5%증가하였고, GPL2계통은 6%감소하였으며, GPL3계통은 진부벼와 수량성이 비슷하였다. GPL1계통은 진부벼보다 등숙율이 낮는데 수량성이 증가한 이유는 주당수수가 많아졌고, 수당립수가 많아졌으며, 천립중이 증가한데 기인한 것으로 생각된다. 미질특성에서 내병충성복합계통들은 단백질함량, 아미로스함량 및 알카리붕괴도는 진부벼와 유사하였으나, 심복백이 다소 많이 보이는 경향이였다. GPL2와 GPL3계통은 이삭선단이 퇴화된 표현형을 보였고, 수발아율이 16%이상으로 높았고, 내냉성도 진부벼에 비해 다소 약하였다. GPL1계통은 진부벼와 비교하여 수량성도 다소 높고, 표현형도 우수하며, 내냉성과 수발아율도 양호하여 내병충성육종에 유용한 중간모본으로 활용할 수 있을 것으로 기대된다.

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OC-03

Development of diagnostic DNA markers for eating quality of *indica* rice

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Rice eating quality is considered to be one of the top priorities in determining the agronomical value of rice. Thus the rapid evaluation of eating quality at early breeding generations in breeding programs for better eating quality is of great importance. However, it has been limited due to the complex nature of eating quality and the absence of standard evaluation method. In our previous study, we developed a evaluation method with a set of DNA markers that allows to predict the eating quality for *japonica* rices. Here we successfully developed another marker set for the eating quality of *indica* rices. We used multiple regression analysis to test 54 markers, which were preselected for their possible association with eating quality, using 24 *indica* varieties with different palatability scores. Of these markers, eighteen markers were found to be significantly associated with palatability according to sensory evaluation. Accordingly, a marker set in the model regression equation with a high R^2 (0.997) was formulated to estimate *indica* rice palatability. Validation suggests that markers and the statistical parameters formulated by the equation could be a potential tool to predict the palatability of cooked Indonesian *indica* rice and could be reliable in developing country-dependent model equations for eating quality. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008125), Rural Development Administration, Republic of Korea.

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OC-04

QTL mapping for agronomic traits with a RIL population derived from a dent corn x waxy corn cross

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In this study, 80 F_{7.8} recombinant inbred lines (RIL), derived from a cross between dent corn and waxy corn, were evaluated for 10 grain yield and eating-related traits over a two-year period. A total of 39 quantitative trait loci (QTLs) and 74 epistatic interactions were confirmed in 2011 and 2012. All QTLs detected in 2011 and 2012, qAC9 (amylose content), qEH4 (ear height), qSEL6 (setted ear length), and q100KW10 (fresh 100 kernel weight) had higher phenotypic variance and were observed in both years; therefore, they may be considered major QTLs. We reported that the QE interaction affects (QTLs and environmental changes) for qEH4, qSEL6, and q100KW10 in discussion. Some new QTLs identified in this study were located on different loci compared with other studies. The genetic region (bin 4.08) strongly controls plant height and ear height, and results from pleiotropy and/or tight linkage. qST3 (including stem thickness) and qEH3 were co-located within two common adjacent simple sequence repeat (SSR) markers (umc2275 and umc1273), whereas qEL6 (ear length) and qSEL6 were co-located within two common adjacent SSR markers (umc2309 and bnlg238). Thus, these SSR markers are a useful selection tool for screening grain yield and yield component traits.

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OC-05

Development of InDel markers to discriminate common (*Fagopyrum esculentum*) and tartari (*F. tataricum*) buckwheat content based on the chloroplast genome sequencesKwang-Soo Cho^{1*}, Young-Ho Yoon², Su-Young Hong¹, Bong-Kyoung Yun¹, Hong-sik Won¹, and Jeong-Ki Jeon¹¹Highland Agriculture Research Center, National Institute of Crop Science, Rural Development Administration, Pyeongchang 232–955, Korea²Functional Cereal Crops Research Div. National Institute of Crop Science, Rural Development Administration, Milyang, 627–803, Korea

Bitter buckwheat, also called tartari buckwheat (*F. tataricum*), contains large amount of rutin and it has antioxidant activity compared to common buckwheat. But after harvesting and processing, the discrimination of two species through visual inspection was almost impossible. Therefore we developed InDel markers to identify common and tartari buckwheat content based on the chloroplast genome sequence. We conducted complete full chloroplast genome sequence of tartari buckwheat and compared with common buckwheat chloroplast genome sequence (NC010776). Based on the mVISTA alignment, we found eight big InDel (above 50bp) regions. Among the InDel, 6 regions are intergenic region and two are genic region in *ycf1*. We designed InDel specific primers and applied to PCR with buckwheat genomic DNA to check the discrimination of two species. These InDel specific primers also applied to buckwheat germplasm, 75 tartari and 21 common buckwheat. Among the primers, 5 markers could be successfully amplified in all germplasm species specific amplicon. And we can detect 10pg/ul of DNA and processed food such as tea and noodle. These results could improve the QC (Quality control) of tartari buckwheat food.

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포스터발표



1. 수량 및 저항성육종
2. 품질 육종 및 유전변이
3. 분자육종 및 유전공학



PA-01

QTLs for high grain with long panicle under low phosphorus input rainfed condition in rice (*O.sativa*)

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New QTLs were identified for high grain yield with long panicle in rice. A total of 137 F₁₅ recombinant inbred lines (RILs) derived from a cross between Dasanbyeol (Tongil) and TR22183 (japonica), together with the parents were evaluated for 16 agronomic traits at IRRI in dry and wet seasons under different phosphorus (P) and irrigation conditions. A linkage map was constructed using 236 polymorphic markers in 384-plex Bead Xpress indica-japonica single nucleotide polymorphism (SNP) platform. P and water effects were significant in both wet and dry seasons. Both parents and RILs showed varying degree of sensitivities to scarcities in water and phosphorus in terms of panicle length. Collocating with 20 yield-related QTLs, the panicle QTLs on chromosomes 1 (*pl01*), 2 (*pl02*), 9 (*pl09*), and 11 (*pl11*) under low P and rainfed conditions were identified. RILs with TR22183 allele at *pl11* showed longer panicle length under low P input rainfed condition in dry and wet seasons. The whole-genome sequences of the two varieties are being compared to design the molecular markers for fine-mapping and candidate gene identification. Based on Nipponbare MSU 7.0 annotation, a total of 1464 genes with predicted function were identified within the four QTL regions. Candidate genes identified in other studies for QTLs under low P and water conditions, such as calmodulin and dehydrin genes, were targeted for designing molecular markers for fine-mapping and expression analysis. Pyramiding the panicle length QTLs correlating with yield QTLs will provide an opportunity of improving yield traits.

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PA-02

Rice breeding strategy for Africa through KAFACI program in Korea

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In Africa, rice is the fastest demanding staple food with a high growth rate of consumption at 4.5% per annum. Currently Africa occupies 32% of world rice imports, and pressure on rice is expected to rise in the near future. Faced with this deficit, Korea has launched the rice breeding project through Korea-Africa Food & Agriculture Cooperation Initiative (KAFACI) of which goal is to increase rice productivity through accelerated development of improved germplasm and varieties in Africa. As of 2013, the ten African member countries joined the rice breeding projects of KAFACI program; they are Cameroon, DR Congo, Ghana, Kenya, Malawi, Mali, Nigeria, Sudan, Tanzania, and Uganda. We adopted the breeding strategy of intervarietal cross and anther culture to speed up high-yielding secondary populations using the Korean and African germplasm. Korean germplasm is composed of 1) temperate japonicas adaptable to tropical conditions of short-day length and high temperature 2) wide-cross derivatives from African wild species, *O. glaberrima* and *O. longistaminata*, and 3) tongil-type varieties. These germplasm is evaluated for adaptability in Africa and African partners make crosses with local germplasm with the best selections. Korea produce double-haploid populations from these crosses for another cycle of selection for high-yielding lines in Africa. Inter-varietal crosses and double-haploid technology could accelerate the development of high-yielding germplasm and new rice varieties in Africa within short project period.

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PA-03

내병성, 고품질 참깨품종 “중모5005” 육성

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참깨 “중모5005(밀양43호)”는 내병 다수성 품종육성을 목적으로 모본 “한섬깨”와 부분 “SIG950033-2-2-1”을 2000년 인공 교배하여 계통육종법으로 육성한 품종이다. “중모5005”의 주요 형태적 특성을 보면 초형은 소분지형이고 꼬투리는 3과성 2실 4방형이며 화색은 백색이다. “중모5005”의 개화기는 7월 6일로 표준품종인 “양백깨”보다 2일 늦고 성숙기는 8월 24일로 1일이 늦었다. 경장은 142cm로 “양백깨”보다 17cm 컷으며 착삭부위장도 컷고, 주당삭수는 76개로 1개가 적은 경향이다. “중모5005”의 종실수량은 103kg/10a으로 “양백깨”와 같았다. 또한 “중모5005”는 표준품종인 “양백깨”보다 역병, 도복에 강한 특성을 나타냈다. “중모5005”의 품질 특성을 보면 조지방함량은 50.1%로 높았으나 단백질 함량은 23.4%로 낮았고, 인체의 노화억제와 항암 효과가 있는 기능성 리그난성분인 세사민 함량은 4.4mg/g으로서 표준품종 “양백깨”보다 1.3mg/g 많은 품종이다.

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PA-04

준조숙 내도복 특성의 장류·두부용 콩 신품종 ‘태선’

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콩의 특성 중 작부체계 및 기계화 적응성은 재배적 측면에서 경제성을 향상시키는 주요 요인이다. 조숙화로 인한 생육기간의 단기화는 9월 하순 파종, 6월 중하순 수확하는 양파나 마늘 같은 후작 작물의 작부체계 구성을 유리하게 한다. 또한 착협고의 증가와 내도복성은 콤팩트 또는 바인더 등 기계화 수확 시 수량손실 감소에 기여할 수 있어 생산비 절감 등 수익 증대를 위해 조숙 기계화 적응성 품종의 개발이 필요하다. 이에 국립식량과학원에서는 2003년 ‘신기’를 모본으로 ‘태광콩’을 부분으로 인공교배하여 2004년~2005년 F₁, F₂ 세대를 양성하고, F₃부터 계통 전개 및 선발하여 준조숙 고착협 내도복 특성의 장류 및 두부용 콩 신품종 ‘태선(밀양230호)’을 육성하여 2014년 품종보호 출원 및 국가품종목록으로 등재하였다. ‘태선’은 경장이 68cm에 화색은 농자색, 모용색은 회색, 종실은 황색 구형, 배꼽색은 황색이며 100립중은 22.2g이다. 병해충 저항성 검정 결과 불마름병 저항성은 표준품종인 대원콩보다 강하였다. 특히 성숙기는 2011년에서 2013년의 지역적 응시험 평균 10월 4일로 표준품종인 대원콩보다 10일 빨라 생육기간이 짧아졌지만 수량은 303kg/10a로 표준품종인 대원콩보다 10% 증수하였고 착협고는 18cm로 대원콩보다 7cm높으며 내도복성 또한 시험포장과 검정 포장에서 대원콩보다 강하였다.

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PA-05

Evaluation of Introgression lines derived from a cross between *Oryza sativa* and *O. glaberrima* for drought tolerance

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Drought stress is one of the major stress 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 a backcrossing using Milyang23, a Korean Tongil-type rice variety as the recurrent parent and *O. glaberrima* (IRGC Acc. No. 103544), an exotic collection from Mali, West Africa as donor parent. 141 SSR markers were used to genotype 55 introgression lines. The 55 introgression lines with the Milyang23 were evaluated for physiological traits such as Fresh shoot weight (FSW), Fresh root weight (FRW) and Dry shoot weight (DSW) under control and 20% PEG-treated condition. Three lines (IL9, 12, 55) showing significant difference with Milyang23 were selected. The genetic background of the three lines were similar to Milyang23 and it has four, four and two *O. glaberrima* homozygous segments, respectively. IL9 performed better than Milyang23 in all traits measured in the 20% 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. IL12 contains four *O. glaberrima* introgressions on chromosomes 3 and 6. And IL55 contains two *O. glaberrima* introgressions on chromosomes 2 and 6. *O. glaberrima* segment delimited by markers OSR19-RM225 at chromosomes 6 was commonly present in these three lines. This region corresponds to the QTL region for drought tolerance reported by other previous studies. A set of introgression lines are being developed containing only few chromosomal segments from *O. glaberrima* in the Milyang23 background. These would be useful not only in developing drought tolerant lines in the breeding program but also in fine-mapping the genes/QTLs for drought resistance.

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PA-06

항혈전활성이 우수한 중생 다수성 찰수수 '중모4002' 육성고지연¹, 정태욱^{1*}, 김정인¹, 이재생¹, 우관식¹, 송석보¹, 김기영¹, 오인석¹, 곽도연²¹농촌진흥청 국립식량과학원 잡곡과, ²농촌진흥청 연구운영과

수수(*Sorghum bicolor* L. Moench)는 탄닌, 안토시아닌 등이 다량 함유되어 있어 기능성이 우수한 작물로 육종의 방향은 수량뿐만 아니라 기능성 품종의 개발이 필요하다. 수수 중모4002는 항혈전활성이 우수한 찰수수로 2013년 육성된 신품종으로 고유특성은 이삭 측면 모양이 타원형으로 밀수형의 형태를 가지며, 이삭밀도는 중간이다. 종실의 받침껍질색은 짙은 갈색이고 종실색은 적갈색이며, 배유특성은 찰성이다. '12년 2개소에서 실시한 평균 출수일수는 중모4002는 68일로 63일인 황금찰수수보다 5일정도 길었으며, '13년 6개소에서 실시한 평균 출수일수는 중모4002이 65일, 황금찰이 58일로 7일정도 차이를 보여 '12~'13년 6개소 평균 출수일수는 중모4002는 67일, 황금찰이 61일로 6일 정도 늦었다. 간장은 164 cm로 황금찰에 비해 9 cm 크며, 이삭길이와 폭은 큰 차이가 없다. 줄기직경은 황금찰에 비해 2.1 cm가 더 굵어 도복에 강하고 엽장은 길지만 엽폭은 비슷하다. 중모4002의 주당 이삭수는 1.1개로 황금찰과 비슷하고 1수당 이삭중은 53.9 g, 이삭당 종실중은 35.4 g, 천립중은 20.3 g으로 황금찰과 비슷하다. '11~'12년 밀양 지역에서 실시한 생산력 검정시험에서 중모4002의 현곡 평균 수량이 182 kg/10 a으로 황금찰수수(175 kg/10 a)와 비슷하였다. '12~'13년 6개소에서 실시한 지역적응시험에서 중모4002 현곡 평균 수량이 316 kg/10 a으로 황금찰(323 kg/10 a)과 비슷하였다. 중모4002은 황금찰수수보다 단백질, 칼륨, 칼슘, 마그네슘, 나트륨 함량은 약간 높게 나타났으며, 항산화활성에 관여하는 폴리페놀, 플라보노이드 및 탄닌 함량과 라디칼 소거활성은 황금찰보다 높았다. 혈액의 응고능력을 측정하는 상대적 트롬빈(thrombin) 시간을 측정한 결과 지표물질인 아스피린 보다 적은 농도인 5 mg/mL에서 중모4002가 190.5%로 황금찰보다 12% 높은 활성을 보였다.

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PA-07

Giant head형 밀 육성 계통의 흰가루병, 붉은곰팡이병 저항성 검정김경훈¹, 강천식¹, 서세정², 손재한¹, 신상현¹, 김학신¹, 박종철¹, 현종내³, 정영근¹, 이춘기¹, 박광근¹, 박기훈¹, 박철수⁴¹전라북도 익산시 평동로 457, 국립식량과학원 벼맥류부 맥류사료작물과²경기도 수원시 권선구 수인로 126, 농촌진흥청 기술협력국 국제기술협력과³경상남도 밀양시 점필재로 20, 국립식량과학원 기능성작물부 잡곡과⁴전라북도 전주시 덕진구 백제대로 567, 전북대학교 농업생명과학대학 작물생명과학과

Giant head(GH)형 밀은 보통 밀(금강)보다 이삭이 길고 립수가 많아서 생산량을 늘릴 수 있는 잠재력이 매우 높아 밀 생산 농업인들에게 큰 관심을 받고 있다. 그러나 이상기상에 대비한 병해및 재해안정성을 갖추고 있지는 못한 실정이다. 이에 GH형 밀 계통의 병에 대한 평가를 통한 저항성 계통을 육성하고 안정적인 생산을 할 수 있는 품종을 개발하고자 연구를 수행하였다. 2013년 주요 GH형 밀 19계통과 2014년 GH형 밀 176계통을 밀에서 주로 문제가 되는 흰가루병과 붉은곰팡이병 저항성 검정을 하였다. 흰가루병 검정 결과, 2013년 GH형 계통 중 GHW109는 유묘 검정에서는 R, 성체검정에서 1로 저항성을 나타냈고, 2014년 유묘검정에서는 GHW012, GHW018 2계통이 1반복에서는 R, 2반복에서는 S로 반복간에 차이가 있었고, 이는 년차간 재현성이 낮았다. 붉은곰팡이병 검정 결과, 2013년 19계통에서는 76.4~100.0%, 2014년에는 176계통에서는 12.0~100.0%를 나타냈다. 176계통 중에서 GHW135 계통은 12%, GHW114 계통은 22%, GHW53 계통은 40%, GHW011 계통은 39% 순으로 금강밀 100.0% 이병율에 비해 낮게 나타났다. 향후 이삭이 길고 립수가 많은 GH형 계통 중에서 붉은곰팡이병에 중도 저항성을 보인 4계통은 유전자원으로 활용할 계획이며, 붉은곰팡이병과 흰가루병에 대한 저항성 유전자원을 GH형 밀에 집적하여 국산 밀의 병 저항성 증진 연구를 계속 수행할 계획이다.

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PA-08

국내 품종의 중국 운남과 한국 진부에서 작물학적 특성 비교

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우리나라의 벼 재배지역은 북방한계 지역으로 파종기에서 등숙기까지 전 생육기간을 통하여 냉해에 노출되어 있고, 지구의 온난화가 도래하는 과정에 돌발적인 저온 내습의 잠재적 위험성 내재하고 있다. 그래서 지구온난화 등 기후 변화에 대응 우리 품종의 내냉성에 대하여 안정성을 증진시키고자 2013년 중국 운남성 마룽(해발 2,124m)과 국내 진부(해발 576m) 지역에서 국내 벼 6품종 및 계통을 시험지별 표준재배법으로 관리 재배하고 이들 품종의 출수일수, 작물학적 특성 및 내냉성 등을 조사하였다. 시험 품종들의 평균 출수일수는 중국 운남에서는 73일 한국 진부에서 70일로 중국 운남에서 3일 정도 길었다. 간장은 중국 운남과 한국 진부에서 63~64cm로 거의 비슷한 경향이였다. 주당수수는 한국 진부에서 14개로 중국 운남에서 보다는 5개가 많은 반면, 수당입수는 중국 운남에서 102개로 한국 진부에서 보다는 43개가 많았다. 또 현미천립중은 중국 운남에서 25.5g인 반면 한국 진부에서는 23.0g으로 중국 운남에서 현미천립중이 다소 무거운 편이었다. 내냉성과 관련된 입실율은 중국 운남에서 60.3%, 한국 진부에서는 65.7%로 한국 진부에서 다소 높은 경향이였고, 등숙율은 한국 진부에서 90.3%로 중국 운남의 55.7%에 비하여 매우 높은 편이었다.

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PA-09

벼 조생종 흰잎마름병 저항성 중간모본 ‘중모1031’

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벼 품종 ‘중모1031’은 기상이변으로 조생벼 재배지대의 재해 및 병해 발생 증가에 대비 벼 조생 품종의 내재해성 및 내병성을 증진할 목적으로 국립식량과학원에서 2002년 하계에 조생종인 상미벼와 운봉31호와 인공교배하여 2003년에 F₁세대, 2004년에 F₂세대, 2005년 F₃세대 이후부터는 포장에서 계통육종법에 의해 선발하면서 주요 병해충 및 미질검정을 병행하였다. 선발된 우량계통에 대해 2008~2010년 3년간 생산력검정시험을 실시한 결과 조생종이면서 도열병 및 흰잎마름병에 강하면서 쌀 외관이 양호한 SR28111-27-3-2 계통을 철원84호 계통명을 부여하여 2011~2013년 3년간 지역적응시험 실시한 결과 도열병과 흰잎마름병에 저항성이 인정되어 2013년 12월 농촌진흥청 농작물직무육성신품종선정위원회에서 중간모본 ‘중모1031’으로 명명하였다. ‘중모1031’은 출수기가 보통기 보비재배에서 7월26일로 오대벼와 비슷한 조생종이다. 벼 키는 오대벼보다 12cm 작은 단간종으로 쓰러짐에 강하고, 주당수수는 13개로 오대벼와 같으나 수당입수는 80개로 오대벼의 67개보다 13개가 많다. 잎도열병과 흰잎마름병 K1, K2 그리고 K3에 강한 편이다. 저온발아성에는 양호하였으며, 수발아도 잘 안되는 편이다. 쌀알의 크기는 현미 천립중이 22.0g으로 오대벼 26.3g보다 적은 소립이고 쌀의 외관은 맑은 편이다. 쌀수량성은 5.47톤/ha으로 오대벼보다 5% 증수되었다. 최근 지구 온난화로 인하여 조생벼 재배지대에서 흰잎마름병 발생이 빈번한데 ‘중모1031’은 향후 흰잎마름병 저항성 조생품종 육성에 중간모본으로서 역할이 클 것으로 기대된다.

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PA-10

우리나라의 귀리 BYDV 발병

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전북 세 지역의 귀리포장(익산, 전주, 김제)에서 귀리의 보리황화위축바이러스(Barley yellow dwarf virus, BYDV) 병징을 관찰한 후 이를 면역혈청학적 방법 및 분자생물학적 방법으로 진단하여 귀리의 BYDV 감염을 확인하였다. 귀리는 BYDV의 기주식물이며 감염 시 잎과 잎집이 붉은색으로 변하고 생육이 위축되는 특징을 보이므로 감염 여부를 육안으로 쉽게 확인 가능하기에 지금까지 귀리 육종 및 재배시험 과정 중 귀리의 BYDV 감염을 관찰하여 왔으나 병징 육안관찰 외의 방법으로 귀리의 BYDV 감염을 진단 및 보고하지 않았기에 아직 한국식물병명목록에 귀리의 BYDV 감염이 등재되지 않았다. 그러므로 세 지역에서 전형적인 BYDV 감염 병징을 나타내는 귀리를 채집하여 RT-PCR 진단 및 염기서열 분석을 통해 세 지역에서 수집한 귀리 모두가 BYDV에 감염되어 있음을 확인하여 우리나라에서 귀리의 BYDV 감염이 이루어짐을 확인하였다. 귀리 재배포장에서 올해 특히 BYDV 감염 병징이 확연히 드러난 것과 올겨울이 4월 상순까지 평년에 비해 1.5°C 따뜻하였던 결과로 미루어볼 때 따뜻한 겨울조건에서 매개충인 진딧물의 월동률이 높아지고 생육시기가 빨라졌기에 진딧물 매개 BYDV 감염이 증가하였으리라 추정 가능하며, 전지구적 기후변화와 맞물린 귀리의 BYDV 발병증가에 대비하기 위한 귀리의 BYDV 저항성 검정과 이를 위한 검정체계 개발이 요구된다.

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PA-11

Selection of salt-tolerant common wheat (*Triticum aestivum* L.) and durum wheat (*T. turgidum* L. subsp. *durum*) from Korea and Tunisia

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Soil salinity limits crop productivity in many regions. This problem would be more serious as the global climate changes and worldwide water shortages would accelerate soil salinization. This study is fulfilled with aim on resolve crop cultivation in dry/saline land as an international joint research project with Tunisia. Total 48 lines of wheat cultivars including 32 common wheat (16 Korean wheat, 16 Tunisian common wheat) and 16 Tunisian durum wheat were incorporated in this study. Salt stress was applied for 2 weeks by submerging the pots into 500 mM NaCl at 3-leaf stage followed by re-watering for restoration in greenhouse. Numerous agronomic/growth parameters were scored for tolerance. SSR primers that have been known to be related to salt tolerance were applied to explain selected population. The correlation between PCR-based length polymorphism of selected lines and their resistance were evaluated. The obtained information will aid selection for salt tolerance hexa/tetraploid wheats.

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PA-12

다수성 흰색 참깨 ‘건백’

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‘건백(밀양44호)’은 고품질, 다수성 참깨 품종 육성을 목적으로 2001년 모본 ‘성분’과 부분 ‘SIG950006-4-1-1’를 인공 교배하여 계통육종법으로 육성한 품종이다. 주요 형태적 특성을 보면 초형은 소분지형이고 꼬투리는 3과성 2실 4방형으로 달리며 꽃과 종피는 흰색이다. ‘건백’의 개화기와 성숙기는 7월 6일과 8월 24일로 표준품종인 ‘양백’보다 조금 느리다. 반면에 경장은 149 cm로 크고 주당삭수가 90개로 많으며 역병 및 도복에도 강한 특성을 나타내었다. 종실수량은 전국 7개 지역 평균 119kg/10a으로 표준품종인 ‘양백’보다 15% 증수하여 국내 참깨 육성 품종 중 최대 수량성을 보였다. ‘건백’의 품질 특성을 보면 조지방 함량은 50.2%이며, 리그난의 주요성분인 세사민 함량은 396 mg/100g을 나타내었다.

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PA-13

Expression profiling and genome mining for selected candidate genes for heat and cold tolerance in rice

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To obtain a better insight into a possible common regulatory mechanism shared in response to heat and cold stresses in model monocot plant, expression profiling for several selected transcripts of rice (*O. sativa* L.) was examined from meiotic stage panicle samples of a number of different cultivars including both heat/cold tolerant and susceptible varieties. Induction of several of these genes in response to heat stress treatment was observed across all different rice varieties tested, but no differential induction kinetics between the heat-tolerant and susceptible varieties was discernable for these genes. On the other hand, a few genes that are known to be involved in ROS signaling showed different induction kinetics between the tolerant and susceptible varieties, suggesting that these genes might be playing a key role in conferring the heat/cold stress tolerance at reproductive stage of tolerant rice varieties. This approach was also augmented by comparative gene expression data analyses, utilizing expression data of other monocots and dicots model plants available in the database. Based upon these results, a preliminary gene pyramiding effort to estimate contributing factor of several selected alleles after putting these genes together is underway. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No.PJ009076), Rural Development Administration, Republic of Korea.

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PA-14

벼멸구 저항성 유전자의 유묘기 저항성 반응

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국내 Biotype 1 벼멸구에 대해 각각 서로 다른 벼멸구 저항성 유전자를 가진 계통의 저항성 반응을 검토하여 벼멸구 저항성 품종 육성에 필요한 정보를 알고자 본 실험을 수행하였다. 공시충은 남평벼(저항성 유전자 없음)에서 10세대 이상 누대사육한 Biotype 1 벼멸구를 사용하였다. 벼멸구에 대한 유묘저항성 반응은 벼가 3~4엽기에 개체당 10마리를 접종한 후 조사하였다. *Bph1*, *Bph3*, *Bph18* 유전자를 보유한 계통은 매우 강한 저항성 반응을 보였으며 *Bph2*, *Bph6*, *bph7*, *Bph9* 유전자 보유 계통은 중도저항성을 나타냈다. *bph5*, *bph8* 유전자 보유 계통 및 남평벼는 벼멸구에 매우 약한 감수성 반응을 보였다. 벼멸구 비선호성(antixenosis)을 접종 후 24시간 마다 3번 조사한 결과 72시간 후에 남평벼는 50% 이상, *bph5*, *bph8* 유전자는 40% 이하, *Bph6*, *bph7*, *Bph9* 유전자는 30% 이하, *Bph1*, *bph2*, *Bph3*, *Bph18* 유전자는 20% 이하의 식이선호성을 보였다. 벼멸구의 비선호성은 유묘저항성 반응과 비슷한 결과로 저항성 유전자별 그룹화 되었다. 접종 10일 후 벼멸구 생존율은 저항성 유전자를 가진 계통은 30% 이하인데 반해 남평벼는 70% 이상이었다. 본 실험결과 저항성 유전자 다양화 및 향상을 위해 저항성 반응이 뛰어난 *Bph3*, *Bph18* 유전자를 이용한 벼멸구 저항성 품종의 육성이 유용할 것이다

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PA-15

Breeding of Light Purple Standard Rose 'Violetta' with Good Vase life

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A new light purple rose cultivar 'Violetta' was bred from the cross between light purple standard cultivar 'Ocean Song' and yellow standard cultivar 'golden gate' at the National Institute of Horticulture & Herbal Science. The cross was made in 2010 and 'Violetta' was finally selected in 2013 after investigating characteristics for three years from 2011 to 2013. 'Violetta', a light purple color standard cultivar grows vigorously and has good shape and good vase life. The major characteristics of this cultivar are 167.1 stems/m²/year in yield, 77.9±6.0 cm in length of cut flower, 12.8±0.3 cm in flower diameter, 55.5±4.9 in petal number, and 13.1±1.6 days in vase life. This cultivar can be propagated by both cutting and grafting. The consumer's preference of this cultivar is relatively higher than that of control cultivar, 'Aqua'.

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PA-16

직파 초기생육과 재배안전성의 상관관계

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직파재배의 장점은 노력시간을 절약하여 생산비를 이앙재배대비 8%를 줄일 수 있는 효과적인 재배법으로 알려져 있다. 그러나 우리나라에서 직파재배는 '95년 118천 ha (벼재배면적의 11%)를 정점으로 계속 감소하였다. 이러한 배경에는 직파적응성 품종, 잡초, 앵미, 미질 등 재배여건 등이 크게 관여 했는데 품종적 측면에서는 저온발아성, 담수토중출아성 등 초기입모관련 특성과 내도복성, 균집의 균일성 등 재배안전성이 가장 큰 요인이다. 본 연구에서는 초기 입모와 관련한 저온발아성 (13℃, 15일, 유아장 1mm이상), 담수토중출아성 (5월 중순, 토중 1cm, 수심 10cm, 15일후 입모조사), 도복검정(담수직파)을 실시하여 실제 담수직파재배 생육과의 연관성을 조사하였다. 저온발아성은 담수직파 포장에서의 입모율과는 직접 연관이 적으며 담수토중출아성은 상관성이 인정되었다. 초기신장성은 입모와 관련 중요한 특성이며 이후 제초제 처리 등 포장관리 측면에서도 매우 중요한 특성이다. 그러나 초기 신장성이 우수한 계통은 후기생육까지 영향을 주어 도복에 취약한데 HR27035-23-2-4, HR27035-39-3-1은 초기 신장성이 우수하고 성숙기 간장이 73cm로 양호하였다.

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PA-17

벼 중만생 복합저항성 직파적응성 '중모 1035호'

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중모1035호는 생산비 절감을 위한 직파적응성이 우수한 고품질 품종개발을 목적으로 2005/2006년 동계에 국립식량과학원 벼백류부에서 단간, 복합내병성, 다수성인 익산488호 (IT235282)을 모본으로 하고 HR21050-B-50-1을 부본으로 육성되었다. 육성방법은 인공교배 후 F₂ 및 F₃는 집단으로 F₄ 이후부터는 계통육종법에 의하여 육성선발하면서 주요 병해충 및 미질특성을 조사하였다. 2010~2011년 생산력검정을 실시한 결과 초형이 우수한 고품질 직파적응성 HR26399-B-14-1-4 계통을 선발 "익산541호"로 계통명을 부여하였다. 주요 특성으로 출수기는 8월 17일로 중만생종이며 간장이 73cm로 단간이고, 수수는 328개/m²이다. 13℃에서 15일간 실시한 저온발아성은 88%로 높았고 적고에도 강했으나 수발아가 40.1%였다. 주요 병해충 특성은 도열병에는 중도 저항성이고, 흰잎마름병 K1, K2, K3 및 줄무늬잎마름병에는 강하나 해충에 대한 저항성은 없다. 수량성은 보통기 보비재배에서 525kg/10a, 담수직파에서 523kg/10a이다. 직파관련 특성으로 저온발아성이 우수하고 입모가 123개/m²로 양호하며 도복에 강하다. 그러나 담수토중출아성, 밥맛, 수량성 등이 미흡하여 2011~2013년 지역적응시험을 실시한 결과 "중모1035호"로 명명하였다.

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PA-18

저온발아성 및 담수토중출아성이 우수한 벼 유전자원 선발

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직파재배는 노력시간 및 생산비 절감 등의 장점이 있으나 입모율 저하 및 도복에 의한 수량 감소 등의 문제로 계속 감소하고 있는 추세이다. 본 연구는 담수직파 전용 벼 품종육성을 위한 교배모본을 탐색하기 위해 국립농업과학원 유전자원센터에서 분양받은 저온발아성이 우수한 유전자원 및 보유하고 있는 유전자원의 저온발아성 및 담수토중출아성을 평가하였다. 522점의 유전자원을 이용하여 13°C에서 15일간 처리한 후 발아율을 조사하고 저온발아성이 우수한 유전자원에 대해 파종 후 1cm 복토하고 10 cm 담수상태에서 15일 후 발아율 및 초장을 조사하여 담수토중출아성을 평가하였다. Dao ye qing, IR63295-AC209-7 등 13°C 저온에서 전혀 발아가 되지 않는 유전자원도 있었으나 400여점이 저온발아율 60% 이상으로 저온발아성이 양호하였다. 저온발아성이 우수한 유전자원 308점을 이용하여 담수토중출아성을 평가한 결과, 토중출아율의 범위는 0~80%, 평균 17.8%를 나타냈고 출아한 유전자원의 초장은 평균 8.8 cm, 최대 20.7 cm로 담수토중에서도 출아 및 초기신장이 양호한 유전자원을 선발할 수 있었다. 그 중에서 Yunjing4, Lan dao, Annapurna 및 자광도는 저온발아성 및 담수토중출아성이 우수하여 담수직파 전용 벼 품종육성을 위한 모본으로 활용 가능할 것으로 생각된다. 자포니카 형인 Yunjing4의 저온발아율, 토중출아율 및 초기신장성(초장)이 각각 99.0%, 55%, 7.4 cm이었고 Lan dao는 100.0%, 80.0%, 9.8 cm이었다. 인디카형인 자광도는 98.0%, 76.0%, 11.3 cm이었으며 Annapurna는 99.5%, 60%, 7.3 cm이었다.

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PA-19

Development of salt tolerant soybean by marker assisted selection.

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A total area of reclaimed land in Korea is about 135,100 ha, which occupies 9 % of total arable land. Soybean is one of the most important crop in Korea and demand for the crop is increasing, while the country's self-sufficiency is very low, around 9 %. If it's possible to cultivate soybean in reclaimed land, it would increase self-sufficiency of the soybean. However, there are difficulties to cultivate soybean in reclaimed land because of excessive level of salinity in the soil, to prevent this barrier in saline soils, it is necessary to develop salt tolerant soybean cultivar. This research was conducted to select salt tolerant lines derived from PI 483463 (salt tolerant wild soybean accession). The F₁ (Hutcheson × PI 483463) was backcrossed with Hutcheson and Wooram (salt sensitive soybean cultivar). For marker assisted selection and salt reaction phenotyping, randomly selected BC₁F₁ seeds from two backcross populations were planted in 11 cm tall tray. At the V1 growth stage, DNA was sampled with FTA card. The genomic DNA and SSR marker, BARCSOYSSR_03_1348, were used for PCR amplification and the result was checked through electrophoresis. The trays with BC₁F₁ plants were immersed in 100 mM NaCl solution up to the bottom third of the trays directly after the DNA extraction. After two weeks, phenotype was measured depending on leaf scorch degree. Through this research, 25 dominant homozygote lines and 22 heterozygote lines from Hutcheson backcross population and 28 dominant homozygote lines and 37 heterozygote lines from Wooram backcross population were selected. These lines will be used for developing soybean with salt tolerance.

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PA-20

호두나무 신품종 ‘정월’, ‘보름달’ 및 ‘칠선’

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고품질 다수확성 호두나무 품종을 육성하기 위해 호두나무 주산지를 대상으로 병해충 피해가 없고 과실형질이 우수한 우량개체들을 선발하였다. 선발된 후보목들은 경기도 수원에 위치한 국립산림과학원의 재배포지에 식재하였고 품매검정을 통하여 제특성을 검정하여 형질이 우수한 ‘YD1’, ‘MP10’ 및 ‘ET1’ 개체를 선발하였다. 우량개체로 선발된 YD1, MP10 및 ET1을 대상으로 2009~2011년까지 결실 및 과실특성에 대한 안정성 검정을 수행한 결과 우수한 특성들이 안정적으로 발현되어 각각 ‘정월’, ‘보름달’ 및 ‘칠선’으로 최종 명명하였다. 신품종 ‘정월’은 과실의 종경과 횡경이 각각 44.3mm와 35.6mm, 입중과 인중은 14.0g과 6.6g, 인중비와 과피 두께는 46.9%와 1.5mm이다. ‘보름달’은 과실의 종경과 횡경이 각각 40.2mm와 39.1mm, 입중과 인중은 15.8g과 6.5g, 인중비와 과피 두께는 41.3%와 1.7mm이다. ‘칠선’은 과실의 종경과 횡경이 각각 44.8mm와 41.0mm, 입중과 인중은 19.7g과 11.2g, 인중비와 과피 두께는 53%와 1.7mm로 과실형질이 우수하다.

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PA-21

종신품위가 우수하며 수량이 높은 장류 · 두부용 콩 신품종 ‘선풍’

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국내 콩의 재배면적은 증가하지 못하고 있는 반면 연간 1인당 소비량은 8kg을 유지하고 있어 식용콩의 자급율이 30% 이상 증가하지 못하고 있다. 따라서 정부에서는 콩의 생산성 향상을 위해 수량성이 높은 품종을 개발하여 왔으며, 2002년 ‘신팔달콩2호’의 수량성을 이용한 ‘대풍’이 평균 3MT/ha 이상의 다수성 품종으로 개발되었으나 종자의 배꼽색이 갈색이며 크기가 작아 보급이 확대되지 못하였다. 이러한 문제점은 개선하기 위해 2012년 ‘대풍’을 모본으로 하여 종자상의 단점을 개선한 ‘진풍’이 개발되었으며, 2013년에는 ‘진풍’보다 종자가 굵고 품위가 우수한 다수성 ‘선풍(밀양231호)’을 개발하였기에 그 특성을 보고하고자 한다. ‘선풍’은 ‘신팔달콩2호’에 ‘화엄꽃콩’을 교배하여 대립화한 ‘수원 224호’에 ‘동산121호’와 ‘Sprite87’의 교잡후대로서 종신품위가 우수한 계통을 교배하여 계통육종법에 따라 육성한 품종이다. ‘선풍’은 성숙기가 10월 19일로 현재 가장 많이 재배되는 ‘대원콩’보다 5일 늦으며, 불라름병과 SMV에 저항성이다. 종자의 배꼽색이 없고 100립중이 ‘대원콩’보다 1.7g 무거운 대립이면서 내탈립성이 강하다. 지역적응시험을 실시한 전 지역에서 ‘대원콩’보다 수량이 높았으며 특히 중남부지역에서 평균 3.4MT/ha로서 대원콩 대비 21% 증수하였다.

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PA-22

벼흰잎마름병 K3a 균계 저항성 최고품질 ‘해품’

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쌀 개방화 대응 최고품질 벼 품종의 다양화와 남부지역을 중심으로 확산되고 있는 벼흰잎마름병, 줄무늬잎마름병에 대응하기 위하여 복합내병성 품종 개발이 필요하다. 이에 국립식량과학원 벼맥류부에서 2007년 하계에 고품질 이면서 K3a에 저항성 계통인 익산493호(진백)를 모본으로 하고 벼멸구저항성 계통 익산495호(다청)와 직파적응 계통인 익산496호를 교배한 F₁을 부분으로 하여 삼원교배 하였다. 조기에 우량 품종을 개발하고자 F₁세대에서 약 배양을 수행하여 우량계통을 선발 고정하여 2013년에 ‘해품’을 개발하였다. ‘해품’은 출수기가 8월 11일로 ‘남평’보다 3일 빠른 중생종이며 남평’보다 8cm 작은 단간 내도복 품종이다. ‘해품’은 벼흰잎마름병(K₁~K₃, K_{3a})과 줄무늬잎마름병에 강하고, 쓰러짐에 강하며 수발아가 안 되는 편이다. 쌀 수량성은 2010~2013년 3개년 간 실시한 지역 적응시험 보통기 보비재배에서 5.27MT/ha로 남평에 비해 2% 적으나, 벼흰잎마름병 발병상습지 검정에서는 5.25MT/ha으로 이병성인 남평벼에 비해 26%의 증수효과가 있다. 또한 ‘해품’은 이모작재배에서 5.25MT/ha, 만식재배에서는 5.05MT/ha의 수량성을 보이는 최고품질 벼 품종이다. ‘해품’의 적응지역은 충남이남 평야지 및 남서해안지이다.

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PA-23

Doubled Haploid Corn Breeding and Introduction of the Technology for Practical Inbred Line Development in Korea

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Maize breeding is mainly divided by two steps; line development and hybrid selection. Line development is very important procedure to make good hybrids and this line development in Korea is fully depend upon conventional methods like pedigree selection, back-cross, etc. For development of pure line, we have to do self-pollination for at least seven cycles. This line development system is tedious, labor-intensive, and time-consuming procedure. Doubled Haploid technology for maize is a new system to develop inbred lines within short period and many maize research institutes in foreign advanced countries have been actively using this technology. Using Doubled Haploid technology, we can greatly reduce the period of line development and strengthen maize research ability in Korea. Key requisite for Doubled Haploid breeding is possession of inducer lines which can produce haploid when source population is crossed with them. Maize Research Institute in Gangwon Province secures the right of using inducer lines and is trying to introduce Doubled Haploid breeding in Korea. Doubled Haploid breeding system is as follows; crossing between population and inducer, separation haploid seeds from F₁ seeds, chromosome doubling, doubled plant management, self-pollination, seed multiplication, and assessment. We expect our breeding capacity will be progressed by introduction of Doubled Haploid technology. When this technology comes to combine with marker assisted selection, we can increase competitiveness against global institutes.

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PA-24

Genome Wide Association Study (GWAS) approach for the blast disease resistance in rice

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One of the biotic stresses in rice production is rice blast disease caused by *Magnaporthe oryzae*, which is one of the most destructive fungal diseases in rice. We outlined an approach towards genome wide association study for the blast disease resistance in rice. In total, 295 rice accessions including 137 Heuristic Set accessions (HS) and 158 Korean Bred varieties (KB) were screened for the rice blast disease resistance. Firstly, *Magnaporthe oryzae* were inoculated to the rice seedlings of two weeks after germinations. Then, evaluation of the disease symptoms and checking the crossing point (CP) value were conducted one week after inoculation. To quantify the CP value, real-time polymerase chain reaction (PCR) was employed in combination with the primer pair and Taqman probe specific to *Magnaporthe oryzae* HYDROPHOBIN class 1 (*MHPI1*) which is an indispensable unigene encoding HYDROPHOBIN for normal virulence expression. Based on these CP values from the PCR reactions containing a series of increasing concentration of cloned amplicon or fungal genomic DNA, correlation among the template's copy number or its amount and amplification pattern was calculated. Reliability of this equation was further confirmed using the DNA samples from the rice leaves infected with compatible or incompatible strains of *M. oryzae*. These steps are still being undertaken, and after the complete process of disease resistance phenotyping for the whole population containing 295 accessions, GWAS will be performed to examine the associated genes involving in blast resistance mechanism using the whole genome resequencing data of 295 accessions. This approach would be a useful technique for identifying genetic loci responsible for natural variation in rice blast disease resistance and ultimately, new R genes which can improve the blast resistance in rice.

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Selection of Field Maize Hybrids for Adaptation to Southern Asia

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With the economy development, people have an increasing demand for meat and eggs. Hence the market demand for cereal crop keeps increasing. maize is the major crop to meet the conditions of market demand. As a part of the Golden Seed Project, we are planning to develop maize varieties for adaptation in Southern Asia, especially in India. This project was started at 2013 and has been collaborated with Nongwoo Bio Co. Our project is based on overseas maize breeding in Bangalore, India. At first year, we tested 40 maize hybrids to investigate adaptability, yield capacity, and growing characteristics. Planting materials for this test were developed and selected in Cambodia by researchers of Maize Research Institute. Growing performance is usually quite different by the growing area and seasons, but some of our materials have shown good adaptability and yield at dry season in Southern India. 13IN07 was selected by yield and grain color, 13IN39 was selected by yield and plant type. These two selected hybrids were applied to regional test controlled by Indian Council of Agricultural Research in India. We will see how our hybrids adapt in various regions in India, assess how other tested hybrids perform in those regions, and compare each other. We may also expect one of the selected hybrids can be a candidate variety for some regions in India and we will continuously select good hybrids and develop new varieties in India.

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해외식량기지 기후 및 환경 적응 옥수수 품종 개발

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강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

국내 곡물 옥수수 자급률이 1% 미만이지만 매년 약 800만톤 이상을 소비하고 있는 실정으로 우리의 식량자급은 대단히 위태로운 상황에 직면해 있다. 이에 농림축산식품부의 해외식량기지 구축 및 지원을 위한 우량 옥수수 품종개발을 통하여 식량자급에 보탬이 되고자 본 연구를 수행하였다. 서울대학교 이석하 교수와 현지 진출기업과 공동으로 수행하는 본 과제는 2011년 8월부터 2014년 8월까지 3년간 캄보디아, 러시아 연해주에서 현지 기업 재배 시험포에서 적응하는 품종을 개발하였다. 캄보디아 캄푼에서 에이퍼플 주식회사의 JNJ Bora의 협조로 현재까지 3년간 총 8작기(회) 현지에 상주하면서 육종 및 평가를 추진하였으며, 러시아 연해주 우스리스크에서 서울사료의 협조로 4작기의 평가를 수행하고 있다. 캄보디아는 연구원 현지 상주로 국내 육성 또는 도입 고정계통의 특성평가, 현지 평가용 교잡종의 구성 및 평가, 열대 수집자원을 중심으로 한 분리계통의 육성 등을 추진할 수 있었다. 그 결과 열대지방 지속 육종을 위한 분리 395계통과 교잡종 강원감1, 2, 3호를 선발하였다. 분리 계통은 남부아시아 적응 수출용 옥수수 품종개발 육종 재료로 활용하고 있고 선발된 교잡종 3종은 현지 캄보디아 품종 출원 중에 있으며 신속한 종자공급을 위하여 50a 채종포를 조성하였다. 러시아 연해주에서는 2011년부터 3년간 국내에서 육성 교잡한 225교잡종을 현지에서 평가한 결과 최종으로 강원러1호(종교101호)를 선발하였고, 현지에 채종포 10a를 조성하였다. 현지에 적응하는 품종은 향후 품종실시를 통하여 우리 진출기업이 옥수수 대량 재배에 활용할 수 있도록 지속적인 육종과 종자생산관리를 추진할 예정이다.

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Blast diseases influenced on agronomic and eating quality traits of rice in Korea

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Rice (*Oryza sativa* L.) is one of the most important staple foods that feed more than 50% of the world's population. With the improving of people's living standard, eating quality of rice become the most important aims in current breeding programs. Amylose content (AC) and gelatinization temperature (GT) are the two main measures to estimate the rice grain quality. In rice, a total of 27 genes directly involved the rice starch biosynthesis effecting on the rice eating quality. It clearly identified chromosome 6 to be rich in the genes related to AC and GT properties (*GBSSI*, *SSIIa* and *SBE I*) along with other genomic regions scattered in rice genome. Rice blast, caused by the fungal pathogen *M. oryzae*, is the most devastating disease of rice and severely affects crop stability and sustainability worldwide. Many fungal genes involved in pathogenicity and rice genes involved in effector recognition and defense responses have been identified over the past decade. A total of 99 and 22 blast resistance genes have been identified and cloned; in which 45% were found in *japonica* cultivars, 51% in *indica* cultivars, and the rest 4% in wild rice species. Among them, three major resistance gene clusters have been characterized: the *Pik* locus on Chromosome 11, and the *Pita* locus on Chromosome 12, the *Piz* locus on Chromosome 6 closely to the starch synthesis-related genes. These results could be important clues for studying the relationship between resistance / susceptible materials and eating quality.

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Overexpression of cysteine protease from *Brassica rapa* modulates response of transgenic rice to *Xanthomonas oryzae* pv. *oryzae*

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In spite of the overwhelming number of cysteine proteases in plants, only a few were substantially investigated. Papain-like cysteine proteases (PLCPs) are commonly implicated to disease immunity in some key pathosystems in plants, such as in tomato - *Cladosporium fulvum*, potato/tomato - *phytophthora infestans*, and *Arabidopsis* - *Ralstonia solanacearum*, among the few others. This study demonstrates the function of cysteine protease gene cloned from *Brassica rapa* (*BrCP*) related to resistance to *Xanthomonas oryzae* pv. *oryzae* in transgenic rice lines. The cysteine protease-encoding full-length cDNA was identified and characterized using web-based tools. The gene is 2,267 bp in size with an open reading frame of 1,365 bp that encodes predicted polypeptide of 455 amino acids. Blast analysis of the conserved domain of the gene confirmed its affinity to Peptidase_CIA family. Full-length cDNA of PLCP in *Brassica rapa* was then cloned and co-overexpressed in rice with HPT marker. Introgression of the gene was confirmed in the transformants through genomic PCR assay. RT-PCR analysis showed that the gene was constitutively expressed and present in all tissues. The overexpression rice lines exhibited an enhanced resistance when screened with four Korean *Xoo* isolates.

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벼 중생 고품질 내병 내도복 다수성 신품종 ‘다보’ 육성

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국립식량과학원 영덕출장소에서 2001/2002년 동계온실에서 동해안 및 영남지역에서 출수기가 중생이면서 밥맛이 뛰어나고 재배안정성이 높은 벼 품종을 육성할 목적으로 벼알의 속색이 양호하고, 초형 및 밥맛이 좋은 “영덕31호”를 모본으로 다수성이면서 밥맛이 우수한 “밀양165호”를 부분으로 인공교배를 실시하고, 2002년 하계에 F₁을 양성하여 YR23160의 교배번호를 부여하였다. 2003년에 F₂집단을 포장과 실내 선발하여 2004년 하계에 F₃세대를 육성하고, 이후 F₄-F₈세대를 계통육종법으로 전개하면서 예비선발시험 후 고품질이면서 현미 외관특성이 우수하고 병해 및 재해에 안정적인 저항성을 나타내는 계통을 선발하여 2008년 생산력검정예비시험 2009년 생산력검정본시험을 실시 한 후 중생이면서 다수성이고 완전미율이 높아 외관이 우수하면서 재배 안정성인 YR23160-31-2-1-5-B-3을 선발하여 “영덕53호”로 명명하였다. 2010년~2012년까지 3년간 지역적응시험을 실시한 결과 중생종이면서 쌀 품위 및 밥맛이 좋고 내도복과 내병성이 양호한 것으로 평가되어 2012년 12월 농작물 직무육성신품종선정위원회에서 국가품종목록 “다보”로 명명하였다. 출수기는 보통기재배에서 평균 8월 8일로 “화성벼”보다 6일 빠른 중생종이며 직립 초형이고 탈립은 잘되지 않고 이삭추출은 양호하고 까락이 거의 없다. 수당립수는 “화성벼”보다 많으나 현미천립중은 22.6g으로 “화성벼”보다 약간 가볍다. 도정특성은 “화성벼”와 비슷하고 쌀알 모양이 단원형으로 맑고 투명하며 밥맛은 “화성벼”와 같이 양호하다. 불시출수는 안되는 편이고, 위조현상에 강하고 성숙기 엽노화가 느린 편이며 내병성은 “화성벼”보다 다소 약한 수준이다. 잎도열병은 중도저항성을 보였고 줄무늬잎마름병과 흰잎마름병(K₁, K₂, K₃)에는 강하나 오갈병 및 검은줄오갈병에 약하고 벼멸구 등 충해에는 감수성이다. 쌀수량성은 보통기 보비재배에서 5.90MT/ha로 “화성벼”보다 10% 증수되었으며, 이모작재배에서는 5.37MT/ha로 21%, 만식재배에서는 4.75MT/ha로 20% 증수하여 이모작 및 만식적응성이 높았다. 적응지역은 동해안냉조풍지 및 남부해안지, 영남평야지, 남부중산간지이다.

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RAPD marker conversion into SCAR marker for identifying white rust resistance in chrysanthemum

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Chrysanthemum white rust, caused by *Puccinia horiana*, is one of the most destructive fungal diseases in chrysanthemum cultivation worldwide. For increasing efficiency of resistant breeding, molecular markers linked to chrysanthemum white rust resistance gene were developed in pseudo F₁ cross population between 'Puma White' as susceptible and 'Dancer' as resistant using bulked segregant analysis (BSA). Of 280 RAPD primers (Operon 10 mer), 18 primers found to be polymorphic. After screening of these primers in 20 individual lines, only OPI-13₅₂₀ was selected as closely linked marker to white rust disease resistance. Based on correspondence between phenotypic resistant level and marker in 187 segregation population, the genetic distance between white rust resistance gene and OPI-13₅₂₀ marker assumed to be 3.8 cM. For OPI-13₅₂₀ marker conversion into sequence characterized amplified region (SCAR) marker, the amplified fragment of OPI-13₅₂₀ was purified, cloned and sequenced. Based on the DNA sequence of OPI-13₅₂₀, SCAR maker was generated and verified in 20 individual lines used in BSA-RAPD. The results showed SCAR marker could be used to identify white rust resistance in chrysanthemum.

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자포니카 다수성 벼 드래찬과 보람찬 유래 약배양 계통을 이용한 이삭과 수량 관련 형질 분석 및 다수성 우량 계통 육성

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자포니카 다수성 벼 품종으로 소얼수증형인 드래찬과 다소 수수형 특성을 나타내는 보람찬을 인공교배한 F₁을 약배양하여 220개 약배양 계통을 육성하였고 이 중 출수기가 모부본과 비슷하고 농업형질이 양호한 163계통을 선발하였다. 2011, 2012년에 이삭 및 수량 관련 18개 형질에 대한 특성을 분석하였다. 간이수량은 2차지경 착생립수와 가장 높은 정의상관관계를 나타냈으며 1차지경에 비해 2차지경 관련 형질이 높은 관련성을 나타냈다. 주성분1을 기준으로 간이수량은 이삭관련 형질들과 같은 방향성을 나타낸 반면 수수와 등숙률과는 반대방향을 나타내고 있어 공시된 약배양 집단의 다수성 특성은 2차지경립 확보에 의한 수당립수 증가에 기인한 것으로 생각된다. 군집분석을 통해 분류된 그룹 중 그룹 C의 평균 간이수량이 가장 높았으며 수장, 수수, 수당립수, 지엽장 등이 드래찬과 보람찬의 중간을 나타냈다. 그룹 C에 속하는 13개 계통과 모부본에 대해 2013년 생산력검정시험을 수행하여 이삭과 수량관련 형질들을 조사하였고 이를 이용해 군집분석한 결과 네 개의 그룹으로 분류되었다. 그룹 A는 드래찬 포함 5계통, 그룹 B는 보람찬 포함 6계통, 그룹 C는 HR28832-AC60, AC156 계통, 그룹 D에는 AC152, AC161 계통이 속하였다. 수량성은 D>C>B>A순으로 그룹 C는 수당립수가 다른 그룹에 비해 적고 천립중이 가벼우며 수수가 많고 등숙률이 높은 특성을 나타냈으며 그룹 D는 특히 2차지경립이 많아서 수당립수가 가장 많고 천립중, 수수, 등숙률이 A와 B의 중간을 나타냈다. 그룹 C와 D에 속하는 다수성 4계통을 대상으로 2014년 생산력검정시험을 수행하여 수량성에 대한 재검정과 품질특성에 대해서 조사할 계획이다.

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약배양 이용 DZ78 유래 벼흰잎마름병 저항성 계통 육성

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벼흰잎마름병 저항성 유전자 *xa5*와 *Xa7*을 가지고 있는 것으로 보고된 방글라데시 *aus* 타입 벼 품종 DZ78로부터 벼흰잎마름병 저항성 유전자가 도입된 저항성 계통을 육성하고자 본 연구를 수행하였다. *Xa3* 보유 운광벼를 반복 친으로 하여 육성된 BC₁F₂ 집단에 K3a 균계를 접종하여 선발된 저항성 33개체를 약배양에 이용하여 93개의 약배양 집단을 작성하였다. K1 및 K3a 균계에 대한 저항성 반응을 조사하여 반응에 따라서 그룹을 분류하였다. 이 중 K3a 균계에 저항성인 계통은 1/1 그룹에 속하는 9 계통과 1/3 그룹에 속하는 7계통으로 예상보다 적게 발생하였는데 이는 원연교배와 약배양에 의해서 segregation distortion이 일어난 것으로 생각한다. *Xa7*이 도입된 것으로 추정되는 1/1 그룹에 속하는 계통들의 농업형질 특성을 보면 평균 간장이 49 cm, 수장이 20 cm로 다른 그룹에 비해서 간장과 수장이 짧았고, 수수는 많은 편이었다. 수당립수가 적고 까락이 존재하며 탈립이 심하고 불량한 초형 등 열악형질이 수반되어 육종소재로 활용하는데 어려움이 있을 것으로 판단되었다. 또한 접종 후 2주 후의 진정저항성은 강한 반응을 나타내었으나 시간이 경과함에 따라서 다소 병반이 진행되는 경향을 나타냈다. 적색 종피를 가지고 있는 DZ78의 기능성 효과가 보고되었는데 약배양 계통 중 적색 종피이며 농업형질이 양호하고 K1에 저항성인 계통을 선발하였다. 운광벼에서 저항성유전자가 도입된 것으로 추정되는 이들 계통들은 벼흰잎마름병에 모두 이병성인 적미 품종의 저항성 강화에 기여할 것으로 판단되어 추가적인 농업형질 및 벼흰잎마름병 저항성 성능검정을 실시하고 있다.

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벼흰잎마름병 저항성 유전자 *Xa2*, *Xa3*, *xa5*, *Xa21* 보유 자포니카 조생 찰벼 계통 육성

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자포니카형 조생 찰벼의 벼흰잎마름병 저항성 증진을 위하여 내도복 다수성 조생 찰벼인 상주찰벼 배경에 벼흰잎마름병 저항성 유전자 *Xa2*, *Xa3*, *xa5*, *Xa21*을 도입한 저항성 계통을 여교배와 벼흰잎마름병 생물검정을 통해 육성하였고, 해당 저항성 유전자를 표지하는 DNA 분자 마커를 이용하여 저항성 유전자 도입 여부를 확인하였으며 우리나라 벼흰잎마름병 균계 네 개와 필리핀 11개 균계를 대상으로 저항성 반응을 조사하였다. *Xa2*가 도입된 HR24465 계통은 우리나라 K1, K2 균계와 필리핀 race 9a에 저항성을 나타냈으며 *Xa3*가 도입된 HR24666 계통은 우리나라 K3a와 필리핀 race 6을 제외하고 저항성 및 중도 저항성을 나타냈다. *xa5*가 도입된 HR24668과 HR24673은 필리핀 race 6을 제외하고 모두 저항성 반응을 나타냈으며 *Xa21*이 도입된 HR24669는 우리나라 K1 균계와 필리핀 race 10을 제외하고 저항성 및 중도 저항성을 나타냈다. 육성된 계통들은 상주찰벼와 같이 조생이면서 찰벼였고 출수기와 수장, 수수, 정현비율 및 백미수량이 상주찰벼와 차이가 나지 않았다. 상주찰벼 배경에 *Xa2*, *Xa3*, *xa5*, *Xa21*이 도입된 저항성 계통은 벼흰잎마름병 저항성이 부족한 자포니카형 조생 찰벼의 저항성 강화를 위하여 유용한 육종소재로 활용될 것이다.

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Variation of yield and seed component in delayed planting cultivated in southern region of Korea tested with currently developed soybean cultivars

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In southern region of Korea, double cropping system including soybean as a second crop is widely adopted because prolonged high temperature in October enables soybean maturation even in late autumn. Global warming during decades derives transition of soybean planting dates as late as late-July. Delayed planting beyond the critical time moves reproductive stage to less favorable weather conditions like low temperature and short photoperiod, which can affect soybean yield and seed composition. Therefore selection of appropriate cultivar for changed climate and cultural practice is required. Effects of different eco-type and planting date on soybean yield was investigated for three sowing dates of 20 June, 5 July and 20 July with ten cultivars. Strong interaction between cultivar and sowing date was detected in number of branch, node and pod. No significant interaction was observed in 100-grain weight and yield, and this might be resulted from similar yield reduction pattern. Daepung, Taekwang and Uram recorded the highest yield when planted late, proving that these three cultivars are the most adaptable to delayed planting. Delayed planting results in higher sugar content, especially stachyose and raffinose which have detrimental effect on human health by causing flatulence and diarrhea. Protein content was decreased and oil content was increased in July 20 planting. Decrease in protein content was the largest in Hwangeumol and maintained high in Saedanbaek. This information will provide a guideline when select appropriate soybean cultivar in delayed planting to maintain yield and seed quality.

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직파 초기생육과 재배안전성의 상관관계

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직파재배의 장점은 노력시간을 절약하여 생산비를 이앙재배대비 8%를 줄일 수 있는 효과적인 재배법으로 알려져 있다. 그러나 우리나라에서 직파재배는 '95년 118천ha(벼재배면적의 11%)를 정점으로 계속 감소하였다. 이러한 배경에는 직파적응성 품종, 잡초, 앵미, 미질 등 재배여건 등이 크게 관여 했는데 품종적 측면에서는 저온발아성, 토출출아성 등 초기입모관련 특성과 내도복성, 군집의 균일성 등 재배안전성이 가장 큰 요인이다. 본연구에서는 초기 입모와 관련한 저온발아성(13℃, 15일, 유아장 1mm이상), 담수토중출아성(5월 중순, 토중 1cm, 수심 10cm, 15일 후 입모조사), 도복검정(담수직파)을 실시하여 실제 담수직파재배 생육과의 연관성을 조사하였다. 저온발아성은 담수직파 포장에서의 입모율과는 직접 연관이 적으며 담수토중출아성은 상관성이 인정되었다. 초기신장성은 입모와 관련 중요한 특성이며 이후 제초제처리 등 포장관리 측면에서도 매우 중요한 특성이다. 그러나 초기 신장성이 우수한 계통은 후기생육까지 영향을 주어 도복에 취약한데 HR27035-23-2-4, HR27035-39-3-1은 초기신장이 우수하고 성숙기 간장이 73cm로 양호하였다.

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벼 중만생 복합저항성 직파적응성 ‘중모 1035’

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중모1035는 직파에 의한 못자리 생략으로 생산비 절감을 위한 직파적응성이 우수한 고품질 품종개발을 목적으로 2005/2006년 동계에 국립식량과학원 벼맥류부에서 단간, 복합내병성, 다수성인 익산488호(IT235282)을 모본으로 하고 HR21050-B-50-1을 부분으로 육성도였다. 육성방법은 인공교배 후 F₃는 집단으로 이후부터는 계통육종법에 의하여 육성선발하면서 주요 병해충 및 미질특성을 조사하였다. 2010~2011년 생산력검정을 실시한 결과 초형이 우수한 고품질 직파적응성 HR26399-B-14-1-4 계통을 선발 “익산541호”로 계통명을 부여하였다. 주요 특성으로 출수기는 8월 17일로 중만생종이며 간장이 73cm로 단간이고, 수수는 328개/m²이다. 13°C에서 15일간 실시한 저온 발아성은 88%로 높았고 적고에도 강했으나 수발아가 40.1%였다. 주요병해충은 도열병에는 중간 저항성이고, 흰 잎마름병 K1-3 및 줄무늬잎마름병에 강하며 충에대한 저항성은 없다. 수량성은 보통기 보비재배에서 525kg/10a, 담수직파에서 523kg/10a이다. 직파관련 특성으로 저온발아성이 우수하며 입모가 123개/m²로 양호하며 도복에 강하다. 그러나 담수토중출아서, 밥맛, 수량성 등이 미흡하여 2011~2013년 지역적응시험을 실시한 결과 “중모 1035”로 명명하였다.

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Comparing characteristics of agricultural and physiological of ‘Iksan370’ and ‘Keumkang’

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Characteristics of agronomy, especially good yield productivity is very important in wheat (*Triticum aestivum* L.) as human food crop. Development of elite cultivar having good traits is required for food stability. In 2013, a new wheat line called Iksan370 has been developed by the National Institute of Crop Science, RDA. Iksan370 has hard red winter wheat characteristics and better features like resistance to biotic, abiotic stress and higher yield ability than Keumkang. Heading and maturing date were delayed about ten days and period to flowering date was shorter three or four days than Keumkang. Culm and spike length of Iksan370 were 95cm and 15.3cm, averagely. This means that culm and spike length were longer than Keumkang (79cm and 7cm, respectively). It showed higher milling rate (75.5%), protein content (13.5%) and SDS-sedimentation volume (77.5ml) than Keumkang. Genotypes of six genes, *GBSSA*, *B*, *D*, *PPO18*, *Pina* and *Pinb*, were represented that were similar to Keumkang, respectively. Average yield of Iksan370 in the preliminary trial test was 6.61 tons/ha in upland. We expect that yield productivity and farm income were increased by Iksan370.

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직립 내도복성 조생 소립 녹색종피 ‘연두채’ 육성

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팔 소비와 재배면적 확대를 위해서 전통적인 붉은색 팔만으로는 제품 다양화에 한계가 있다. 새로 개발된 팔 신품종 ‘연두채’는 싹나물 제조가 가능한 녹색 종피의 품질이 우수한 팔 품종이며, 중생종으로 쓰러짐에도 강한 품종이다. 개화기는 빠르지만 성숙기간이 길어 종자가 알차고 험당립수가 많다. 수량성은 지역적응시험에서 평균수량이 212kg/10a로 표준품종 대비 11% 증수하였다. 연두채는 1999년 SA9411-2B-1-1-2와 수원38호를 교배육종법을 통해 2013년 육성된 신품종으로 협색은 황갈색으로 충주팔(황색)과 구별되며, 종피색은 녹색(충주팔은 암적색)이다. 개화기와 성숙기는 8월 7일 및 9월 26일로 충주팔(8월 18일 및 10월 5일)보다 빨랐으며, 백립중은 9.7 g/100립으로 충주팔(14.1 g/100립)보다 작은 소립종이며, 도복 또한 충주팔보다 강하다. ’09~’12년에 실시한 생산력검정시험에서 263 kg/10a로 충주팔(197 kg/10a)보다 34% 증수되었으며, ’10~’13년에 4개소에서 실시한 지역적응시험에서 212 kg/10a로 충주팔(191 kg/10a)보다 11% 증수되었다. 연두채의 단백질 함량은 19.5%로 충주팔과 비슷하였고 폴리페놀 함량은 2.68 mg/g으로 충주팔(1.96 mg/g)보다 높았으며, 연두채의 ABTS 라디칼 소거활성은 650.8 mg TE/100 g으로 충주팔(456.6 mg TE/100 g)보다 높았다. 30°C에서 5일간 싹나물을 제조하여 수율과 싹길이를 측정한 결과 연두채는 각각 681% 및 26 cm로 충주팔(481% 및 18 cm)에 비해 우수하였다. 싹나물용으로 개발된 연두채는 팔의 신수요 창출과 소비 확대에 크게 기여할 것으로 기대된다.

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Distribution of Blast Resistant Genes in Rice (*Oryza sativa* L.) Germplasm

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Rice blast (*Magnaporthe oryza* B.) is one of the most widespread and devastating diseases of rice. Screening of valuable genetic resources harboring resistance genes is one of the most efficient approaches against blast disease. Because the bioassay to rice blast in the field shows high variations, this study has performed to provide DNA profiles in the accessions of diverse countries using major blast resistant genes linked markers, identified and mapped in different genotypes of rice. Because durable resistance to blast is controlled by a combination of major resistance genes, we surveyed the distribution of blast resistant genes in the 1,500 accessions using major 12 blast resistance genes linked markers. These resistant genes found that the frequency distribution of *Pi-39* (66.9%), *Pik-m* (41.9%), *Pit* (40.5%), *Pii* (21%), *Pib* (19.3%), *Pi-d(t)2* (12.7%), but *Pita*, *Pita/Pita-2*, *Pik*, *Piz-t*, *Pi5* genes were identified in less than 10% frequency. Most of accessions contain from 1 to 4 different resistant genes. *Pi39* and *Pik-m* genes amplified in the 69.1% and 51.7% among 356 Korean accessions, *Pi39* (79.6%) and *Pib* (55.8%) in 113 China, *Pit* (80.6%) and *Pib* (32%) in 103 Philippines, respectively. In this study, we evaluated the blast resistance degree and the information about the distribution of rice blast resistant genes in rice germplasm. This study will help to develop effective strategies for managing rice blast disease in rice germplasm.

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Agronomic characteristics of ninety stem rust resistance accessions from worldwide in 2013

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Stem rust of wheat caused by *Puccinia graminis* f. sp. *Tritici* is historically one of the most important diseases of crops worldwide. The objective of this study was to screen the growth habits and yield of wheat accessions in Korea winter condition. We collected ninety stem rust resistant germplasms from USDA-Grain and planted for the characteristics of growth and yield in 2013. We measured the growth characteristics such as the plant type, leaf color, heading date, stem length, spike length, awn length, number of spikelet, number of tiller, and 1,000 kernel weight (g). Early maturity is most important wheat breeding target in double cropping system such as Korea. Heading dates of ninety cultivars ranged from May 17 to June 7. The Keumkang control cultivar headed on May 23. Heading dates of seventeen accessions had as early as Keumkang control (May 23). The numbers of semi-erect and intermediate type for growth habit were 45 and 33 respectively. The 1000 kernel weights were also measured. Mean 1000 kernel weights ranged from 16.7g (Webster) to 41.8g (123 A1C2). The average of stem length was 100.2cm and Keumkang was 58.4cm. These results showed that A4849-60P-7P-1P (Chile), MG 31492 (Ethiopia), 1338.F.6.C.3.B (Kenya), 1203 A1C2 (Kenya), and II-90-20/3-1R-1M-3R (Mexico) were best lines for agronomic characteristic such as early heading date and grain yield.

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맑고 깨끗하며 완전미 생산량이 많은 조생종 벼 “온다미”

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“온다미”는 국립식량과학원 상주출장소에서 중산간지 재배에 알맞은 고품질 벼를 육성하고자 2003년 하계에 고품질인 히토메보레를 모본으로 하고 중산간지 적응성 조생 상주27호를 부분으로 인공교배하여 F3이후 계통육종법에 의하여 육성 선발하면서 주요 농업형질 조사 및 병해충-미질검정을 실시하였다. 2010~2011년 생산력검정을 실시한 결과 내도복이며 수량성이 우수한 YR24905-129-3-1-1-3 계통을 선발하여 “상주46호”로 계통명을 부여하였다. 2011~2013년 지역적응성시험을 실시한 결과 대조품종에 비해 수량성이 높고 내도복성, 내수발아성 및 도열병에 강하며 외관품위와 도정특성이 매우 우수하여 2013년 농작물 직무육성 신품종 선정심의회에서 신품종으로 선정하여 “온다미”라 명명하였다. “온다미”는 보통기 보비재배에서 평균 출수기가 7월 27일로 오대벼와 같은 조생종이며, 등숙비율이 88.8%로 오대벼보다 높으며 현미천립중이 21.7g으로 중소립종이다. “온다미”는 도열병에 중도저항성을 보이거나, 줄무늬잎마름병, 흰잎마름병, 기타 바이러스병 및 해충에는 약하다. 쌀알은 심복백이 없이 맑고 투명하며 도정률 및 완전미 도정수율이 각각 75.8, 73.1%로 오대벼보다 높다. 쌀수량은 지역적응시험의 보통기 보비재배에서 5.29MT/ha로 오대벼보다 4% 증수되었으며, 만기재배에서는 5.12MT/ha로 금오벼보다 10% 증수하였다. “온다미”의 적응지역은 남북부중산간지, 남부고냉지 및 동해안 북부해안지이다.

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Cold Hardiness, Proline Content, and Expression of *P5CS* and *P5CR* Genes among Peach Cultivars in Field Conditions

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Changes in cold hardiness were confirmed with relative electrolyte leakage (REL) method in the shoots of two peach cultivars (*Prunus persica* Janghowon Hwangdo and Odoroki) during cold acclimation and deacclimation. Changes in proline (Pro) content and related gene expressions were also analyzed. Particularly, transcript accumulations of *P5CS* and *P5CR* were examined using quantitative real-time RT-PCR. REL in the shoots of two peach cultivars was significantly different during the entire experimental period. Cold hardiness of two cultivars increased gradually to December 2012, and then decreased to April 2013, whereas Pro contents of 'Janghowon Hwangdo' and 'Odoroki' were reduced from the beginning of the experiment to February 2012 and then increased in the spring. Interestingly, *P5CS* gene encoding an enzyme, which catalyzes conversion from glutamic acid (Glu) into glutamic- γ -semialdehyde (GSA) in the first step of Pro pathway, showed the contrasting patterns with Pro contents of two cultivars. On the other hand, *P5CR* gene encoding an enzyme, which catalyzes conversion from Δ^1 -pyrroline-5-carboxylate(P5C) into Pro in the final step of Pro pathway, showed the similar patterns to Pro contents in two cultivars. Our results demonstrate that Pro responds negatively to low temperatures in the shoot of different peach cultivars, including the supplemental 10 peach cultivars, and expression of both *P5CS* and *P5CR* genes could show contrasting patterns from each other. Our results suggest that identification of both *P5CS* and *P5CR* genes are required necessarily for accurate analysis of Pro biosynthesis because Pro accumulation is affected more by expression of *P5CR* gene.

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가축 기호성 증진 총체사료용 벼 중간모본 '중모1038' 개발안억근^{1*}, 이점호¹, 양창인¹, 정웅기¹, 이상복¹, 원용재¹, 최용환¹, 손지영¹, 신영섭¹, 윤미라¹, 이규성², 정종민¹, 장재기¹, 정국현², 전용희², 이점식¹, 현용조¹, 황기호¹, 모영준¹, 김보경¹¹농촌진흥청 국립식량과학원²농촌진흥청

일반적으로 가축의 기호성은 가축의 선택적인 채식에 영향을 미친다. 또한 사료의 소화율과 가축의 채식량 간에는 높은 정의 상관관계가 있다고 알려져 있다. 벼의 잎이나 종실에 존재하는 강모의 대부분은 규소결정체로 이루어져 있어 이는 가축이 소화하기 어렵다. 이에 가축의 기호성을 증진할 목적으로 잎과 종실에 강모가 없어 매끄러운 특성을 갖는 총체사료용 벼 '중모1038'을 육성하였다. 출수기가 평균 8월23일로 만생종인 '중모1038'은 저온발아성이 높고 잎도열병 검정결과 중정도 이상의 저항성 반응을 보였으며 기타 흰잎마름병, 바이러스 및 멸구류에는 약하다. 보통기 다비재배로 중부, 호남 및 영남평야에서 실시한 지역적응시험 결과 평균 총체건물수량이 1,716 kg/10a로 '녹양'에 비해 21% 증수되었다. 조사료의 소화율 및 섭취량에 관여하는 산성세제불용섬유소(ADF)는 33.5%, 중성세제불용섬유소(NDF)는 48.5%이고 가소화양분총량(TDN)은 62.4%로 '녹양'보다 약간 적은편이나 매끄러운 잎 및 종실을 가지고 있어 가축의 기호성을 증진시킬 것으로 기대된다.

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Fine mapping of the potyvirus resistance gene *Pvr7* in *C. annuum*

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Pepper mottle virus (PepMoV) is frequently occurring virus in pepper field. PepMoV infected plants show symptoms including mosaic leaf, distortion of foliage and fruit deformation. The dominant gene *Pvr7* from *Capsicum annuum* '9093' confers resistance to PepMoV. Previous research reveals that *Pvr7* is located in 10 chromosome and linked to the dominant potyvirus resistance gene *Pvr4* and *Tomato spotted wilt virus* (TSWV) resistance gene *Tsw*. To identify the *Pvr7* gene, we constructed an intraspecific F₂ mapping population from a cross between *C. annuum* '9093' (PepMoV resistant) and *C. annuum* 'Jejujaerae' (PepMoV susceptible). Resistance of F₂ plants were screened with green fluorescent protein (GFP) tagged PepMoV. Genomic DNA was extracted from F₂ individuals and markers were developed using *C.annuum* 'CM334' whole genome sequence (WGS). Several single nucleotide polymorphism (SNP) markers that were co-segregated with *Pvr7* were developed. We are expecting that this *Pvr7* SNP marker can be used to breeding PepMoV resistant cultivars and fine mapping of *Pvr7*.

Keywords: *Pvr7*, PepMoV, dominant resistance, marker development, HRM

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불임성 억새 품종육종을 위한 종별 개화 특성 및 임성 분석

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전남 무안군 청계면 무안로 199, 국립식량과학원 바이오에너지작물센터

억새(*Miscanthus* spp.)는 우리나라가 원산지인 대표적인 섬유질계 바이오에너지 원료작물로 다년생 C₄ 식물이며 배수성이 다른 유전자원이 널리 분포하고 있다. 외국에서는 자연 생태계 교란 방지를 위해 종자번식 억새의 재배를 규제하고 있어 불임성 억새 품종개발이 시급하다. 본 연구는 국내 수집 1,500여 종의 유전자원 중 재배년수가 비슷한 물억새 518점, 참억새 297점 등 총 815점을 대상으로 불임성 억새 품종 육종에 필요한 종별 개화 특성을 조사하였다. 억새의 자가불화합성은 물억새 3종, 참억새 3종 및 3배체 억새 이삭에 봉지를 씌워 개화 후 이삭의 지경수, 총영수 및 결실 종자수를 조사하였다. 억새 유전자원의 개화기(FS3)까지의 전체 생육일수 210일에서 220일 사이에 개화하는 물억새는 전체의 80% 이상, 참억새는 56%였다. 또한 억새 유전자원의 자가불화합성을 검토한 결과, 자연수분 조건에서 참억새의 임실률은 45.7%인 반면, 봉지를 씌운 참억새의 임실률은 8.3%로 매우 낮았다. 한편, 2배체 참억새와 4배체 물억새 중간 교잡종으로 알려진 3배체 억새는 자연수분 조건에서도 임실률이 0.9%로 매우 낮아 기존 보고와 동일한 결과를 얻었다.

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다양한 유전자원 수집 및 평가를 통한 고추 탄저병 저항성 소재 확대

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Colletotrichum spp.에 의해 발생하는 고추 탄저병은 국내외 고추 재배 시에 가장 많은 피해를 주는 병해이다. 현재 가장 많은 분포를 나타내는 종은 *C. acutatum*이며 베노밀 등 일부 살균제에 내성을 가지는 것으로 보고되었다. 그러므로 탄저병 피해 경감을 위한 방법으로 저항성 품종을 재배하는 것이 최선이지만 판매되고 있는 저항성 품종이 극히 일부이며 보급면적이 아직 확대되지 않아 대부분 약제에 의한 화학적 방제가 이루어지고 있다. *C. baccatum* 종에서 저항성 유전자를 도입하고자 많은 연구가 이루어 졌으나 종간교잡으로 인한 임성저하 등의 문제점으로 저항성 품종 육성에 어려움이 있다. 따라서 본 연구에서는 국내외의 다양한 유전자원과 육성계통을 대상으로 무상 처접종법과 포장검정을 통하여 기존에 알려진 저항성 이외의 새로운 저항성 계통을 탐색하여 고추 탄저병 저항성 품종육성에 이용하고자 수행하였다. 고추 육성계통 및 유전자원 932점을 대상으로 수확과실을 이용한 분무접종 방법과 포장검정을 통해 저항성을 평가한 결과 무상처 분무접종결과 강한 저항성을 나타낸 자원은 13A101 등 15 점이었으며 나머지 평가자원들은 감수성으로 확인되었다. 포장결과도 무상처 분무접종과 유사한 결과를 보였으며 저항성으로 13A37 등 28점, 중도저항성으로 18점을 선발하였다. 인공접종결과와 포장저항성 결과를 비교하여 평가방법에 상관없이 저항성이었던 13A263 등 *C. baccatum* 6점과 13A691 등 *C. annum* 2점을 선발하였으며 이는 고추 탄저병 저항성 품종육성 재료로 지속적으로 육성할 계획이다.

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아시아 광지역 적응성 벼 품종 ‘아세미’

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온대지역의 벼 품종을 열대지역 재배시 불수출수로 인하여 수확량이 급감하는 경향을 보이는 데 중·만생종이 이러한 환경변화에 더욱 민감하다. 이러한 장벽을 극복하고자 필리핀 국제벼연구소내 한국지소에서 열대지역에서도 정상적인 생육을 나타내는 ‘진미’와 밥맛이 좋고 병해에 강한 ‘철원46호’를 교배하여 열대지역에서도 잘 생육하여 수량성도 높으면서 병에도 강한 온대벼 ‘아세미(수원574호)’를 개발하였다. 필리핀 현지에서는 간장이 66cm로 작고 주당수수 12개 수당립수 84개였으며 등숙률을 보면 현지 품종(IR 72)의 등숙률이 63%인데 ‘아세미’는 77%로 높았고 수확량도 헥타르 당 4~5 톤으로서, 현지 품종인 ‘IR72’보다 10% 가까이 많았고, 밥맛도 좋았다. 우리나라에서는 출수기가 8월1일로 ‘화성’(8월 12일)보다 11일 빨랐으며 간장은 82cm, 수장 21cm, 수수 12개, 수당립수 109개, 등숙률 83%였고 현미천립중이 22.5g인 중립종이다. 생리장해 저항성으로 유묘적고가가 거의 없고 감수분열기 임실률도 높아 내랭성을 어느 정도 갖추고 있었다. 잎도열병 저항성은 보통 수준이었고 흰잎마름병에는 약하나 줄무늬잎마름병에는 강했다. 또한 심복백정도 백미완전미율 등 미질특성은 ‘화성’과 비슷하였다. 수량성은 중북부 내륙지와 중서부 해안지에서 ‘화성’보다 10%정도 높았고 중북부 산간지에서는 ‘오대’보다 13%높은 수준을 보였다. 이처럼 ‘아세미’는 열대지역이나 우리나라에서 잘 재배되는 것으로 보아 아시아 지역에 재배가 가능한 비감 광성 광지역적응성을 갖춘 벼 품종임이 확인되었다.

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Relationship between cold hardiness and bud opening among peach cultivars during deacclimation at constant warm temperatures

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Recent climate changes due to global warming are gradually introducing adverse circumstances for winter survival of temperate fruit trees. Particularly, late winter or early spring thaws followed by hard freezes can cause severe injury to deacclimated flower buds. Thus, the selection of later or slower deacclimating cultivars is needed to avoid frost injury in late winter or early spring. This study was performed to investigate relationship between cold hardiness and bud development under an experimental deacclimation condition for 10 *Prunus persica* cultivars (Aikawanakajima, Daewol, Izumi Hakuto, Janghowon Hwangdo, Kiraranokiwami, Mihong, Misshong, Soomee, Suhong, and Sun Gold). The rate of deacclimation was not correlated with hardiness before the deacclimation treatment. On the other hand, a strong positive correlation was found between cold hardiness and stage of bud opening.

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친환경 소비재배 및 가공밥 적성 벼 품종 ‘미소미’ 개발

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중부지역에 재배되는 벼 품종은 중생종으로 ‘화성’, ‘대안’, 중만생으로는 ‘삼광’, ‘칠보’ 정도로 농민들이 선택할 수 있는 다양성이 부족하고, 재배안전성이 부족한 외래품종의 재배면적이 넓어 이들을 대체할 수 있는 벼 품종개발이 필요하고, 또한 친환경 재배를 위하여 복합내병성 외에 소비료재배 적성 품종이 필요한데 아직까지 ‘청해진미’와 ‘청청진미’가 개발되었으나 내병성이 부족하다. 복합내병성이면서 소비재배 적성이 우수한 품종을 개발하고자 육성된 ‘미소미’의 출수기는 중부지역 보통기 재배에서 8월 14일이고, 쌀이 맑고 투명하며, 밥맛은 추정 보다 우수하다. 수량성은 지역적응시험 보통기 보비재배(4개소)에서 5.68MT/ha, 소비료재배에서도 5.00MT/ha로 추정, 화성 보다 높다. 도열병, 흰잎마름병 및 줄무늬잎마름병에도 강하여 재배안전성이 높은 품종이다. 특히 ‘미소미’는 밥알의 부착성이 좋고 식은밥 맛이 우수하여 간편식 가공밥으로 적합한 품종이다. ‘미소미’는 중부지역 적응 벼 품종의 다양성을 확보하고, 생산자, 가공업자 및 소비자가 모두 만족하는 특성을 갖고 있어 고품질 쌀 안정생산으로 농가소득증대가 기대된다.

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Morpho-physiological changes of Sorghum seedlings response to heavy metal stress

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Among the abiotic stresses, heavy metal (HM) toxicity is thought to be one of the major abiotic stresses leading to hazardous effects in plants. In spite of its potential physiological and economical significance, morphological alterations induced by heavy metals in plants have so far been grossly overlooked. In the present study, the morphological and physiological changes were observed in the leaf of sorghum plants treated with different concentrations (0, 50, 100, and 150 μM) of CdCl_2 . Results revealed that plants endured reduction in growth and morphological changes amazingly altered by cadmium. The growth of sorghum seedlings treated with 150 μM cadmium was more inhibited than that of sorghum seedlings treated with 100 μM Cd, 50 μM and non-treated plants. The morphological characteristics revealed that the cadmium stress inhibited the root and shoot elongation after growing the rise seedling in the presence of cadmium. In the case of ion concentration, the concentrations of Zn^{2+} , Ca^{2+} were decreased whereas Fe^{2+} concentration was increased except 100 μM under cadmium stress. In confocal microscopy, results showed that the absorption degree of cadmium was increased by the higher concentration of cadmium. The fluorescence intensity of cadmium was also increased. Thus, it seemed that cadmium has an influence on sorghum in the case of early stages of sorghum. This study reported the effects of heavy metal, cadmium on the growth and physiological characteristics of sorghum seedlings, hoping to provide references on the mechanism of heavy metal damaging plants, and phyto-remediation for heavy metal polluted soil.

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Overexpression of CBL-interacting protein kinase 15 improves tolerance to pre-harvest sprouting in rice (*Oryza sativa* L.)

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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 (CIPK15) was isolated from rice flowers. This gene is 2,818 bp long with 1,332 bp coding region that encodes a polypeptide of 443 amino acids. We constructed a recombinant vector carrying the *OsCIPK15* 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 *OsCIPK15* in the regulation of pre-harvest sprouting.

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Phylogenomic analysis and a systematic view of U-Box E3 family in rice

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E3 ubiquitin ligase plays a central role in determining specificity of the ubiquitination system by selecting appropriate candidate proteins. Compared with other eukaryotic species there are significantly more U-box protein-encoding genes in plant genome. The rice genome contain 77 U-box-type E3 encoding genes. The 77 members of the rice plant U-box (PUB) E3 family can be placed into 8 major groups based on their domain organizations. In this study, we generate and analyze phylogenomic data integrating anatomical expression patterns consisting of anatomical and stress responsive expression patterns base on 1150 affymetrix arrays to the phylogenetic tree of rice plant U-box E3 family. We further developed functional gene network mediated by E3 ligases and refined the components in network by integrating gene expression patterns in response to drought stresses. We expect that our analysis will be a useful platform to facilitate the functional identification for each of U-box E3 family.

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종피가 부드럽고 기름함량이 많은 종실용 들깨 신품종 ‘들샘’이명희^{1*}, 정찬식¹, 배석복¹, 황정동¹, 김성업¹, 송득영², 오기원¹, 이병규¹, 이춘기³, 박장환², 백인열¹¹경상남도 밀양시 점필재로 20 국립식량과학원 두류유지작물과²경기도 수원시 권선구 수인로 125 국립식량과학원³전라북도 익산시 평동로 457 국립식량과학원 맥류사료작물과

들깨는 꿀꿀과 1년생 식물로 우리나라 주요 유지작물 중 하나이다. 들깨의 국내 재배면적은 2013년 30.1천ha로 꾸준히 늘어나고 있는 추세이다. 그 이유 중 하나로 들깨의 종실은 기름 함량이 40-50%이며 기름의 지방산 조성 중 60% 이상을 차지하고 있는 알파-리놀렌산이 심장질환 예방, 학습능력 향상, 알레르기 치료 등에 효과가 있는 것으로 알려져 수요가 늘고 있기 때문이다. 들깨는 주로 조미용이나 착유용으로 많이 이용되므로, 종피가 부드럽고 기름함량이 많은 품종을 선호하고 있다. 2013년에 개발된 ‘들샘’은 2003년에 ‘밀양28호/YPS72’ 모본에 ‘대실들깨’를 부분으로 하여 육성된 품종으로 계통육종법에 따라 육성하였으며, 수량 및 종실특성이 우수하여 2011년 ‘밀양57호’로 계통명을 부여하였다. ‘들샘’은 소비자의 기호에 적합한 품종으로, 종피가 갈색이며, 부드럽고 기름함량이 43%로 높으며, 착유량 또한 39%로 많다. ‘들샘’은 성숙기 10월 7일로 기존 품종과 비슷한 시기에 수확할 수 있다. 6월 중하순경 파종하였을 경우, 경장이 134 cm이고, 화방군수가 77개로 많았다. 종실의 수량성은 3년간 지역적응 시험 결과 표준품종인 새엽실들깨보다 5% 증수하였으며, ha당 수량은 1.43MT이다.

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중국 연길지역에서의 카멜리나 표준 재배법 연구박민우¹, 이상협^{2*}¹경상남도 진주시 진주대로 501 경상대학교 농학과²서울특별시 광진구 능동로 209 세종대학교 바이오자원공학과

The objective of this study was comparison of seed yields according to different seeding rates, seeding time and application of chemical fertilizations in Yanji Region of China. The experiment was conducted on commercial farmland at Yanji region in 2013. All the experimental fields were designed following randomized block design with 3 replicates. The plant spacing was applied as 65×1cm distance. To check the effect of seeding rate, two different seeding rate, 0.2kg/0.1ha and 0.5kg/0.1ha were applied. The higher seed yields was observed in low seeding rate(0.2kg/0.1). The application of fertilizer(mixture of N and P) showed different results following different experimental fields. However, there was little positive effects following fertilizer application into commercial farmland. When we compare seed yields between two different seeding dates, 4th May and 29th May, the earlier seeding date(4thMay) showed higher seed yields. In considering these results, low seeding rate and early seeding time is important for getting high camelina seed yields.

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유채 개화기 침수처리에 따른 수량 및 수량구성요소의 변화

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우리나라에서 유채(*Brassica napus* L.)는 논 이모작(벼·유채) 재배가 가능한 동계 유지작물이다. 유채는 종자 기름 함량이 45%로 많고, 올레인산(C18:1) 함량도 65% 정도로 높아 바이오디젤 원료작물로 유망하다. 본 연구는 우리나라 유채 6품종(‘선망’, ‘탐미’, ‘탐라’, ‘내한’, ‘영산’, ‘한라’)에 대해 개화 초기(early flowering stage)에 침수처리(3, 6, 9, 12일)를 통해 개화기 토양 침수에 의한 습해반응과 이에 따른 수량구성요소와 종실수량 변화를 조사하고자 수행되었다. 침수 3일 처리구는 무처리구와 비교해 유채 6품종의 생육에 차이가 없으나, 침수 4~9일 처리구에서는 꽃봉우리 정단부 꺾임현상이 심하게 나타났다. 하지만 ‘내한’과 ‘영산’ 유채는 침수 9일 처리구에서 꽃봉우리 정단부 꺾임현상이 나타나 침수처리에 강한 반응을 보였다. 전반적으로 유채는 개화기에 토양 침수가 4일 이상 지속되면 꽃봉우리 정단부 꺾임, 안토시아닌 과다형성, 도복, 개화기 연장 및 등숙 지연 등 생식생장기 생육에 큰 영향을 주었다. 또한 유채는 개화기에 침수 스트레스가 6일 이상 지속되면 주당협수, 협당립수, 결실율 및 천립중 현저하게 감소하였고, 각각의 수량구성요소에 미치는 영향은 최종적으로 종실수량 감소로 이어졌다. 무처리구 대비 침수 6일 처리구에 대한 품종별 종실수량을 보면 ‘선망’(54%), ‘탐미’(35%), ‘탐라’(33%), ‘내한’(78%), ‘영산’(70%) 및 ‘한라’(32%)로 나타났다. 하지만 침수처리에 따른 종자의 지방산 조성에는 큰 변화가 없었다. 전반적으로 6 시험품종 중에서는 ‘영산’ 유채가 개화기 내습성이 강한 품종으로 나타났다.

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Distribution aspects of organisms by NGS analysis in soybean breeding field

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Generally, the virus was detected by the ELISA using the serological method and RT-PCR based on the genetic information. Recently, NGS (next-generation nucleotide sequencing) has been used in genome analysis and diseases diagnostics. To identify distribution aspects of viruses, we collected diseased samples twice in soybean breeding field. After extraction of total RNA from the collected bulk samples, RNA was sequenced by the NGS method. The NGS data were analyzed using the bioinformatics software. With newly produced NGS data, the identification of distribution aspects of organisms in field was estimated in this study. Sequence based identification method should be more accurate diagnostic tools of the target diseases and be able to predict occurrence of potential and new pathogens. NGS method will also provide the basic data by identifying the distribution of using bacteria. In this study, we analyzed the extracted RNA from the collection of approximately 3000 samples. Consequently, we confirmed the following types: the 7,089 kinds of bacteria including Burkholderiaceae, the 13,397 kinds of Eukaryota, the 952 kinds of viruses from the first bulk samples, the 4,160 kinds of bacteria including Burkholderiaceae, the 10,475 kinds of Eukaryota, and the 576 kinds of viruses from the second bulk samples.

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Detection of Soybean mosaic virus by RT-LAMP

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Soybean mosaic virus (SMV) is a prevalent pathogen that causes significant yield reduction in soybean production worldwide. SMV belongs to potyvirus and causes typical symptoms such as mild mosaic, mosaic and lethal necrosis. SMV is seed-borne and also transmitted by aphid. Eleven SMV strains, G1 to G7, G5H, G6H, G7H, and G7a were reported in soybean varieties in Korea. A reverse transcription loop-mediated isothermal amplification (RT-LAMP) method allowed one-step detection of gene amplification by simple procedure and needed only a simple incubator for isothermal template. This RT-LAMP method allowed direct detection of RNA from virus-infected plants without thermal cycling and gel electrophoresis. In this study, we designed RT-LAMP primers named SML-F3/B3/FIP/BIP from coat protein gene sequence of SMV. After the reaction of RT-LAMP, products were identified by electrophoresis and with the detective fluorescent dye, SYBR Green I, under daylight and UV light. Optimal reaction condition was at 58°C for 60min and the primers of RT-LAMP showed the specificity for nine SMV strains tested in this study.

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재배안정성이 우수한 조생 다수성 황색 메조 ‘다황메’ 육성

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웰빙 트렌드에 따라 잡곡수요는 점차 늘어나고 있으나, 농가에서 재배되고 있는 조의 경우 태풍, 폭우 등 급증하는 환경 재해에 취약하여 수량이 낮은 실정이므로 재해저항성이 강하고 수량이 높은 조 품종의 개발이 필요하다. 다황메는 충북 보은지역에서 2008년 수집된 재래조를 기본집단으로 하여 분리육종법을 통해 2013년 육성된 신품종이다. 다황메의 고유특성은 익은 녹색이나 생육후기에는 황록색으로 변하고 노화속도는 늦고 줄기의 분얼개도는 직립이고 강하며, 마디수는 많은 편이다. 이삭의 형태는 방추형으로 길며 아래로 처지는 자세이고 착립밀도는 보통이고 탈립은 잘 안되며, 낱알은 황색을 띠고 배유특성은 메성이다. 출수기는 대비품종인 황금조보다 보통기에서 3일, 이모작재배시 5일 늦고, 생육일수는 보통기 108일로 황금조(105일)보다 3일 많은 조생종이다. 간장(131 cm)과 수장(20.3 cm)은 황금조(각각 122 및 19.8 cm)에 비하여 큰 편이며, 줄기의 마디수는 17개로 3개 정도 많다. 다황메의 주당 수수는 황금조와 비슷하나 수당 중실무게는 13.3 g으로 황금조보다 2 g 정도 무거우며, 등숙비율은 67.8%로 황금조보다 2% 정도 높다. 천립중은 조곡 2.84 g, 현곡 2.57 g으로 대비품종 황금조(각각 2.74 및 2.44 g)에 비해 무겁다. 도복은 황금조보다 강한 편이고 불임내성 또한 강한 것으로 조사되었으며, 조도열병과 조노균병은 발생하지 않았고 줄무늬잎마름병은 경미한 발생을 보였다. 생산력검정시험 결과 다황메의 조곡 평균수량은 보통기 및 이모작재배에서 각각 400 및 293 kg/10a으로서 대비품종인 황금조에 비하여 각각 17 및 16% 증수되었고 특히 만식재배(257 kg/10a)에서는 62% 증수되어 내만식성이 우수하였다. 지역적응시험에서 전국 7개 지역의 수량은 대비품종 황금조에 비하여 보통기재배 평균수량은 296 kg/10a로 24% 증수되었고 이모작 재배는 263 kg/10a로 23% 증수되었다. 다황메의 제현율은 82.4%, 도정수율 75.6%, 완전미도정수율 71.3%로 대비품종 황금조(각각 79.7, 72.0 및 67.9%)보다 높았다. 품질특성은 대비품종 황금조에 비하여 아밀로스 함량은 약간 높은 편이나 조단백, 칼리, 칼슘 및 마그네슘 함량은 비슷한 함량을 보였다.

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가공용 통일형 중생 다수성 “중모1036” 육성

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‘중모1036’은 떡, 면류 등 쌀을 이용한 가공용에 적합한 통일형 다수성 품종이다. 2002년 하계에 수량이 높고 재배 안정성이 우수한 밀양181호를 모본으로, 천립중이 크고 단간 다수성인 다산벼와 YR22838(다산벼/YR22838(IR66738/가야벼//IR66738/가야벼)의 F₁을 부분으로 이용하여 인공교배를 실시하였다. 2003년 하계에 F₁을 양성하였고, 2005년도 F₃세대부터 2008년도 F₆세대까지 계통육종법으로 고정된 계통을 육성하여 수량성이 우수한 YR24230-27-2-1-1 계통을 선발하였다. 이 후 2009년 하계에 예비선발시험, 2010년부터 2011년까지 2년간 생산력 검정시험을 수행한 후 2011년부터 2013년까지 3년간 지역적응시험을 마치고 2013년 신품종선정위원회에서 다수성 및 가공이용성 등의 우수성이 인정되어 ‘중모1036’으로 명명되었다.

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Classification of rice varieties based on the haplotypes of major genes associated with grain size and shape

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Increasing demand on cereal grains to meet the population growth requires more production of rice as well as other cereals, which is supposed to rise up to 40% until 2030. Grain size and shape are critical factors determining grain yield. Several genes on grain shape and size have been reported, and of them, seven cloned genes were chosen for haplotype analysis, such as *GS3*, *GW2*, *qSW5*, *GS6*, *GW8*, *GS5*, and *TGW6*. We genotyped 218 rice varieties which had diverse grain size and shape originating from 25 countries. As for *GS3* and *qSW5*, PCR markers were developed for point mutation and deletion, respectively. For the other five genes in which functional SNPs were reported, we designed primer sets to distinguish a functional allele for each gene. *GW2* and *TGW6* had two alleles, while the other five genes displayed three alleles which were evenly distributed throughout the population. Analysis on the relationship between haplotype of the genes and grain phenotype is in progress. We expect that desirable allelic combination of genes would assure the optimal grain size and shape for higher grain yield and market quality. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No.PJ009076), Rural Development Administration, Republic of Korea.

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Plant fluorescence image analysis of salt-stressed soybean (*Glycine max*) for high throughput screening of salt stress tolerance

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The purpose of this study was to establish a system for plant fluorescence image acquisition and to verify the possibility of plant fluorescence image analysis as a non-destructive method to screen the salt tolerance of soybean (*Glycine max*). Two-weeks-old seedlings of soybean at the V1 growth stage were treated with 0, 50, and 100 mM of NaCl for salt stress and plant fluorescence images were taken by CCD camera (EOS-600D, Canon, Japan) equipped with band pass filter (XNiteBPPB, LPD LLC, USA) at 0, 15, 30, 60, 120 and 240 second after blue light exposure at 1 day after treatment. Red color intensity was extracted using MatLab 8.1 (The MathWorks Inc., USA) for estimation of plant fluorescence intensity. Red color intensity of soybean image decreased 0 (F_{0-10}) to 240 ($F_{240-250}$) second after blue light exposure irrespective of NaCl concentration, while $F_{0-10}/F_{240-250}$ decreased with NaCl concentration, resulting in significant relationship with plant fluorescence (F_v/F_m) and salt stress intensity. Therefore, our results suggest that our plant fluorescence image acquisition and analysis methods can be a part of high-throughput screening system for salt tolerance of soybean varieties.

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Effects of air temperature and light intensity on the acquisition of thermal image of rice (*Oryza sativa* L.)

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It is assumed that air temperature and light intensity may influence thermal image of plants but little effort has been made to these environmental factors. We conducted this study to investigate the effects of these environmental factors on the thermal image of rice and thus to optimize the condition for thermal image acquisition for high-throughput screening of salt-tolerant rice. Rice (*Oryza sativa* cv. Chuchoeng-byeo) seedlings at the four-leaf stage were treated with 0, 50, and 100 mM of NaCl for salt stress. Thermal images (T420, FLIR, Sweden) were taken at 1 and 2 days after salt treatment under 4 different air temperatures and 3 light intensities. Thermal images were analyzed using FLIR Tools 3.1 (FLIR systems Inc., USA) and MATLAB 8.1 (The MathWorks Inc., USA). Rice leaf temperature increased significantly with increasing air temperature and light intensity, resulting in greater discrimination between salt-stressed and unstressed rice plants. Our results thus conclude that environmental conditions such as air temperature and light intensity affect rice thermal image and their optimization is essential for better image acquisition and high-throughput screening system based on thermal image analysis.

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덩굴쪼김병 저항성, 베타카로틴 고함유 고구마 품종 ‘에스미’

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고구마의 단위면적당 수량은 연작, 병 감수성 품종의 재배면적 증가, 이상기상 등으로 인해 '00년 21.4MT/ha에서 '12년에는 14.9MT/ha까지 꾸준히 감소하였다. 특히 고구마 주산지에서 덩굴쪼김병 피해가 증가하고 있어 덩굴쪼김병 저항성 품종의 개발이 필요하다. 최근에 육성된 ‘에스미’는 덩굴쪼김병 저항성이 강한 품종으로서 육색이 담주황색이고 껍질색은 붉은색이며 괴근의 모양은 장방추형이다. ‘에스미’는 목포34호(IT232329)를 모본, 덩굴쪼김병 저항성 품종인 신건미(IT258213)를 부분으로 하여 2005년에 교배하였으며, 2009년부터 2010년까지 생산력 검정시험, 2011년부터 2013년까지 전남 무안 등 5개 지역에서 지역적응시험을 수행하였다. 생산력검정시험 결과, ‘에스미’의 상품괴근수량은 ha당 45.9MT으로 ‘올미’의 15.5MT/ha 대비 196% 높았다. 지역적응시험 보통기재배 결과, 상품괴근수량이 ha당 23.9MT, 주당괴근수는 2.8개, 괴근평균중은 개당 143g이었다. 전남 무안에서 수행한 지역적응시험 조기재배 결과, 상품괴근수량이 32.5MT/ha, 주당괴근수는 4.2개로 많아 조기재배용으로도 적합하였으며, 괴근평균중은 개당 117g으로 올미의 135g 보다 낮았다. 또한 ‘에스미’는 보통기재배 시 베타카로틴 함량이 15.7mg/100g으로 높았으며, 총유리당 함량과 감미도 역시 각각 30.3g/100g d.w.과 16.9로 ‘올미’ 보다 높았다. ‘에스미’는 덩굴쪼김병이 상습적으로 발생하는 포장에서 재배될 경우 수량 증대로 인한 농가소득 향상에 기여할 수 있을 것으로 보이며, 베타카로틴 함량이 높아 기능성 식품 등 가공 제품으로의 이용도 기대된다.

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Overexpression of *UGE1* from *Brassica rapa* enhances yield and tolerance to drought in transgenic riceHye Jung Lee^{§1}, Sailila E. Abdula^{§1,2}, Marjohn C. Niño¹, Kwon-Kyoo Kang³, Illsup Nou⁴, Yong-Gu Cho^{1*}¹Department of Crop Science, Chungbuk National University, Cheongju 361-763, Korea²Current Address, Philippine Rice Research Institute-Midsayap, North Cotabato 9410, Philippines³Department of Horticulture, Hankyong National University, Ansong 456-749, Korea⁴Department of Horticulture, Suncheon National University, Suncheon 540-742, Korea

UDP-glucose 4-epimerase (UGE) catalyzes the reversible conversion of UDP-glucose to UDP-galactose. To understand the biological function of *UGE* from *Brassica rapa*, the gene hereinafter referred to as was cloned and overexpressed into *Japonica* rice cv. Gopum. Transcriptional profiling showed that the is specific to stem of rice plant. Morphological evaluation of the overexpression lines revealed altered phenotype characters particularly in panicle length, number of productive tillers and filled spikelets which account for an increase in yield. This remarkable agronomic performance was ascribed to higher photosynthetic rate complemented with higher CO₂ assimilation. Interestingly, *BrUGE1* did not only improve plant fitness under optimal condition but also under water deficit stress. The enhanced drought tolerance may be due to the induction of soluble sugar which may act as osmolyte to compensate dehydration during drought stress.

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Breeding of Light Yellow Standard Rose ‘Green star’ with Powdery Mildew ResistanceHye-Jin Lee^{*}, Won-Hee Kim, Su-Young Lee, O-Hyeon Kwon, Kyeong-Seong Cheon.

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A new standard rose cultivar ‘Green Star’ was bred from the cross between pink color standard cultivar ‘Pastel move’ and red color standard cultivar ‘Vital’ at the National Institute of Horticulture & Herbal Science. The cross was made in 2008 and ‘Green Star’ was finally selected in 2013 after investigating characteristics for three years from 2011 to 2013. ‘Green Star’, a light yellow standard cultivar grows vigorously and has good and big shape. The major characteristics of this cultivar are 122.0 stems/m²/year in yield, 77.0±8.0 cm in length of cut flower, 12.1±0.4 cm in flower diameter, 37.7±4.2 in petal number, and 11.0±1.4 days in vase life. This cultivar can be propagated by both cutting and grafting. The consumer’s preference of this cultivar is relatively higher than that of control cultivar, ‘Moonlight’.

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Allelic diversity of genes associated with spikelet number per panicle in rice

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The spikelet number per panicle (SPP) in rice is a quantitative trait controlled by numerous genes. To identify the alleles of these genes, we conducted sequencing of coding region or UTR of 13 genes which are known for controlling SPP trait, subjected to 48 rice cultivars covering 27 Indica, 17 Japonica, and 4 Tongil types. The genes were *EP3*(ERECT PANICLE 3), *RCN1*(REDUCED CULM NUMBER 1), *RCN2*(REDUCED CULM NUMBER 2), *FZP*(FRIZZY PANICLE), *LAX1*(LAX PANICLE 1), *MOC1*(MONOCULM 1) *APO1*(ABERRANT PANICLE ORGANIZATION 1), *APO2*(ABERRANT PANICLE ORGANIZATION 2), *DEP1*(DENSE AND ERECT PANICLE 1), *FON1*(FLORAL ORGAN NUMBER 1), *GHD8*(GRAIN NUMBER, PLANT HEIGHT, AND HEADING DATE 8), *GNIA*(GRAIN NUMBER 1A), and *HDI1*(HEADING DATE1). As a result, 1 synonymous SNP was found in *EP3*, *RCN1* and *RCN2*. In *LAX1* and *MOC1*, 1 non-synonymous SNP was identified. But none of SNP was found from the coding region of *FZP*. Moreover, 3, 6, 7, 8, 9 and 10 alleles were detected in *APO1* and *APO2*, *FON1*, *GHD8*, *GNIA*, *DEP1*, and *HDI1* respectively. The multiple regression analysis revealed that *GHD8*, *DEP1* and *HDI1* had strong effects on spikelet number of primary branch. In addition, *HDI1* had strong effects on spikelet number of secondary branch, and for total spikelet number per panicle as well. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008125), Rural Development Administration, Republic of Korea.

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중북부 고랭지 적응 내랭성 조생 벼 품종 ‘진옥’

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냉해는 벼의 생육저해 및 수량감소를 발생시키는 재해 중 하나이며, 특히 우리나라 고랭지 지역은 냉해로 인한 벼 수량 및 품질저하가 우려된다. 따라서 안정적인 벼 재배를 위해 벼 재배기간 중 저온피해에 대비한 조생 내랭성 고품질 벼 품종개발이 필요하다. ‘진옥’은 고랭지 적응 내랭성 조생 품종 육성을 목적으로 ‘태봉’을 모본으로 하고 ‘운봉31호’를 부분으로 인공교배 하여 육성과정을 거쳐 2013년 신품종으로 선정되었다. ‘진옥’의 출수기는 7월 23일로 조생종이며 간장이 62cm 정도로 ‘진부’보다 7cm 짧고 수당립수는 84개 정도이다. 불시출수와 수발아는 안 되는 편이다. ‘진옥’은 저온발아성이 양호하고 냉수처리 내랭성 검정 결과 출수지연일수는 진부에 비해 짧으며 냉수구입실율이 양호하여 강한 내랭성을 나타내었다. 쌀 수량은 지역적응시험 보통기(4개소)에서 550Kg/10a로 진부벼보다 6% 증수되어 향후 중북부 고랭지 지역의 품종 다양화 및 수량성 개선에 부응할 것으로 기대된다.

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고온등숙성 및 도열병 저항성 조생종 벼 “중모1024” 육성

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최근 지구온난화로 인한 쌀의 품질저하가 큰 문제로 대두되고 있다. 특히 등숙기간의 고온은 쌀의 품위를 상당히 저하한다. 이로 인하여 고온에서도 좋은 외관 품위를 유지할 수 있는 품종 개발이 요구되고 있다. 중모1024는 야생종인 남일에 아지드화 나트륨을 처리하여 육성된 남일 돌연변이이다. 중모1024는 출수기가 보통기재배에서 대조품종인 오대와 같고 화성보다 9일 빠른 조생이다. 수량성은 보통기재배에서 498kg/10a로 오대와 동일한 수준이며, 화성보다는 낮다. 수수는 16개로 화성보다 많고 수당립수는 82개로 적은편이며 등숙율과 현미천립중은 22.3kg으로 화성과 비슷하다. 간장은 69 cm로 단간이며 수장과 숙색은 화성과 유사하다. 도복에 대해서는 좌절중이 높고 도복지수가 낮아 우수하다. 병해충에 대해서는 도열병에 매우 강하다. 반면, 흰잎마름병 및 바이러스병과 멸구류에는 약하다. 외관 품위에서는 심복백이 없어 우수하며, 이화학적 특성으로 단백질 함량은 6.2%이며 아밀로스 함량은 18.4%로 화성에 비해 다소 낮다. 도정율은 화성과 비슷하나 백미완전립율 및 완전미 도정수율은 화성에 비해 높다. 고온등숙성은 고온에서 현미 완전립율이 39.7%로 19.0~30.0%를 보인 대조품종들에 비해 높으며, 포장에서도 82.4%로 66.8~75.2%인 대조품종들에 비해 높다. 도열병에 강하며 고온등숙성을 보이는 중모 1024는 기후변화에 대응하는 육종모재로서 또한 돌연변이 육종을 이용한 유전인자에 대한 지적재산권 확보에 기여할 것으로 사료된다.

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중생 초다수 가공용 벼 품종 “팔방미”

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쌀의 식품형태 다양화를 통한 쌀 소비용도가 다양해짐에 따라 쌀 가공 시장의 규모와 가공용 이용량이 점점 커지고 있으나, 원료곡 가격, 가공적성, 그리고 제분 및 가공비용이 제한요인이 되고 있다. 따라서 수량성과 재배안정성이 높고, 배유전분 성능이 가공공정에 적합한 품종의 개발이 필요하다. 초다수이며 복합저항성 가공용 벼 품종인 팔방미는 병해충에 강한 서부아프리카 야생벼인 글라베리마 (*O. glaberrima*)와 통일계인 밀양 23호를 교배하여 육성하였다. 팔방미는 대조품종인 국내 초다수 품종인 다산과 동일한 수준의 수량성 (633kg/10a)을 보이며, 수수는 12개로 다산과 같으나 수당립수는 148개로 월등이 많다. 출수기는 다산에 비해 평균 3일정도 늦다. 또한 저온발아성은 다산에 비해 양호한 편이나 유묘냉해에 다소 약하다. 간장은 평균 74 cm로 다산보다 3 cm 짧고 수장은 25 cm로 길며 숙색이 양호하다. 도복지수는 다산보다 높으나 간장과 3절 간장이 짧아 포장도복에 강하다. 병해충에 대해서는 벼멸구와 애멸구에 저항성이 있으며, 도열병 및 줄무늬잎마름병에는 강하나 흰잎마름병과 오갈병 및 검은줄오갈병에는 저항성이 없다. 이화학적 특성으로 아밀로스함량이 29.5%로 매우 높으며, 단백질 함량은 7.9%로 다산과 유사한 수준이다. 쌀가루의 호화특성은 최고점도, 최종점도, 치반점도가 대조품종인 고아미보다 매우 유의하게 높았다. 또한, 10분 정도 삶았을 때의 압출물의 물성은 경도와 탄성 및 점성이 고아미보다 유의하게 높았다. 높은 수량 및 복합저항성 그리고 가공용으로 높은 적합성을 보이는 팔방미는 신규유용형질의 실용화 및 육종모재로 기대된다.

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기계화 수확이 가능한 중생 찰수수 ‘소담찰’ 육성

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농가에서 재배되고 있는 수수는 태풍, 폭우 등 급증하는 환경 재해에 취약하여 수량이 낮은 실정이므로 재해저항성이 강하고 수량이 높은 수수 품종의 개발이 필요하다. 소담찰은 2007년 황금찰수수와 증모4001을 교배육종법을 통해 2013년 육성된 신품종으로 고유특성은 이삭 측면 모양이 역삼각형으로 산수형의 형태를 가지며, 이삭밀도는 성긴 편이다. 종실의 반침껍질색은 짙은 갈색이고 종실색은 적갈색이며, 배유특성은 찰성이다. '12년 3개소에서 실시한 소담찰의 출수일수는 70일로 64일인 황금찰수수보다 6일정도 길었으며, '13년 6개소에서 실시한 평균 출수일수는 소담찰이 67일, 황금찰이 58일로 9일정도 차이를 보여 '12~'13년 7개소 평균 출수일수는 소담찰은 69일, 황금찰이 61일로 8일 정도 늦었다. 간장은 91 cm로 황금찰에 비해 58 cm 정도 작으며, 이삭길이는 3.2 cm 정도 길지만 이삭폭은 큰 차이가 없다. 줄기직경은 황금찰에 비해 4.5 cm가 더 굵어 도복에 강하고 엽장과 엽폭은 긴 편이다. 소담찰의 주당 이삭수는 1.1개로 황금찰과 비슷하고 1수당 이삭중은 48.9 g로 황금찰에 비해 무겁지만 이삭당 종실중은 32.5 g, 천립중은 21.1 g으로 황금찰과 비슷하다. '12년 밀양 지역에서 실시한 생산력 검정시험에서 소담찰의 현곡 평균 수량이 244 kg/10 a으로 황금찰수수(136 kg/10 a)보다 79% 증수되었다. '12~'13년 7개소에서 실시한 지역적응시험에서 소담찰 현곡평균수량이 295 kg/10 a으로 황금찰(299 kg/10 a)과 비슷하였다. 소담찰은 황금찰수수보다 단백질, Mg, Na 함량은 약간 높았고 아미로스 및 Ca 함량은 낮은 편이다. 항산화활성에 관여하는 폴리페놀과 탄닌 함량은 소담찰이 각각 14.00 및 3.55 mg/g이 약간 높았고 DPPH 및 ABTS 라디칼 소거활성 또한 황금찰수수(각각 3.69 및 8.65 mg TE/g)에 비해 소담찰이 각각 5.17 및 11.73 mg TE/g으로 높은 활성을 보였다.

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강원지역에서 호밀 “곡우”의 파종량이 종자 채종에 미치는 영향

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호밀은 추위에 강하고 단위 면적당 생산성이 높으며 불리한 토양환경에도 잘 자라는 매우 중요한 사료 및 녹비작물이다. 그러나 호밀은 타식성이고, 결실기에 도복에 약해 국내 채종이 어려워 대부분 종자를 수입에 의존하고 있다. 따라서 호밀의 국내 종자자급과 증수요인을 분석하기 위하여 국내 육성품종인 “곡우” 호밀의 재배환경과 초기 생육특성을 조사하였다. 시험장소는 강원도 영월군에 소재한 농가 채종포에서 수행하였으며, 시험처리는 파종량에 따라 10a당 3, 5, 7 kg 3처리구 3반복으로 2013년 10월 8일에 25 cm 간격으로 세조파기를 이용하여 기계 파종하였다. 시비는 국립농업과학원 휴토람 프로그램을 이용하여 진단 시비하였다. “곡우” 호밀의 출현기(2013년 10월 20일)와 출현양부(90% 이상)는 3처리구 모두 동일한 결과를 보였다. 생육재생기(2014년 2월 25일)와 출수기(2014년 4월 26일)도 3처리구 모두 비슷한 결과를 나타냈다. 초기 주간엽수는 파종량이 늘어날수록 감소하는 경향을 보였고, 반면에 m²당 경수와 이삭수는 파종량이 늘어날수록 증가하는 경향을 나타냈다. 초기 분얼수는 파종량 5 kg/10a 처리구(17.6개)에서 가장 높게 나타났고, 3 kg/10a 처리구에서 17.0개, 7 kg/10a 처리구에서 15.8개였다.

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벼 속기별 품종의 종자 발아율 변이

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최근 육성한 벼 품종을 대상으로 조생종, 중생종, 중만생종 품종에 대한 발아세 및 발아율에 대한 차이를 알아보고자 본 연구를 수행하였다. 시험재료는 국립식량과학원 벼 재배 시험포장 신흥통(사양토)에서 재배한 메벼로 조생종 11, 중생종 15, 중만생종 15품종 등 41품종에 대하여 조사하였다. 시험처리는 생육상(한백과학, HB-503LF)에서 25°C 항온으로 품종당 100립을 페트리디쉬에 치상하여 3반복 조사하였다. 발아세는 치상 후 5일에, 발아율은 치상 후 14일에 조사하여 발아립수를 총 시험립수로 나누었다. 시험결과 화왕벼 등 조생종의 발아세는 설레미 67.3%~조평벼 97% 범위였으며, 평균 발아세는 86.6%였다. 치상 후 14일후의 발아율은 운광벼 86.0%~조평벼 98.7%였으며, 평균 발아율은 91.8%였다. 중생골드 등 중생종의 발아세는 신백벼 53.7%~청운벼 97.3% 범위였고, 중생종 15품종에 대한 평균 발아세는 91.1%였다. 치상 후 14일후의 발아율은 신백벼 91.7%~청운벼 99%로 평균 발아율은 95.4%였다. 현품벼 등 중만생종의 발아세는 소다미 74%~삼광벼 99.7%였으며, 평균 발아세는 94.7%였다. 치상 후 14일 후의 발아율은 황금노들 94.3%~삼광벼 100%였다. 중만생종 15품종의 평균 발아율은 97.8%였다. 벼 속기별 발아세 및 발아율은 중만생종> 중생종>조생종> 순으로 높았다. 총 41 품종중에서 발아세가 높았던 품종은 삼광벼로 99.7%였다. 품종에 대한 발아세 및 발아율에 대한 정보를 활용해 본답 결주율을 사전에 방지할 수 있다. 최근 농촌 일손 부족을 해소하고 생산비를 절감 시키기 위하여 벼 무논점파 재배기술이 널리 확산 보급되고 있으므로 발아율이 높은 품종은 초기 신장성과 연계해 벼 무논점파용 품종으로 적응성이 높을 것으로 사료된다.

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콩 씨스트선충 감염지 작부체계에 의한 콩 생육 특성

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콩씨스트선충은 전세계적으로 콩 재배지에서 이어짓기 피해의 가장 중요한 요인중 하나로, 선충이 심하게 감염된 포장에서 콩의 수량 감소율은 69-72%이고, 우리나라 콩 농가포장의 50%가 콩씨스트선충에 감염돼 재배적방법(윤작, 태양열 소독, 답전윤환 등)이나 살선충제를 반드시 처리하여 씨스트선충 피해를 감소시켜야 한다. 경남농업자원관리원에서 20년 정도 콩+맥류를 계속 재배하고, 콩씨스트 선충의 밀도가 높을 것으로 추정되는 포장에서 실험을 실시하였다. 동계작물로 유채는 '선망', 밀은 '금강밀', 헤어리벤티는 '벳치1호', 여름작물로 들깨는 '다유', 콩은 '대원'을 시험재료로 하였다. 콩 씨스트선충 조사는 우리나라에서 가장 많이 발견되는 HG-type 2.5에 대하여 실시하였다. 콩 재배시 동계작물로 유채, 여름에 콩 재배시 수량이 16% 증수되었고, 겨울철 유채 재배가 어려운 경우 하계에 들깨를 윤작으로 재배시 콩 수량이 12% 증수되어 선충 피해를 경감할 수 있었다. 동계작물로 밀 재배는 콩씨스트선충의 피해 경감효과가 없었다.

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PA-74

남부지방 강낭콩의 파종기에 따른 생육 및 종실 특성

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남부지방에서 강낭콩의 2기작 재배를 위한 파종기별 생육과 수량성 및 종실의 외관 품질 등의 변화를 알아보고자 본 연구를 수행하였다. 시험재료로 ‘선강’ 품종, 파종기는 9시기로 4월 2일부터 8월 27일까지 흑색유공비닐 피복하여 재식거리는 55 x 15cm, 1주 2본으로 파종하였다. 파종기별 개화소요일수는 평균 38일이고 33일(8월 6일 파종)에서 51일(4월 2일 파종) 범위였다. 성숙일수는 평균 45일이고, 39일(4월 2일 파종)에서 59일(6월 25일 파종) 범위였다. 생육일수는 평균 83일이고, 71일(6월 4일 파종)에서 93일(6월 25일 파종) 범위였다. 8월 27일 파종시 11월 12일 서리로 인하여 생육이 중단되었다. 파종시기가 늦어짐에 따라 경장, 분지수, 마디수, 협수가 함께 감소하다 다시 증가하였다. 풋콩의 100립중은 평균 85.0g이고 50.5g(6월 4일 파종)에서 99.5g(4월 2일 파종) 범위였다. 춘계파종시 풋협과 종실 수량은 4월 2일 파종에 비하여 6월 4일까지 감소하였다. 추계파종시 8월 16일 파종한 시험구만 수확이 가능하였다. 6월 4일 파종은 8월 초 성숙기의 장마로 인하여 병해립이 많이 발생하여 종실의 외관 품질이 크게 저하되었다.

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PA-75

멜론 흰가루병 Race 판별계통을 이용한 국내 수집 흰가루병균으로부터 신규 Race 분리

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멜론 재배에 있어서 덩굴쪼김병과 더불어 흰가루병은 매우 중요한 병해로 멜론의 생장이나 수량 감소에 크게 영향을 끼쳐 농가 소득에 큰 피해를 주고 있다. 멜론 흰가루병의 병원균에는 *E. cichoracearum* 및 *S. fuliginea*가 보고되어 있으며, 2 종류의 사상균은 발아관의 형태, 피브로신(fibrosin)체의 유무를 관찰함으로써 차이점을 판별할 수 있다. *E. cichoracearum*는 프랑스 및 수단에서 처음으로 발생되어 보고되었지만, 1970년대부터는 *S. fuliginea*의 발생이 많이 보고되었고 근년에는 프랑스를 포함하여 미국, 이스라엘, 일본 등 세계 각국에서 흰가루병의 주요한 병원균으로 보고되고 있다.

흰가루병균은 1999년 Bardin 등이 PMR 45, WMR 29, PI 124112, PMR 5, MR-1 등의 판별품종을 이용하여 7개의 Race를 동정하여 발표하였으며, 최근 일본에서는 Race들의 분화에 의해 다수의 Race가 동정되어지고 있다. 그러나, 우리나라의 경우 Race 1이 광범위하게 발병하고 있다는 것 이외에 국내에서 발병하고 있는 멜론 흰가루병균에 대한 체계적인 연구가 아직 미비한 실정이다. 이에 본 연구는 국내에서 발병하고 있는 흰가루병균을 안성, 이천, 영암, 순천, 울촌 등에서 수집하여 사상균의 종류 및 판별품종을 이용하여 국내에서 발병하고 있는 흰가루병 Race를 확인하였다. 그 결과 국내 흰가루병균의 종류는 *S. fuliginea*였으며, 안성과 이천에서 수집한 흰가루병균은 Race 1뿐만 아니라 기존에 보고된 Race들이 아닌 새로운 Race의 흰가루병균이었다. 이 결과는 국내에도 다양한 흰가루병 Race의 존재 가능성을 시사하므로 다양한 Race 저항성 품종 개발이 요구되어진다.

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PA-76

Rice Small GTPase Rab11 is involved in Pathogen Defense Signaling

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Small GTP binding protein, Rab GTPases are a large family of proteins with a variety of regulatory functions in membrane traffic and development. Previously, we characterized OsRab11, which in concert with OsGAP1 and OsGDI3 regulates vesicular trafficking from the trans-Golgi network (TGN) to the plasma membrane or vacuole. To further elucidate the physiological function of OsRab11 in plants, we performed yeast two-hybrid screens using OsRab11 as bait. OsOPR8 was isolated and shown to interact with OsRab11. A co-immunoprecipitation assay confirmed this interaction. The green fluorescent protein-OsOPR8 fusion product was targeted to the cytoplasm and peroxisomes of protoplasts from *Arabidopsis thaliana*. OsOPR8 exhibited NADPH-dependent reduction activity when 2-cyclohexen-1-one (CyHE) and 12-oxo-phytodienoic acid (OPDA) were supplied as possible substrates. Interestingly, NADPH oxidation by OsOPR8 was increased when wild-type OsRab11 or the constitutively active form of OsRab11 (Q78L) were included in the reaction mix, but not when the dominant negative form of OsRab11 (S28N) was included. OsRab11 was expressed broadly in plants and both OsRab11 and OsOPR8 were induced by jasmonic acid (JA) and elicitor treatments. Overexpressed OsRab11 transgenic plants showed resistance to pathogens through induced expression of JA-responsive genes. In conclusion, OsRab11 may be required for JA-mediated defense signaling by activating the reducing activity of OsOPR8.

Keywords: OsRab11, GTPase, trafficking, OsOPR8

PA-77

고랭지 적응 조생 우량계통 ‘진부59호’현용조^{1*}, 정종민¹, 이상복², 윤영환¹, 정응기², 김보경²¹강원도 춘천시 충열로 251 국립식량과학원 춘천출장소²경기도 수원시 수인로 125 국립식량과학원 답작과

냉해는 벼의 대표적인 자연재해중 하나이며 쌀 수량 감소의 주요 원인이다. 우리나라에서도 1980년 냉해발생으로 국내 벼 재배면적의 64.2%에 결정적인 피해를 주고 약 32%의 수확량 감소를 가져왔다. 최근 잦은 기상이변이 발생함에 따라 저온으로 인한 안정생산이 우려되고 있다. 벼 냉해를 막는 가장 좋은 방법은 내랭성이 우수한 벼 품종의 개발이다. ‘진부59호’는 내랭성이 우수하고 쌀수량 및 품질이 향상된 고랭지지역에 적응하는 조생품종 육성을 목적으로 ‘진부’를 모본으로 하고 ‘운광’을 부분으로 2006년에 인공교배 하였다. 계통육종법에 의해 세대를 진전시킨 후 고정세대에서 실시한 생산력검정 시험에서 쌀수량이 525kg/10a로 진부보다 9% 증수하였다. ‘진부59호’의 출수기는 7월 29일로 조생종이며 간장이 62cm 정도로 ‘진부’보다 7cm 짧고 수당립수는 77개 정도이다. ‘진부59호’는 저온발아성이 92%로 양호하고 유묘내랭성이 매우 강한 특성을 보였다. 향후 지역적응시험을 통해 계통의 안정성 및 특성을 검정할 계획이다.

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PA-78

진도 지역 월동 양배추 품종별 특성 조사

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본 연구는 우리나라 진도지역에서 재배하고 있는 월동 양배추 품종의 포장 생육특성을 조사하기 위해서 일본품종 7종, 국내 품종 12종 등 19품종을 공시하여 파종은 7월 27일, 정식 8월 30일에 하고, 생육조사는 12월 28일에 품종별 초장, 초폭, 엽장, 엽폭, 엽중 그리고 구중, 구폭, 구고, 결구진도등을 조사하였다. 양배추의 초장은 23-32cm, 구중은 2-3kg등 다양성을 보였으며, 결구 진도는 품종별 유의적 차이를 보이지 않았다. 양배추의 외관은 결구의 정도에 따라 품종간 조금씩 차이를 보였지만 대체적으로 타원형의 모양을 보였고, 구고는 8-13cm, 구폭은 18-25cm까지 다양성을 보였다. 특히, 이번 조사에서는 현재 문제가 되고 있는 위황병 발병 정도도 함께 조사하였다. 위황병 발병 정도는 양배추의 형태적 특징을 보고 판단하였으며, 조사한 전체 20품종 중 4개의 품종에서는 전체적으로 위황병이 나타났으며 8개 품종에서는 전혀 발병하지 않았다. 전반적으로 위황병의 발생 빈도는 낮은 것으로 조사되었다.

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PA-79

수박 유전자원의 저온신장성 평가 및 관련유전자 발현분석

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수박(*Citrullus lanatus*)은 대표적인 고온성 채소이지만 대부분이 저온기에 정식하여 재배 하기 때문에 유묘기 저온으로 인하여 생육 불량하여 고품질 안정생산에 많은 장애 요인이 되고 있어 유묘기 내저온성 품종개발 필요성이 커지고 있다. 따라서 본 연구에서는 수박유전자원 16개 계통을 NDVI영상분석을 통하여 선발된 저온 신장성 우수 계통(PI299379, PI482261)과 시판품종삼복꿀, 수피금천을 식물생장상 28°C/18°C에서 20일간 육묘하여 3일간 15°C에서 순화 시킨 후 10°C에서 2일간 저온 처리(순화구)와 순화 없이 10°C로 2일간 저온처리(급저온구) 하였고 대조구는 주야간 온도를 28°C/18°C로 하여 유전자 발현의 차이를 분석하였다. 그 결과 대조구와 저온처리구의 발현양상 차이를 보이는 17개의 단편의 염기서열 분석을 통하여 확인하였다. 단편 서열을 바탕으로 한 RT-PCR 분석을 통하여 저온신장성 우수계통에서만 특이적으로 발현하는 calcium-binding EF hand family protein, trypsin inhibitor, Sigma factor binding protein, 등 4개의 유전자를 확인하였다

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PB-01

A new white wheat variety, “Joongmo2012” with low amylose and resistance to winter hardiness and moderate pre-harvest sprouting

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“Joongmo2012”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “Sinmichal/Keumkang” during 2006. “Joongmo2012” was evaluated as “Iksan357” in advance yield trial test in 2010. It was tested in the regional yield trial test between 2011 and 2013. Its heading date was May 2 in upland and May 1 in paddy field conditions, and Maturing date was June 8 in upland and June 8 in paddy field, which were similar to Keumkang, respectively. It showed 628 in number of spikes per m², 34 of grain number per spike, 47.6g of 1,000 grain weight, and 762g of test weight. “Joongmo2012” showed susceptible to Fusarium head blight (Scab) in test of specific character although “Keumkang” is susceptible to scab. “Joongmo2012” had lower flour yield (68.4%) than “Keumkang” (73.5%, respectively). “Joongmo2012” showed similar ash (0.40%), lower protein content (11.7%), SDS-sedimentation volume (39.8ml) and gluten content (8.1%) than “Keumkang” (0.41%, 12.7%, 55.8ml and 9.2%, respectively). It showed higher lightness (92.70) in flour color than “Keumkang” (91.51, respectively). “Joongmo2012” exhibited lower hardness (3.19N), similar springiness and higher cohesiveness of cooked noodles (0.90 and 0.66) compared to “Keumkang” (4.21N, 0.90, and 0.62, respectively). The average grain yield in the regional yield trial was 5.48MT/ha in upland and 4.47 MT/ha in paddy field, which were higher 5% and similar than those of the check cultivar, Keumkang, respectively.

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PB-02

A new white wheat variety, “Joongmo2004” with high milling rate and moderate resistance to Fusarium head blight

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“Joongmo2004”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “Bacanora88/Keumkang//Keumkang” during 1996. “Joongmo2004” was evaluated as “Iksan320” in advance yield trial test in 2006. It was tested in the regional yield trial test between 2007 and 2009. Its heading date was April 26 in upland and April 23 in paddy field conditions, and Maturing date was June 5 in upland and June 4 in paddy field, which were similar to Keumkang, respectively. It showed 830 in number of spikes per m², 35 of grain number per spike, 44.9g of 1,000 grain weight, and 806g of test weight. “Joongmo2004” showed moderate to Fusarium head blight (Scab) in test of specific character although “Keumkang” is susceptible to scab. “Joongmo2004” had higher flour yield (75.5%) than “Keumkang” (72.5% and 0.42%, respectively). “Joongmo2004” showed similar ash (0.42%), lower protein content (12.3%), SDS-sedimentation volume (43.0ml) and gluten content (10.3%) than “Keumkang” (0.42%, 13.1%, 57.8ml and 10.8%, respectively). It showed higher lightness (89.97), redness (-1.38) and yellowness (10.76) in flour color than “Keumkang” (89.61, -1.15 and 9.46, respectively). “Joongmo2004” exhibited lower hardness (3.50N), similar springiness and higher cohesiveness of cooked noodles (0.92 and 0.65) compared to “Keumkang” (4.54N, 0.93, and 0.63, respectively). The average grain yield in the regional yield trial was 5.17MT/ha in upland and 5.34 MT/ha in paddy field, which were lower 11% and higher 3% than those of the check cultivar, Keumkang, respectively.

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PB-03

A new white wheat variety, “Joongmo2003” with early maturity, good noodle quality and resistance to winter hardiness

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“Joongmo2003”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “SW86054/Keumkang” during 1997. “Joongmo2003” was evaluated as “Iksan318” in advance yield trial test in 2006. It was tested in the regional yield trial test between 2007 and 2009. Its heading date was April 24 in upland and April 21 in paddy field conditions, which were two days earlier than those of the check cultivar Keumkang, respectively, and Maturing date was June 4 in upland and June 2 in paddy field, one or two days earlier than those of Keumkang, respectively. “Joongmo2003” showed resistance to winter hardiness and pre-harvest sprouting, which lower withering rate on the low ridge (0.3%) and rate of pre-harvest sprouting (18.5%) than “Keumkang” (9.2 and 25.8%, respectively). “Joongmo2003” showed similar protein content (13.2%), lower SDS-sedimentation volume (54.0ml) and higher gluten content (11.7%) than “Keumkang” (13.1%, 57.8ml and 10.8%, respectively). It showed higher lightness (89.85) of flour and noodle dough sheet than “Keumkang” (89.81 and 80.28, respectively). “Joongmo2003” exhibited similar hardness (3.84), springiness and cohesiveness of cooked noodles (0.92 and 0.63) compared to “Keumkang” (4.54N, 0.93, and 0.63, respectively). The average grain yield in the regional yield trial was 5.55MT/ha in upland and 4.85 MT/ha in paddy field, which were 4% and 7% lower than those of the check cultivar, Keumkang, respectively.

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PB-04

A new red wheat variety, “Sooan” with good noodle quality and resistance to winter hardiness and pre-harvest sprouting

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“Sooan”, a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA. It was derived from the cross “Keumkang/Eunpa//Keumkang” during 1997. “Sooan” was evaluated as “Iksan319” in advance yield trial test in 2006. It was tested in the regional yield trial test between 2007 and 2009. “Sooan” is an awned, semi-dwarf and hard winter wheat, similar to “Keumkang” (check cultivar). The heading and maturing date of “Sooan” were similar to “Keumkang”. “Sooan” had similar test weight (817 g/L) and lower 1,000-grain weigh (43.7g) than “Keumkang” (817 g/L and 46.2g, respectively). “Sooan” showed resistance to winter hardiness and pre-harvest sprouting, which lower withering rate on the low ridge (0.2%) and rate of pre-harvest sprouting (0.2%) than “Keumkang” (9.2 and 25.8%, respectively). “Sooan” showed lower protein content (12.7%), SDS-sedimentation volume (42.0ml) and gluten content (10.5%) than “Keumkang” (13.1%, 57.8ml and 10.8%, respectively). It showed higher lightness (90.08) and lower redness (-1.11) and yellowness (8.80) in flour color than “Keumkang” (89.81, -1.15 and 9.46, respectively). “Sooan” showed higher lightness (81.34) of noodle dough sheet than “Keumkang” (80.28). “Sooan” exhibited lower hardness (3.84N) and similar springiness and cohesiveness of cooked noodles (0.91 and 0.65) compared to “Keumkang” (4.54N, 0.93, and 0.63, respectively). Average yield of “Sooan” in the regional adaptation yield trial test was 5.94 MT/ha in upland and 5.63 MT/ha in paddy field, which was 3% and 8% higher than those of “Keumkang” (579 MT/ha and 520 MT/ha, respectively).

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PB-05

극대립 황색자엽 검정콩 ‘중모3011호’ 개발

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‘중모3011호(밀양228호)’는 극대립 검정콩의 품종 육성을 목적으로 초형이 양호하고 다수성인 ‘청자3호’를 모본으로 극대립 검정콩인 ‘단파흑두’를 부분으로 2002년 인공교배하여 계통육종법으로 육성되었다. 자엽은 황색이고 종피색은 검정색이다. 2013년 1년간 전국의 7개소에서 지역적응시험을 실시한 결과 ‘중모3011호’의 성숙기는 11월 17일로 표준품종인 ‘청자3호’보다 22일 늦은 극만숙종이고, 경장은 80cm로 청자3호보다 15cm 크고 도복지수는 6으로 약하다. 종자의 100립중은 66.4g으로 ‘청자3호’보다 32.0g 무거운 극대립종이며, 수량성은 10a당 157kg으로 대비품종의 55% 수준이었다. 불마름병과 검은뿌리썩음병에 비교적 강했다. 경실종자는 없으며, 12시간 침종시 종자의 수분흡수율은 153%로 대비품종보다 25% 높았다. 또한 조단백질 함량은 40.5%이고 조지방 함량은 16.8%로 대비품종의 42.0%와 17.1% 보다 낮았다. 또한 기능성 성분인 이소플라본과 안토시아닌 함량은 각각 1,682 μ g과 15,556 μ g으로 대비품종 보다 낮았다. 재배상의 유의점은 표준 재식거리의 재배시 도복이 나타므로 소식재배를 준수하고 성숙기가 매우 늦으므로 조기에 파종하는 것이다.

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PB-06

국내 콩 유망 장려품종의 종실 Saponin 함량변이

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국내 콩 유망 장려품종 중 2009년까지 육성된 120품종의 종실 Saponin 함량의 변이를 구명하여 기능성 콩 품종개발의 기초자료로 활용코자 본 연구를 수행하였다. 콩 종실의 Group A와 B saponin을 합한 Total saponin 함량은 2431.1~8231.3 $\mu\text{g g}^{-1}$ 의 범위였고, 평균은 4910.5 $\mu\text{g g}^{-1}$ 이었다. Total saponin 중, Group A saponin은 225.6~1,193.3 $\mu\text{g g}^{-1}$ 의 범위였고, 평균은 592.5 $\mu\text{g g}^{-1}$ 이었다. Group B saponin은 2168.6~7270.0 $\mu\text{g g}^{-1}$ 범위였고, 평균은 4318.0 $\mu\text{g g}^{-1}$ 이었다. 각종 생리활성 효과를 나타내는 물질로 인식되는 Group B saponin이 높은 상위 품종은 원황콩, 녹채콩, 부광콩, 장기콩 및 흑미콩이었다. 콩 Saponin 함량은 품종, 육성연대, 용도, 종실크기 및 육성모지에 따라서 유의한 차이를 보였다. 육성연대는 2000년도 이후가, 용도는 나물콩이, 종실크기는 소립종이, 육성모지는 익산이 Total saponin 함량이 가장 높았다. Total saponin 함량과 Group B saponin의 함량 간에는 정의 상관이었다.

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PB-07

국내산 고구마 잎의 유용성분 함량 비교

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고구마의 주된 이용부위는 괴근으로 보조식량 및 간식용으로 이용되어 왔고, 엽병은 표피를 벗겨 나물용과 김치 용으로도 활용되고 있다. 하지만 최근에는 엽신 부분에 lutein과 β -carotene을 비롯한 여러 기능성 물질이 많이 함유되어 있어 가공식품 및 건강기능 식품으로 그 이용도가 확대되고 있다. 고구마의 이용부위의 확대는 고구마의 경제적 가치를 제고 시킬 수 있는 수단뿐만 아니라 국민 식생활 개선을 통한 건강증진에도 큰 도움을 줄 것으로 기대된다. 본 연구에서는 국내산 몇 가지 고구마 품종들을 대상으로 엽내 lutein, β -carotene 및 total polyphenol 함량을 조사하였다. 품종별 고구마 잎의 lutein 함량은 105~391 $\mu\text{g/g}$ 로 품종에 따라 큰 차이를 보였으며, 주황미, 진홍미, 진미, 울미 등이 각각 391, 348, 343, 310 $\mu\text{g/g}$ 으로 다른 품종들에 비해 높게 나타났다. 품종별 고구마 잎의 β -carotene 함량은 240~1,038 $\mu\text{g/g}$ 으로 나타났으며, 주황미, 울미, 진홍미, 신자미 등에서 각각 1,038, 803, 772, 737 $\mu\text{g/g}$ 으로 다른 품종들에 비해 높았다. 품종별 total polyphenol 함량은 16.6~34.1 mg/g으로 유사하게 나타났으며, 다호미, 대유미, 신울미, 신황미 등에서 각각 34.1, 28.7, 27.9, 27.1 mg/g으로 다른 품종들에 비해 높았다. 품종별 잎의 수량성은 신황미, 주황미, 신자미, 다호미, 대유미 등의 순으로 높게 나타났다.

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PB-08

다수성 가공용 향미품종육성 및 선발표지 개발

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가공용 쌀의 소비량은 2005년 이후 꾸준히 증가하고 있는 추세로서 국내 쌀 소비 기반 확대를 위해서는 기존 밥쌀 시장을 유지하는 것과 함께 다양한 쌀 가공식품 시장 개척을 통한 소비기반 확충이 필요하다. 본 연구는 향기 성분에 대한 간이 평가법을 개발하고, 다수성 향미 신품종 개발을 목표로 수행하였다. 향기 계통의 조기 선발을 위해 벼 식물체 잎을 채취하여 Solid Phase Micro Extraction(SPME)를 이용한 향기성분 검출법을 확립하였고, 벼에서 주요한 향기성분으로 알려진 2-acetyl-1-pyrroline (2AP)의 methyl ketone기에 특이적으로 반응하는 DNPH (2,4-di-nitrophenyl hydrazine)을 이용하여 향미계통과 무향 계통을 차별화 가능한 2AP-DNPH간 고유 발색반응을 조건을 설정하였고, 이를 활용한 향의 유무 및 간이 수준의 2AP함량 추정이 가능할 것으로 판단되었다. 향미품종 개발을 위해 고세대 육성계통의 생산력 및 지역적응성 시험을 통해 복합저항성 향미 계통 및 가공용 다수성 향미 계통 등 우수 계통을 육성하였다. 예농3호는 수원지역에서 8월 22일경에 출수하는 중만생종으로 간장이 78.4cm로 화영벼와 비슷하고, 현미의 단백질함량과 아밀로스 함량은 각각 6.9%, 18.6% 수준이며, 현미 천립중은 19.4g정도 이고, 장폭비는 2.79의 장원형이다. 내냉성, 목도열병, 흰잎마름병 및 줄무늬잎마름병에 중 정도의 저항성을 보였으나 멸구에 대한 저항성은 없었으며, 10a 당 수량은 417kg 수준이었다. 효원5호는 수원지역에서 8월 14일경에 출수하는 중생종으로 간장이 81cm로 다산벼 보다 크고, 이삭길이가 26.1cm로 긴 편이었다. 현미의 단백질 함량과 아밀로스 함량은 각각 8.4%, 19.4% 수준이고, 장폭비는 2.9의 장원형이다. 현미천립중은 20.8g이며 10a 당 수량은 627kg 수준이다. 육성 향미계통 및 품종은 떡볶이용 떡, 볶음밥 등 조리 가공용으로 활용이 가능할 것으로 기대 된다.

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PB-09

‘Haeoreum’, a new variety of *Hibiscus syriacus* L., suitable for street trees

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‘Haeoreum’, a new variety of *Hibiscus syriacus* was selected from the progenies of artificial breeding between ‘Bulkot’, as a mother plant, and ‘Wonhwa’, as a pollenizer, at the Korea Forest Research Institute in 2006. The preliminary, advanced and regional trials for evaluation and selection of this variety were carried out from 2012 to 2013. Investigated morphological characteristics showed that ‘Haeoreum’ is a simple flower type and has bell shape in open type of corolla. The diameter of flower is about 12.8mm, and the white petals are slightly folded each other. The length of red eye zone is very long, about 26.0mm. Leaf type is in oval shape, and leaf thickness, glossy level and the shape of leaf base is medium, medium and rounded, respectively. Its blooming period each year lasted more than 80 days, and the quantity of bloom is large in normal condition. In addition, it showed faster growth performance compared to the similar varieties, about 90cm per growing season in tree height. According to all these characteristics, the new variety ‘Haeoreum’ could be useful for large container plants or street trees.

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PB-10

유색밀의 도정비율별 취반 특성 분석

김경훈, 유인영, 강천식, 김학신, 최인덕, 김영진, 신상현, 손재한, 정영근, 이춘기, 박광근

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최근 다양한 소비자의 기호를 충족하기 위해 국산밀의 가공 이용성을 다양하게 하고, 이와 함께 소비촉진 정책이 같이 추진되고 있다. 이에 유색밀의 도정비율별 취반 특성을 분석하였다. 시험재료는 메성인 금강밀, 유색밀과 찰성인 유색찰밀을 이용하였으며 40분간 취반 후 흡습성, 퍼짐성, 경도, 탄성, 껌성, 씹힘성과 응집성을 분석하였다. 금강밀과 유색찰밀 모두 취반 후 도정비율이 높아질수록 흡습성, 퍼짐성이 높아졌으나, 도정비율 30% 이상에서는 낮아졌다. 경도와 껌성은 도정비율이 높아질수록 감소하였고, 금강밀이 유색찰밀보다 높았다. 금강밀의 경도는 13.5~138.5N, 유색밀은 20.8~131.2N, 유색찰밀은 12.8~112.6N을 나타냈다. 씹힘성도 도정비율이 높아질수록 감소하는 경향을 보였으나, 25% 이상에서는 큰폭으로 감소하지는 않았다. 탄성, 응집성은 도정비율과 유의성이 없었고, 금강밀, 유색찰밀 간에도 차이가 없었다. 향후 유색/유색찰밀 계통 중에서 농업적 특성이 우수한 찰성을 가진 계통을 선발하여 그에 따른 취반 특성을 측정하여 식미와 취반 적성 모두 적합한 계통 선발 및 도정비율을 선별할 예정이다.

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PB-11

바이오디젤 및 경관용 내도복성 유채 ‘중모 7002’

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유채(*Brassica napus* L.)는 오래 전부터 기름을 이용하기 위해 재배되어 왔으나, 최근에는 지역자치단체의 축제와 홍보를 목적으로 경관용 유채 재배가 증가하고 있다. 유채는 월동이 가능한 전남북, 경남, 제주도 등의 남부지방에서 주로 재배되었으나 최근에는 구리, 삼척 등의 중부지방 지방자치단체에서도 하천의 고수부지와 공원 및 동계 유희농지에 경관을 목적으로 유채를 재배하여 유채를 주제로 한 축제를 개최하여 관광객 유치, 지역사회홍보 및 농가소득증대를 유도하고 있다. 경관용 내도복성 유채 ‘중모 7002’은 농촌진흥청 국립식량과학원 바이오에너지작물센터에서 [(RS10×Erra)×Tower]를 모본으로, ‘RS10’을 부분으로 인공교배하여 육성하였다. 1984년에 교배하여 F₁을 양성한 후 1985년과 1986년에 F₁과 F₂를 전개하여 집단으로 선발하였고, 1987년 F₃ 부터 1990년에 F₆ 까지 4년 동안 계통선발 과정을 거쳐 우량계통인 ‘목포116호’(84013-B-6-3-3-6)을 선발하였다. 선발한 ‘목포116호’를 2009년과 2010년에 전남 무안의 바이오에너지작물센터 포장에서 생산력검정시험을 실시한 후, 2011-2013년에 3년 동안 무안(전남), 익산(전북), 진주(경남) 및 애월(제주) 등 4개 지역에서 유채 고정 품종인 ‘한라유채’와 비교하여 지역적응시험을 실시한 결과, 이형주가 발견되지 않아 품종으로서 균일성 요건을 충족하여 안정성을 갖춘 것으로 판단되어 ‘중모7002’(Jungmo7002)으로 명명하였고, 국립종자관리원에 품종보호출원(출원 2014-221)을 마쳤다. ‘중모7002’ 기존 유채 고정품종인 ‘한라’에 비해 개화균일성이 우수하고 내도복성과 내병성(균핵병)에 강하여 바이오디젤 및 경관용으로 적합하다.

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조숙, 논재배 적응 유채 1대잡종 ‘해안’

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십자화과(Cruciferae)에 속하는 동계작물인 유채(*Brassica napus* L.)는 예로부터 어린 식물체는 나물로, 종자는 식용유로 사용하기 위해 제주도를 포함한 남부지역에서 재배되어 왔다. 최근 지구온난화와 유가상승으로 바이오디젤을 생산하기 위해 유채기름에 대한 관심의 증가와 함께 재배면적이 증가하고 있다. 유채는 밭작물이지만 대량 재배와 기계화를 위해서는 논재배가 필수적이며 논재배에 강한 유채 품종육성이 절실하다. 이에 따라 2008년도에 국립식량과학원 바이오에너지작물센터에서 모본으로 ‘목포-CGMS’(웅성불임)와 부분으로 ‘8516-B-5-6-1-2’(임성회복화분친)을 교배하여 1대잡종인 ‘단교70호’를 양성하고 유채 1대잡종 품종인 ‘선망’을 대비품종으로 하여 2009~2010년에 걸쳐 생산력검정시험을 실시하였으며, 2011~2013년에 전남, 전북, 경남 및 제주 등 4개 지역에서 지역적응시험을 실시하였다. 생산력검정과 지역적응 기간 동안 농업적인 특성, 종자 내의 지방함유량, 지방산의 조성 및 글루코지놀레이트의 함량 등을 분석한 결과, ‘단교70호’는 대비품종인 ‘선망’에 비해 조숙이며, 논재배에 대한 적응성이 강하며 내병성 및 내도복성이 강하여 해안(Hae-an)으로 명명하였고, 2014년에 국립종자관리원에 품종보호출원(출원 2014-2222)을 마쳤다. ‘해안’의 엽형은 하부익상전열이며, 결각은 중간, 엽색은 녹색, 종피색은 흑색으로 대비품종인 ‘선망’(Sunmang)과 비슷하나 꽃색은 선황색이다. ‘해안’의 추대기는 3월 23일, 개화기는 4월 11일로 ‘선망’과 비슷하였으나 성숙기가 6월 4일로 ‘선망’보다 4일 빨랐으며, ‘해안’은 경장이 115 cm로 선망과 같았으며, m²당 주수는 103본으로 ‘선망’보다 5본 많았고, 1수협수는 53개로 ‘선망’보다 2개 많았다. 천립중은 ‘해안’이 4.1 g으로 ‘선망’보다 0.2 g 더 무거웠다. ‘해안’은 기름함량이 44.2%로 ‘선망’보다 0.9% 높으며, 올레인산 함유 비율이 69.8%로 ‘선망’보다 2.5%가 높았고, 에루신산은 전무하며, 구루코지놀레이트 함량이 1.84 mg/g으로 국제 허용기준치인 3.0 mg/g 이하이다. 수량은 10a 당 272 kg로 ‘선망(256 kg/10a)’에 비해 약 6%가 증수되었으며 도복과 균해병에 비교적 강하다.

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PB-13**Genetic diversity for gliadin subunits of Korean and Tunisian wheat**

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Gliadins are the main class of wheat seed storage proteins. Since gliadins show a high level of polymorphism as well as genetically fixed, it can be used as a marker for the genetic identification. Gliadin subunit diversity information can be useful for wheat quality breeding programs. Tunisia is a country in the North Africa bordered with the Mediterranean Sea to the north and the east but with the Sahara desert to the south, which represent extremely different growth climate. Therefore, there may be a numerous variation in Tunisian common wheat and durum wheat. Total 48 lines of wheat consisted of 32 common wheat (16 Korean wheat and 16 Tunisian common wheat) and 16 Tunisian durum wheat were incorporated in this study. Gliadins were extracted with 70% ethanol and fractionated by acid polyacrylamide gel electrophoresis (A-PAGE) at 8% in aluminum lactate buffer (pH 3.1). The gel was stained with 0.25% Coomassie Brilliant Blue (CBB) R-250. The presence of each gliadin subunit band was scored and cluster analysis was carried out. The cluster showed that wheat varieties were classified into some groups and their genetic distance could be identified. The obtained information will be helpful to the future breeding program of tetraploid durum wheat as well as hexaploid common wheats.

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쌀귀리(*Avena sativa* L.) 춘파재배시 파종시기별 출수반응

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맥류는 대부분 추파(가을 파종)하나 파종기에 잦은 비로 인하여 파종을 하지 못할 경우가 발생된다. 이에 따른 대책으로 춘파(봄 파종)하는 경우가 보리와 밀 등에서 이루어지고 있다. 그러나 춘파 파종하면 불리한 점이 많다 추파보다 출수가 늦고 수확량도 낮고, 논 2모작 작부체계에서 후작물 재배에 어려움을 초래하는 단점이 있으나 최근 맥류 재배기간 이상고온으로 출수가 빨라져 2모작 재배에 지장을 초래하지 않는 선에서 재배가 가능성을 확인을 위해 최근 밀 춘파 재배시험이 이루어지고 있다. 또한 내한성이 약한 쌀귀리 재배지에서도 일부 춘파재배가 이루어지고 있는 실정이다. 이와 관련하여 쌀귀리 재배품종의 춘파재배시 출수반응을 알아보기 위한 시험결과로 춘파시험은 2월 26일부터 5일 간격으로 4월 5일까지 9회 파종하였으며, 품종은 조숙종인 조양, 만숙종인 대양 등 2품종을 시험품종으로 하였다. 그 결과 춘파재배시 출현까지의 소요일수는 조양 10~20일, 대양 11~21일로 조숙종과 만숙종이 비슷한 출현일수를 보였다. 출현일수는 춘파시기가 늦어질수록 온도상승에 따른 출현일수는 3~10일 정도 단축되었고, 파종부터 출현기까지 적산온도는 조양 75.7~114.3℃, 대양 85.5~123.9℃ 이었다. 추파(10.15)한 경우보다 조양 7~19일, 대양 11~24일 늦은 출수를 보였다. 출현부터 출수기까지 소요일수는 조양 45~61일, 대양 55~70일로 조숙종인 조양에서 9~10일 정도 짧았다. 출수는 춘파시기가 늦어짐에 따라 출수 일수가 단축되는 경향이나 4월 1일 이후 파종된 경우에는 변화가 없었다. 출현부터 출수기까지 적산온도는 조양 616.7~689.8℃, 대양 820.3~968.7℃로 만숙종인 대양은 출수기까지 적산온도가 203.6~278.9℃ 더 필요한 것으로 나타났다. 따라서 익산지역과 비슷한 기상을 보이는 지역에서는 조숙종인 조양은 3월 중순이내로 파종하면 출수가 5월 중순경으로 6월 하순 전·후로 수확이 가능하나 만숙종인 대양은 출수가 5월 하순경으로 논 2모작 작부체계에서 춘파재배는 곤란할 것으로 생각된다.

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PB-15

Induction of Microspore-derived Embryos According to Heat Shock, Dark Incubation, and Washing Medium

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Heat shock pretreatment, dark culture period and washing medium could have marked effects on microspore embryogenesis. A heat shock pretreatment of microspores at 32.5°C for 48 hours gave high production rate of microspore-derived embryo (MDE) when compare to shorter and longer period. The yield of MDE increased significantly when microspore cultured for 15 days at 25°C in dark condition followed by heat shock pretreatment. MDE were browned and lost vitality when dark treatment period extended longer than 15 days. This is caused by an insufficient oxygen and light for growing embryo which already formed during dark treatment period. The vitality of a microspore isolated from flower bud stored at 4°C become decreased at the very first day and the vitality of microspore stored at 4°C in the form of flower bud itself become decreased from the 5th day after storage. This shows the possibility of getting a certain period of storage for a suitable flower bud in MDE formation. The yield of MDE was most effective when isolated microspore was had with MS medium compared to B-5 and NLN medium and also showed most effective result with sucrose 130 g·L⁻¹ in additional sucrose concentration. The above result is thought to be very useful for the development of a new cultivar of radish and other many crops including *Brassica* using haploid breeding technology.

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PB-16

밀 반수체 육종 시스템을 이용하여 육성한 조숙 밀 계통의 농업특성

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본 연구는 밀x옥수수 원연교잡을 이용한 반수체 육종 시스템을 이용하여 조숙 밀 계통을 생산하고 그 농업특성을 비교한 것이다. 조숙 밀 품종 개발을 목적으로 수원283/조은밀, 수원287/조은밀 2조합의 인공교배를 실시하여 30 이삭 222립을 수확하였다. 밀 반수체 생산을 위해서 모본인 밀 F₁은 2010년 10월 22일에 포장에 파종하고, 부분인 옥수수(cv. 광평옥)는 2011년 2월 5일부터 3월 30일 까지 5일 간격으로 유리온실(32/20°C, 12hr 일장)에 파종하였다. 2011년 5월부터 밀x옥수수 원연교잡을 실시하여 미숙배를 생산하고, 배배양을 통해 미숙배를 재분화시켜 반수체를 얻었다. 반수체 개체는 온실에서 순화처리 후 재배하였으며, 콜히친 처리를 통해 염색체를 배가하여 28개의 정상적인 식물체를 얻었다. 반수체 육종시스템을 통해 생산된 식물체의 증식 및 개체 특성을 파악코자 2012년 10월에 포장에 전개하여 2013년 여름에 종자를 수확하였다. 그 중 농업특성이 우수한 개체를 선발하여 2013년 10월에 생산력검정 예비시험에 공시하여 종실 등 농업특성을 조사하였다. 출수기와 성숙기는 14wPYTs-36(수원283/조은) 계통이 4월17일과 5월 27일이었으며, 14wPYTs-37(수원287/조은) 계통은 4월18일과 5월 28일이었는데 이는 교배 모, 부분에 비해서 출수기와 성숙기가 1주일 이상 빨랐다. 현재 재배되고 있는 밀 장려품종 중 가장 속기가 빠른 조품밀 보다도 성숙기가 1~2일 빠른 경향을 보였다. 종자의 임실률은 14wPYTs-36 계통이 80%, 14wPYTs-37 계통이 92%를 나타냈다. 천립중은 조품이 37.5g, 조경이 39.8g인 반면, 14wPYTs-36(수원283/조은) 계통은 45.5g, 14wPYTs-37(수원287/조은) 계통은 43.6g을 보여 상대적으로 대립종이었다.

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PB-17

Bud germination rates of four gamma ray-irradiated Citrus species

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we analyzed the survival rate through the measurement of germinability of the gamma-ray irradiated buds of 4 Citrus species, *C. hybrid* 'Kiomi', *C. hybrid* 'Setoka', *C. hybrid* 'Kanpei', and *C. junos*, in greenhouse. To induce mutation, spring buds of Citrus with 0, 10, 20, 40, 60, 80 and 100 Gy of gamma radiation were irradiated and then were vgrafted onto trifoliolate orange rootstock. The rootstock number per gamma ray dosage was two hundreds. After after 6 months growth, the shoot germination rate from gamma ray-irradiated buds presented lower viability than those of non-irradiated buds. Higher dossage of irradiation more inhibited bud germination at all experimental groups of citrus. The viability of unirradiated citrus plants was *C. junos* > 'Setoka' > 'Kiomi' > 'Kanpei'. We have determined LD50 of gamma ray-irradiation.

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PB-18

SELDI-TOF/MS를 이용한 초다수성 밀 계통의 저분자 펩타이드 탐색

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초다수성 밀 계통의 프로테옴 분석에 의한 생태생리대사를 해석해 보고자 본 연구를 수행하였다. 초다수성 밀 계통의 저분자 단백질 변화를 SELDI-TOF/MS로 CM10과 Q10의 두 단백질 칩을 이용하여 2kDa ~ 15kDa의 범위에서 분석하였다. 저분자 단백질을 분석하여 검출된 단백질 결과는 CM10을 사용하여 총 106개, Q10을 사용하여 총 84개의 바이오마커 가능성을 가진 단백질을 검출할 수 있었다. 총 190개의 저분자 단백질을 탐색하여 금강밀과 초다수성 밀계통간의 단백질을 비교하였다. Q10에서 $p < 0.01$ 의 유의성을 가진 피크 클러스터들로 PCA 분석을 통해 3차원적 군집화하여 그 군집분포를 통하여 Q10에서 금강밀을 제외한 나머지 13GHW059, 78, 80, 143의 밀계통이 군집화되는 것을 확인할 수 있었다. CM10에서 $p < 0.05$, Q10에서 $p < 0.01$ 의 유의성을 가진 피크 클러스터들로 heat map한 결과 각 칩별로 CM10에서 2,182 kDa, 2,411 kDa, 2,542 kDa, 2,629 kDa, 2,775 kDa, 2,857 kDa, 2,964 kDa, 3,002 kDa, 3,511 kDa, 4,040 kDa, 4,379 kDa, 4,818 kDa, 5,479 kDa, 5,739 kDa, 6,257 kDa, 7,104 kDa, 7,988 kDa, 11,659 kDa, 16,404 kDa, 25,270 kDa 총 20개의 바이오마커를 찾았고, Q10에서 2,967 kDa, 3,831 kDa, 4,075 kDa, 5,374 kDa, 5,409 kDa, 5,424 kDa, 7,774 kDa, 8,161 kDa, 13,128 kDa, 16,336 kDa, 24,614 kDa, 25,162 kDa, 25,615 kDa, 25,917 kDa, 27,635 kDa 총 15개의 바이오마커를 찾아, 각 칩별 초다수성 밀 계통의 바이오마커를 유추할 수 있었다.

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PB-19

두릅나무 선발개체의 새순특성과 선발효과

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기능성 산채로 부가가치가 높은 두릅나무의 우량 품종을 육성하기 위하여 경기 가평 등 21지역에서 새순의 특성이 우수한 192개체를 선발하였다. 기존에 육성된 충북1호, 건국1호, 논산1호 그리고 일본도입종 자오 등 4개의 품종을 대조구로 하여 새순의 수확시기, 무게 등 새순특성을 분석하였다. 새순의 수확시기는 길이가 15~20cm일 때를 적기로 판단하였으며, 최적 수확시기는 4월 29일부터 5월 13일까지 15일 정도로 나타났다. 선발개체의 전체평균 특성은 새순길이 14.0cm, 새순굵기 13.7mm, 새순무게 12.0g으로 나타났으며, 새순색은 녹색, 적녹색, 적색으로 각각 나타났다. 새순 특성이 우량한 개체선발을 위하여 새순의 무게를 기준으로 상위 5% 및 10%에 해당하는 새순이 크고 무거운 개체를 각각 10본, 19본을 선발하였다. 선발효과는 각각 210%, 193%로 나타났으며 특히, 대조품종인 건국1호, 충북1호, 논산1호 및 자오에 비해서 새순특성이 우수한 것으로 나타났다.

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PB-20

정금나무 선발개체 열매의 총 플라보노이드 및 안토시아닌 함량

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정금나무의 기능성 품종을 육성하기 위하여 우량집단으로 선발되어진 4집단에서 각각 6개체씩 선발하여 총 24개체의 열매에 대한 형태적 특성, 총 플라보노이드 및 안토시아닌 함량을 조사·분석하였다. 총 플라보노이드 함량 측정에는 Davis법을 변형한 방법, 안토시아닌의 함량은 AOAC에 의한 pH differential method를 응용하여 측정하였다. 열매의 형태적 특성에서는 태안 집단의 개체들의 과지당 열매수, 크기, 무게에 있어 높게 나타났으며, 논산 집단의 개체들은 당도가 평균 12.5%로 다른 집단에 비해 높게 나타났다. 총 플라보노이드 함량은 2.2~8.1 mg/g의 범위를 나타냈으며, 집단별로는 구미와 논산 집단이 높은 함량을 보였고, 광주 집단이 낮은 함량을 보였다. 개체별로는 논산36이 8.1 mg/g으로 가장 높았고, 다음으로 논산32, 구미12, 구미31 개체가 유사하게 높게 나타났다. 총 안토시아닌 함량은 232.5~684.3 mg/100g의 범위로 나타났다. 집단별로는 구미 집단이 가장 높게 나타났으며, 광주 집단은 안토시아닌 함량이 가장 적은 특성을 보였다. 특히, 가장 높은 수치를 나타낸 구미 집단이 가장 낮게 나타낸 광주 집단에 비해 1.3배 이상의 함량을 나타냈고, 개체별로도 한 집단 내에서 약 2.4배 이상의 차이를 보였다. 개체별로는 태안1, 태안34, 논산36 개체가 각각 684.3, 678.9, 636.1 mg/100g으로 상대적으로 높았다. 또한 대조구로 사용한 국내재배 블루베리(246.4 mg/100g)와 북미산 블루베리의 안토시아닌 함량(228.1 mg/100g)에 비해 정금나무 전체 집단의 평균 안토시아닌 함량(474.5 mg/100g)이 각각 1.9배와 2.1배 높게 나타났다. 종합적으로, 구미 집단이 총 플라보노이드 및 안토시아닌 함량이 높게 나타났으며, 개체별로 볼 때 논산36이 당도가 높으면서 유용성분 함량이 높아 육종 소재 및 기능성 성분 소재로서의 이용가치가 높을 것으로 사료된다.

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PB-21

중대륜계통의 파스텔톤 분홍색 반겹꽃 절화용 거베라 ‘Pinkever’ 품종 육성

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거베라 ‘Pinkever’는 2007년 수원 국립원예특작과학원에서 분홍색 반겹꽃 ‘Stefani’와 분홍색 홑꽃 ‘Selma’를 교배하여 획득한 종자로부터, 2008년 실생 계통을 양성하여, 화색이 선명하고 화형이 안정된 중대륜계통의 분홍색 반겹꽃 거베라 ‘08B3-42’를 개체 선발하였다. 선발된 계통에 대하여 2008년부터 2010년까지 분주 및 조직배양으로 개체를 증식한 후 2011년부터 2012년까지 1·2차 생육특성검정을 수행하고, 2013년에 ‘원교B3-52호’로 계통명을 부여하여 3차 특성검정, 안정성·균일성에 대한 연차별 재현성 및 기호도 평가를 수행한 결과, 화색 및 화형에 대한 기호도가 우수하고, 절화장이 길며 연간채화량이 많은 다수성 품종으로 그 우수성이 인정되어, ‘원교B3-52호’는 2013년 농촌진흥청 직무육성품종심의회를 거쳐 ‘Pinkever’로 명명되고 직무육성품종으로 등록되었다. ‘Pinkever’의 생육 및 개화특성은 화색과 화형이 유사한 ‘Eta’를 대조품종으로 하여 조사하였다. ‘Pinkever’는 녹색 화심의 RHS color chart R49B의 파스텔톤 분홍색 반겹꽃으로, 대조품종(RHS R52C) 보다 밝은 분홍색 품종이다. 평균 화경은 11.4cm로 대조품종(11.1cm)와 비슷한 중대륜계 품종이며, 설상화의 길이와 폭은 각각 5.3cm와 1.1cm로 비교적 길고 넓다. 꽃대 굵기가 꽃목부위 3.9mm, 중간부위 5.2mm로 비교적 굵고 등글어 경할현상이나 꽃목굵음 등의 생리장애 발생이 적고, 절화수명도 평균 10.0일로 길다. 절화장이 평균 61.3cm로 대조품종(49.8cm)보다 11.5cm 정도 길어 절화 품질이 우수하며, 연간 채화량도 54.9본/주로 대조품종(49.3본/주)보다 주당 5.6본 더 많은 다수성 품종이다.

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PB-22

Isolation of microsatellite loci from ramie, *Boehmeria nivea* (L.) Gaudich and their application to the genetic resource analysis

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Ramie (*Boehmeria nivea* L. Gaudich.) 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 microsatellite molecular markers of ramie. To do this, we generated microsatellite-enriched genomic DNA libraries using magnetic bead hybridization selection method. 216 contigs containing microsatellite repeat 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 26 microsatellite markers, possibly showing polymorphism among the genetic resources. Results on the genotype analysis of the ramie genetic resources using the microsatellite markers will be presented.

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PB-23

Change of Nutritive Value and Fermentation Quality of the Silage of Kenaf Cultivars by Different Harvest stage

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This study was carried out to determine the effects of different harvesting stage on nutritive value and the quality of ensiled kenaf after fermentation among six kenaf cultivars. Six kenaf cultivars including two different maturity groups, mid-late maturing (Auxu, Jangdae and Jinju) and early-maturing (Baekma, Jeokbong and C14), were planted on May 14, 2013. Four harvesting times were made at intervals of 20 days from 15 July to 16 September, 2013. In all cultivars, the CP (crude protein) contents were decreased by a delayed harvest; the CP contents of kenaf silage were ranged from 92 to 184 g kg⁻¹. Interestingly, there were no significant difference of NDF (neutral detergent fiber) and ADF (acid detergent fiber) content between the cultivars, however NDF and ADF content of kenaf silage were significantly increased by a late harvest. The silages of all cultivars displayed a low pH ranges less than 4.0, which is sufficient for stable storage. The lactic acid contents in Auxu were from 2.57 to 3.21%, which is higher than other cultivars. The harvesting stages did not affect to the concentrations of butyric acid and acetic acid in all cultivars. These results indicate that the harvesting stage is more important for the quality of kenaf silage than cultivar differences. And kenaf silage could be also used as fodder for ruminants.

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PB-24

SELDI-TOF/MS를 이용한 초다수성 밀 계통의 저분자 펩타이드 탐색

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초다수성 밀 계통의 프로테옴 분석에 의한 생태생리대사를 해석해 보고자 본 연구를 수행하였다. 초다수성 밀 계통의 저분자 단백질 변화를 SELDI-TOF/MS로 CM10과 Q10의 두 단백질 칩을 이용하여 2kDa ~ 15kDa의 범위에서 분석하였다. 저분자 단백질을 분석하여 검출된 단백질 결과는 CM10을 사용하여 총 106개, Q10을 사용하여 총 84개의 바이오마커 가능성을 가진 단백질을 검출할 수 있었다. 총 190개의 저분자 단백질을 탐색하여 금강밀과 초다수성 밀계통간의 단백질을 비교하였다. Q10에서 $p < 0.01$ 의 유의성을 가진 피크 클러스터들로 PCA 분석을 통해 3차원적 군집화하여 그 군집분포를 통하여 Q10에서 금강밀을 제외한 나머지 13GHW059, 78, 80, 143의 밀계통이 군집화되는 것을 확인할 수 있었다. CM10에서 $p < 0.05$, Q10에서 $p < 0.01$ 의 유의성을 가진 피크 클러스터들로 heat map한 결과 각 칩별로 CM10에서 2,182 kDa, 2,411 kDa, 2,542 kDa, 2,629 kDa, 2,775 kDa, 2,857 kDa, 2,964 kDa, 3,002 kDa, 3,511 kDa, 4,040 kDa, 4,379 kDa, 4,818 kDa, 5,479 kDa, 5,739 kDa, 6,257 kDa, 7,104 kDa, 7,988 kDa, 11,659 kDa, 16,404 kDa, 25,270 kDa 총 20개의 바이오마커를 찾았고, Q10에서 2,967 kDa, 3,831 kDa, 4,075 kDa, 5,374 kDa, 5,409 kDa, 5,424 kDa, 7,774 kDa, 8,161 kDa, 13,128 kDa, 16,336 kDa, 24,614 kDa, 25,162 kDa, 25,615 kDa, 25,917 kDa, 27,635 kDa 총 15개의 바이오마커를 찾아, 각 칩별 초다수성 밀 계통의 바이오마커를 유추할 수 있었다.

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PB-25

속잎색이 노랗고 작은 구를 형성하는 배추 '원교20045호' 육성

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배추는 우리나라에서 김치, 국, 무침, 찌개 등 다양한 요리의 재료가 되는 주요 전통 채소이다. 60년대 후반부터 일대잡종 품종 육성 연구를 시작하여 현재는 대한민국 품종의 우수성이 중국, 일본 및 동남아 지역까지 인정되고 있다. 따라서 종자의 수출을 확대코자 중국 소비자의 요구에 부합되는 소재의 개발이 필요하다. 중국의 배추 시장은 '북경3호'처럼 대형의 구를 형성하며 잎이 억센 북음용 품종이 주류를 이루었으나, 최근 우리 소형 배추를 데쳐서 이용하는 '와와채' 시장이 성장하고 있다. 따라서 구가 작고 조숙형이며 잎의 색이 진한 품종의 요구가 증가하고 있다. 국립원예특작과학원에서는 다양한 배추 자원을 수집, 평가 후 선발된 자원을 소포자 배양하여 다양한 계통을 육성해오고 있다. 2009년에 다양한 국내외 배추 품종을 수집하여 그 중 속잎색이 노란 개체를 선발하였다. 선발된 개체들은 후대 종자 채종을 위해 성숙모본의 형태로 하우스에 이식하였으며, 이듬해 2010년 봄부터 여름까지 뇌수분 방법으로 종자를 증식하였으며, 증식된 종자는 가을동안 채종하였다. 100립 이상 증식된 개체의 후대는 2011년 가을에 노지 포장에서 재배하였다. 이들 중 속잎색이 노란 개체를 다시 선발하여 성숙모본의 형태로 하우스에 이식한 후, 이듬해 봄부터 소포자 배양을 실시하였다. 2012년 여름에 다양한 Doubled-Haploid(DH) 개체를 획득하였으며, 획득된 식물체는 춘화처리를 한 후 화분에 정식하여 뇌수분 하였다. 2013년 여름에 다양한 개체로부터 종자를 100립 이상 채종하였으며, 이들을 2013년도 가을에 노지 포장에 심어 특성검정을 실시하였다. 특히 종묘회사와 공동으로 특성평가 결과 중국 수출에 용이하도록 속잎과 겉잎의 색이 진하고 대조(불암3호)의 2.2kg보다 작은 1.7kg의 작은 구를 형성하여 신품종으로 선발하게 되었다. 선발된 품종은 2013년 겨울에 직무육성품종 심의회를 통과하여 '원교20045호'로 명명되었으며, 현재 품종보호 출원을 위해 종자를 증식하고 있다.

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PB-26

EMS 처리에 의한 group A 사포닌 결핍 돌연변이 콩 특성 검정

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콩은 40% 단백질과 20% 지방을 가지는 중요한 작물중 하나이다. 또한 이소플라본, 사포닌 펩타이드, 피틴과 같은 여러 생리활성 물질은 가지고 있다. 사포닌은 콩의 중요한 2차대사 물질중 하나로 콩에는 0.6-6.2%의 사포닌을 가지고 있다. 콩 사포닌은 그룹 A, B, E 그룹으로 나뉘어진다. 그룹A 사포닌은 콩에서 쓴맛과 떼은맛을 내는 것으로 알려져 있어 그룹 A 사포닌을 제거하려는 노력이 이루어지고 있다. Group A 사포닌이 제거된 콩을 개발한다면 콩 식품의 맛을 개선할 수 있을 것으로 기대가 된다. 본 연구의 목적은 풍산나물콩 EMS 처리집단에서 group A 사포닌 결핍 개체를 선발하고, group A 결핍에 관한 유전현상을 밝히는 것이다. TLC(thin layer chromatography)방법을 통해 M4 834개체에서 한 개의 group A 사포닌 결핍 개체를 선발하였다. 선발한 개체의 Sg-1 유전자 염기서열 분석에서 non-sense mutation을 발견하였고 이를 검출할 수 있는 SNP마커를 개발하였다. Group A 사포닌 돌연변이개체와 풍산나물콩과 인공교배를 통해 F2 종자를 생산하였다. TLC와 HPLC로 사포닌 표현형을 결정하였고 SNP마커를 이용하여 유전자형을 결정하였는데, 정상적인 group A 사포닌(wild type)과 결핍 개체는 3:1로 분리하였다. 이 연구를 통해 육성된 group A 돌연변이 사포닌 계통은 콩 품종육성의 재료로 이용할 예정이다.

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PB-27

Variation in Antioxidant Activity and Flavonoid contents in Leaves and Fruits of Eggplant (*Solanum melongena* L.) Germplasm

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Eggplant (*Solanum melongena* L.) is an excellent source of vitamin A and C as well as flavonoid compounds, which are important antioxidant components that may reduce the risk of diseases. In this study, we investigated ABTS, DPPH activity and flavonoid contents in eggplant leaves and fruits to identify genetic resources with high antioxidant capacity for use in food or as feed additives. A total of 102 eggplant accessions were classified into four groups by latitude of their origins: 0°~15° N (8 accessions), 15°~30° N (19 accessions), 30°~45° N (34 accessions), and 45°~60° N (41 accessions). The accessions originated from 45°~60°N showed the highest flavonoid contents (AVG. = 15.4 $\mu\text{g mg}^{-1}$) followed by accessions originated from 30°~45° N (AVG. = 13.0 $\mu\text{g mg}^{-1}$), 15°~30°N (AVG. = 11.0 $\mu\text{g mg}^{-1}$) and 0°~15°N (AVG. = 9.5 $\mu\text{g mg}^{-1}$). Same pattern was also found in ABTS and DPPH antioxidant activities. High ABTS, DPPH activity and flavonoid contents were found in the early-flowering accessions. All flavonoids of the greenish violet leaves were significantly higher than those in green leaves. The flavonoid concentration in eggplant leaves with an average of 15.6 $\mu\text{g mg}^{-1}$ increased from 10- to 20-fold as compared with their fruit (AVG.=0.9 $\mu\text{g mg}^{-1}$). In conclusion, eggplant leaves represent a potential source of natural antioxidants due to their very high flavonoid contents.

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PB-28

A New Short Stem and Lodging Resistant Peanut Variety “Danwon”

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A new peanut (*Arachis hypogaea* ssp. *fastigiata* L.) variety “Danwon(Milyang51)” with short stem length and lodging resistance was developed at the Department of Functional Crop, NICS, in Miryang in 2013. This variety was developed from the crossing line between cultivar “YG 75” with large grain and fewer branch number and “SP9617” with short stem length. “Danwon” which is Shinpung plant type has 32cm 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 40 mature pods of per plant, 91g of 100-seed weight, 77% of pod shelling ratio in the regional yield trials(RYT). Seed quality show 48.7% of crude oil and 26.9% of protein content. “Danwon” has resistance to lodging in even double dense planting without yield reduction. This is more resistant to early and late leaf spot, web blotch and stem rot, compared with check variety “Daekwang”. In the regional yield trials “Danwon” outyielded check variety by 6% with 4.52 MT/ha for kernel.

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PB-29**A New High Oleate Peanut Variety “K-OI”**

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High oleate oil enhance flavors and shelf life and decrease coronary heart disease mortality. A new peanut(*Arachis hypogaea* ssp. *fastigiata* L.) variety “K-OI(Milyang56)” with high oleic acid of fatty acid composition was developed at the Department of Functional Crop, NICS, in Milyang in 2013. This variety was developed from the crossing line between cultivar “Baekseon” with large grain and erect plant type and “F435-5” with high oleate and runner type. “K-OI” which is Shinpung plant type has 43cm of main stem length and 10 branch number per plant. This also show more resistant to late leaf spot, web blotch and stem rot, compared with check variety “Daekwang”. Each pod has two grains with short ellipse shape of brown testa and yield components is composed of 46 mature pods of per plant, 74g of 100-seed weight, 76% of pod shelling ratio in the regional yield trials(RYT). For 3 year regional yield trials the average yield of “K-OI” had 4.45 MT/ha for kernel similar to that of check variety. Seed quality show 50.7% of crude oil and 82.9% of oleic acid. The oil acidification of “K-OI” measured by acid value(P-A value) variation for 3 hours at 180 °C showed one-ninth as low as ‘Daekwang’ do. This variety is expected to develop new demand area such as the improvement of cardiovascular disorders and shelf-life, and import substitution of olive oil.

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PB-30**A New Peanut Variety “Hwaseon” with High Yield and Large Grain**

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A new peanut(*Arachis hypogaea* ssp. *fastigiata* L.) variety “Hwaseon(Milyang50)” with the high yield potential was developed at the Department of Functional Crop, NICS, in Milyang in 2013. This was developed from the crossing line between cultivar “Iksan 31” with large grain and high quality and “SP9614” with short stem. “Hwaseon” which is Shinpung plant type has 41cm of main stem length and 10 branch number per plant. Each pod has two grains with long ellipse shape of brown testa and yield components is composed of 45 mature pods of per plant, 84g of 100-seed weight, 79% of pod shelling ratio in the regional yield trials(RYT). Seed quality showed 47.3% of crude oil and 27.6% of protein content. This variety also showed more resistant to early leaf spot, and stem rot, compared with check variety “Daekwang”. In the regional yield trials “Hwaseon” outyielded check variety by 12% with 4.78 MT/ha for kernel.

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PB-31

Induction of Microspore-derived Embryos According to Light Quality Treatment on Donor Plant of Broccoli

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Investigation of flowering time, flower structure, microspore density, microspore vitality and microspore-derived embryo (MDE) formation rate according to the light quality treatment on broccoli donor plant was accomplished. The material was 08-8-3 line yielding high MDE production rate having 4.0 ± 0.5 mm flower bud length. The donor plant was cultivated with light quality treatment of red LED light, red+blue+white LED light and fluorescent light. The light intensity was $50 \mu \text{mol m}^{-2} \text{s}^{-1}$ and photoperiod was 16/8 hours (light/dark). The flowering time was fastest at red LED light treatment compared to the other light treatment condition. 100.0, 36.4 and 18.2% of flower bud with longer stigma length than floral leaf which reported high MDE production rate were found under red LED light, Red+Blue+White LED light and fluorescent lights respectively. The microspore density and MDE production rate per single flower bud was highest at Red LED light. Suitable flower bud and high MDE production rate could be achieved in a short period if using LED light to broccoli donor plant cultivation. The above result is thought to be very useful for the development of a new cultivar of broccoli and other many crops including *Brassica* using haploid breeding technology.

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PB-32

영남 평야지 소득작물 전후작용 극단기성 신품종 '중모1032'

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지구온난화에 따른 기온상승은 작물 재배기간을 증가시켜 1년 2모작 및 3모작 작부체계가 확대될 것으로 보인다. 이러한 추세에 따라 시설 및 노지에서 재배되는 소득작물 전후작지에 2모작 및 3모작 작부체계에 적용이 가능한 극단기성 품종이 요구되어왔다. “중모1032”는 2005년 하계에 중만생종이면서 고품질인 남평벼와 극조생이면서 저아밀로스인 Aya를 부분으로 인공교배한 것에 남평벼를 반복친으로 2회 여교배 하였다. 2005/2006년 동계에 BC₂F₁ 개체를 양성하여 약배양으로 세대를 조기 고정시킨 계통들 중에서 출수기가 빠르고 미질이 양호한 YR25786Acp13-1을 선발하여 밀양255호의 계통명을 부여하였다. 2010~2011, 2013년 3년간 지역적응시험을 거쳐 ‘중모1032’를 육성하였다. 출수기는 만기재배에서 8월13일로 표준품종인 금오벼보다 12일 빠르고, 조기재배에서는 7월 11일로 대비품종인 조운보다 4일 빠른 극단기성 품종이다. 수당립수는 50개로 적으며, 현미천립중은 21.1g이다. 쌀수량은 만기재배에서 평균 2.71MT/ha, 조기재배에서 3.60MT/ha이다. ‘중모1032’는 영남 평야지 소득작물 재배지에서 소득작물의 출하시기를 조절할 수 있는 극단기성 품종에서 농가소득증대에 기여할 것이다.

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PB-33**A New Hybrid *Cymbidium* 'Beauty Smile' with Orange Colored Flower and Medium Type**

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A new hybrid, *Cymbidium*(*C.*) 'Beauty smile' was developed as new hybrid by National Institute of Horticultural & Herbal Science, Rural Development Administration, Suwon, Korea in 2013. This hybrid came from the progenies crossed between *C.* '2113'(Accession No.) and *C.* Lucky Rainbow 'Randevious' in 2000. Finally, eighty seven seedlings were obtained after planting and acclimatization in green house. In 2007, one line was selected by their performance such as flower color, leaf shape, flower stalk, and vigorous growth and named 'Wongyuo F1-43. The line code 000550-78 had uniformity and excellent characteristics. The selected line after second characteristics test was named as 'Beauty smile'. This hybrid had bright pink colored petal and lip (RP63D)and large sized flower(diameter 8.3cm). A 'Beauty smile' had about 13.3 flowers per flower stalk and medium sized flower and plant. General impression of petals and sepals showed some incurved shape. The attitude of peduncle was half-erect. Bloom was started from middle of November under optimal culture condition.

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PB-34**A New Hybrid *Cymbidium* 'Sunny Bell' with Fragrant of Small Type**

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A new hybrid, *Cymbidium*(*C.*) 'Sunny Bell' was developed as new hybrid by National Institute of Horticultural & Herbal Science, Rural Development Administration, Suwon, Korea in 2013. This hybrid came from the progenies crossed between *C. karan* and *ebruenum* in 2000. Finally, one hundred-one seedlings were obtained after planting and acclimatization in green house. In 2007, one line was selected by their performance such as flower color, leaf shape, flower stalk, and vigorous growth and named 'Wongyuo F1-47. The line code 000390-46 had uniformity and excellent characteristics. The selected line after second characteristics test was named as 'Sunny Bell'. This hybrid had light purple colored petal and lip (RP59B)and large sized flower(diameter 7.9cm). A 'Sunny Bell' had about 7.8 flowers per flower stalk and small sized flower and plant. General impression of petals and sepals showed some incurved shape. The attitude of peduncle was erect. Bloom was started from February under optimal culture condition.

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PB-35

A New Forage Barley(*Hordeum vulgare* L.) Short Awn Spike type with Lodging and Disease resistance, 'Jungmo2506'

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'Jungmo2506' (*Hordeum vulgare* L.), a new ruminant-palatability forage barley cultivar, was developed by the breeding team at the Department of Rice and Winter Cereal Crop, National Institute of Crop Science, RDA in 2013. It was derived from the cross between 'Sunwoo' and 'Milyang 34'. Among the cross made in 2002, a promising line, SB02T2020-B-B-B-64, showed good characteristics in potential forage yield in the yield trial tested at Iksan in 2009 to 2010 designated as Iksan 463. The line in the Regional Yield Trials(RYT) tested in eight locations around Korea for three years from 2011 to 2013, and was released as the name of 'Jungmo2506'. It has the growth habit of group IV, erect plant type, green leaf and short awn spike. Its average heading and maturing dates were on May 3, and June 2, respectively, with similar to check cultivar 'Youngyang'. The cultivar had 99cm of culm length, 692 spikes per m² and it showed better rate of leaf, winter hardiness, and resistance to BaYMV than those of the check cultivar. The average forage yield of 'Jungmo2506' was about 11.8 ton ha⁻¹ in dry matter in paddy field. 'Jungmo2506' also showed 6.6% of crude protein content, 27.4% of ADF (Acid Detergent Fiber), 49.2% of NDF (Neutral Detergent Fiber), and 67.2% of TDN (Total Digestible Nutrients), including higher grade of silage quality for whole crop barley.

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PB-36

A New Forage Barley(*Hordeum vulgare* L.) Awnless Spike type with Good quality and Disease resistance, ‘Muhan’

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‘Muhan’ (*Hordeum vulgare* L.), a new ruminant-palatability forage barley cultivar, was developed by the breeding team at the Department of Rice and Winter Cereal Crop, National Institute of Crop Science, RDA in 2013. It was derived from the cross between SB921011-3B-16-2/IT0188556 and ‘Suwon 365’. Among the cross made in 2002, a promising line, SB02T2097-B-B-B-18, showed good characteristics in potential forage yield in the yield trial tested at Iksan in 2009 to 2010 designated as Iksan 465. The line in the Regional Yield Trials(RYT) tested in eight locations around Korea for three years from 2011 to 2013, and was released as the name of ‘Muhan’. It has the growth habit of group IV, erect plant type, green leaf and awnless spike. Its average heading and maturing dates were on May 4, and June 4, respectively, with similar to check cultivar ‘Youngyang’. The cultivar had 102cm of culm length, 711 spikes per m² and it showed better rate of leaf, winter hardiness, and resistance to BaYMV than those of the check cultivar. The average forage yield of ‘Muhan’ was about 12.4 ton ha⁻¹ in dry matter in paddy field. ‘Muhan’ also showed 6.6% of crude protein content, 28.6% of ADF (Acid Detergent Fiber), 50.1% of NDF (Neutral Detergent Fiber), and 66.3% of TDN (Total Digestible Nutrients), including higher grade of silage quality for whole crop barley.

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PB-37

Change of quality characteristics of foxtail millet, proso millet, and sorghum with storage temperature

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The change of quality characteristics with storage temperature (room (25°C), low (15°C) and cold (4°C) temperature) and period of unhulled foxtail millet (*Setaria italica* Beauv. cv. Samdame and Gyeongkwon 1), proso millet (*Panicum miliaceum* L. cv. Hwanggeum-gijang and Manhongchal) and sorghum (*Sorghum bicolor* (L.) Moench cv. Hwanggeumchal and Donganme) were evaluated. The 1,000 grain weight, lightness, redness, yellowness and moisture content with storage temperature and period of unhulled foxtail millet, proso millet and sorghum were not showed difference. Germination percent and milling recovery of foxtail millet, proso millet and sorghum decreased with increasing storage temperature and period. Fat acidity of stored foxtail millet, proso millet and sorghum was increased with increasing storage period, and the higher temperature increased more. The results of this study show that the storage of foxtail millet, proso millet and sorghum at the low and cold temperature is better than the room temperature. Especially, in mind of the economics, the storage method is good low temperature than cold temperature.

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PB-38

Selection of soybean mutant lines changed seed coat color and identification of their flavonoid contents

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In this study, the concentrations of isoflavones, anthocyanins and total phenol content (TPC) in 19 soybean mutant lines changed seed coat color from yellow to black or brown were determined. Among 19 soybean mutant lines, 5 soybean mutant lines with black pigment were detected 3 anthocyanins (delphinidin-3-O-β-D-glucoside, D3G; cyaniding 3-O-β-D-glucoside, C3G; petunidin 3-O-β-D-glucoside, Pt3G). The highest concentration of anthocyanins among 5 soybean mutant lines was D-16 (1280.0 ± 19.4 mg/100g seed coat) derived from cv. Danbaek. Although isoflavone contents of all soybean mutant lines showed lower levels compared to original cultivars, glycitein was detected only 5 soybean mutant lines (DP-37-2, DP-38, DP-39, DP-40, and DP-41 derived from cv. Daepung). In TPC of 19 soybean mutant lines, DP-10 was increase levels compared to original cultivar, while DP-37-2, DP-40, and DP-41 were decrease levels of TPC. Using reduction of DPPH, we measured the free radical scavenging activity (FRSA) among 19 soybean mutant lines. Five black and 4 brown soybean mutants showed significant increase in FRSA. On the basis of these results, it was concluded that gamma irradiation may change the isoflavone, anthocyanin, and total phenol contents of soybean. These mutant lines using in this study can be useful for the breeding of soybean varieties altering the nutritional values.

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PB-39

Proteome analyses reveal new insights on heteromorphic self-incompatibility in Common Buckwheat

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The different forms of flowers in a species have drawn thoughtful attention of many evolutionary botanists, including Charles Darwin. Common buckwheat (*Fagopyrum esculentum* Moench.) is regarded as a dimorphic self-incompatible plant which bears either a pin or a thrum flower. It is revealed that the S supergene the key element to govern the self-incompatibility, flower morphology, and pollen size. Already, we have produced self-incompatible buckwheat lines by an interspecific cross between *F. esculentum* and *F. homotropicum* by using embryo rescue. We also notice that the self-compatibility allele, S^h , keeps up the heteromorphic incompatibility. In the past decades, two dimensional gel electrophoresis based proteomics approaches have been applied systematically to identify and profile proteins expressed during pollen development of model plant species. Proteome techniques have vastly been applied in the fields of plant genetics, plant development, and plant physiology and ecology to reveal plant genetic diversity, plant development, differentiation of plant tissue and organ, separation and functional identification of novel component of various organelles, mechanisms of plant adapted to abiotic or biotic stresses including high temperature, low temperature, high salt, drought, and pathogens and insects, and interaction of plant with microbe. However, the plethora of studies related to heteromorphic has added remarkably to our knowledge in the field of the multiple aspects of the breeding system and many researches have provided evidence for the connection between these two components. But in spite of its potential biological significance, the high throughput proteomics analysis of this connection has so far been grossly overlooked. So our attempts are to unravel the proteome investigation in common buckwheat.

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PB-40

Proteome responses of diploid and tetraploid roots under various hormones in *Platycodon grandiflorum*

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Platycodon grandiflorum, known as Doraji in Korea, is used in various medications and traditional cuisine in Korea. This study was conducted to characterize the hormonal effects of diploid and tetraploid roots of *P. grandiflorum* using proteomics technique. Prior to proteome analysis, different kinds of growth hormones; IBA (1mg/L), NAA (1mg/L) and IAA (1mg/L) were applied in the adventitious (Diploid and tetraploid) roots for investigation. Solid (1/4MS) and liquid (1/2MS) medium were performed in the present study to investigate the hormonal effects. In diploid roots, two dimensional gels stained with CBB, a total of 1154 protein spots were identified using image analysis by Ludesi REDFIN 3 programme (Ludesi AB, Lund, Sweden: www.ludesi.com). Out of 1154 differential expressed protein spots, a total of 33 protein spots (≥ 2 -fold) were selected for mass spectrometry. Among the 33 protein spots, 7 protein spots were up-regulated in IBA, 12 proteins in NAA and 14 proteins in IAA. In the case of tetraploid roots that performed under solid medium, a total of 842 differentially expressed protein spots were identified of which 34 proteins spots (≥ 1.5 -fold) were selected for mass spectrometry. Out of 34 protein spots, 11 proteins were up-regulated in IBA, 10 proteins in NAA and 13 proteins in IAA. However, a total of 659 differentially expressed proteins were confirmed from the liquid medium of tetraploid roots from which 32 proteins spots (≥ 1.5 -fold) were sorted for MS analysis. Out of these 32 proteins, a total of 3 proteins were up-regulated in IBA, 7 proteins in NAA and 22 proteins in IAA. The identified proteins may provide insight clues for better understanding of the characteristics of proteins and biological activity from adventitious roots of *Platycodon grandiflorum*.

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PB-41

Proteome profiling unraveling the characterization of diploid and tetraploid roots in *Platycodon grandiflorum*Hye-Rim Kim¹, Soo-Jeong Kwon², Swapan Kumar Roy¹, Jung-Hee Ko¹, Hag-Hyun Kim², Hee-Ock Boo³, Sun-Hee Woo^{1*}¹Department of Crop Science, Chungbuk National University, Cheongju 361-763, Republic of Korea²Department of Flower Floral Plant Coordination and Landscape Architecture, Woosong Information College, Daejeon, 300-715, Republic of Korea³WellPhyto Co. Ltd., BI Center, GIST, Gwangju 500-712, Republic of Korea

Platycodon grandiflorum is a perennial flowering plant, known as Chinese bell flower, widespread in northeast Asia. The roots of this species are used for centuries to treat diseases, and have extensive pharmacological effects such as reducing adiposity, hyperlipidemia as well as anti-atherosclerotic disorder. In this study, systematical and targeting proteome analysis were executed from the 3, 4 and 5 months aged diploid and tetraploid roots of *Platycodon grandiflorum* and the proteins were separated by 2-DE and stained by CBB. In diploid roots, a total of 30 protein spots (≥ 2 -fold) were analyzed using MASCOT search engine according to the similarity of sequences with previously characterized proteins along with the UniProt database. Among the 30 differentially expressed proteins, 21 proteins spots were identified as up-regulated and 9 proteins were identified as down-regulated. In contrary, a total of 40 differentially expressed proteins were confirmed from tetraploid roots whereas 28 protein spots were confirmed as up-regulated and 12 proteins were identified as down-regulated. However, the differentially expressed proteins from diploid and tetraploid roots were classified into 12 and 14 possible functional categories respectively using Protein Information Resources. The results revealed that the identified proteins from diploid and tetraploid roots were mainly involved in oxidoreductase activity, nucleotide binding, transferase activity and catalytic activity in bellflower roots. In conclusion, the exclusive proteins from diploid and tetraploid roots may provide insight clues for better understanding the characteristics and functions of proteins and metabolic activity of *Platycodon grandiflorum*.

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PB-42

Variation of seed germinability in diverse rice genetic resources

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Rice (*Oryza sativa* L.) is important crop as a staple carbohydrate sources and was regarded as domesticated in Asia region. The seed dormancy is one of the domesticated traits, and this character allows that plants survive in various environment. The degree of dormancy have been targeted for controlling in breeding program while weak dormancy cause pre-harvest sprouting contrary to the nonuniform seed germination by strong dormancy. In this study, we surveyed the variation of germinability in diverse rice genetic resources including japonica and indica ecotype. Overall, the degree of seed dormancy of rice germplasm was distinguished into four groups and admixed types; first group(G-1) included accessions revealing high germinability, the accessions of second group(G-2) acquired the high germinability by after-ripening process, third group(G-3)'s accessions showed high germinability after dormancy breaking process and the accessions of last group(G-4) maintained the low germinability in spite of the dormancy breaking process. Among the 51 japonica accessions G-1, G-2, G-3 and G-4 included 15, 15, 11 and 10 accessions, respectively, and among 40 indica accessions, G-1, G-2, G-3 and G-4 groups included 15, 15, 9 and 1 accessions, respectively. Based on these primary test, we plan to detail examine the seed germinability and survey the genetic factors affecting the degree of germinability in representative accessions of each group.

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PB-43

Fine mapping of gem controlling the enlarged embryo character in rice (*Oryza sativa* L.)

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Rice embryo contains valuable materials which are related to human health and industrial material, thus controlling embryo size is more and more important in the field of rice breeding. Especially, main health-aid components such as γ -aminobutyric acid (GABA), tocopherol and vitamins showed positive-correlation with embryo size. We obtained three enlarged embryo character mutants derived from Hwacheongbyeon (Korean japonica cultivar) by treatment of chemical mutagen, N-methyl-N-nitrosourea(MNU). These three mutants were named according to their embryo size as ge-m, ge, ge-s. The result of allelism test between Hwacheongbyeon, ge-m, ge and ge-s represented that the embryo size of ge and ge-s was controlled by the same gene(Giant embryo, GE). Through GE locus sequencing of three mutants, we found that each of ge and ge-s mutant has a point mutation, causing non synonymous amino acid substitution. On the other hand, ge-m mutant, the embryo of which featured intermediate size in between those of Hwacheongbyeon and ge, turned out to be non-allelic to the GE locus, suggesting it is likely a novel gene, which influences rice embryo development through a different mechanism than GE gene. Fine mapping of ge-m is currently in progress. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008125), Rural Development Administration, Republic of Korea.

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PB-44**Composition of Korean colored barley varieties with the different degree of pearling**

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Anthocyanins are the primary pigments in black, blue, and purple cereal grains. Recently, anthocyanins have been recognized as health-enhancing substances due to their antioxidant activity. Anthocyanin-pigmented barley grains can be a stable source of anthocyanins as well as β -glucan. Colored barley as purple, blue and black barley consumptions are rapidly growing presently due to their healthy functional food ingredients in Korea. Color barley cultivars accumulate purple pigments in the stem, awn, lemma, palea, and pericarp during seed maturation. The large consumption of barley in human foods is almost pearled products. Here we investigated composition of pearled barley and pearling by-products of Korean colored barley varieties by degree of pearling. Barley grains from four hull-less colored barley varieties, Zasoojeongchal, Boseokchal Ganghochung and Huknarae were pearled to various degrees (5-50%). The composition (β -glucan, total phenol, proanthocyanidin and total anthocyanin) of pearled barley fractions flour and pearled barley grain was determined. β -glucan content was not changed seriously in pearled barley grain according to increasing pearling degree. Total phenol and proanthocyanidin content was decreased. β -glucan content was increased in pearling by-products according to increasing pearling degree and total phenol and proanthocyanidin content was decreased. Total anthocyanin content also was decreased in pearled barley fractions flour by the degree of pearling.

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PB-45**Naked non-waxy barley cultivar “Dahan” with good properties for noodle containing barley flour**

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Current consumers have interest in nutrition and health. So, the interest in barley for other food and industrial applications is increasing. Noodles, which have been consumed largely in Korea, are usually made from wheat flour, salt and appropriate amount of water. A New Six-rowed Naked Barley Cultivar “Dahan” was developed in 2012, have high winter hardness, lodging tolerance and good noodle property. It was crossed in 2001, and an elite line was selected in 2010 and designated as ‘Iksan 106’. It showed good agronomic performance in the regional yield trials (RYT) from 2010 to 2012. The average heading and maturing dates of “Dahan” were April 29 and June 3 in paddy field, which were two days earlier than those of the check cultivar ‘Saessalbori’ respectively. The new cultivar, “Dahan”, had 92cm of culm length and 3.9cm of spike length. It showed 625 spikes per m², 54 grains per spike, 31.3 g of 1,000-grain weight, and 815 g of test weight. “Dahan” showed better resistance to BaYMV (Barley yellow mosaic virus) than those of the check cultivar. Its average yield of the pearled grain in the regional yield trial was 4.32 MT/ha in paddy field, which were 16% higher than those of the check cultivar. It showed higher breakdown and setback than those of the check cultivar. Texture properties of noodle were better in hardness, adhesiveness, chewiness. This cultivar would be suitable for the industrial application as noodle and bread.

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PB-46

Antioxidant and anti- α -glucosidase activities of Korean traditional fermented soybean (Doenjang) made by 9 different cultivar

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Doenjang is one of the most favorite traditional food which was produced by the fermentation process of soybean with various microbes such as *Aspergillus oryzae*, *Bacillus subtilis* and so on. The aim of this research is to analyse the antioxidant and anti- α -glucosidase inhibitory activities of doenjang made by 9 different cultivar (Daewonkong, Taekwangkong, Daepungkong, Hwangkeumkong, Saedanbaek, Hanolkong, Pungsannamulkong, Cheongja-3 and Cheongdu-1). Doenjang samples were made by traditional manner using rice straw. Each samples were extracted with 40% methanol and extract were used Among them, cheongja-3's doenjang showed a significant highest antioxidant and anti- α -glucosidase inhibitory activities because of its anthocyanin. Except for cheongja-3's Doenjang, antioxidant activity had positive correlation with isoflavone content. But no relationship observed between isoflavone content and anti- α -glucosidase activity. The highest anti- α -glucosidase activity was observed in Saedanbaek's Doenjang with highest protein content.

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PB-47

Genetic variation in High Molecular Weight glutenin subunit of Glu-1 loci in Wheat Landrace accessions originated from Korea, China, and Japan

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This study is to raise the utilization of genetic resource of wheat (*Triticum aestivum*) landrace by evaluating genetic variation related to end use quality of the Far East. Allelic composition of HMW-glutenin subunits encoded by genes of Glu-1 loci associated with bread baking quality was investigated in 324 wheat landrace genetic resources originated from Korea, China, and Japan. The most frequent combination of HMW-glutenin subunits were Glu-A1c, Glu-B1b in Korean and Japanese resources, but Glu-A1a and Glu-B1c were the most in Chinese resources. By using the Glu-1 score system, 24 accessions were evaluated as 10 out of 10. As for genetic diversity, represented by polymorphic information content(PIC) index, the level of variation of Korean landrace(0.245) was lower than that in China(0.569) and Japan(0.294). When it comes to unique composition, Glu-B1f(13+16) and Glu-D1f(2+10) subunits are only in Chinese resources. Glu-B1d(6+8), Glu-B1e(20), Glu-D1b(7+8), and Glu-D1c (7+9) subunits are only in Korean resources. Consequently, this study showed that Chinese landrace collection was the most highly diverse and had distinctive characteristics compared to Korean and Japanese one. Especially, some resources having preferable genetic stock or high Glu-1 score can be valuable for wheat breeding program.

Keywords: wheat, Genetic variation, HMW-glutenin subunit, Korea, Japan, China, landrace

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Total phenolics and antioxidant activity of radish: reference to breeding variety 'Bordeux'Han Yong Park¹, Kyung Hyun Seok², O New Lee¹, Awrarid D Assefa³, Shivraj Nile³, Eun Young Ko³, Se Won Park^{3*}¹Department of Bioresource Engineering, Sejong University, Seoul 143-747, Republic of Korea²Syngenta Korea, Icheon 467-902, Republic of Korea³Department of Molecular Farming and Food Science, Konkuk University, Seoul 143-701, Republic of Korea

Anthocyanins are very important constituent of human diet. In recent years, they have gained much attention due to their antioxidative properties. As the radish (*Raphanus sativus* L.) has rich content of anthocyanins, the study is aimed to develop increased functional radish from selected radish varieties. 'Bordeux' is a hybrid variety of breeding between one accession derived from 'Oharu' as a maternal variety and 'Chungpihongsim' as a paternal variety. In this study, we investigated the new varieties of radish commonly consumed in Republic of Korea for their total phenolic content (TPC) and antioxidant activities using three (DDPH, FRAP and CUPRAC) different assays. The selected radish varieties like 'Bordeux', 'Chungbok', '3209', 'Chungwoon', 'Oharu', and 'Chungpihongsim' were procured from the company Syngenta Korea. Among the selected radish varieties, 'Bordeux' (289 µg/g FW) and 'Chungpihongsim' (276 µg/g FW) revealed maximum amount of phenolics; whereas '3209' (103 µg/g FW) and 'Chungwoon' (166 µg/g FW) showed the lower amount of phenolics content, respectively. Extracts from these studied radishes showed good to moderate antioxidant activities. The varieties 'Chungpihongsim' and 'Bordeux' revealed maximum antioxidant activity for all assays as demonstrated. However, some varieties like '3209' and 'Oharu' exhibited the lowest antioxidant activity in all the tested assays, viz; DPH, FRAP and CUPRAC in µg TE/g FW, respectively. The antioxidant activities may be attributed to the higher phenolic acid contents as a linear relation was observed between the two components and the antioxidant parameters.

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신규 무 유전자원(꼬투리무 및 노란꽃무)의 수집 및 증식

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무의 핵심집단 구축을 위해 국내외의 유전자원을 수집하여 평가 중, 국내에 잘 알려져 있지 않은 꼬투리무 및 노란꽃무를 발견하였기에 그 형태적 특성을 조사하여 보고하고자 한다. 꼬투리무는 십자화과 무속(*Raphanus sativus* L.)에 속하는 1년생 초본으로, 어린꼬투리를 이용하는 채소이다. 인도, 파키스탄, 아프가니스탄 지역으로부터, 타이, 인도네시아 등 동남아시아 지역에 걸쳐서 분포하며, 식물체가 성장해도 뿌리의 비대는 이루어지지 않는다. 꼬투리무는 파종 후 약 45일-70일경에 화서가 신장하여 추대하고, 열은 보라색 꽃을 피우며, 개화 후 꼬투리는 콩처럼 얇고 길게 신장한다. 일반무는 화아분화 및 추대에 저온을 요구하나, 꼬투리무는 저온감응을 필요로 하지 않는 것이 특징이다. 주당 다수의 꼬투리가 달리며, 종자를 맺을 때에는 콩처럼 꼬투리가 20cm 이상까지 신장한다(일반무의 꼬투리는 5cm 전후). 동남아시아에서는 10cm 전후의 어린 꼬투리를 샐러드, 볶음요리 혹은 카레의 재료로 이용하며, 맛은 어린꼬투리일수록 더욱 매운맛을 보인다. 무꽃은 전형적인 십자화과 꽃의 모습으로, 4장의 꽃잎이 십자모양으로 개화한다. 화색은 일반적으로 백색이나 열은 자색이 많으나, 매우 드물게 노란꽃을 피는 무도 있다. 본 연구실에서는 노란꽃 무를 수집하여, 형질 고정을 위해 4세대 이상 자식 후 증식 중에 있다. 노란꽃 무는 F3세대를 공시하여 형질 평가를 실시한 결과, 시험한 100주 전부에서 노란꽃이 보였으며, 파종 후 약 37일경에 개화하였다.

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항산화 성분 고함유 호박종자 자원 선발

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채소종자는 채소생산을 주목적으로 사용되고 생산목적 이외의 활용도가 매우 낮는데 그 이유는 채소종자는 부산물로 인식되어 대부분 폐기되기 때문이다. 그러나 채소종자 중 호박, 수박 등의 박과채소 종자는 중국, 미국, 유럽 등지에서 간식, 식용유, 에센셜오일 등으로 많이 이용되고 있다. 호박씨의 경우에는 단백질과 불포화지방이 풍부하며, 머리를 좋아지게 하는 레시틴과 필수아미노산이 많이 들어있고 파미틴산과 같은 지방산은 비만을 방지하고 암이나 동맥경화 등 성인병을 예방하는 것으로 알려져 있다. 호박 유전자원의 종자를 대상으로 유용한 항산화 성분이 높은 자원을 선발하여 호박자원의 활용성과 부가가치를 향상하기 위하여 본 연구를 수행하였다. 호박 유전자원 58점의 종자에 대한 항산화활성(DPPH 소거능)을 조사한 결과 항산화성의 범위가 30.1~77.2%이었으며 평균 44.7%이었고 60% 이상인 자원이 전체의 19%를 차지하였다. Total phenol 함량에 있어서는 함량범위가 건물중 6.1~81.2 mg/100g이었으며 평균 26.2 mg/100g이었고 40 mg/100g이상인 자원이 전체의 83%를 차지하였다. Total Flavonoid의 함량은 그 범위가 건물중 22.2~74.8 mg/100g이었으며 평균 41.3 mg/100g이었고 50 mg/100g이상인 자원이 전체의 31%를 차지하였다. 항산화 활성(DPPH 소거능)이 47.6% 이상인 'P54' 등 16계통, total phenol 함량이 30 mg/100g 이상인 'P38' 등 13계통, total flavonoid함량 45 mg/100g 이상인 'P38' 등 15계통을 선발하였으며 선발된 자원은 다양한 종자크기와 종피색을 보였다. 선발된 호박 유전자원 중 'P54' 등 7점은 동시에 항산화 활성, total phenol 및 total flavonoid 함량이 높은 자원이었다.

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기장 적정 수확시기 판단을 위한 등숙 적산온도

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기장은 농업기후대, 품종의 특성 및 재배시기 등에 따라 수확시기가 상이하나 농가에서는 재배지역, 시기 및 품종 특성 등에 상관없이 획일적으로 수확하고 있는 실정이다. 기존 식량원의 연구에 따르면 도정수율 및 품질향상을 위한 적정 수확적기는 출수 후 45일로 보고하였다. 현재 출수 후 등숙일수에 따른 수확적기 설정기술은 개발되어 있으나 농업지대 및 재배시기는 고려되어 있지 않은 실정이다. 농업현장에서는 이와 관련된 정보가 부족하여 적기수확이 이루어지지 않아 생산된 잡곡의 손실 및 품질저하의 한 원인으로 알려져 있다. 따라서 본 연구에서는 수확된 기장의 도정수율의 변화를 조사하고 등숙 적산온도를 산출하여 적정 수확시기를 제시하고자 하였다. 그 결과 기장의 완전미 도정수율 향상을 위하여 적정수확에 필요한 출수 후 등숙 적산온도는 조생종(황금기장)은 1,050℃, 중생종(이백찰)은 950℃, 만생종(황실찰)은 1,000℃로 조사되었다. 또한 이에 해당되는 적정 등숙일수는 내륙 평야지(밀양)에서는 조생종은 38일, 중생종은 35.5일, 만생종은 39일이었으며, 중부중산간지(원주)는 각각 45, 44 및 48.5일로 조사되었다. 이상의 결과는 잡곡재배농가와 잡곡 도정관련 업체에 정보 제공과 지역특성화사업에 정책지원을 통해 잡곡생산 및 수요에 대한 통계자료 미흡으로 정확한 경제성분성은 곤란하나 약 3~5% 가격 및 품질 경쟁력 향상이 가능할 것으로 판단된다.

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Study of Grain Appearance and Sensory Preference of African on Rice Ecotype

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The objective of this study was to evaluate grain appearance and cooked rice taste preferred by Africans for the rice ecotype of one Japonica variety, one Indica variety, and two varieties of Tongil type as compared with Korean's preference. The preferred grain appearance by Africans who have participated as panelists was in the order of grain length, aroma, and shape, while Korean preferred rice quality in the order of appearance(head rice) and grain length. Africans preferred imported Indica rice from Thailand the most, while Korean preferred Japonica Haimi the most. Overall, African preferred aromatic rice with long grain, while Korean preferred short grain rice with high head rice ratio. In the evaluation of cooked rice taste, there was no significant statistical difference between varieties preferred by Africans. Whereas, Koreans showed clear preference in the order of Haimi > Dasan 1 = Hanareum > Indica rice. The preference analysis results of cooked rice taste subjected to Japonica and Indica which showed clear preference by Koreans revealed that Africans from Cameroon, DR Congo, and Tanzania preferred Haimai. Meanwhile, the Africans from Uganda, Mali, and Nigeria preferred imported Indica rice from Thailand. The Africans from Kenya, Malawi, Ghana, and Sudan showed similar preference among Japonica and Indica varieties. The study results indicated that Africans had different preference of cooked rice taste for eco-type rice varieties by different nations. It is regarded that additional research would be conducted to evaluate cooked rice taste by the appropriate numbers of panelists from various field and by the various rice varieties including rice variety preferred by different African countries.

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Development of soybeans with high and low α -linolenic acid

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Soybean has around 20% oil in total seed compound. Fatty acid concentration of soybean oil is about 12% palmitic acid, 4% stearic acid, 23% oleic acid (ω -9), 54% linoleic acid(ω -6) 54% and 8% linolenic acid(ω -3). To improve oxidative stability and quality of oil, the breeding programs mainly focused on reducing saturated fatty acids, increasing oleic acid and reducing linolenic acid in soybean oil. In plant oil, an essential fatty acid omega-3 fatty acid is in the form of α -linolenic acid (ALA) therefore, increasing ALA in soybean oil became one of the breeding goals for human health. In our research group, we have two breeding programs for concentration of ALA in soybean oil. Wild soybeans have almost twice ALA than that in cultivated soybeans. Introgression of alleles from wild soybean to cultivated soybean may lead to the increase of ALA in soybean seed oil for various applications. We developed several backcross populations by elite cultivars x wild soybean to select high ALA with good agronomic traits. In the case of low linolenic acid program, we developed an EMS (ethyl methane sulfonate) mutation population to select low ALA concentration line and found a mutant line with low ALA in seed oil. The scheme for developing high ALA concentration from wild soybean and molecular characterization for low ALA line will be discussed.

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Assessment of agricultural traits and phenolic compound composition of induced onion (*Allium cepa* L.) germplasm.

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Onion(*Allium cepa* L.) is one of the most important crops to the fresh vegetable spices and the food processing industry in Korea. To evaluate genetic variation in onion, major agricultural characteristics and biochemical characteristics such as flowering day, harvest day, brix and so on. Phenolic compound compositions were analyzed for 44 accessions. Accessions in white color was about 92% which is the largest one followed by standard criteria. The sweetness of juice ranged from 6.1 to 19.3(in brix), and Brix range of 117 accessions was from 10.1 to 14.0. High performance liquid chromatography(HPLC) was used to identify the phenolic profile and quantify phenolic content in bulbs: quercetin, quercetin 7, 4'-diglucoside, quercetin 3-glucoside and quercetin 4'-glucoside were detected as major components. The total Quercetin and Quercetin glycoside content ranged between 123.59 and 1155.84 mg/100mg bulb freeze dried weight. The quercetin contents was up to 16.7mg/100g, and 7.41mg/100g in average. It is expected that the result of this study can be used for breeding more competitive species with respect to contents in functional chemicals.

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벼의 이삭 특성과 도정특성간의 관계

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기후변화에 의한 온도상승으로 인해 벼는 등숙기간 중 고온에 의한 벼 품질과 수량이 저하될 것으로 예상하고 있고 이에 따라 기후온난화에 대처하기 위한 고온 적응형 품종개발이 요구되고 있다. 기후변화 대응한 고온 적응형 고품질 품종개발을 위해서는 등숙율 향상과 도정수율이 향상된 고품질 우량계통을 육성하는 것이 중요하다. 본 실험은 국내 품종 및 계통에 대하여 수형과 관련 있는 항목 및 도정특성들 간의 상관관계를 분석하여 등숙율과 도정수율에 관계하는 특성과 우수계통을 선발하고자 수행되었다. 40품종 및 계통을 보통기 보비 재배하여 1, 2차지경수, 임실율, 수당립수, 수수, 수장 등 농업형질과 제현율, 현백율, 도정율, 완전미율 등 도정특성을 조사하였다. 시험결과, 수수는 2차지경수, 등숙율과 부의 상관성이 인정되었다. 1차지경수는 등숙율과 부의상관, 수당립수와 정의상관이 인정되었고 2차지경수는 수당립수와 정의 상관성이 인정되었으며 1차지경수, 2차지경수와 도정특성간에는 상관관계가 인정되지 않았다. 도정특성은 천립중과 정의 상관성이 인정되었고 완전미율은 등숙율, 현백율, 도정율과 정의 상관성이 인정되었다. 등숙율과 상관성이 있는 것으로 알려진 2차지경수에서 유의성이 없었는데 향후 도정율과 등숙율이 양호한 품종과 계통을 대상으로 이상형태별로 도정율과 등숙율에 대한 정밀한 분석을 실시할 필요가 있을 것으로 생각된다.

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Analysis of Eleutherosides B and E in *Acanthopanax divaricatus* and *A. koreanum* by Different Fertilizer RatioJeong Min Lee^{1,2}, Dong-Gu Lee¹, Sunghun Cho¹, Jung Jong Lee³, Myoung-Hee Lee², and Sanghyun Lee^{1*}¹Department of Integrative Plant Science, Chung-Ang University, Anseong 456-756, Korea²Department of Functional Crop, NICS, RDA, Miryang 627-803, Korea³Yeongcheon Agricultural Technology & Extension Center, Yeongcheon 770-270, Korea

Acanthopanax species is known commonly as Siberian ginseng, touch-me-not, devil's shrub, prickly eleutherococc, eleutherococc and wild pepper. A diverse group of chemical compounds isolated from *Acanthopanax* species was named 'eleutherosides'. Among eleutherosides, eleutherosides B and E were widely known in *Acanthopanax* species. *Acanthopanax* species are cultivated and grow wild in a various area of Korea and have a variety of pharmacological effects. But, there are a lot of difficulties on producing excellent *Acanthopanax* species, according to the cultivated method is different pharmacological ingredients. This study, therefore, analyzed eleutherosides B and E in *A. divaricatus* and *A. koreanum* by different fertilizer ratio using HPLC. We will be investigated a high content of eleutherosides B and E by different fertilizer ratio and suggest an efficient fertilizer ratio of *A. divaricatus* and *A. koreanum*. All samples of *A. divaricatus* and *A. koreanum* were collected at Yeongcheon Agricultural Technology & Extension Center, Yeongcheon, Korea. The sample was prepared by upper and lower parts. The fertilizer ratio are N-P-K(10.5-8.5-8.5: 50 kg/10a), 2N-P-K (21-8.5-8.5: 50 kg/10a), N-2P-K (10.5-17-8.5: 50 kg/10a), N-P-2K (10.5-8.5-17: 50 kg/10a), and 2N-2P-2K (21-17-17: 50 kg/10a), respectively. To analyze eleutherosides B and E, 5 g of *A. divaricatus* and *A. koreanum* was extracted with 50% MeOH (3 × 100 ml) by reflux and evaporated *in vacuo*. The residue was dissolved in 1 ml of MeOH. The resulting solution was used for HPLC analysis. HPLC separation of eleutherosides B and E for qualitative and quantitative analysis was performed using a reverse phase system. A Discovery[®]C18 (4.6 × 250 mm, 5 μm) column was used with a mobile phase that consisted of water and acetonitrile. A gradient solvent system of water and acetonitrile (90:10 to 70:30 for 20 min) was used for the elution program. UV detection was conducted at 350 nm. The injection volume was 10 μl and the flow rate was 1 ml/min. All injections were performed in triplicate. The different fertilizer ratio yielded total eleutherosides B and E contents of 4.417-6.905 and 3.652-7.227 mg/g in the upper and lower parts of *A. divaricatus*, respectively. In *A. koreanum*, the total eleutherosides B and E contents were 4.591-10.108 and 3.834-9.079 mg/g in the upper and lower parts, respectively. The best conditions to increase eleutherosides B and E content in *A. divaricatus* was determined to be with N-2P-K fertilizer ratio, on the other hand, in *A. koreanum* was 2N-2P-2K fertilizer ratio.

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SSS1 gene may improve the eating quality by changing the starch composition in rice grain

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An increasing preference for good eating quality of rice among consumers has become one of the important considerations in rice breeding. Amylose content of starch is one of the important factors of rice eating quality. Amylose composition is determined by the relative activity of soluble starch synthase (*SSS*) and granule-bound starch synthase (*GBSS*). This study focuses on modifying the expression of *SSS1* gene which is responsible for amylopectin and amylose synthesis in rice by using RNA interference (RNAi) and antisense technology. The transgenic rice plants showed various amylose content (9-17%) in rice seed. Candidate rice lines were selected according to PCR, RNA expression and amylose contents analyses. A semi-quantitative RT-PCR was carried out to determine the expression level of *SSS1* gene at several time points after the flowering of transgenic plants. Downregulation of *SSS1* gene in transgenic rices was evident in the decreasing expression in rice grains over time. Accordingly, SEM micrographs analysis revealed uniform size with smooth curves starch granules in downregulation rice lines, in contrast with the non-uniform granules in wild type.

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Modification of Starch Composition Using Downregulation of *GBSS1* gene in *Japonica* Rice

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There is a great consideration on rice eating quality aside from improving its tolerance to various stresses. High yielding and pest and disease tolerant rice is highly desirable but it is more commercially important if it also has a high eating quality. There are various factors contributing to the good eating quality of rice. This study focuses on modifying the expression of *GBSS1* genes which are responsible for amylopectin and amylose synthesis in rice by using RNAi and antisense techniques. We have developed 40 transgenic plants with RNAi-*GBSS1* gene and 60 transgenic lines with antisense-*GBSS1* gene. The transgenic plants show diverse amylose contents in rice seed. We selected candidate lines according to PCR, RNA expression and amylose contents. A semi-quantitative RT-PCR was carried out to measure the expression level of *GBSS1* gene at several time points after the flowering of transgenic plants. The expression level of *GBSS1* gene in rice grains decreases over time and the mRNA expression among the transgenic plants were lower compare to its wild type. In the SEM analysis, the starch granule of wild type Gopumbyeon has very large structures accompanied with small ones around the area. However, the starch structures in transgenic plants were smaller and more uniform in size and shape throughout the viewing area.

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Studies on Biological Effects of Gamma-ray in *Sorghum bicolor* M.

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This study was conducted to determine the optimal dose of gamma-ray for mutation breeding in sorghum (*Sorghum bicolor* M.). Gamma-rays irradiated to dry seeds with various doses (0 to 1000 Gy) at Korea Atomic Energy Research Institute. Lethal dosage (LD₅₀) was approximately 256 Gy. Significant decreases in growth characteristics (plant height, tiller number and fresh weight) were observed by dose of increased over 300 Gy. Reduction doses (RD₅₀) was approximately 363 Gy in plant height. We also conducted comet assay to observe nucleus DNA damage due to gamma irradiation. In comet assay, a clear difference was identified over 100 Gy treatments. With increasing doses of gamma-ray in the range of 100 to 400 Gy, the rate of head DNA was decreased significantly from 93.52% to 67.57%. The most of the Sorghum cells were severely damaged in the integrity of DNA by gamma-ray. These data provide valuable information when the optimal dose should be chosen for purpose of mutation breeding program of Sorghum.

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오렌지색 반겹꽃 대륜화 절화용 거베라 ‘선셋드림’ 육성

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경상남도농업기술원 화훼연구소에서 2013년 화색이 선명한 오렌지색 절화용 거베라 ‘선셋드림’을 육성하였다. 교배조합 육성을 위하여 2005년부터 국내 재배농가에서 유전자원 수집 후 특성을 검정하였다. 2009년 3월 교배 후 우수개체를 선발하여 2011년부터 2013년까지 3회의 특성검정을 거친 다음, 화색과 화형이 우수한 계통 경남교 G-48호를 선발하였다. 이 계통은 절화특성이 우수하고 화색 등 소비자의 기호도가 높아 2013년 11월 농촌진흥청 농작물 직무육성 신품종 선정 심의회의 심의를 거쳐 ‘선셋드림(Sunset Dream)’으로 명명하였다. ‘선셋드림’ 품종의 생육 및 개화특성 조사를 위하여 대조품종으로 교배모본인 ‘엔토라지(CFG0061)’를 사용하였다. ‘선셋드림’ 품종은 복색계의 ‘엔토라지(CFG0061)’와 적색계의 ‘알버트’(CFG0058)와의 교잡에서 육성된 품종으로, 화색이 선명한 오렌지색(RHS, 30D/40B) 반겹꽃으로, 화폭이 12.2cm 정도인 절화용 대륜화이다. 또한 포기당 연간 평균절화수량은 50.7송이 정도이며, 절화수명은 약 12.1일 정도이다. 개화소요일수는 92.8일로 대비품종 ‘엔토라지’의 94.1일에 비하여 약 1.5일 정도 빠르며 이때 개화엽수는 약 8.8매 정도이다. ‘선셋드림’ 품종의 설상화의 길이는 5.2cm 정도로 대조품종 ‘엔토라지’의 4.7cm에 비하여 길며, 설상화의 폭은 1.1cm 정도로 대조품종 ‘엔토라지’의 1.0cm와 비슷한 편이다. 화경 직경은 상부는 0.4cm 정도이고, 하부는 0.6cm 정도로 대조품종 ‘엔토라지’의 상부 0.5cm, 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.

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Detection of New Source of High Eating Quality in Korean *Japonica* Rice Germplasm

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Eating and cooking qualities are the most important trait in *japonica* rice breeding program in Korea. More improvements in grain quality to meet the demand of consumers are needed to develop new rice germplasm of high grain quality. In this study, we performed genetic analysis and grain quality evaluation in 96 Korean *japonica* rice germplasm including 26 varieties with 4 Japanese *japonica* high eating quality, 24 landraces, 22 weedy rices, and 14 breeding lines. These germplasm were analyzed using 13 DNA markers related to eating quality to conjecture the palatability of cooked rice (Lestari et al. 2009). Most varieties of high eating quality were clustered with germplasm of high expected quality (eq) varieties of similar genetic background of pedigree. The expected quality (eq) values of high eating quality varieties, Gopum, Ilpum, Samgwang, and Sugwang were 99.6 ~ 104.5, and Koshihikari was 103.5. The eq of two weedy rices, Hoengseongaengmi 3 and Namjejuaengmi 6 were 101.9 and 101.6, respectively. However, Haiami of high eating quality was clustered with 15 weedy rice and 11 landrace germplasm of low eq value. The eq values of Haiami and Wandoaengmi 6 were 66.9 and 40.8, respectively, but they has 2 and 3 of palatability of cooked rice, and 73.6 and 78.6 of glossiness of cooked rice, respectively. We expect these germplasm would be new source for rice grain quality to develop *japonica* rice of high eating quality.

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Map-based cloning of *SUI4* gene which controls internode elongation in rice

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Internode elongation is an important agronomic trait in rice that is associated with lodging, yield, and flooding adaptation. We identified a novel rice mutant line showing shortened uppermost internode among the rice Ac/Ds insertional mutant population and named it *shortened uppermost internode 4 (sui4)*. The phenotypes of F1 plants and F2 plants from the cross of *sui4* with its original variety, Dongjin, indicated that the *SUI4* gene shows incomplete dominance or semidominance. Because the Ds genotypes did not co-segregate with the *sui4* phenotypes, we performed mapping of this gene with 273 F2 plants from a cross between *sui4* and Milyang23. Primary mapping revealed that the *SUI4* locus was located between the *S07012* and *S07015* markers on rice chromosome 7. Further fine mapping narrowed down the location of *SUI4* to the 1.1-Mbp interval of *RM1253-S07015*. Using re-sequencing data of this mutant along with its original variety, Dongjin, and five other varieties, we found six *sui4* specific SNPs occurred within the genic region of five genes in the fine-mapped interval. Among them, one SNP is in exon, while the other five SNPs are in intron. This SNP in exon occurred in the *miR172* binding site of a gene encoding AP2 domain transcription factor, which seems to interrupt suppression of this gene activity by *miR172*. We isolated the genomic region of this gene from *sui4* and transformed the wild type variety, Dongjin. The transgenic plants showed remarkably shortened internodes, which indicates that this AP2 domain transcription factor gene is the *SUI4* gene.

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Glucosinolate variation in Korea *Brassica rapa* core collection and their application for genetic studyMina Jin^{1*}, Mi-suk Seo^{1*}, Sun-Ju Kim², Jin-Hyeok Chun², Beom-Seok Park¹, Seong-Han Sohn¹, Jung Sun Kim¹¹National Academy of Agricultural Science, RDA, Suwon, Republic of Korea²Department of Bio-Environmental Chemistry, Chungnam National University, Daejeon, Republic of Korea

Glucosinolates of *Brassica rapa* collection from Korea genebank were measured to determine total glucosinolate content and their variation of diverse glucosinolates; Around 100 accessions representing the different morphotypes and geographical origin of *Brassica rapa* were analysed. The principal component analysis was performed to evaluate the differences among morphotypes using the profiles of 14 glucosinolates identified from the leaves. DMRT test and box plots showed the significant difference between total glucosinolates of subspecies. Most of turnip accessions had higher gluconilates compared to the other type accessions, Chinese cabbage and pak choi. These accessions will be used for GWAS study for glucosinolate. Now they are being finger-printed by genotyping by sequencing (GBS). Among these accession, we selected a turnip accession with high amount of glucosinolate, K0466 and two Chinese cabbage accession with low amount of glucosinolate, K0015 and K0621. To analyse quantitative traits loci (QTL) for glucosinolate synthesis, these three accessions were fixed through microspore culture. Finally, six homozygous lines were selected and were crossed each other to make F1 hybrids. We just harvested F2 seeds and transferred doubled haploid plants to pots. QTL analysis for glucosinolate will be performed these F2 and DH population.

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황색 홑꽃 화형의 조기개화성 분화용 국화 ‘가야글로리’ 육성진영돈^{1*}, 황주천¹, 정용모¹, 안동춘¹, 이병정¹, 신현열²¹경남 창원시 의창구 대산면 경남농업기술원 화훼연구소²경남 진주시 경남농업기술원 연구개발국

‘가야글로리’는 2013년 육성된 홑꽃 화형 진한 황색의 분화용 국화로 개화가 빠르며 분지수가 많은 품종이다. 교배는 2010년 10월에 분지성은 많으나 연한 황색의 ‘가야엘로우’을 모본으로, 진한 황색이나 분지성이 적은 ‘그린문’을 부본으로 교배한 조합으로부터 220여개 종자를 획득하였다. 채종 즉시 벤레이트수화제 1,000배액에 소독하여 페트리디쉬에 파종한 후 25°C 정도의 조식배양실에 넣어 발아된 유묘를 원예상토로 채운 플러그 트레이(200공)에 옮겨 심고 1개월 정도 육묘하여 화훼연구소 비닐온실내의 10cm 포트에 정식하였다. 재배방법은 정식 2주후에 적심하였고 적심 2주 후 13시간으로 단일처리를 재배하였다. 개화된 실생계통들 중에서 화색이 우수하고 분지수가 많은 우수개체를 1차로 4개체 선발하여 모주를 증식하고 1차 특성검정을 실시한 결과 GYGM -160개체를 선발하였고, 2011년도부터 2013년까지 3회에 걸쳐 축성, 억제, 자연재배의 생육 및 개화특성을 농촌진흥청 농사시험연구 조사기준과 국립종자원의 신품종 출원 및 심사를 위한 국화 특성조사요령에 의거하여 조사하였다. 그 결과 기호성이 좋고 화색과 화형 등 품질이 우수하다고 판단되어 2013년 농작물직무육성신품종선정위원회의 심의를 거쳐 ‘가야글로리’로 명명하였다. ‘가야글로리’는 가을에 개화하는 홑꽃 화형 황색(Y9A) 꽃잎의 분화용 국화이다. 개화 소요일수는 평균 39일 정도로 6주 이하의 조기개화성 품종이며, 10cm내외의 화분에서 적심 후에 일반적인 분화국화 재배법으로 재배가 가능하다. 꽃직경은 3.1cm 정도로 작으며, 초장은 12.9cm 정도의 소형 분화용 국화이다. 특히 착화수와 분지수가 32.7개와 5.1개로 많아 상품성이 높고 상품화하기 좋은 품종이다. 재배상의 유의사항은 여름철 고온기의 화색퇴화 및 개화지연 방지를 위하여 차광을 해주고 서늘하게 관리하는 것이 좋다.

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A Yellow Single Freesia ‘Song of Angel’ with Middle Petals

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A freesia (*Freesia hybrida* Hort.) ‘Song of Angel’ was developed for the cut flower in the National Institute of Horticultural and Herbal Science in 2013. This hybrid was crossed and selected from a seedling of three-way crossing ‘Golden Flame’ and the seedling of ‘Athene’ and ‘Yvonne’ in 2006 and 2007, respectively. Morphological characteristics of the selected freesia hybrid were investigated for 5 years from 2008 to 2012, and then it was named ‘Song of Angel’ in 2013. ‘Song of Angel’ has single flower and yellow petals (RHS, YG13B) with yellow center color (RHS, YG13A). The average flower width is 5.8 cm and the average yield is 4.3. The growth of the plant shows vigorous and the average height is 95.3cm, and it is higher than about 30cm that of control cultivar ‘Yvonne’. The average number of floret per stalk and stalk length, 14.3, and stalk was 11.1 cm length is higher than the ‘Yvonne’, 9.7 and 8.3cm length, respectively. The average days to first flowering of ‘Song of Angel’, 141 days, was approximately 10 days earlier than the control cultivar. It’s average vase life and yield is 10.7 days and 6.2 cormlets per plant, respectively.

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자주색 홑꽃화형 스프레이국화 ‘에스루비’ 육성

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스프레이국화 ‘에스루비(Yes Ruby)’는 2010년 10월 충남농업기술원 예산국화시험장에서 고온기 화색발현이 우수하고 고성장성인 스프레이국화 신품종 개발을 위해 연분홍색 홑꽃화형의 ‘보라미(Borami)’ 품종을 모본으로 하고 자주색 홑꽃화형의 ‘에스라인(Yes Line)’을 부분으로 인공 교배하여 얻어진 500개의 종자를 2011년에 파종하였고, 이 중에서 성장 세력이 빠르고 화색이 선명한 320번째 개체를 선발하여 ‘SP11-148-01’으로 계통명을 부여하였다. 이 품종의 주년재배 특성검정을 위하여 2011년부터 2012년까지 1, 2차 생육특성 검정을 수행하였고, 2013년 안정성, 균일성 등 3차 특성검정 및 기호도 평가를 수행한 결과 기호도가 4.21/5.0(n=90)로 높아 ‘예산SP-44호’로 명명하였다. 2013년 농촌진흥청 농작물 직무육성 신품종선정위원회 심의를 거쳐 ‘에스루비(Yes Ruby)’로 명명하고 품종등록 출원을 하였다. ‘에스루비(Yes Ruby)’의 생육 및 개화특성은 구미시설공단 수출품종인 ‘킹피셔(Kingfisher)’를 대조품종으로 하여 조사하였다. ‘에스루비(Yes Ruby)’는 자주색(RP71A)의 화심이 녹색인 고성장형 절화용 스프레이국 품종이다. 착화수는 20.0개/본으로 대조품종 19.5개와 비슷하였으나 꽃직경이 6.2cm이고 설상화의 꽃잎수는 25.7매로 대조품종의 5.0cm에 23.3매와 비교하여 화형이 크고 꽃잎수가 많아 볼륨감이 우수하였으며, 절화장이 94.9cm로 대조품종의 89.2cm보다 커 초세 및 줄기가 강건하였다. ‘에스루비(Yes Ruby)’는 자연개화기가 10월 24일로 대조품종보다 평균 5일 빠른 경향을 보였고 개화반응주수는 7.0주로 빠른 편이며 주년재배가 가능하였다. 재배상 유의사항은 동계 재배시 균일한 개화 및 개화자연 방지를 위하여 적정온도를 유지해 주어야 한다.

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PB-67

Molecular Analysis of Genes Related to Tryptophan Biosynthesis and Grain Quality Evaluation in High Tryptophan Rice

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Fortification with vitamins in crops like rice is a continuing endeavor for geneticists and rice breeders. Tryptophan is one of the essential amino acids needed in human diet. In this study, we developed rice mutant lines using ethyl methane sulfonate (EMS) treatment in Korean cv. Donganbyeon and candidate rice lines were selected by insensitivity to the tryptophan analog, 5-methyltryptophan. One of the mutants has a 20-25 fold higher tryptophan level in mature seeds than wild type. To identify the mutations in anthranilate synthase genes, OASA1 and OASA2 sequences were generated. Moreover, mRNA expression levels of tryptophan biosynthesis related genes were examined. To further qualify the tryptophan fortification in rice, comparative assessment of cooking and eating quality was conducted with mutant lines and wild type. The moisture, viscosity, taste quality, protein content, amylose content and amino acid composition were similar with wild type. However, tryptophan contents in the mutant lines were higher than wild type as we targeted. The mutation present in AS gene of 5MT resistant rice may prove useful for the generation of crops with increased tryptophan contents and the mutation differences in AS sequences can be used for selection of mutant lines with high tryptophan level from large population.

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PB-68

Quantitative Analysis of the Major Aliphatic Glucosinolates in Doubled Haploid Lines of Radish Plant (*Raphanus sativus* L.) Obtained by Microspore Culture

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Glucosinolates (GLS) are secondary metabolites commonly occurring in Brassica crops and more than 130 different GLS have been reported in diverse plants. Recent studies have indicated that isothiocyanate (ITC) derived from GLS by hydrolysis had a potential for anticancer activity against several tumor cells on human. In addition, it was found that glucoraphenin (GRE) and glucoraphasatin (GRH) were abundant and differently regulated in radish plant, depending upon organs and developmental stages. Microspores isolated from flower buds of radish were cultured in vitro to obtain doubled haploid (DH; but homozygous) lines in a short time period. The present study was conducted to determine the concentration of GRE and GRH, an immediate precursor of ITC from DH lines of radish plant. Total 41 DH lines were selected based on flow cytometry analysis. The seeds, obtained by bud pollination from the DH lines, were planted and 3-weeks-old young seedlings were used for the major aliphatic GLS analysis. Amounts of GRH were highly variable from the DH lines ranging from 2.3 to 31.5 mg·g⁻¹ dry weight (DW). The donor plant (DP) contained 18.4 mg·g⁻¹ DW. It was noticed that there were 6-fold differences in the amounts of GRE between the highest and lowest DH lines. Among 41 lines tested, 14 DH lines of radish plant were significantly reduced in the amount of sum of GRH and GRE compared those of the donor plant (P<0.05), whereas only three lines increased. The results obtained in the present study will lend to select genotypes with low and high GLS contents of radish plant. In addition, those DH lines will aid to elucidate a biosynthetic pathway of the aliphatic GLS in radish plant, which remain for the most part unsolved.

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PB-69

잎자루 채소용 고구마 우수 계통의 생육 및 품질 특성

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고구마는 주로 괴근(덩이뿌리)을 식용으로 이용하지만 최근 고구마 줄기에 대한 영양성분이 알려지면서 다양한 요리 재료로 이용되고 있다. 고구마 줄기(잎, 잎자루)에는 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 잎자루 채소용 고구마의 육종 선발 지표를 개발하고 이를 통해 우수 계통을 선발하고자 수행되었다. 시험품종은 ‘신미’(잎자루색 녹색)와 ‘하얀미’(자주색+녹색)를 대조품종으로 하여 온실에서 15일 간격으로 6차례 수확한 후 우수한 7계통을 선발하여 생육 및 품질특성을 조사하였다. 잎자루 생체수량은 계통 MI 2010-01-18가 신미 62,150kg/10a에 비해 57,167kg/10a로 낮았으나, 잎자루 갯수는 5,730천개로 ‘신미’와 비슷하였다. 잎자루 길이는 ‘신미’가 6회 평균 34cm인 반면 MI 2009-33-12는 38cm로 길었다. 잎자루의 당도는 수확시기에 따라 큰 차이는 보이지 않았으나 MI 2009-33-12는 6회 평균 3.0Brix°로 ‘신미’ 2.7, ‘하얀미’ 2.72Brix° 보다 높았다. 총폴리페놀 함량은 자주색을 띠고 있는 하얀미가 8.8mg/100g(건물중)으로 가장 높았고 MI 2010-01-18이 5.5 mg/100g으로 신미 4.5 mg/100g 보다 높았다. 잎자루 경도는 신미 0.134kg에 비하여 MI 2010-05-03 이 0.086kg으로 가장 유연하였고 MI 2009-33-12는 0.177로 가장 단단하였다. 고구마 잎자루용 품종을 육성하기 위해서는 생육 및 수량 특성 뿐만 아니라 당도, 생체 경도 및 데친 후 경도, 무름성, 껍질 벗김성 등 여러 가지 부분을 고려한 지표 개발이 필요할 것으로 사료된다.

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PB-70

지베렐린 처리에 의한 유핵 포도 품종의 무핵화 및 자방 비대 효과

홍미향^{1*}, 정찬진¹, 허윤영¹, 정성민¹, 남중철¹, 류명상¹¹경기도 수원시 장안구 천천로 203 국립원예특작과학원 원예작물부 과수과

2배체 유핵(seeded) 포도 품종에 개화 14일 전(14 DBF, days before flowering) 지베렐린을 1차 처리하면 무핵(seedless) 과립의 생장이 유도되고, 무핵 과립의 비대를 위해 개화 14일 후(14 DAF, days after flowering) 지베렐린을 2차 처리하면 종자는 없지만 과립은 정상적으로 비대 된 씨 없는 포도가 생산된다. 수량과 직결되는 과립 비대는 지베렐린 2차 처리에 의한 효과라고 알려져 있으며 지베렐린 처리에 의한 과립 비대와 관련된 연구가 활발히 진행되고 있다. 그러나 무핵과를 유도하기 위해 개화 전 지베렐린을 한 번 처리한 경우에도 무처리구에 비해 씨방과 자방이 비대되며 화분관 신장이 저해되어 수정이 일어나지 않는다는 것이 보고되었다. 이에 본 연구에서는 2배체 유핵인 ‘탐나라 (*Vitis* spp.)’ 품종에 개화 14일 전 지베렐린을 처리하여, 개화 전 지베렐린 처리가 포도 꽃과 자방 발달에 미치는 영향을 살펴보고자 하였다. 개화 7일 전부터 개화 2일 전까지, 무처리구의 자방은 종적으로는 지속적으로 신장하였고 횡적 성장 속도는 감소하였다. 반면, 지베렐린 처리구에서는 종적, 횡적 생장이 지속적으로 증가하여 자방 크기가 무처리구에 비해 약 10% 증가하였다. 화관이 벗겨진 개화부터 개화 2일 후까지, 지베렐린 처리구는 무처리구에 비해 20% 이상 자방이 비대되었으며, 개화 5일 후에는 30% 이상 자방의 크기가 증가하였다. 이러한 결과는 지베렐린 처리구가 무처리구에 비해 성장 속도가 빠르다는 것을 나타내는 것이다. 또한 pedicle도, 만개 7일 전부터 지베렐린 처리구가 무처리구에 비해 40% 이상 빠르게 신장되는 것을 관찰하였는데 이러한 결과는 개화 전 지베렐린 처리가 자방뿐만 아니라, pedicle의 신장에도 영향을 끼친다는 것을 의미한다. 그러나 지베렐린 1차 처리에 의한 자방 비대와 pedicle의 신장 효과는 개화 후 9일째에 감소되었다. 이 시기는 지베렐린 처리에 의한 성장 촉진 효과가 사라지면서 동시에 무처리구의 수정된 배(embryo)에서 지베렐린이 분비되기 시작하는 시점임을 시사한다. 이상의 관찰을 통해, 지베렐린 1차 처리에 의해서도 포도 꽃과 자방의 발달이 촉진됨을 알 수 있었으며, 지베렐린 처리에 의한 씨방과 자방의 조기 발달이 수분 후 화분관 신장 환경에 영향을 끼쳐 화분관 신장이 저해됨을 추정할 수 있었다.

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PB-71

Transcriptional changes of three *Vitis* PIN genes in grapevines during inflorescence development upon gibberellin application at pre-bloom

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The tight regulators of fruit set initiation, gibberellin (GA) and auxin, have been applied for decades to induce parthenocarpy, fruit set without fertilization. The integration of GA and auxin signaling mediated by either GA or auxin application during parthenocarpy has been actively reported in tomato, and recently we reported that GA application at pre-bloom also activating auxin signaling and down-regulated negative regulators of fruit set initiation in grapevines. However, the activation of auxin signaling upon GA application without up-regulation of auxin biosynthesis is still unclear. In this study, expression patterns of three auxin efflux transporter genes, *VvPIN1a*, *VvPIN2* and *VvPIN4*, were monitored during inflorescence development in ‘Tamnara’ grapevines with or without GA application. Without GA application, transcription levels of *VvPIN1a* and *VvPIN4* gradually increased from 14 days before full bloom (DBF) to 2 and 5 days after full bloom (DAF), respectively, except down-regulation of *VvPIN1a* during 5 DBF to full bloom. However, *VvPIN2* expression declined steadily after peaking at 10 DBF. With GA application, *VvPIN1a* did not show significantly different expression patterns when compared to no GA application, with the exception of 4-fold up-regulation at full bloom, but transcription of *VvPIN4* was reduced between 5 and 2 DBF. In addition, *VvPIN2* was down-regulated between 12 and 10 DBF by more than 50% compared to levels in the absence of GA application. These reductions of both *VvPIN2* and *VvPIN4* with GA application prior to pollination suggest that GA application might regulate auxin distribution, instead of auxin biosynthesis, to activating auxin signaling during parthenocarpic fruit initiation.

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PB-72**Characterization of the Agronomic traits in the Inbred line derived from Double Haploid line using Pollen of Maize in the Crossing between Geumgang and CIMMYT's wheat**

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Wheat is one of the most important food crops in the world and provides 20% of nutritional requirement to the consumers in developing countries. The consumption per capita of wheat is persistent but the self-sufficiency has decreased owing to the less competitive world market and double cropping system with rice in Korea. This study was conducted to obtain baseline data on the selection lines with early maturity and good agronomic traits. Geumgangmil, a leading Korean variety, was crossed with CIMMYT's line, and a DH (double haploid) line was released using pollens of Maize in Mexico. The 71 inbred lines were grown in fields at NICS, Miryang. The culm length of inbred lines were normally distributed from 37cm to 106cm, though that of the P1 (Geumgangmil) was 71 and P2 (CIMMYT's Line) was 77cm. Especially, some lines were very short and measured below 50cm. The spike lengths of most of the lines were longer than that of P1 (7.5cm), but were normally distributed. The number of spikelet was less than that in P2 (19ea.), but was more than P1 (10ea.). The heading day of most of the lines was between P1 (11th April) and P2 (25th April) and the maturity day of the lines was similar to P1 (1st June) but 5 lines showed 2~6 days shorter maturity period than that of P1. However, 20 lines were found to have 2~10 days longer maturity period than that of P2.

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PB-73

Colchicine, Oryzalin 처리에 의한 *Cymbidium* Mystery Island ‘Silk Road’ 선발계통의 기내 배수화

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본 연구는 심비디움의 배수성 육종의 기초자료를 얻기 위하여 실시하였다. 서양란 심비디움 품종인 *C. Mystery Island ‘Silk Road’*를 자가수분하여 얻은 선발계통(*Silk Road-4*)의 성장점배양을 통하여 생산된 PLBs(Plant like bodies)에 뽕족한 핀셋으로 10회 찢러 상처를 준 후 oryzalin을 3, 5, 10, 20mg L⁻¹를 첨가한 액체배지에서 3, 6, 9일간 진탕처리하였다. 모든 처리농도에서 처리시간이 길어질수록 생존율이 낮아지는 경향을 보였으며 배수화의 정도는 4배체 뿐 아니라 2배체와 4배체, 4배체와 8배체의 혼수체, 기타 염색체키메라도 처리에 따라 나타났다. 그중 10mg L⁻¹ 농도로 3주간 처리했을 때와 20mg L⁻¹ 농도로 1주간 처리했을 때 4배체 출현빈도가 12.5%로 가장 높았으나 생존율이 상대적으로 낮아 효율은 0.27로 나타났고 3mg L⁻¹ 농도로 2주간 처리했을 때는 4배체 출현빈도가 4.5%였지만 상대적으로 생존율이 높아 효율이 0.83으로 가장 높게 나타났다. 콜히친의 경우 50, 100, 300, 500mg L⁻¹ 농도로 1, 2, 3주 처리하였다. 그중 300mg L⁻¹ 농도로 3주간 처리했을 때 4배체 출현빈도가 25%로 가장 높았으나 생존율이 상대적으로 낮아 효율은 0.13로 나타났고 50mg L⁻¹ 농도로 1주간 처리했을 때는 4배체 출현빈도가 13.8%였지만 상대적으로 생존율이 높아 효율이 3.87로 가장 높게 나타났다. 배수화가 된 식물은 2배체 식물보다 생육이 더났고 잎의 길이는 짧은데 비해 넓이가 넓고 두께가 두껍게 나타났으며 기공의 크기는 2배체 식물에 비해 커지고 면적당 기공의 수는 감소하였다.

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PB-74

Colchicine, Oryzalin 처리에 의한 *Cymbidium* Show Girl ‘Silky’의 기내 배수화

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본 연구는 심비디움의 배수성 육종의 기초자료를 얻기 위하여 실시하였다. 서양란 심비디움 품종인 *C. Show Girl ‘Silky’*의 성장점배양을 통하여 생산된 PLBs(Plant like bodies)에 뽕족한 핀셋으로 10회 찢러 상처를 준 후 oryzalin을 3, 5, 10, 20mg L⁻¹를 첨가한 액체배지에서 1, 2, 3주간 진탕처리하였다. 모든 처리농도에서 처리시간이 길어질수록 생존율이 낮아지는 경향을 보였으며 배수화의 정도는 4배체 뿐 아니라 2배체와 4배체, 4배체와 8배체의 혼수체, 기타 염색체키메라도 처리에 따라 나타났다. 그중 20mg L⁻¹ 농도로 2주간 처리했을 때 4배체 출현빈도가 46.7%로 가장 높았으나 생존율이 상대적으로 낮아 효율은 34.21로 나타났고 5mg L⁻¹ 농도로 2주간 처리했을 때는 4배체 출현빈도가 44.4%였지만 상대적으로 생존율이 높아 효율이 40.0으로 가장 높게 나타났다. 콜히친의 경우 50, 100, 300, 500mg L⁻¹ 농도로 1, 2, 3주 처리하였다. 모든 처리시간에서 100%의 생존율을 보인 50mg L⁻¹ 농도를 제외하고 oryzalin 처리와 마찬가지로 처리시간이 길어질수록 생존율이 낮아지는 경향을 보였으며 배수화 정도의 종류도 oryzalin 처리와 마찬가지로 나타났다. 그중 500mg L⁻¹ 농도로 2주간 처리했을 때 4배체 출현빈도가 63.6%로 가장 높았으나 생존율이 상대적으로 낮아 효율은 46.67로 나타났고 100mg L⁻¹ 농도로 2주간 처리했을 때는 4배체 출현빈도가 63%였지만 상대적으로 생존율이 높아 효율이 56.67로 가장 높게 나타났다. 배수화가 된 식물은 2배체 식물보다 생육이 더났고 잎의 길이는 짧은데 비해 넓이가 넓고 두께가 두껍게 나타났으며 기공의 크기는 2배체 식물에 비해 커지고 면적당 기공의 수는 감소하였다.

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PB-75**A high isogomaketone perilla cultivar 'Atom-Ketone'**

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Perilla frutescens (L.) is an annual herbaceous and ornamental plant in the Lamiaceae family. *Perilla frutescens* (L.) Britt.cv.Chookyoupjaso were irradiated using a 200 Gy gamma ray in 1995. By HPLC analysis, this new cultivar significantly induced isogomaketone content compared with 'Chookyoupjaso' control. The phenotypical difference was the changed leaf color of the 'Atom-Ketone' from violet to green. The yield potential of this cultivar (106 kg/10a) was 1.83 folds higher than that of 'Chookyoupjaso' (57.65 kg/10a). The methanol extracts of 'Atom-Ketone' inhibit nitric oxide (NO) production in LPS-stimulated RAW 264.7 cells. This extract was further partitioned using ethyl acetate (EtOAc), butanol (BuOH), and water. The EtOAc fraction (EF-Atom-Ketone) was evaluated for antiinflammatory activities. These results indicated that the EF-Atom-Ketone reduced NO production by inhibiting inducible nitric oxide synthase (iNOS) expression. The EF-Atom-Ketone treatment also significantly diminished expression of MCP-1 and IL-6. Therefore, 'Atom-Ketone' reveals the potential therapeutic use of bioactive.

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PB-76**A new perilla cultivar 'Atom-Ros' with high content of rosmarinic acid**

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Perilla frutescens (L.) is an edible plant, not only used as a food ingredient, but also in skin cream, soaps, and medicinal preparations. 'Atom-Ros', a perilla (*Perilla frutescens* (L.) Britt. cv. Chookyoupjaso) was developed in 1995 by 200 Gy gamma irradiation-mutagenesis. This new cultivar has high rosmarinic acid content more than two fold compared with 'Chookyoupjaso' control. The observed phenotypical difference was changed leaf color of the 'Atom-Ros' from violet to green. The yield potential of this cultivar (123.5 kg/10a) was 2.14 fold higher than that of 'Chookyoupjaso' (57.65 kg/10a). The methanol extracts of 'Atom-Ros' were tested for inhibition of nitric oxide (NO) production in lipopolysaccharide (LPS)-stimulated RAW 264.7 macrophage cells. Atom-Ros showed significant inhibition of NO production. This rosmarinic acid extracted from 'Atom-Ros' has a good potential to be developed as an antioxidant agent.

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PB-77

복색 홑꽃 화형의 절화용 스프레이국화 ‘매직스타’ 육성

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스프레이국화 ‘매직스타’는 2009년 10월에 경남농업기술원 화훼연구소에서 복색 홑꽃인 ‘Delmont(CFC0007)’를 모본, 초세가 좋고 흰녹병에 강한 복색 홑꽃 화형의 ‘Moulinrouge (CFC0063)’를 부분으로 인공교배하여 획득한 571개의 종자로부터 실생계통을 양성하여 착화성이 좋고 화형이 안정되며, 화색이 우수한 홑꽃 화형의 복색(RP60A/Y8A) 스프레이국화 ‘DM10-99’를 개체 선발하였다. 삼목에 의해 개체증식 후 화훼연구소 비닐온실 내에 정식하였으며, 2011년부터 2012년까지 2년간에 걸쳐 1~2차 생육특성검정을 통해 안정성, 균일성과 흰녹병 저항성 등을 조사하였고, 2013년에는 계통번호 ‘경남CS-36호’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 초세 강하면서도 화색이 좋아 소비자들의 기호성이 우수하며, 화색 및 화형 등 품질이 우수하다고 판단되어 2013년 농작물 직무육성신품중심의회 심의를 거쳐 ‘매직스타’로 명명하고 국립종자원에 품종보호출원 하였다. 국화 ‘매직스타’ 품종의 자연개화기는 10월 하순이며, 선명한 자주색(RP60A) 꽃잎 가장자리 부분에 황색(Y8A) 테두리를 두른 복색 홑꽃 화형인 스프레이국화이다. 화형이 안정되고 화색이 우수하며, 생육이 균일하고 동시개화 한다. 초장 115.3cm, 줄기 직경 6.5mm로 대조품종 113.5cm, 5.7mm 보다 약간 길고 굵으며, 꽃 크기는 7.1cm로 대조품종 보다 약간 작다. 꽃자루 길이는 8.4cm로 약간 길지만 견고하여 부러짐이 없고 설상화의 주된 형태는 대조품종은 선단모양이 뾰족한 반면에 둥근 모양이며, 꽃잎 수는 37.1개로 많다. 평균 착화수는 11.3개로 대조품종 보다 1~2개 많고 절화수명은 21.7일로 긴 편이며, 휴면에는 약하다. ‘매직스타’ 품종은 비닐하우스 내에서 연중재배 할 수 있으며, 재배상 유의사항은 하계 고온기에는 화색 발현을 위해 한 낮엔 차광율 30% 정도의 한랭사로 차광하여 온도상승을 막아주고 환기도 충분히 해 주는 것이 좋다.

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PB-78

Transcription factor for gene function analysis in maize

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Maize is one of the most important food and feed crops in the world including Southeast Asia. In spite of numerous efforts with conventional breeding, the maize productions remain low and the loss of yields by drought and downy mildew are still severe in Asia. Genetic improvement of maize has been performed with molecular marker and genetic engineering. Because maize is one of the most widely studied crop for its own genome and has tremendous diversity and variant, maize is considered as a forefront crop in development and estimation of molecular markers for agricultural useful trait in genetics and breeding. Using QTL (Quantitative Trait Loci) and MAS (Marker Assisted Breeding), molecular breeders are able to accelerate the development of drought tolerance or downy mildew resistance maize genotype. The present paper overviews QTL/MAS approaches towards improvement of maize production against drought and downy mildew. We also discuss here the trends and importance of molecular marker and mapping population in maize breeding.

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PC-01

A Bioinformatics Approach for Identification, Evolution and Expression Analysis of Rapid Alkalinization Factor Gene Family in Plant Species

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Receptor mediated signal carriers play a critical role in regulation of plant defense and development. Rapid Alkalinization Factor (RALF) is an important signaling family which has a role in plant growth and development. However, only few RALF polypeptides have been identified till date, mainly because of enormous efforts required for their isolation or identify their gene through mutational analysis. In this study, an extensive database search yield 39, 43, 34 and 23 potential RALF genes in Arabidopsis, rice, corn and soybeans, respectively. RALF genes are highly conserved across the plant species. A comprehensive analysis including the chromosomal location, gene structure, subcellular location, conserved motif, protein structure and promoter analysis was performed. RALF genes from four plants under study were divided in 7 groups based on phylogenetic analysis. *In silico* expression analysis of these genes, using microarray and EST data, revealed that these genes exhibit a variety of expression pattern. Furthermore, RALF genes showed distinct expression pattern under nitricoxide (NO) stress in Arabidopsis. This suggests a role of RALF genes in plant defense regulation. Our comprehensive analysis of RALF genes is a valuable resource that further elucidates the roles of RALF family members in plant growth and development. In addition, comparative genomics analyses deepen our understanding of the evolution of RALF gene family and will contribute to further genetics and genomics studies of other monocot and dicot plant species.

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PC-02

Evaluation of Soybean [*Glycine max* (L.) Merr.] Germplasm for Tolerance to flooding at early developmental stage

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Soybean [*Glycine max* (L.) Merr] is one of the most important legumes in the world. However, soybean varieties are sensitive to flooding stress and their seed yields are substantially reduced in response to the flooding stress. 192 soybean germplasm collection was screened to identify flooding tolerant germplasm at an early vegetative growth stage (V1). Soybean plants at V1 stage were waterlogged for 4 to 10 days. To evaluate flooding tolerance, survival rate were investigated as a time dependent manner. Jangbaegkong, Danbaegkong, Sowonkong, Socheong2 and Suwon269 showed flooding tolerance, while Shillog, T201, T181, NTS1116 and HP-963 showed flooding sensitivity. We also investigated effects of flooding stress on soybean morphology. The adventitious root development was greatly increased in flooding tolerant plants compared to it in flooding sensitive plants. In addition, root length and root number were analyzed. The significant reduction of root length and root number was observed in flooding sensitive plants. Thus, these results indicate that the morphological changes in roots are important for acclimation to flooding stress. Taken together, the relationship between the morphological changes in the roots and flooding tolerance may be useful in selecting a flooding tolerant soybean germplasm.

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PC-03

Genome Wide Association Study on the Preharvest Sprouting Resistance in RiceAye Aye Khaing¹, Min-Young Yoon¹, Byung-Kook Yun², Tae-Sung Kim¹, Chang-Yong Lee², Yong-Jin Park^{1,3*}¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340-702, Republic of Korea²Department of Industrial & Systems Engineering, Kongju National University, Cheonan 330-717, Republic of Korea³Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340-702, Republic of Korea

Preharvest sprouting resistance (PHS) causes the reduction of grain yield and also affects the quality of grains, resulting significant economic losses. PHS and its related traits were evaluated and observed in wide range among the 137 diverse rice accessions. To mine the associated signals for PHS resistance, genome wide association study (GWAS) was performed using phenotype data and whole genome resequencing data of 137 diverse rice accessions. This study not only could detect the previously identified dormancy and PHS associated genes but also explore the new candidate genes associated with the PHS and related traits. An example of them is seed dormancy 4 (Sdr4) gene which was found to be associated with germination % at day 14 (D14). This study provided the potential associated candidate genes which might be very useful to improve the PHS resistance in future rice breeding.

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PC-04

Transcriptome analysis of grain-filling caryopses reveals the potential formation mechanism of the rice *sugary* mutantFeng-peng Li¹, Won-Hee Ra¹, Min-Young Yoon¹, Soon-Wook Kwon², Tae-Sung Kim¹, Il-Pyung Ahn³, Yong-Jin Park^{1,4*}¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340-702, Republic of Korea²Department of Plant Bioscience, College of Natural Resources and Life Science, Pusan National University, Milyang 627-706, Republic of Korea.³National Academy of Agricultural Science, Rural Development Administration, Suwon 441-107, Republic of Korea.⁴Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340-702, Republic of Korea

A *sugary* mutant with low total starch and high sugar content was compared with its wild type Sindongjin for grain-filling caryopses. In the present study, developing seeds of Sindongjin and *sugary* mutant from the 11th day after flowering (DAF) were subjected to RNA sequencing (RNA-Seq). A total of 30,385 and 32,243 genes were identified in Sindongjin and *sugary* mutant. Transcriptomic changes analysis showed that 7,713 differentially expressed genes (DEGs) (\log_2 Fold change ≥ 1 , false discovery rate (FDR) ≤ 0.001) were identified based on our RNA-Seq data, with 7,239 genes up-regulated and 474 down-regulated in the *sugary* mutant. A large number of DEGs were found related to metabolic, biosynthesis of secondary metabolites, plant-pathogen interaction, plant hormone signal transduction and starch/sugar metabolism. Detailed pathway dissection and quantitative real time PCR (qRT-PCR) demonstrated that most genes involved in sucrose to starch synthesis are up-regulated, whereas the expression of the ADP-glucose pyrophosphorylase small subunit (*OsAGPS2b*) catalyzing the first committed step of starch biosynthesis was specifically inhibited during the grain-filling stage in *sugary* mutant. Further analysis suggested that the *OsAGPS2b* is a considerable candidate gene responsible for phenotype of *sugary* mutant.

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PC-05

QTL analysis of the *qBK1*, a major QTL for bakanae disease resistance in rice

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Bakanae disease is one of the most serious and oldest problems of rice production, which was first described in 1828 in Japan (Ito and Kimura 1931). This disease may infect rice plants from the pre-emergence stage to the mature stage, with severe infection of rice seeds resulting poor germination or withering (Iqbal et al. 2011). Under favorable environmental conditions, infected plants have the capacity to produce numerous conidia that subsequently infect proximate healthy plants, resulting in major yield loss (Ou 1985). One hundred sixty nine NILs, YR28297 (BC₆F₄) generated by five backcrosses of Shingwang with the genetic background of susceptible *japonica* variety, Ilpum were used for QTL analysis. Rice bakanae disease pathogen, CF283, was mainly used in this study and inoculation and evaluation of bakanae disease was performed with the method of the large-scale screening method developed by Kim et al. (2014). A major QTL for resistance against bakanae disease on chromosome 1 was identified using SSR marker, RM9, which explaining 65 % of the total phenotype variation. The major QTL designated as *qBK1* and mapped to a 4.4 Mbp region between RM24 (19.30 Mb) and RM11295 (23.72 Mb). The results of this study are expected to provide useful information toward developing resistant rice lines to this detrimental fungal disease.

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PC-06

Variation and haplotypes of NaCl salinity on rice at germination stage based on Genome-wide association study

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Salt toxicity is the major factor limiting crop productivity in saline soils. Rice is an important staple food crop of nearly half of the world population and is well known to be a salt sensitive crop. The completion and enhanced annotations of rice genome sequence has provided the opportunity to study functional genomics of rice. With the rapid development of the biotechnology techniques, we can use more accurate and reliable methods to study the mechanism and function in different stress conditions. In present study, 295 rice accessions of diverse origin were re-sequenced and used for genome-wide association study (GWAS) with several germination-related traits, including germination percentage (GP), germination energy (GE), germination rate (GR), germination index (GI), salt tolerance index (STI) in salt tolerant germination stage. Phenotyping of the rice accessions were carried out at 200mM NaCl to screen salt tolerance levels. GWAS was applied to detect the associated genes related to salt tolerance in rice germination stage. Variations and haplotypes of the associated genes were detected and correlation between the phenotypes and genotypes were validated using qRT-PCR.

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PC-07**Characterization of *OsLPS* gene in heterologous plant system**

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OsLPS is pollen specific gene that express at late stage of pollen development in rice. Based on microarray database, promoter region of two genes Os03g0106900 and Os03g0106500 were identified. The sequence of 2287bp and 2468bp upstream region of these genes were amplified and designated as *OsLPS10* and *OsLPS11*. These promoters were fused with GUS-GFP reporter gene in a destination vector, pKGWFS7 and introduced into rice (Dongjin cultivar) and Arabidopsis (Col-0). The results of GUS assay showed different pattern of gene expression in pollen of rice and Arabidopsis. In Arabidopsis, the *OsLPS10* gene strongly activated in young anther and not expressed in mature pollen. Pollen development analysis revealed GUS expression was detected at unicellular stage and strongest at the bicellular pollen developmental stage. No GUS signal was recorded in mature pollen. In case of *OsLPS11*, no GUS signal was detected in during pollen development of inflorescent. By contrast, in rice, the GUS expression pattern of *OsLPS10* and *OsLPS11* exhibited similar. GUS expression was first detectable in the anthers of spikelets at the bicellular stage and intensity increased in tricellular and mature pollen. The GUS signal was not detected in the anthers in unicellular microspores in both genes, *OsLPS10* and *OsLPS11*. The results suggested that these genes were different activity in heterologous plant system, monocot and dicot. Complementation analysis and Cis-regulatory elements will be examined to illuminate the characteristic of these genes.

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PC-08**Identification and characterization of microspore-specific rice promoters during pollen development**

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Based on the results of microarray analysis we selected ten candidate genes that express in pollen at the early pollen developmental stage. By PCR amplification, the promoter region of these genes were amplified from rice genomic DNA (Nipponbare) and cloned into the destination pKGWFS7 vector via an entry vector, pDONR201. The characteristic of promoters were evaluated in *Arabidopsis thaliana* (Col-0) through GUS expression analysis. Fifty T2 plants respectively from each promoter were tested. Whole inflorescence of individual plant was stained with 1mM X-Gluc solution to observe tissue-specific GUS expression patterns. The results showed that all 10 promoters activated in pollen tissues. Among them six promoters expressed at the early developmental stage (unicellular) of pollen and the others expressed at both early (unicellular) and late pollen developmental stage (mature pollen). The results indicated that these promoters would be potential applicable for the studies of pollen function. Currently, we are performing these promoters analysis in rice transgenic plants as well as molecular characterization.

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PC-09

Resequencing 295 accessions of heuristic and Korean breeding rice deciphers the milestones for breeding and domestication history of Korean rice

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As one of the most important crop, rice is not only a staple food of half world's population but a wonderful model plant, which has been leading the evolution and functional genomics study. The next-generation sequencing technology are expediting rice genomic study, by providing a simple but powerful way. In this study, we re-sequenced a core collection of 137 rice accessions from all over the world along with 158 Korean breeding varieties. Finally, 6.3G uniquely mapped reads were obtained, and about 10 million SNPs and ~1.2 million InDels were identified with average sequencing depth of 7.5X. These will help us to maximize our germplasm utilization and assists all the deep research in population dynamics and functional studies. Here, we'd like to show the approaches applied to resequencing data mining and on-going activities.

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PC-10

Haplotype analysis and functional study of *badh2*, a gene responsible for fragrance in aromatic rice

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2-acetyl-1-pyrroline (2AP) was widely known as the principal aroma compound, its development in rice has been reported due to the loss of function of betaine aldehyde dehydrogenase gene (*badh2*) on chromosome 8. In previous study, a lot of haplotypes have been found of this gene, while only limited haplotypes have been proved as functional mutations. A total of 137 core set accessions, and additional 45 germplasms have been employed in this study. Finally, two new mutations have been found (3bp deletion in exon12 and C/A SNP in exon 10), and 23 haplotypes have been detected, most of them had strong relations with aroma formation. According to the sequence results, five functional markers have been developed, the markers showed a highly efficient in discriminating the special aromatic rice varieties, and displayed perfect co-segregation with the trait of fragrance in F2 population. Those new markers developed in the present study would be useful in molecular breeding of fragrant rice varieties. Based on the haplotypes, the further research is in progress.

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PC-11**Identifications of DNA polymorphism associated with signaling pathway in arsenic tolerance rice mutants**

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In order to select a rice population with useful trait such as arsenic tolerance for crop improvement, we have developed 3000 M₇ Targeting Induced Local Lesions IN Genomes (TILLING) lines by gamma ray (GR) irradiation treatment to a rice variety (cv. Donganbyeon). A total of 2 M₇ lines exhibited the arsenic (AsV) tolerant phenotype (hereafter, named Arsenic Tolerant TILLING line 1 and 2, and designed as ATT1 and 2), in which the shoots and roots length of ATT lines were significantly longer than those of wild type (WT) during As(V) treatment. To survey the DNA polymorphism of these plants, we conducted the Whole genome resequencing with 10x coverage in ATT lines. By comparative analysis among ATT lines, we have identified the common DNA polymorphism such as 11,817 SNPs (49.83% in ATT1 and 48.35% in ATT2) and 30,618 InDels (86.72% in ATT1 and 86.23% in ATT2). Also, these mutants were showed the close relationships more than WT. To further study the changed amino acids of genes, we commonly identified the 758 genes for non-synonymous SNPs and 249 genes for changed codon InDels. These genes were mainly exhibited the enriched GO functions such as catalytic activity, nucleic acid binding and transferring phosphorus-containing groups. To determine the genes associated with arsenic-related mechanism in DNA polymorphism of ATT lines, we have retrieved the two structurally altered genes (Os11g47870 and Os03g19900) for metalloid As(V) detoxification toward induced genes in response to arsenic treatments by public microarray datasets. We suggest that As(V) tolerant phenotypes of ATT lines are certainly affected by structurally altered genes associated with phosphorus transferring and As(V) detoxification during GR treatment.

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PC-12

Molecular breeding of a pepper cultivar (*Capsicum annuum*) containing high capsinoids

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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 *p-aminotransferase (p-AMT)* gene. In the previous study, SNU11-001 (*C. chinense*) containing high levels of capsinoids was found in germplasm collections of Seoul National University. We found that this collection has a unique mutation in the *p-AMT* gene. In order to develop a cultivar containing high capsinoids contents, marker-assisted foreground and background selection were performed in this study. Backcrossing is an effective breeding method for introducing useful traits to an elite cultivar. Compared to conventional backcrossing, marker-assisted backcrossing (MABC) is extremely useful for recovery of a recurrent parent's genetic background. To obtain background selection markers, a total of 412 single nucleotide polymorphism (SNP) markers was screened to obtain polymorphic SNP markers between 'Takanotsume (*C. annuum*)' and 'SNU11-001'. Of the 412 SNP markers, 96 polymorphic SNP markers evenly distributed in pepper genome were finally selected. Plants carrying the *pAmt/pamt* genotype were selected from a BC₁F₁ population using SCAR markers derived from the unique *p-AMT* mutation of SNU11-001. BC₁F₁ plants carrying the *pAmt/pamt* genotype were subjected to background selection. Multiple genotype analysis was done using Fluidigm platform (BioMark). Once we obtain plants carrying most similar genetic background to recurrent parent, capsinoids contents will be measured and another round of MABC be done to obtain plants containing high levels of capsinoids.

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PC-13

Haplotype variation in *Submergence 1 (SUB1)* contributing to the anaerobic germination (AG) in rice

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Anaerobic germination (AG) is plays important role in submergence resistance which is an important trait for rice production in flood-prone lowland areas. Slow seed germination and delayed seedling establishment due to flooding become major problem for modern sowing methods such as direct seeding and environmental friendly good agricultural practices especially using young seedling age. In total, 137 diverse rice accessions were evaluated for anerobic germination ability. *Submergence 1 (SUB1)* which is induced ethylene response factors is suggestive because genes belonging to this gene family play a crucial role in rice tolerance to submergence. In this study, haplotype variations of three AG related genes, *SUB1 (SUB1A, SUB1B, SUB1C)* were examined using whole-genome resequencing data of 137 accessions of rice core set. The new SNPs and InDels found in the exon of the *sub1* loci would be useful in developing markers to screen the varieties with strong anaerobic germination ability in the future molecular breeding.

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PC-14

Insights from 295 diverse origin rice to elucidate chloroplast variation and evolution based on whole genome re-sequencingWei Tong¹, Tae-Sung Kim¹, Yong-Jin Park^{1,2*}¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340-702, Republic of Korea²Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340-702, Republic of Korea

Chloroplast (cp) DNA sequence data are a versatile tool for plant identification, barcoding and establishing genetic relationships among plant species. Different chloroplast loci have been utilized to infer evolutionary relationship of plant species. Although the overall structure of the chloroplast genome is generally well conserved, a number of mutations have been observed. Thus, documentation of chloroplast sequence variation has also been an valuable asset in plant population and evolutionary studies for over two decades. Recently, advance in chloroplast genome assembly from whole genome NGS data has become available. In the present study, chloroplast variations among 295 diverse origin accessions were detected based on *Oryza rufipogon*, which thought to be the progenitor of cultivated rice.. Variation calling was carried out using the whole genome re-sequencing data of those accessions along with the five rice reference cp genomes. Phylogenetic and evolution analysis of the six references and 295 accessions were performed using the whole reference genome sequence and the variation data, respectively. Also, nucleotide polymorphisms of 295 rice accessions were validated by using previously characterized 50 ecotypes. Differential SNP frequency across the rice cp genome suggests a regional dependent preferential high variation occurrence during the evolution of chloroplast.

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PC-15

Genetic Analysis and Phenotypic Performance over Multi-generations for Resveratrol RiceYang Qin¹, Hong-Il Ahn¹, Yong-Woon Jeong¹, Myung-Ho Lim¹, Soo-Yeun Park¹, Jin-Hyoung Lee¹, Kong-Sik Shin¹, Hee-Jong Woo¹, Bum-Kyu Lee¹, So-Hyeon Baek², Soon-Ki Park¹, and Soon-Jong Kweon^{1*}¹Biosafety Division, National Academy of Agricultural Science, RDA, Suwon 441-707, Korea²Rice Breeding and Cultivation Research Division, National Institute of Crop Science, RDA, Iksan 570-080, Republic of Korea

Resveratrol rice Iksan526 was developed by overexpression of T-DNA (RB::P-Ubi::RS::T-NOS::P-35S::PAT::T-35S::LB) in rice variety Dongjin. To confirm one locus insertion of T-DNAs, Mendelian genetic analysis was carried out on selection marker bar gene and objective RS gene separately by using a F2 population derived from a cross of Dongjin/Iksan526 (T6). A total of 450 four-leaf-old plants from F2 population were treated by 0.3% basta, and a phenotypic separation ratio of 3:1 (321 survival: 129 dead, p>0.90) complied with Mendelian inheritance indicating one locus insertion of bar gene. Genotypic separation was analyzed by using PCR with specific primers for 300 plants, which were selected from 321 survival plants after phenotypic separation. Results revealed a ratio 1:2 of homologous to heterozygous (92:208, p>0.90), which further confirmed one locus insertion of RS gene. In addition, comparison on agronomic traits and resveratrol contents between transgenic rice and the donor variety were launched to evaluate the phenotypic performance over multi-generations (years).

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PC-16

Association study of vitamin E content in rice using whole genome re-sequencing

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Rice is the major food for half of the world population. The nutrition component in rice is critical for improvement of people's health. Vitamin E serves as important antioxidant by quenching the free radical intermediates and thus protects the cell membrane. Because of the high nutritional value and the benefits of vitamin E in human health, increasing the tocopherol content of major agricultural crops has long been in the focus of breeding programs and genetic engineering approaches. The key genes involved in tocopherol biosynthesis have been elucidated in Arabidopsis and other model organisms. Quantitative trait locus (QTL) study performed in Arabidopsis suggested that some of these key genes and a few additional loci contribute to natural tocopherol variations. Identifying such genetic variations in rice, enrich our understanding of the genetic mechanisms controlling tocopherol variation, which can be directly applied to rice breeding programs. In this study, we used genome-wide association mapping with high-resolution density SNPs of rice core set to identify natural allelic variations, which contribute to tocopherol increase in rice.

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PC-17

Progeny Selection and Molecular Characterization for Transgenic PAC Soybean

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Two carotenoid biosynthetic genes, phytoene synthase (Psy) and carotene desaturase (CrtI) linked via synthetic 2A sequence under control of CaMV 35S promoter (two T0 plants 5 and 6) or β - conglycinin promoter (three T0 plants 7, 13 and 16) were transformed into soybean variety Kwangan. After agronomic and phenotypic selection at early generations, T5 progeny of PAC soybean were analyzed by Southern blot to confirm T-DNA copy numbers. A total of 27 homologous lines derived from one of three T0 plants (line 7 under the control of β - conglycinin promoter) with one copy T-DNA insertion, were separated and planted into greenhouse. Flanking sequence analysis was carried out on one of homologous line 6-2-3 and results indicated the T-DNA was intergenic inserted into chromosome 14 from 10,873,131 to 10,872,998 base of soybean chromosome. T-DNA insertion structure, flanking sequence and inserted gene expressions need to be analyzed in the further study.

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PC-18

Genome sequence of mungbean and insights into evolution within *Vigna* species

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Mungbean (*Vigna radiata*) is a fast-growing, warm-season legume crop that is primarily cultivated in developing countries of Asia. We constructed a draft genome sequence of mungbean to facilitate genome research into the subgenus *Ceratotropis* and to enable a better understanding of the evolution of leguminous species. The draft genome sequence covers 80% of the estimated genome, of which 50.1% consists of repetitive sequences. In total, 22,427 high confidence protein-coding genes were predicted. Based on the de novo assembly of additional wild mungbean species, the divergence of what was eventually domesticated and the sampled wild mungbean species appears to have predated domestication. Moreover, the de novo assembly of a tetraploid *Vigna* species (*Vigna reflexo-pilosa* var. *glabra*) provided genomic evidence of a recent allopolyploid event. To further study speciation, we compared de novo RNA-seq assemblies of 22 accessions of 18 *Vigna* species and protein sets of *Glycine max* and *Cajanus cajan*. The species tree was constructed by a Bayesian Markov chain Monte Carlo method using highly confident orthologs shared by all 24 accessions. The present assembly of *V. radiata* var. *radiata* will facilitate genome research and accelerate molecular breeding of the subgenus *Ceratotropis*.

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PC-19

강낭콩 유전자원의 종피색에 따른 항산화 활성 비교

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경상남도 밀양시 점필재로 20 국립식량과학원 기능성작물부 두류유지작물과

본 연구는 강낭콩(*Phaseolus vulgaris*, PV)의 종피색에 따른 항산화 활성 차이를 알아보기 위하여 수행하였다. 유전자원에 따른 16가지의 강낭콩을 적색 3종, 황색 1종, 적색얼룩무늬 3종, 흰색 얼룩무늬 1종, 회갈색얼룩무늬 2종, 흰색 2종, 회갈색 2종, 흑색 2종으로 총 8가지 색으로 나누어 진행하였다. 연구결과를 요약하면 16가지 강낭콩을 콩 전체, 콩 종피 그리고 종피를 제외한 콩으로 분리하여 각각 80% 메탄올에 48시간 추출하였다. 추출 후 원액을 필터하여 실험에 사용하였다. 강낭콩에서 종피가 차지하는 비율은 6.93~10.20%이었으며, 총 폴리페놀 함량은 종피에서 7.05~180.33mg GAE/mL, 콩 전체에서 17.96~61.23mg GAE/mL, 그리고 콩 알맹이 16.58~22.24mg GAE/mL이었다. 종피 추출물에서 PV-151(적색얼룩무늬)이 180.33mg/mL로 가장 높은 폴리페놀 함량을 보였고, PV-132(회갈색)에서 164.67mg/mL, PV-78(회갈색얼룩무늬)에서 158.36mg/mL, PV-133(회갈색얼룩무늬)에서 158.19mg/mL, PV-126(적색)에서 147.93mg/mL, PV-343(흑색)에서 121.49mg/mL으로 나타났다. 흰색 강낭콩은 폴리페놀 함량이 미비하였다. DPPH 라디칼 소거능은 종피 추출물 2.5배 희석 하였을 때, PV-151(적색얼룩무늬), PV-343(흑색), PV-78(회갈색얼룩무늬), PV-132(회갈색)에서 90%이상 소거능을 보였으며 농도 의존적으로 활성이 감소하는 것을 확인하였다. ABTS 라디칼 소거능은 종피 추출물을 10배 희석 하였을 때, PV-78(회갈색얼룩무늬)가 88.16%, PV-132(회갈색)가 81.29%, PV-151(적색얼룩무늬)가 95.26%, PV-343(흑색)이 80.11%의 소거능을 보였다. 이상의 결과로 보아 색이 다른 강낭콩 종피마다 가지고 있는 폴리페놀 함량이 다르며 각각 다른 항산화 활성을 나타냈다. 적색얼룩무늬, 회갈색얼룩무늬, 회갈색 그리고 흑색처럼 강낭콩 종피의 색이 진할수록 총 폴리페놀 함량과 더불어 항산화 활성이 높은 것으로 나타났다.

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PC-20

SSR 마커를 이용한 국내 콩 육성품종의 유전적다양성과 품종판별

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국내에서 육성된 콩 91품종에 대하여 SSR마커를 이용하여 품종판별의 기초자료로 이용하고자 다형성이 높은 5개의 Primer(Sat_043, Sat_036, Sat_022, Sat_088, Satt045)를 이용하여 5단계로 판별하였다. 5개마커의 총 대립인자수는 64개이었고, 범위는 10-15개이었으며, 평균대립인자수는 12.8개이었다. 판별 1단계의 Sat_043으로 판별 하였을 때 육성품종 91품종 중에서 부석콩(172bp)의 1품종이 판별되었고, 판별 2단계의 Sat_036으로 판별하였을 때 호장콩(90bp)등 34품종이, 3단계의 Sat_022로 단경콩(230bp)등 29품종이, 4단계의 Sat_088로신팔달콩(160bp)등 12품종이, 5단계의 Satt_045로 새별콩(132bp) 등 6품종이 판별되었으며, 82품종이 판별되었다. 판별되지 않은 9품종은 형태적특성에 의하여 서로간에 판별되었다.

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PC-21

Validation and Application of a Qualitative Real-Time Polymerase Chain Reaction Method for Detecting Genetically Modified Papaya line 55-1 in Papaya Products

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Genetically modified (GM) papaya (*Carica papaya* L.) line 55-1 (55-1), which is resistant to papaya ringspot virus infection, has been marketed internationally. Many countries such as the European Union, Japan, and Korea have a mandatory safety assessment, approval and labeling regulations for GM foods. Thus, there is a need for specific methods for detecting 55-1. In this study, we established a real-time PCR detection method applicable to 55-1 for a variety of papaya products. The limit of detection was possible for fresh papaya fruit up to dilutions of 0.005% and 0.01% (weight per weight [w/w]) for homozygous SunUp and heterozygous Rainbow cultivars, respectively, in non-GM papaya. The 55-1 event-specific detection method observed parallelism ($r^2 > 0.99$) between the concentration of line 55-1 cultivars and Ct values obtained in amplification plots at concentrations of 0.005-10% for SunUp DNA and 0.01-10% for Rainbow DNA. The method was applicable to the qualitative detection in various types of processed products (cocktail fruit, dried fruit, juice, etc.) containing papaya as a main ingredient. Monitoring papaya products for the presence of GM papaya were demonstrated using a P35S and T-nos real-time PCR detection method but no amplification signals were detected.

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PC-22

QTL mapping related to grain shattering using DH population in rice (*Oryza sativa* L.)

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The seed shattering played a key role in the crucial step of rice domestication. Because it has been important to increase the yield human had to select the rice varieties and species with low shattering degree. The shattering habit of rice is considered to be under the relatively simple genetic control compared with other characteristics related to domestication. Several recessive genes associated with the formation of an abscission layer, *sh2*, *sh4* and *sh-h* on chromosomes 1, 3 and 7, have been reported. In addition, the grain shattering of rice is considered to be caused by seed abscission. The morphology of the abscission layer can differ in many different rice varieties that show varying degrees of shattering. Accordingly, it is important to elucidate the molecular mechanism to determine why some varieties do not have abscission layers and have an easy-shattering trait. In this study, analysis of QTL for grain shattering was performed to determine the location of QTLs on the whole chromosomes of rice. Also, we tried to construct a physical map for qPs6.

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PC-23

Analysis of QTL Associated with WBPH and Identification of WBPH Mediated Compounds in Rice (*Oryza sativa* L.)

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The White backed planthopper (WBPH), *Sogatella furcifera* (Horvath) is one of the serious insect pests in rice growing region in Asia. When rice is attacked by the insect it releases secondary metabolites for self-defense. In this study, we identified WBPH-mediated compounds from a cross 'Cheongcheongbyeo/Nagdongbyeo' doubled haploid (CNDH). The compounds were located in chromosome. Leaves and stem of CNDH lines were infected by 2~3 instar of 3 weeks WBPH and samples were extracted by 90% methanol. Extracted compounds were analyzed through HPLC. TLC was used in separating the target compounds. QTL analysis of compound was done using winQTLcart 2.5 program. Chrysoeriol was highly contained in Cheongcheongbyeo. QTL location is found on chromosome by winQTLcart 2.5. QTL associated with compound7 was detected on chromosome 4, 7 and 12. qFla4 was detected on chromosome 4 in RM280-RM6909 at LOD 3.5 with 30% of variation. qFla7 was detected on chromosome 7 in RM248-RM1134 with LOD 3.0 with 30% of variation. qFla12 was detected on chromosome 12 in RM1226-RM12 with LOD 2.7 with 40% of variation. Cochlioquinone was detected on chromosome 8, qFla8 in RM23230-RM3689 with LOD 2.5 with 30% of variation. Chrysoeriol and Cochlioquinone separated to condition of (Chloroform: Methanol: 1-Butanol: Water=4:5:6:4). Separated compounds were analyzed by LC/MS and NMR. These results, investigation is being done to determine how the secondary metabolites come lead to pathways of genes and its effect on WBPH relation.

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PC-24

Studies on the optimum screening time for improved WBPH-associated QTL analysis in riceSoheap Yun¹, Hyun-Suk Lee¹, Gihwan Yi², Kyung-Min Kim^{1*}¹Division of Plant Biosciences, School of Applied Biosciences, College of Agriculture and Life Science, Kyungpook National University, Daegu 702-701, Republic of Korea²Department of Farm Management, College of Agriculture and Life Science, Kyungpook National University, Gunwi-gun, Gyeongbuk 716-821, Republic of Korea

The whitebacked planthopper(WBPH), *Sogatella furcifera* is a serious pest of rice. The nymphs and adults suck phloem sap which causes reduced plant vigor, stunting, yellowing of leaves, delayed tillering in rice. This study was conducted to identify the optimum screening time for improved WBPH-associated QTL analysis and to develop the markers for use in breeding WBPH resistance. Resistance after 7 days infestation was observed in 100 lines(83.3%), after infestation for 14 days, resistance was observed in 14 lines(11.7%), and after infestation for 21 days, resistance was observed in 10 lines(8.3%). However, no after 14 days infestation was as similar as normal distribution in WBPH resistance. QTLs associated of the resistance detected in four regions on *qWBPH1* and *qWBPH8* in the intervals marker. After 7 days of infestation, the *qWBPH1* was located in the interval RM3482-RM11966 and RM3709-RM11694 with LOD 4.0 and RM3709-RM11694 with LOD 3.5. After 14 days of infestation, The *qWBPH1* was located in the interval RM3709-RM11694 with LOD 3.3. and RM3709-RM11694 with LOD 3.3. After 21 days of infestation, The *qWBPH8* was located in the interval RM17699 with LOD 3.3. The QTLs on chromosome 1 was the most effective RM11694-RM11669 (LOD 3.3, variance 30%). The resistance lines were collected 10 plants of phenotypic variation with genotype. The ratios of coincidence were used to determine resistance in 10 plants with phenotypic variation and a genotype of 8 markers. 3 markers were used: RM3482 on chr.1 represented 100%, RM8235 and RM11694 represented 80%, 90%, respectively, RM17699 on chr.8 represented 80% of the coincident ratio. These selected markers will be useful to rice breeding programs interested in new sources of WBPH resistance.

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PC-25

A cleaved amplified polymorphic sequence(CAPS) derived from a conserved missense mutation of the *CmACS-7* for selecting monoecious melon plants (*Cucumis melo* L.)

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Most of the melon(*Cucumis melo* L.) breeding lines in Korea show andromonoecious (male-perfect flowers) sex expression, which requires laborious hand emasculatation to produce the F1 seeds. There is a high demand for developing monoecious (male-female flowers) elite germplasm. The present study was carried out to develop molecular markers for selecting monoecious plants based on the *CmACS-7* gene [*a* locus with 1-aminocyclopropane-1-carboxylic acid synthase(ACS) activity] responsible for ethylene synthesis and sex determination in melon. The full length sequences of the *CmACS-7* were cloned from a monoecious inbred 'Mo23' and an andromonoecious inbred 'Am24'. Sequence alignment revealed a major SNP(C170T) in exon1 and 18bp indel in intron4 of the *CmACS-7*, and a CAPS (SNP-C170T) and SCAR (ID4-18) were developed from the SNP and indel, respectively. A total of 453 F2 plants derived from 'Mo23' x 'Am24' were determined for their sex expression and genotyped using the SCAR marker. A Mendelian ratio of 3(monoecy): 1(andromonoecy) was observed from the F2 population, and sex type of 449 plants (except for four plants that showed incomplete monoecy) cosegregated with the SCAR marker, demonstrating that *CmACS-7* is a single dominant gene conferring monoecy of 'Mo23'. Allele variation of the *CmACS-7* was evaluated by genotyping 114 melon accessions with diverse geographical origins using the CAPS and SCAR. C170T-SNP in exon1 of the *CmACS-7* was highly conserved in melon germplasm and perfectly matched with the phenotype, whereas the 18bp-indel mutation in intron4 existed in various forms. The results demonstrated that CAPS marker SNP-C170T can be useful for marker-assisted selection(MAS) of monoecious melon plants.

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PC-26

Molecular analysis of transgenic rice overexpressing UDP-glycosyltransferase from *Brassica rapa*Me-Sun Kim¹, Hye-Jung Lee¹, Joonki Kim¹, Dal-A Yu¹, Sanguk Byeon¹, Kwon-Kyoo Kang², Illsup Nou³, Yong-Gu Cho^{1*}¹Department of Crop Science, Chungbuk National University, Cheongju 361-763, Korea²Department of Horticulture, Hankyong National University, Ansong 456-749, Korea³Department of Horticulture, Suncheon National University, Suncheon 540-742, Korea

Secondary plant metabolites undergo several modification reactions, including glycosylation and physiological functions. Glycosylation, which is mediated by UDP-glycosyltransferase (UGT), plays a role in the storage of secondary metabolites and in defending plants against stress. In this study, a UDP-glycosyltransferase cDNA was isolated from *Brassica rapa* hereinafter referred to as *BrUGT*. It has a full-length cDNA of 1,236 bp that contains a single open reading frame of 834 bp which encodes a polypeptide of 277 amino acid residues with a calculated mass of 31.19 kDa. BLASTX analysis hits a catalytic domain of glycos_transf_1 super family (c112012) that belongs to the glycosyltransferases group 1 with tetratricopeptide (TPR) regions. UGT gene expression analysis showed high mRNA transcripts in pistil, followed by petal, seed and calyx of flower in *Brassica rapa*. Furthermore, we constructed a recombinant pFLCIII vector carrying the *BrUGT* gene under the control of ubiquitin promoter and NOS terminator and transformed into rice using *Agrobacterium tumefaciens*. The *UGT* overexpressing rice lines were then characterized at the physiological and molecular levels. To further understand the biological function of *BrUGT*, transcriptional profiling of the gene in transgenic rice lines under cold, salt, PEG, H₂O₂, ABA and drought stress condition is underway.

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PC-27

Development and Selection of CGMMV Resistant Watermelon by Crossing CGMMV Resistant GM Rootstock

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Many viruses infect cucurbits. One of the well-known symptoms is mosaic disease. Those that cause mosaic are cucumber mosaic virus (CMV), squash mosaic virus (SqMV), watermelon mosaic virus (WMV), zucchini yellow mosaic virus (ZYMV) and cucumber green mottle mosaic virus (CGMMV). WMV resistant GM squash was developed many years ago in the United States and it was on the market, but no further information was available by now pertinent to commercial aspect. Usually these viruses are not easily controlled by frequent applications of chemicals that target the insect as carriers of viruses. Therefore, it is necessary to develop commercial varieties possessing resistance against viral diseases. We have developed GM watermelon rootstocks called gongdae, using a coat protein gene of CGMMV as transgene. Those GM watermelon rootstocks showed highly resistant to CGMMV, and have been crossed to get the several BC and T generation. In order to obtain the virus resistant watermelon, watermelon lines were crossed to the selected GM watermelon rootstock. Here, we present the successful watermelon cultivars that show resistance to CGMMV. The resistance must have obtained by transferring the transgene from the GM watermelon rootstock to watermelon line.

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PC-28

Distribution of Single Nucleotide Polymorphism(SNP) in Major Domestic Rice Cultivars compared to Japonica and Indica Reference Genomes

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With the development of next generation sequencing (NGS) technology, the variation of sequences represented as SNP between cultivars becomes available at genome level. The major domestic cultivars with high yield have been developed by breeding of indica and japonica, it is important to localize the region of origin according to the genotype for further characterization of unique features of cultivars. For the localization of SNP at genome level, the paired end sequences of 6 major domestic rice cultivars, Ilmi, Ilpoom, Sulgaeng, Baekjinju1ho, Hwayoung and Woongwang were compared against Japonica and Indica Rice Genomes as reference genomes. The genomic DNAs were prepared from callus tissues and paired-end of the fragments were sequenced with NGS Sequencer, Illumina HiSeq2000. About 50x coverage of paired-end sequences were trimmed according to the quality of the sequences, and errors were corrected with statistical analysis of kmers of 15. The trim-corrected sequences were mapped and variants were analyzed against reference genomes. The overall change rate of Ilmi against Nipponbare IRGSP 1.0 and Indica BGI 93-11 reference genomes were 0.92 base/1kb (1/1,079 base) and 8.09 base/1kb (1 base/123 bases), respectively. Among 6 cultivars, overall rate of Baekjinju1ho showed the lowest overall change rate of 0.53 base/1kb, and Hwayoung showed highest frequency of 0.92 base/1kb. Compared to high level in the range of change rate of 7.0-9.3 base/1kb against indica, domestic cultivars showed lower range of change rate 0.2-3.3 base/1kb with unique local high peak against japonica genome depend on the chromosomes. Compared to assembly of genome sequences, the variation of nucleotides compared to reference sequences is much faster and simple to characterize the genotype. The types of variation and the effect on functional categories will be presented.

PC-29

Development of Drought Tolerant Gourds (Chambak) Developed by Crossing GM Gourds (Jorong bak)

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Unfavorable environmental stresses are major limiting factors that affect plant productivity. Plants perceive and respond adaptively to an abiotic stress condition, and the adaptive process is controlled mainly by phytohormone, consequently, changing in gene expression pattern. Transcriptional regulator ABF3 (Abscisic acid response element Binding Factor 3) mediating the ABA-responsive gene expression plays important roles in drought and temperature tolerance. Here, we report an event of drought tolerant GM gourd in which *abf3* was inserted in the genome. For drought stress experiment, T₀ plants were self-pollinated and back-crossed to select cultivars for drought stress experiment. The drought tolerant GM gourds were selected for last 3 years and have been crossed to get the several BC and T generation consecutively. In this year, BC3T1, F1 (Bak x GM gourd), BC1F1 and control plants were subjected to drought stress, that is no watering for 12 days and rehydration afterwards. The GM gourds showed high tolerance to drought while the non-transformed plants were totally dried. When the plants were subjected to rehydration, the GM bottle gourds were completely revived and recovered from the drought stress. Tolerance levels to drought of BC3T1, F1 (Bak x GM gourd) and BC1F1 were 92.5%, 50.0% and 65.0%, respectively.

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PC-30

Development and Selection of GM Cabbage Resistant to Diamondback Moth

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Bt gene derived from the *B. thuringiensis* has been used for developing GM crops, and corn, cotton and soybean producing *B. thuringiensis* toxins have been on the market for last 17 years or so creating a huge GM seed industry. One of the notorious pests in brassica crops is diamondback moth (DBM). In order to protect the insect plague of crops from DBM, 4-5 billion dollars have been wasted annually for applying integrated measures in worldwide. Major prevention is use of pesticides that may build the contamination level of chemicals in the ground and this practice threats the environment and ecosystem. An alternative is to develop GM brassica crops and therefore we have developed GM cabbages resistant DBM using bt gene. Lots of T₀ cabbages were tested for resistance and independent GM cabbages resistant to DBM were selected. Molecular analysis was conducted to find if GM cabbage holds one copy transgene and intergenic insertion. We found an independent GM cabbage and it contained a singly copy of the transgene without disturbing the insertion site. This one called C95 line with an status of event have been self-crossed for two generation (T₂). Also we are working the development of GM cabbage with different vector that contains bar gene as a selection marker. So far 17 T₀ cabbages have been obtained by bar selection.

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PC-31

Molecular Tagging of the Gene Controlling Fruit Peel Color in Tomato (*Solanum lycopersicum* L.)

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Fresh market tomato cultivars are divided largely based on fruit color appearance (red or pink), which is attributed by the trait of peel. It had been reported that mutation of the *Slmyb12* gene suppresses synthesis of yellow-colored flavonoid (naringenin chalcone) in peel and causes pinkish tomato fruit. Whereas wild-type tomato plants synthesizing naringenin chalcone produce yellow-colored peel, which resulting in the fruit appearance to be red. The present study was performed to investigate the association between the *Slmyb12* and fruit color of domestic tomato inbred lines. A SCAR marker was developed from an Indel mutation site (72bp insertion in exon3) of the *Slmyb12*, and tested on 22 and 18 red and pink-fruited inbred lines, respectively. Unexpectedly, the results showed that all inbred lines tested had wild-type *Slmyb12*. The full length sequences of the *Slmyb12* were cloned from two inbred lines (FCR1 and FCP1), but the sequence alignment did not identify any nucleotide variations within this gene. Furthermore, scanning of SNPs between FCR1 and FCP1 using SolCAP Tomato SNP array) found no SNPs for *Slmyb12*. To delimit the genomic region of the gene conferring fruit color of domestic tomato lines, we are analyzing SNPs in the genes adjacent to the *Slmyb12* using an F₂ population derived from FCR1 x FCP1. So far, one SNP located at 1,750kbp downstream from the stop codon of *Slmyb12* was mapped using 54 F₂ plants and 83% of phenotype-marker association was revealed, demonstrating that the fruit color is controlled by *Slmyb12* indeed, or other neighboring gene(s) involved in the pathway of naringenin chalcone synthesis. Further study with more SNPs will clear up this question.

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PC-32

QTL mapping of a tolerance gene for germination under anaerobic conditions in riceSuk-Man Kim¹, Endang Septiningsih³, Kyung-Ho Kang², Bo-Kyeong Kim², Nguyen Thi Lang⁴, Russell Reinke^{1*}¹IRRI-Korea Office, National Institute of Crop Science, Rural Development Administration, Suwon 441-857, Republic of Korea²National Institute of Crop Science, Rural Development Administration, Suwon 441-857, Republic of Korea³Plant Breeding, Genetics, and Biotechnology Division, International Rice Research Institute, DAPO Box 7777, Metro Manila, Philippines⁴Cuu Long Delta Rice Research Institute, Thoi Lai, Can Tho Province, Vietnam

Rice cultivation by direct seeding allows reduced labour and production costs in addition to other benefits. However the success of this rice production method can be limited by uneven fields with poor drainage or heavy rainfall at sowing leading to early flooding conditions slowing germination and hindering crop establishment. Hence, the need to improve tolerance to anaerobic conditions in both rainfed and irrigated rice ecosystem after direct seeding. In this study QTL analysis was performed to identify QTLs associated with tolerance derived from Vietnamese variety Tai Nguyen (TN) under anaerobic conditions during germination. The population derived from a cross between TN (tolerance indica lines) and Anda (susceptible japonica), was used for collection of phenotypic data based on the survival rates of the seedlings at 21 days after sowing under 10cm of water. A total of 286 F_{2:3} families of the population were used for QTL mapping and the genotyping was carried out with the Infinium 6K SNP-chip based on the illumina Infinium platform. Two significant QTLs associated with the AG trait were detected on chromosomes 1 and 11, respectively. In Particular, the QTL on chromosome 1 had an LOD score of 7.45 and R² of 14.21%. We plan to confirm the identified QTLs in further studies and develop varieties with improved anaerobic germination ability using advanced backcross lines.

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PC-33

The Establishment of a Standard SSR System Fitting for Pear Germplasm Management

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Pear (*Pyrus* spp.) is one of the most important temperate fruit species in the world. The identification of *Pyrus* spp. based on analysis and comparison of their phenotypes has been causing a number of synonyms and homonyms among *Pyrus* spp. For accurate identification, genotype analysis with molecular marker such as microsatellite is necessarily to use. However, It is difficult to share and compare of microsatellite profiles obtained among different laboratories because no effort has made to standardize equipment or protocols. A strategy for data comparison by dint of reference to the alleles detected in well-known cultivars will be helpful for co-work with laboratories and developing international databases. Thus the study was performed to compare results between laboratories of microsatellite DNA profiling for reproducibility and standardize allele scoring by defining reference alleles efficiently. In this study, ninety pear species including forty-four comparison Asian pears, six of comparison suspicious Asian pears and reference pears, seven basic pear species, and twenty-seven Korean native pear cultivars to development of a standard set of SSR reference alleles. Twelve primers covering most of pear genome were chosen, which are CH02b10, CH03g07, CH04e03, CH03d12, EMPc117, CH01f07a, EMPc11, CH01d09, GD147, CH01d08, CH05c06, and GD96 located in pear chromosome of 2, 3, 5, 6, 7, 10, 11, 12, 13, 15, 16, and 17 respectively. Genotyping was conducted with Fragment Analyzer. After genotyping, a set of defined standard alleles based on reference pear cultivars can facilitate data comparison among laboratories and will permit the improvement of a common international database.

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PC-34

A codominant molecular marker in linkage disequilibrium with a restorer-of-fertility gene (*Ms*) and its application in reevaluation of inheritance of fertility restoration in onions

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To reveal the linkage relationship between the *Ms* locus, a restorer-of-fertility gene for cytoplasmic male-sterility (CMS) caused by CMS-S cytoplasm in onion (*Allium cepa* L.) and previously reported molecular markers linked to the *Ms* locus, 11 recombinants selected from 4,273 segregating plants originating from the cross between male-sterile maternal and male-fertile paternal lines were analyzed. Results showed that genotypes of a codominant marker, jnurfl2, were perfectly matched with the male-fertility phenotypes in all recombinants, but that this marker was not applicable in diverse breeding lines due to multiple band patterns. For the development of more reliable markers, a 12-bp indel was identified from the sequences which were obtained by genome walking, and was used to develop a simple PCR marker which was designated jnurfl3. When 104 diverse breeding lines containing CMS-S cytoplasm were analyzed with the jnurfl3 marker, male-fertility phenotypes of all breeding lines were perfectly matched with marker genotypes. To our surprise, phenotypes of 153 breeding lines containing CMS-T-like cytoplasm were also matched with genotypes of the jnurfl3 marker which was linked to the *Ms* locus for the CMS-S system. Furthermore, phenotypes of four F₂ populations containing CMS-T-like cytoplasm co-segregated perfectly with jnurfl3 genotypes. Allelic segregation distortion was detected in two F₂ populations using the jnurfl3 marker. The results of this study were in conflict with a previous model for inheritance of fertility restoration in the CMS-T system. Therefore, we proposed a new model based on the data analyzed with the jnurfl3 marker, which was in linkage disequilibrium with restorer-of-fertility genes for both CMS systems.

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PC-35

A putatively stress-related gene *BrTSR53* isolated from Chinese cabbage (*Brassica rapa*) confer salt tolerance in Yeast

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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.

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PC-36

Response of NBS encoding resistance genes linked to heat and fungal stress in *Brassica oleracea*

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Numerous environmental stresses, such as abiotic and biotic stresses, cause significant yield loss in crops and can significantly affect their development. Un the field conditions, crops are exposed to a variety of concurrent stresses. Combined high temperature and linked diseases can cause considerable damage that eventually leads to crop death. Hence, this study was conducted to characterize the genes encoding the nucleotide-binding site (NBS) motif obtained from transcriptome profiles of two cabbage genotypes with contrasting responses to heat stress. We selected 80 up-regulated genes form a total of 264 loci, among which 17 were confirmed to be complete and incomplete members of the TIR-NBS-LRR (TNL) class families, and another identified as a NFYA-HAP2 family member. Expression analysis using qRT-PCR revealed that 8 genes showed significant responses to heat shock treatment and *F. oxysporum* infection. Additionally, in the commercial *B. oleracea* cultivars with resistance to *F. oxysporum*, *Bol007132*, *Bol016084*, and *Bol030522* genes showed dramatically higher expression levels in the *F. oxysporum* resistant line than the intermediate and susceptible lines. The results of this study may facilitate the identification and development of molecular markers based on multiple stress resistance genes related to heat and fungal stress under field conditions in *B. oleracea*.

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MAS를 위한 벼멸구 저항성 유전자 *Bph3* 연관마커 탐색

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기상조건의 변화로 우리나라에 벼멸구의 발생이 점차 증가하며 피해가 커지고 있다. 다양한 벼멸구 저항성 유전자를 가진 벼 품종의 육성이 필요하다. 본 연구는 Marker-assisted Selection(MAS)을 통한 벼멸구 저항성 유전자 *Bph3* 보유 벼 품종 육성을 위해 *Bph3* 연관마커 탐색을 수행하였다. 각각 서로 다른 벼멸구 저항성 유전자를 가진 9개 품종의 DNA를 추출한 후 6번 염색체의 *Bph3* 유전자 인근의 8개의 SSR 마커를 가지고 PCR을 수행하였다. 8개 SSR 마커중 *bph4*를 제외한 나머지 유전자와 다른 위치의 밴드를 나타내는 RM586이 가장 적합한 마커로 판단되었다. 선발된 RM586의 MAS 능력을 검증하기 위해 벼멸구에 감수성인 벼 품종 새누리과 *Bph3* 유전자를 보유한 저항성 벼 품종 BG367-2를 교배하여 F1을 육성하였고 다시 새누리를 반복친으로 여교배 하여 BC₁F₁ 80개체를 얻었다. 80개체를 벼멸구 저항성 검정 결과 1:1의 저항성과 감수성 분리비를 보였으며, 이들 개체의 DNA를 분리하여 RM586 마커로 PCR 후 전기영동 했을시 저항성 개체와 감수성 개체는 서로 다른 크기의 밴드를 형성 하였다. RM586로 생성된 PCR 산물의 크기는 2% agarose gel로 쉽게 분석이 가능하다. 따라서 RM586은 *Bph3* 유전자를 가지는 벼멸구 저항성 품종 육성에 MAS를 사용하는데 적합한 마커로 확인되었다.

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PC-38

Variation block-based genomics method for the detection of functional lociYul Ho Kim^{1*}, Hyang Mi Park¹, Tae-Young Hwang¹, Ho-Sung Yoon², Dongwoo Lee³ and Sunghoon Lee³¹National Institute of Crop Science, Rural Development Administration²Department of Biology, Kyungpook National University³Theragen Bio Institute, TheragenEtex

In contrast with wild species, cultivated crop genomes consist of reshuffled recombination blocks, which occurred by crossing and selection processes. Accordingly, recombination block-based genomics analysis can be an effective approach for screening target loci with agricultural 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. Finally, the genomes are compared using the variation blocks. The variation block method identified recurring recombination blocks accurately and successfully represented block-level diversities in the publicly available genomes of 31 soybeans and 23 rice accessions. The practicality of this approach was demonstrated by the identification of a putative locus determining soybean hilum color. 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.

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PC-39

알로에 품종 35개 유전자원의 RAPD 마커를 이용 유연관계 분석이성훈¹, 김인중^{2*}¹제주특별자치도 서귀포시 김정문알로에 제주농·공장²제주특별자치도 제주시 제주대학교 생명공학부

김정문 알로에 제주농·공장에서는 알로에 베라와 알로에 아보레센스를 중심으로 450여종의 알로에가 보존되어져 오고 있으며, 알로에 중 일부는 전시용으로 활용되고 있다. 전세계 500여종의 알로에가 알려져 있는 가운데 제주농·공장의 알로에 보존 현황은 원산지가 아님에도 불구하고 많은 종수를 보유하고 있으며 보존 또한 잘 이루어지고 있다. 또한 변종 및 아종과 더불어 교잡종 등의 분류가 제대로 이루어진다면 분류군은 증가하리라 예상된다. 따라서 제주농·공장에 보존되고 있는 다양한 알로에 종을 김정문 알로에의 경제적 자원으로서 활용하기 위해서 이들의 유연관계를 분자생물학 기술을 활용하여 분석하고 품종 구분에 대한 기술을 확보하는 것이 필요하다. 이에 따라 김정문 알로에 제주농·공장에 보존되어 있는 품종 중 경제성이 있을 것으로 판단되는 35종의 품종을 대상으로 하여 Operon 사의 OPF 프라이머 5종, OPD 프라이머 15종을 사용하여 RAPD 분석을 수행하였다. 이를 통해 품종별 유연관계를 분석하였고, 10개의 그룹으로 알로에가 분류될 수 있음을 확인하였다. 이와 같은 연구를 통해 품종판별용 RAPD 마커 제작도 가능할 것으로 기대된다.

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PC-40

The promoter from the *Citrus unshiu* carotenoid isomerase gene directs differential GUS expression in transgenic *Arabidopsis*

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Carotenoid isomerase (CRTISO) catalyzes the isomerization of polyycopene to all-trans-lycopene in the carotenoid biosynthetic pathway. We isolated a full-length promoter region of CuCRTISO from *Citrus unshiu*. We determined if the promoter encoded organ-specific or developmental-specific expression, and identified possible *cis*-acting promoter elements. The full-length promoter and two truncated versions were fused to the β -glucuronidase (GUS) gene and transformed into *Arabidopsis thaliana*. Transgenic lines expressing the full-length promoter (pCiso-Prom1) and truncated promoters (pCiso-Prom2 and pCiso-Prom3) showed the same developmental and organ-specific activity. GUS expression was detected in the cotyledon and root at 5 and 10 days after germination, mature leaf, and anther. The CuCRTISO promoter contained several *cis*-acting elements involved in hormonal and environmental stress. Drought stress or abscisic acid treatment did not induce GUS expression in any transgenic lines. Heat stress induced GUS expression in the pCiso-Prom1 line; this promoter construct contains the heat-stress responsive element (HSE). Ethylene and cold-stress treatments induced GUS expression only in the pCiso-Prom3 line, although all transgenic lines contained the same *cis*-acting ethylene and low-temperature response elements, which could indicate the existence of unknown repressor element(s) in the CuCRTISO promoter. These studies indicate that CuCRTISO promoter activity is regulated in a developmental and organ-specific manner that responds to heat, cold, and ethylene. These results provide new insights into the role of *cis*-acting element(s) in CuCRTISO promoter activity. (This research was supported by the Basic Science Research Program of the National Research Foundation of Korea (NRF) funded by the Ministry of Education (NRF-2010-0007627 and 2009-0094059), and by Golden Seed Project, Ministry of Agriculture, Food and Rural Affairs (MAFRA), Ministry of Oceans and Fisheries (MOF), Rural Development Administration (RDA) and Korea Forest Service (KFS), Republic of Korea)

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PC-41

Characterization of Cinnamyl alcohol dehydrogenase activity in *Citrus platymamma* hort. ex Tanaka

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Cinnamyl alcohol dehydrogenase (CAD) catalyzes cinnamyl aldehydes into cinnamyl alcohols, the final step in lignin biosynthesis. In this study, the purification, identification and characterization of a new cinnamyl alcohol dehydrogenase gene isolated from *Citrus platymamma* hort. Ex Tanaka. We expressed CAD potential gene in *E. coli* and then characterized its features in variety of specificity aldehydes substrates. The recombinant CAD protein was shown highest efficiency toward cinnamyl and coniferyl aldehydes and the shown lowest efficiency toward sinapyl aldehydes. We used a new improved analytical HPLC method in CAD enzymatic assay for fast and accurately measurement in various aldehydes substrates. In conclusion, our studies indicated the enzymatic activity of cDNA cloned CAD protein from *Citrus platymamma* hort. Ex Tanaka.

Keywords: Cinnamyl alcohol dehydrogenase; Cinnamyl alcohols; Cinnamyl aldehydes; Subtropical plant development; *Citrus platymamma* hort. Ex Tanaka

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PC-42

Miraculin gene transformation in embryogenic Citrus callus and regeneration

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Miraculin can modify a sour taste into a sweet taste and is an alternative to traditional sweeteners. Miraculin gene was introduced into the Miyagawa Wase Satsuma mandarin (*Citrus unshiu* Marc.) callus by *Agrobacterium*-mediated transformation to produce citrus transgenic plant. Transgenic plant candidates were selected via hygromycin resistance. Transformation was confirmed by Polymerase Chain Reaction, Southern blotting, and Western blot analysis. Expression of this gene in transgenic citrus resulted in the accumulation of miraculin protein in the leaves. Multiple Shoots of transgenic citrus planets were micrografted onto trifoliolate rootstocks in the sterile soil. Plants were established in the greenhouse 2 years after planting.

Keywords: *Agrobacterium*-mediated, embryogenic callus, Miraculin, Miyagawa Wase, ovule

PC-43

Somatic embryogenesis and plant regeneration in Korea Native Citrus Species

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Somatic embryogenic calli were obtained from different native citrus species in Jeju island, South Korea. Undeveloped ovules were cultured on 5 different media, respectively; MSI (MS, modified, with the addition of malt extract 500 mg·L⁻¹ and sucrose 50 g·L⁻¹ and agar 2 g·L⁻¹), MSII (MS, modified, with the addition of malt extract 500 mg·L⁻¹, kinetin 1 mg·L⁻¹ and sucrose 50 g·L⁻¹ and agar 2 g·L⁻¹), MSIII (MS, modified, with the addition of malt extract 500 mg·L⁻¹, 6-benzyladenine, 3 mg·L⁻¹ and sucrose 50 g·L⁻¹ and agar 2 g·L⁻¹), EME-S (MT, modified, with the addition of malt extract 500 mg·L⁻¹ and sucrose 50 g·L⁻¹ and agar 2 g·L⁻¹), 1/2 EME-S (half concentration of MT macronutrients, half concentration of BH3 macronutrients, malt extract 500 mg·L⁻¹, glutamine 1.55 g·L⁻¹ and sucrose 50 g·L⁻¹ and agar 2 g·L⁻¹). Embryogenic calli were induced in the surface of undeveloped ovules in different manners, depending on citrus species and culture conditions. Somatic embryos developed into plantlets with a high frequency. Citrus embryogenic calli can be applied widely to somatic hybridization, genetic transformation, and in vitro germplasm conservation.

Keywords: Somatic embryogenic calli, undeveloped ovules, germplasm conservation

PC-44

Enhanced drought tolerance of transgenic rice plants expressing a pepper methionine sulfoxide reductase B2 in chloroplast

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The perturbation of the steady state of reactive oxygen species due to biotic and abiotic stresses in a plant could lead to protein denaturation through the modification of amino acid residues, including the oxidation of methionine residues. Methionine sulfoxide reductases (MSRs) catalyze the reduction of methionine sulfoxide back to the methionine residue. To assess the role of this enzyme, we generated transgenic rice using a pepper CaMSRB2 gene under the control of the rice Rab21 promoter with/without a selection marker, the bar gene. A drought resistance test on transgenic plants showed that CaMSRB2 confers drought tolerance to rice, as evidenced by less oxidative stress symptoms and a strengthened PSII quantum yield under stress conditions, and increased survival rate and chlorophyll index after the re-watering. The results from immunoblotting using a methionine sulfoxide antibody and nano-LC-MS/MS spectrometry suggest that porphobilinogen deaminase (PBGD), which is involved in chlorophyll synthesis, is a putative target of CaMSRB2. The oxidized methionine content of PBGD expressed in *E. coli* increased in the presence of H₂O₂, and the Met-95 and Met-227 residues of PBGD were reduced by CaMSRB2 in the presence of dithiothreitol. An expression profiling analysis of the overexpression lines also suggested that photosystems are less severely affected by drought stress. Our results indicate that CaMSRB2 might play an important functional role in chloroplasts for conferring drought stress tolerance in rice.

PC-45

Identification of multiple binding motifs and genome-wide target genes of the *OsSMF1* transcription factor during rice seed maturation

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Spatial- and temporal-specific expression patterns are primarily regulated at the transcriptional level by the promoter. Therefore, it is important to determine the binding motifs of transcription factors to understand the networks associated with embryogenesis. Here, we used a protein-binding microarray (PBM) to determine the binding motif of OsSMF1, which is a basic leucine zipper transcription factor that is involved in the regulation of rice seed maturation. OsSMF1 (previously called RISBZ1) is known to interact with GCN4 motifs (TGA(G/C)TCA) to regulate seed storage proteins (SSPs). In addition, OsSMF1 (also known as OsbZIP58) functions as a key regulator of starch synthesis in the rice seed. Quadruple 9-mer-based PBM (Q9-PBM) and electrophoretic mobility shift assay (EMSA) experiments revealed that OsSMF1 binds to the ACGT (CCACGT(C/G)), GCN4 (TGA(G/C)TCA), and GCN4-like (GGATGAC) motifs with K_d values of 0.3353 μM, 0.6458 μM, and 1.117 μM, respectively. We also identified 60 putative OsSMF1 target genes using a combination of data from expression microarrays and RiceArrayNet (RAN) analysis. Of these OsSMF1 target genes, 20, 22, and 17 genes contained ACGT, GCN4, and GCN4-like motifs within the 2-kb promoter region, respectively. In addition to known target genes, we also identified 35 potential OsSMF1 target genes that have not been previously described in immature seeds. We also confirmed that OsSMF1 directly regulates Os03g0168500 (thioredoxin-related protein), RPBF, NAC6, and two hypothetical proteins (Os12g0621600 and Os11g0582400) *in vivo*. This study suggests that OsSMF1 functions in a wide range of seed development processes with specific binding affinities for three DNA binding motifs.

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PC-46

Molecular dissection of the salt stress-induced *OsNRFP* genes in rice roots.

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Rice is a staple food for over one-half of the world population, especially in Asian countries. Recently, the growth and yield of crop plants was affected by various abiotic stresses, such as salt, drought, and high temperature due to change of climate environment. To study molecular functions of *Oryza sativa nuclear-targeted RING Finger Proteins (OsNRFPs)* in response to abiotic stresses, we selected 44 *OsNRFPs* genes, whose subcellular localizations are predicted to the nuclear, on the basis of expression patterns of a microarray dataset. A total of 44 *OsNRFPs* were grouped into two types such as RING-HC and RING-H2 via phylogenetic analysis of their RING domains structures. Subsequently, we surveyed the expression patterns of 44 genes in response to salt stress via qRT-PCR in roots. We found 10 salt stress-induced *OsNRFPs* and then examined their subcellular localizations. These genes were clearly localized to the nucleus (*OsNRFPHC-10*), cytoplasm (*OsNRFPHC-17* and *OsNRFPH2-16*) and microtubule (*OsNRFPHC-23*, *OsNRFPH2-17* and *OsNRFPH2-05*), respectively. These results might provide a key clue for understanding molecular functions of the *OsNRFP* genes associated with salt stress-related signaling pathway.

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PC-47

QTL analysis related to grain qualities under high temperature during ripening stage in riceJeong-Ju Kim^{1*}, Young-Jun Mo², Woon-Cheol Shin³, Ki-Young Kim¹, Jeom-Ho Lee¹¹Rice Breeding and Cultivation Research Division, NICS, RDA, Iksan 570–080, Republic of Korea²Rice Research Division, NICS, RDA, Suwon 441–857, Republic of Korea³Sangju Sub-Station, NICS, RDA, Sangju 742–862, Republic of Korea

This study was conducted to identify quantitative trait loci (QTL) related to grain qualities under high temperature during ripening stage using 187 Korean rice varieties. To analyze grain qualities under high temperature during ripening stage, grain appearance such as head rice and chalky grains percentage and physicochemical characteristics were investigated and SNP genotyping of 187 Korean varieties was conducted for association analysis related with grain qualities under high temperature. Five traits exhibited continuous distributions in the non-glutinous Korean varieties, indicating that these traits are controlled by multiple genes. Association mapping among non-glutinous Korean varieties was conducted using 223 markers showed polymorphism among 384 SNP markers. Six QTLs for chalk grains percentage were mapped to chromosomes 1, 4, 10 and 11. These six QTLs were linked to the SNP marker id1014176 on chromosome 1, id4010924 on chromosome 4, id10000644 on chromosome 10 and id11011505 on chromosome 11, and explained approximately 21, 61, 50, 23, 23 and 21% of the total phenotypic variance. Four QTLs for head rice percentage in chromosomes 4, 10 explained the total phenotypic variance by over 47% and around 20%. Fifteen QTLs for RVA characteristics including hot paste viscosity, peak viscosity and setback viscosity were mapped to chromosome 1, 6, 7, 12 and QTLs were explained around 20% of the total phenotypic variance.

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PC-48

Identification of sound wave induced genes in *Arabidopsis thaliana*

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Sound and communication through it have significantly contributed to study the ecology, evolution, behavior in animal. Plants may also use sound, but until now, we have been unable to effectively research what the ecological, evolutionary and molecular implications might be in plant. So, we wonder what genes are regulated under sound wave conditions. In particular, our research was centered to increase functional materials including vitamins and anthocyanin in plants. First, we investigated up- and down-regulated genes under sound wave treatments (250, 500, 800, 1000 and 1500Hz) by RNA-seq in *Arabidopsis thaliana*. In these results, we selected genes of over 8-fold increase and below 8-fold decrease and especially, focus on vitamin and anthocyanin-related genes in RNA-seq level. Second, we confirmed that these up- and down-regulated genes under sound wave treatments by qRT-PCR. Finally, we selected 13 interesting genes. To confirm these results, now, we are performing promoter assay by using promoter-GUS in plant and by using promoter-luciferase in protoplast. After then, we will find to interacting partners of these genes in sound wave signal. Our final goal is understand signaling network under sound wave treatment condition in plant. We hope that if we do find results that suggest that sound wave have a beneficial effect on crop yield and quality, acoustic biology can then have some viable application in agriculture. This could bring new discoveries into development of farming methods.

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PC-49

The Expression Pattern Characterization of *SENESCENCE 1* Gene from Poplar (*Populus alba* × *P. glandulosa*)

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Plant senescence is a final process of growth and a survival strategy to use limited nutrients efficiently during development and adaptation. Tree, however, runs senescence annually for winter dormancy. Therefore understanding senescence procedure and mechanism is striking issue for tree breeding and wood productivity. In this study, we isolated a *SENESCENCE 1* (*PagSENI*) gene from *Populus alba* × *P. glandulosa* and determined its expressional characteristics under various conditions. The *PagSENI* encodes a putative 243 amino acid protein containing a rhodanese domain. Southern blot analysis suggested that two copies of the *PagSENI* gene are present in the poplar genome. The *PagSENI* is expressed most strongly in mature leaves but most weakly in roots. The gene is significantly up-regulated by treatment with mannitol, NaCl, ABA and JA, but not by cold, SA and GA₃. These results indicate that the *PagSENI* is involved in senescence response induced by natural aging and environmental stresses. This research will provide valuable information for senescence study. To clarify *SENI* gene in poplar, we will make *PagSENI* over-expressed poplar to understand senescence procedure in detail.

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PC-50

Identification of candidate genomic region associated with seed longevity by re-sequencing in rice

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It is well known that Dharial (Bangladesh origin and weedy rice line) has longer seed longevity than indica and japonica rice varieties. To study the genetic basis of seed longevity of Dharial, we developed 240 BC₃F₇ backcross recombinant inbred lines derived from the crosses between Dharial (a donor parent) and two Korea rice accessions (recurrent parents) including Ilmi and Gopum, respectively. Among these lines, we selected two introgression lines with longer seed longevity and named them Ilmi-NIL and Gopum-NIL. Also, we developed an EMS-induced mutant line from Dharial which has shortened seed longevity, and named it Dharial-EMS. We performed re-sequencing of four rice accessions that are Dharial, Dharial-EMS, Ilmi-NIL, and Gopum-NIL. A total of 706×10⁶ raw reads were generated which provided sequence data over 46x rice genome coverage per each accession. We did genome-wide variation analysis comparing produced re-sequencing data and the re-sequencing data of Ilmi from NABIC database with the Nipponbare reference sequence. By graphical analysis of SNP distribution in rice genome of the five accessions, we could select candidate chromosomal segments introgressed from Dharial in Ilmi-NIL and Gopum-NIL. The introgressed chromosomal segments were in seven regions in Ilmi-NIL and eight regions in Gopum-NIL, and four common introgressed regions between Ilmi-NIL and Gopum-NIL were identified. 2,758 SNPs between Dharial and Dharial-EMS were found in the introgressed regions. Also, we detected 450 genes including at least one SNP among these SNPs. This result will facilitate identification of genes and development of molecular markers for improvement of seed longevity.

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PC-51

Mapping of QTLs for stem diameter in MGRIL using CAPS markers

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The next-generation sequencing (NGS) technology is being used for more effective genetic mapping and genome analysis. In this study, we performed whole-genome sequencing on the genomic DNA of Milyang23 and Gihobyeo using NGS and developed new cleaved amplified polymorphic sequence (CAPS) markers based on the single nucleotide polymorphisms (SNPs) in coding sequence between these varieties. Approximately, sequences of 60x coverage of the Nipponbare reference genome on average were obtained following Illumina sequencing. Totally, 1,726,798 SNPs between Milyang23 and Gihobyeo were detected. Among them, 149 SNPs were selected for CAPS markers and located on genetic map with previously reported 219 PCR-based DNA markers. This map was applied to the detection of quantitative trait loci (QTLs) for stem internode diameters, culm length and panicle length in rice with MGRIL population. Newly 6 QTLs were detected for culm length (CL) and stem diameter (ID) traits including the first internode diameter (I1D), third internode diameter (I3D), and fourth internode diameter (I4D). Among those QTLs, qI1D5 and qCL5 had relatively higher LOD score and explained 8.99% and 4.24% of total variation. This study showed that the NGS allowed the rapid discovery of a large number of SNPs for CAPS marker. Only very small portion of SNPs through re-sequencing were used in this study. Furthermore, the results of QTL analysis described above shows relevance of molecular markers in mapping genes for useful traits.

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PC-52

Genetic Relationship Analysis of Four Major Cucurbitaceae crops Using Expressed Sequence Tag-Simple Sequence Repeats of Watermelon [*Citullus lanatus* (Thunb.) Mastum. & Nakai]

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This study was performed to analyze genetic relationship of the four major Cucurbitaceae crop. We used 120 Expressed Sequence Tag(EST)-Simple Sequence Repeat(SSR) primer sets of developed from watermelon and published in International Cucurbit Genomics Initiative (ICuGI) database. Among 120 EST-SSR primer, 51(49.17%) EST-SSR primer set successfully amplified and 49(40.8%) EST-SSR primer set showed polymorphisms among eight cultivars of Cucurbitaceae. In the first instance, amplified PCR products analysis was conducted by the agarose-gel electrophoresis then further analyzed by using Fragment Analyzer. A total 382 PCR band were produced by 49 EST-SSR primers in 24 plant panels, used the analysis of pairwise similarity and dendrogram construction. Assessment of the genetic relationships resulted in similarity index with range of 0.0103 to 0.8452. In dendrogram, 24 plant panels were formed three major groups (A, B, C) and 7 subgroups (A-1, A-2, B-1, B-2, B-3, C-1, C-2). Major group A was comprised of 2 subgroups, subgroup A-1 (6 watermelon cultivars, *Citrullus lanatus* var. *vulgaris* Schrad.) and subgroup A-2 (3 wild type watermelon, *Citrullus lanatus* var. *citroides* Mats. & Nakai). Major group B was comprised of 3 subgroups, subgroup B-1 (4 melon cultivars, *Cucumis melo* var. *cantalupensis* Naudin.), subgroup B-2 (2 oriental melon cultivars, *Cucumis melo* var. *conomon* Makino.) and subgroup B-3 (5 cucumber cultivars, *Cucumis sativus* L.). Major group C was comprised of 2 subgroups, subgroup C-1 [2 squash/ pumpkin cultivars, *Cucurbita moschata* (Duch. ex Lam.)/Duch. & Poir. and *Cucurbita maxima* Duch.] and subgroup C-2(2 squash/pumpkin cultivars, *Cucurbita pepo* L./*Cucurbita ficifolia* Bouche.)

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PC-53

Fine mapping of suppressor of the fruit shape gene OVATE using SNP markers in tomato

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The fruit shape is an important character in tomato. OVATE is one of genes controlling fruit elongation in tomato. Two loci suppress the *ovate* mutation, *sov1* and *sov2*, on chromosome 10 and chromosome 11 respectively. *sov1* appears to control neck constriction in the fruits (Rodriguez et al, 2013). We sequenced the genomes of Gold Ball Livingston and Yellow Pear using the Illumina Hiseq 2000 generating 101 PE reads and developed molecular markers tightly linked to *sov1*. The locus was confirmed by fruit shape index analysis, marker genotyping and progeny testing of recombinants. We find mapped *sov1* to a 145 kb interval corresponding to a region comprising two candidate genes. One of the candidate genes for *sov1* is *SIOFP20* another member of the Ovate Family Protein class. Although there is no difference expression of *SIOFP20* in the parents at anthesis, when the gene is expressed very high, the mutation appears to be a 34 kb promoter deletion of *SIOFP20* in Yellow Pear, conferring a pear shaped and neck-constricted fruit.

PC-54

Cytogenetic Analyses of Six Food crop species by DAPI Staining and Fluorescence *in situ* Hybridization Methods

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Genome sequencing researches for considerable numbers of crops and wild plants are being developed. Cytogenetic researches according to chromosome number and size are essential to confirm and comprehend ploidy level and genome size before genome sequencing project is actually conducted. Cytogenetic researches on six food crop plants were carried out by DAPI staining and fluorescence *in situ* hybridization (FISH) method. *Fagopyrum esculentum* Moench showed $2n=2x=16$, each chromosome length of 1.42 μ m to 1.77 μ m, total chromosome length of 13.31 μ m, and karyotypic formula of $2n=8m$; *Phaseolus angularis* W.F. Wight, $2n=2x=22$, 2.01 μ m to 3.84 μ m, total 28.03 μ m, $2n=9m+2sm$, *Perilla frutescens* var. *japonica* Hara, $2n=2x=40$, 1.73 μ m to 2.76 μ m, total 44.36 μ m, $2n=5m+13sm+2st$. Chromosome sizes of the other three species such as, *Panicum miliaceum* L., $2n=2x=36$, total chromosome length of 30.83 μ m, *Sesamum indicum* L., $2n=2x=26$, 27.39 μ m, *Ipomoea batatas* L., $2n=2x=30$, total 33.51 μ m were too small for each chromosome type to be identified and analyzed. The result of FISH analysis using 5S and 45S rDNA probe showed species-specific chromosome locations in the genome. These preliminary analyses were carried out to decide which food crop to prioritize for genome sequencing. This work was supported by the "Cooperative Research Program for Agriculture Science & Technology Development (No.PJ009837), Rural Development Administration, Republic of Korea.

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PC-55

FISH karyotype and GISH meiosis analyses of a fertile *xBrassicoraphanus* and its parental lines

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xBrassicoraphanus, a new synthetic intergeneric hybrid between *Brassica rapa* L. ssp. *pekinensis* and *Raphanus sativus* L., also locally known as 'Baemoochae', is an interesting subject for studying polyploidy and genome plasticity in the family Brassicaceae, but very few genomic and cytogenetic information. Here, we analysed the chromosome complements and pairing of the most fertile lines, BB1 and BB5, using dual-color fluorescence *in situ* hybridization (FISH) and genomic *in situ* hybridization (GISH) to check their chromosomal segregation stability. The somatic chromosome complement of *B. rapa* was confirmed to be $2n=20$ (2.8~4.8 μ m), of *R. sativus*, $2n=18$ (2.0~3.3 μ m), and of *xBrassicoraphanus*, $2n=38$ (2.2~5.0 μ m). There were eight, eight, and seventeen metacentric pairs and two, one, and two submetacentric pairs in *B. rapa*, *R. sativus*, and *xBrassicoraphanus*, respectively. Additionally, three, two, and five pairs of 5S rDNA and five, three, and eight pairs of 45S rDNA were observed in *B. rapa*, *R. sativus*, and *xBrassicoraphanus*, respectively. This suggests that both *B. rapa* (AA) and *R. sativus* (RR) genomes, particularly the rDNA arrays, co-exist in *xBrassicoraphanus* (AARR) genome. In meiosis I, nineteen bivalents were most frequent, and GISH analysis showed ten bivalents from the A genome. This study would provide a useful information for further genomic study of *xBrassicoraphanus* and its improvement as a new promising breeding variety.

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PC-56

Cytogenetic mapping of *Panax ginseng* major DNA repeats: Evidence for allotetraploidy and utility for chromosome identification

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There is a growing number of plant genomes that are being sequenced, but most of these available assemblies do not cover the entire genome mainly due to the highly repetitive sequences found in most plant genomes. Nevertheless, these repeats, although a challenge in assembly algorithms, provide relevant information about a genome's history that could help explain its structure and complexity. Here, we cytogenetically mapped previously and presently characterized major repeats of *Panax ginseng* genome, including several LTR retrotransposons (PgDel2, PgDel3, PgTat1, PgTat2, PgTork) and one tandem repeat, PgTR. Fluorescence *in situ* hybridization (FISH) results showed differential accumulation of *Ty3/gypsy* LTR retrotransposons into different chromosomal regions or subgenomes, suggesting a non-random preferential amplification of retrotransposons in these regions and an allopolyploid origin of *P. ginseng*. *In silico* analysis based on 1x whole genome sequence reads suggests that PgTR is the most abundant tandem repeat in ginseng, which was further corroborated by FISH analysis. More importantly, its unique distribution pattern among the 24 ginseng chromosomes, coupled with the non-random distribution of LTR retrotransposons and rDNA arrays, allowed us to discriminate and characterize each individual ginseng chromosome. These different newly characterized cytogenetic markers allowed reorganization of previously reported ginseng karyotype with better resolution, demonstrating the utility in ginseng chromosome identification. These information give us insight about the genomic structure of *P. ginseng*, and should be useful for future comparative cytogenetics studies among closely related species to unravel its genomic history. This work was supported by the Next-Generation BioGreen21 Program (No. PJ008202), Rural Development Administration, Republic of Korea.

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PC-57

Soybean transgenic plants with Coat protein and HC-Pro using RNAi method showed enhanced resistant to Soybean mosaic virus (SMV)

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Soybean mosaic virus (SMV), a member of *Potyviridae* family, is one of the most typical viral diseases and results in yield and quality loss of cultivated soybean. Due to the depletion of genetic resources for resistance breeding, a trial of genetic transformation to improve disease resistance has been performed by introducing *SMV-CP* and *HC-Pro* gene by RNA interference (RNAi) method via *Agrobacterium*-mediated transformation. Transgenic plants were infected with SMV strain G5 and investigated the viral response. As a result, two lines (3 and 4) of *SMV-CP*(RNAi) transgenic plants and three lines (2, 5 and 6) of *HC-Pro*(RNAi) transgenic plants showed viral resistance. In genomic Southern blot analysis, most of lines contained at least one T-DNA insertion in both *SMV-CP*(RNAi) and *HC-Pro*(RNAi) transgenic plants. Subsequent investigation confirmed that no viral CP and HC-Pro gene expression was detected in two SMV-resistant lines of *SMV-CP*(RNAi) and three lines of *HC-Pro*(RNAi) transgenic plants, respectively. On the other hand, non-transgenic plants and other lines showed viral RNA expression. Viral symptoms affected seed morphology, and clean seeds were harvested from SMV-resistant line of *SMV-CP*(RNAi) and *HC-Pro*(RNAi) transgenic plants. In addition, strong viral gene expression was detected from seeds of SMV-susceptible non-transgenic plants and SMV-susceptible transgenic lines. When compared the viral resistance between *SMV-CP*(RNAi) and *HC-Pro*(RNAi) transgenic plants, soybean transgenic plants with the *HC-Pro* gene using RNAi strategy showed much stronger and higher frequency of viral resistance.

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PC-58

Characterization of Dihydroflavonol 4-Reductase (*DFR*) Genes in Association with Cold and Freezing Stress in *Brassica rapa*

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Flavonoids including anthocyanins provide flower and leaf colors and other derivatives that play diverse roles in plant development and interactions with the environment and dihydroflavonol 4-reductase (*DFR*) is part of an important step in the flavonoid biosynthesis pathway of anthocyanins. This study characterized 12 *DFR* genes of *Brassica rapa* and investigated their association with anthocyanin coloration, cold and freezing tolerance in several genotypes of *B. rapa*. Sequences of these genes were analyzed and compared with *DFR* gene sequences from other species and a high degree of homology was found. Constitutive expression of them in several pigmented and non-pigmented lines of *B. rapa* showed a correlation with anthocyanin accumulation only for *BrDFR8* and *9*. Conversely, *BrDFR* genes also showed responses to cold and freezing stress treatment in *B. rapa*. *BrDFRs* were also shown to be regulated by two transcription factors, *BrMYB2-2* and *BrTT8*, contrasting with anthocyanin accumulation and cold and freezing stress. Thus, the above results suggest the association of these genes with anthocyanin biosynthesis and cold and freezing stress tolerance and might be useful resources for development cold and/or freezing resistant *Brassica* crops with desirable colors as well. The findings presented here may also help explore the molecular mechanism that regulates anthocyanin biosynthesis and its response to abiotic stress at the transcriptional level in plants.

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PC-59

The overexpression of *PagBEE3* promotes growth, biomass production and proliferation of xylem cells in poplar

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Brassinosteroids (BRs) play important roles in many aspects of plant growth and development. BR-induced *AtBEE3* (*brassinosteroid enhanced expression 3*) is required for a proper BR response in *Arabidopsis*. Here, we identified a poplar (*Populus alba* x *P. glandulosa*) *BEE3* homolog encoding a putative basic helix-loop-helix (bHLH)-type transcription factor through microarray analysis. Transcripts of *PagBEE3* were mainly detected in stems, with the internode having a low level of the transcripts and the node having a relatively higher level. The function of the *PagBEE3* gene was investigated through the phenotypic analyses with *PagBEE3*-overexpressing (ox) transgenic lines. This work mainly focused on a potential role of *PagBEE3* in stem growth and development of poplar. The *PagBEE3*-ox poplar showed thicker and longer stems than wild-type plants. The xylem cells from the stems of *PagBEE3*-ox plants revealed remarkably enhanced proliferation, resulting in an earlier thickening growth than wild-type plants. Microarray analysis revealed that the expression of many genes involved in xylem cell proliferation and development was altered in the *PagBEE3*-ox plants. Therefore, this work suggests that xylem development of poplar is accelerated in *PagBEE3*-ox plants and *PagBEE3* plays a role in the stem growth by increasing the proliferation of xylem cells to promote the initial thickening growth of poplar stems.

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PC-60

Genome-wide analysis of the Shaggy-like kinase genes in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*)

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Shaggy-like kinases (SKs), also known as Glycogen synthase kinase 3 (GSK3) proteins, play many important roles in cellular signaling in animals, fungi and amoebae. In particular, SKs participate in key developmental signaling pathways and also regulate the cytoskeleton. SKs -encoding genes are also present in all land plants and in algae, raising questions about possible ancestral functions in eukaryotes. Unlike in animals and *Dictyostelium*, land plant SKs are encoded by relatively large multi-gene families whose members share high sequence similarity. Along with the studied 10 ASKs (*Arabidopsis* shaggy-like kinases) indicate that plant SK proteins are actively implicated in hormonal signalling networks during development as well as in biotic and abiotic stress responses. In this study, 18 *BrSKs* are identified from Chinese cabbage, and they are classified into four groups according to the classification of *Arabidopsis*. The characterization, classification, gene structure and phylogenetic construction of *BrSK* proteins are performed. Distribution mapping shows that *BrSKs* are absent in A02 and A10 chromosome. 8 orthologous gene pairs are shared by Chinese cabbage and *Arabidopsis*. The expression patterns of *BrSK* genes exhibit differences in five tissues based on RNA-seq data in public data base. Specially, *BrSK β -1* and *BrSK β -2* show floral buds specifically expressed, which indicate that *BrSK β* may play a key role during flower or pollen development. We demonstrated that suppression of *Arabidopsis* orthology of *BrSK β* impaired the late pollen in *Arabidopsis* plants. Taken together, our analyses provided insights into the characterization of the *BrSK* genes in Chinese cabbage, providing foundation of further functional studies of those genes. [This work was supported by a grant from the Next-Generation BioGreen 21 Program (the Next-Generation Genomics Center No. PJ008118), Rural Development Administration, Republic of Korea]

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PC-61

Screening the Tomato Yellow Leaf Curl Virus Resistance Gene *Ty-3* in tomato (*Solanum lycopersicum*)

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Tomato yellow leaf curl disease is a devastating disease of tomato (*Solanum lycopersicum*), which is caused by begomoviruses generally referred to as tomato yellow leaf curl virus (TYLCV). The breeding for TYLCV resistance has been based on the introgression of the *Ty-3* resistance locus. Knowledge about the exact location of the *Ty-3* on tomato chromosome 6 is needed to understand the genomic organization of the *Ty-3* locus. In this study, we conducted a genetic analysis using a segregating population derived from a cross between resistant accession *S. lycopersicum* "A45" and susceptible accession *S. lycopersicum* "A39". The F1 plants showed resistance to TYLCV and F1 was self-pollinated to produce F2 progeny. To screen the TYLCV resistance in 145 F2 plants, a leaf agroinfiltration method was used. F2 plants showed a classical Mendelian segregation (106 resistance : 39 susceptibility) for resistance to TYLCV respectively. SCAR and CAPS markers linked to the *Ty-3* were tested for genotyping F2 plants and genotyping and agroinfiltration results were cosegregated in the newly developed F2 population.

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PC-62

Variation of sugar accumulation and gene expression of transcription factors at different stages of *Allium cepa* under long and short photoperiod condition

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Onion is one of the most widely consumed vegetables. There are many cultivars, which are grouped according to skin color as yellow, white or red. Onions can also be classified as sweet or non-sweet. Their importance in cooking comes from their typical taste and flavour. The sugars, pyruvic acid accumulation and transcript level of some transcription factors involved in the biosynthesis of high sugars and pyruvic acid was analyzed at different stages of bulb onion (*Allium cepa*) growing under light and dark condition using High Performance Liquid Chromatography (HPLC) and Quantitative real time PCR. A genetic map and cultivar lines 36101 and 36122 were used to identify transcription factors controlling pungency and sugar. We compared 2 different lines for low pungency and high sugars during water and photoperiod stress, which showed significant positive phenotypic and genetic correlations. These results could be presumably used as useful information to obtain onion varieties rich in sugars.

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PC-63

A Map-based Cloning Approach for the Identification of a Low Temperature Sensitive Gene *sy-2* in Chilli pepper (*Capsicum chinense*)LiLiu¹, Jin-Ho Kang¹, Yeong Deuk Jo¹, Sota Koeda², Munetaka Hosokawa², Doil Choi³, Byoung-Cheorl Kang^{1*}¹Department of Plant Science and Plant Genomics and Breeding Institute, Seoul National University, Seoul 151-921, Korea²Department of Agronomy and Horticultural Science, Graduate School of Agriculture, Kyoto University, Sakyo-ku, Kyoto 606-8502, Japan³Department of Plant Science, College of Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea

sy-2 (*Seychelles-2*) is a temperature sensitive 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 lower than 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 of 1,010 F₂ plants derived from crossing *sy-2* and the wild type *C. chinense* 'No.3341'. *sy-2* gene is located on chromosome 1, 0.3 cM and 0.1cM away from cosII markers C2_At4g29120 and C2_At1g09070, respectively. The tomato genome sequence between those two markers was compared with pepper genome sequence. We found three of pepper scaffold sequences in this region. We developed seven single nucleotide polymorphism (SNP) markers on the pepper scaffold sequences, among which five SNP markers were co-segregated with *sy-2*. To fill the gap between the scaffolds which contains co-segregating markers, we screened a bacterial artificial chromosome (BAC) library, and end-sequences of total of 22 AC clones were identified. We found that five clones were overlapped to cover the gap. We fully sequenced four AC clones and found that the physical distance between C2_At4g29120 and C2_At1g09070 is 343kb. This region contains 70 putative genes such as HSP90-like ATPase family proteins, lipid-transfer proteins, calmodulin-domain protein kinases, and zinc finger proteins (ZFPs). To identify the *sy-2* gene, we performed RT-PCR and found that a ZFP-like gene is differentially expressed between WT and *sy-2* leaves. This result suggests that the ZFP-like gene is a strong candidate for the *sy-2* gene. We are currently characterizing this candidate gene.

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PC-64

Development of EST-SSR markers for toxic and non-toxic jatrophas

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Toxic (high phorbol esters) and nontoxic (low phorbol esters) jatropha accessions cannot be distinguished morphologically. Their seeds must be chemically analyzed through a complex and costly process using HPLC method. EST-SSR markers can be used to classify jatropha accessions with high and low phorbol esters. In this study, ninety-seven EST-SSR markers amplified the genomic DNA and showed polymorphism among 5 high phorbol esters accessions and 10 low phorbol esters accessions. These markers can be further exploited for jatropha improvement through marker-assisted breeding.

Keywords: EST-SSR, jatropha, phorbol esters

PC-65

Gene Identification and Molecular Marker Development Related to High-Temperature Tolerance in Cabbage

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To select genes associated with the high-temperature tolerance from *Brassica*, two transcriptomic analyses have been used: microarray and RNA Seq. Using two contrasting inbred lines of *B. rapa*, Chiifu and Kenshin, version 3 microarray (135 K microarray) was conducted to RNA samples extracted from series of 45°C-treated leaves and 29 genes were selected for genomic DNA cloning of cabbage. Of 29 genes, 8 genes contain 40 SNPs, 11 SSRs and 23 In-Del markers that distinguish high-temperature tolerant and susceptible cabbages, BN1 and BN2. These 8 genes include a unknown gene, *AP2*, *SMP*, *FBD*, *SKP2B*, *IAA16*, *HSP21* and *OLI2-2*. We also selected 16 cabbage genes from RNA Seq analysis using two inbred lines, BN1 and BN2: 5 genes for BN1-high expression, 5 genes for BN1-specific expression, 5 genes for BN2-specific expression, and *BoCaMB*. Using RNA sequences, genomic DNAs corresponding to 16 genes have been clones and analyzed to find out molecular markers. Markers were further transformed into PCR-based marker and confirmed with additional cabbage genetic lines. We are currently transforming PCR-makers into SNP markers. To examine function of high-temperature tolerant genes, we also transformed 5 genes into *Arabidopsis* plants. We will describe detailed methods and results in a poster. [This work was supported by a grant from the Next-Generation BioGreen 21 Program (the Next-Generation Genomics Center No. PJ009085), Rural Development Administration, Republic of Korea]

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PC-66

양배추 자색관련 분자마커 개발을 위한 안토시아닌 합성관련 유전체 분석

문명일¹, 노일섭², 허윤강^{1*}¹대전광역시 유성구 충남대학교 생명과학과²전라남도 순천시 순천대학교 원예학과

양배추 엽색을 결정하는 주요한 요인은 안토시아닌의 합성 유무 또는 축적된 양의 차이에 기인한다. 양배추의 엽색 관련 분자마커 개발을 위하여 안토시아닌 색소의 축적이 다른 양배추 계통을 이용하여 RNA Seq을 수행하고 분석하였다. 양배추 시료는 자색양배추, 녹색양배추, 저온에서 안토시아닌 발현되는 양배추, 저온에서 안토시아닌 발현이 없는 양배추를 각 2종씩 사용하여 색 관련 유전자 마커의 선별과 분류를 용이하게 하였다. RNA Seq 데이터 분석을 통해 안토시아닌 합성관련 유전자의 발현 양상을 확인한 결과 자색양배추에서 *MYB2*, *TT8*, *F3'H*, *DFR*, *ANS* 유전자의 발현이 많았다. 또한 RNA Seq 데이터를 기반으로 SSR 마커로 활용가능한 프라이머 45개 세트를 선별, 작성하고 PCR방법으로 검정한 결과 9개의 프라이머 세트를 선별하였다. 그 중 1개를 양배추 F1 품종을 대상으로 검정하여 자색양배추 또는 저온에서 자색을 나타내는 양배추를 구분할 수 있었다. 안토시아닌 합성과 관련된 상류유전자와 구조유전자들의 게놈 구조를 분석하고 상류유전자 18개, 구조유전자 15개의 염기서열을 분석하기 위해 각각 33개, 21개 프라이머 세트를 작성하였다. 염기서열 분석한 결과, *F3'H*, *DFR*, *MYB2*, 유전자에서 총 10개의 SNP(Exon 4개, Intron 6개)와 1개의 SSR(Intron)을 발굴하였다. [본 연구는 농림축산식품부-해양수산부-농촌진흥청·산림청 Golden Seed 프로젝트 사업(원예종자사업단, 과제번호 : 213003-04-2-SB230)에 의해 이루어진 것임]

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PC-67

Relationship Between Heterosis and Genetic Distances based on SSR markers in *Allium Cepa* L.Sunyoung Lee^{*}, Jinseong Moon, Injong Ha, HaeJoon Hwang and Hyeonyeol Shin

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This study was carried out to analyze correlation between heterosis of F1 hybrids and the genetic distance of parental lines. Growth characteristics such as number of leaves, plant height, bulb diameter, bulb height, bolting rate and marketable yield were examined in 15 F1 hybrids. The genetic distance among one male sterile line and fifteen restorer lines were analyzed with SSR markers. 21 primer pairs amplified polymorphic band and the average number of polymorphic allele was 3.4. As a result of UPGMA cluster analysis, the similarity coefficient value among parental lines ranged from 0.43 to 0.63. Combination of M1 and R14 is high similarity and number of leaves, plant height and yield are 10.2, 66.7cm and 6,818kg·10a⁻¹. The case of the lowest value combination, they are 9.0 and 63.7cm and 7,728kg·10a⁻¹, respectively. The results showed that there are no significant correlations between genetic distance and heterosis of F1 hybrids and only molecular marker does not predict growth traits and yield of onion.

Keywords: *Allium cepa* L., SSR, genetic distance, heterosis

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PC-68

Cambial Meristematic Cell Specific Homologous Gene, *At1G71110* May Play a Role in R Gene Mediated Defense Signaling Pathway

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Cambial meristematic cells (CMCs) are innately undifferentiated cells located in the meristems of plant with function as a stem cell to renew itself or replace specialized tissues. Another interesting feature of plant stem cells is controlling the plant defense in response to various stresses. Several groups have studied for stem cell triggered immunity signaling however, the molecular basis of the stem cell triggered immunity remains unclear. We previously obtained differentially expressed 563 stem cell specific gene profiles from transcriptome analysis between two different cell types, CMC and dedifferentiated cells (DDCs) of yew tree (*Taxus cuspidate*). In a line of comparative genomics approach, we have selected 30 Arabidopsis homologous immune regulator candidate genes that showed significantly enriched GO terms ; at “response to stress” and “defense response”. We obtained one of homologous knock-out (KO) Arabidopsis mutant line on the locus *At1G71110* whose cognate yew homologous gene showed predominantly expressed in CMCs compared to DDCs (20 times higher). For the assessment of basal disease resistance KO mutant plants were inoculated with *Pseudomonas syringae* pv. *tomato* (*Pst*) DC3000 and counted pathogen isolated from inoculated leaves. Interestingly, the KO mutant plants were not compromised in basal disease resistant, however, the hypersensitive response was significantly enhanced in the mutant compared to wild type in response to *Pst*avrB, suggesting R-gene mediated defense response involved. We also investigated their response to the small reactive redox molecules such as reactive oxygen species (ROS) and reactive nitrogen species (RNS) that associated significantly in plant immune response. Notably the KO mutant plants exhibited hypersensitivity specifically under nitrosative stress condition derived by S-nitrosylglutathione (GSNO), anitrioxide (NO) donor. Taken all together, putative endomembrane components *At1G71110* may play a pivotal role in R gene mediated plant immune system. To further investigate its role(s) and molecular signaling network various defense gene expression profiles and functional genomics approach are ongoing for the long term aim of multi-stress tolerant crop development

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PC-69**Variation and haplotypes in *LOX1*, *LOX2*, and *LOX3* genes related to the seed longevity in rice**Sun-Kyung Min¹, Aye Aye Khaing¹, Win Htet Oo¹, Tae-Sung Kim¹, Yong-Jin Park^{1,2*}¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340-702, Republic of Korea²Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340-702, Republic of Korea

Rice is the most important staple food crop of almost half of the world's population. In rice, seed longevity is major factor for production and storage potential of seeds. But it is faced with grain degradation and loss of seed viability. Lipoxygenases(LOX) are a family of enzymes related to the seed longevity. LOX activity in rice grain is present in a bran-milling fraction. It is also observed that rice embryos contains three isozymes activities, Lox1, Lox2 and Lox3. Among those, the Lox3 isozyme is known as the major component in the embryonic tissue. In this study, genetic structure variability of three seed longevity related genes, Lox1, Lox2 and Lox3 were examined by using whole-genome resequencing data of 137 accessions of rice core set. The new SNPs and InDels in the exon regions identified through haplotyping analysis would be useful to develop new varieties with improved storage ability of rice in the future molecular breeding.

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PC-70**Development of Isaac and CACTA derived Ti-SCARs in Maize**Neha Roy¹, Ji-Young Choi¹, Sung-Il Lee¹, Min-Ji Lim¹, Kyong-Cheul Park², and Nam-Soo Kim¹¹Department of Molecular Bioscience²Department of Agricultural Life Science, Kangwon National University, Chuncheon 200-701, Korea

Transposon elements are widely distributed in the plant genomes. Maize genome consists of various transposable elements that constitute as much as 80% of the genome. Transposon display (TD) is a modified from AFLP, and can be used to generate and display hundreds of genomic fragments affixed to transposons, consequently tagging transposons. We developed maize specific transposon insertion- sequence characterized amplified regions (Ti-SCAR) using Isaac and CACTA transposons. Currently, we have developed 58 dominant Ti-SCAR markers. Validation of the Ti-SCARs is being carried out using a various maize germplasm. Since AFLP is tedious and unsuitable for large scale application in MAS, the Ti-SCAR markers displayed simple binary presence or absence pattern. Thus, the Ti-SCARs can provide a fast, cheap and reliable PCR based assay. A pipeline in developing the Ti-SCAR will be presented in the poster.

PC-71

Over-expression of PsGPD, a mushroom glyceraldehyde-3-phosphate dehydrogenase gene, enhances salt tolerance in rice plants

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Transgenic potatoes expressing glyceraldehyde-3-phosphate dehydrogenase (*GPD*), isolated from the oyster mushroom, *Pleurotus sajor-caju*, had increased tolerance to salt stress (Jeong et al. 2001). To examine the physiological mechanisms enhancing salt tolerance in *GPD* transgenic rice plants, the salt tolerance of five *GPD* transgenic rice lines (T1-T5) derived from Dongjin rice cultivar was tested in a fixed 150-mM saline environment in comparison to two known wild-type rice cultivars, Dongjin (salt sensitive) and Pokali (salt tolerant). Transgenic lines T2, T3, and T5 showed a substantial increase in biomass and relative water content compared to Dongjin. Stomatal conductance and osmotic potential were higher in the *GPD* transgenic lines and were similar to those in Pokali. The results are discussed based on the comparative physiological response of *GPD* transgenic lines with those of the salt-sensitive and salt-tolerant rice cultivars.

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PC-72

배추과 채소의 Core Collection 소포자배양을 통한 소재개발

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네덜란드 와게닝건대학 식물육종연구실에서는 배추과 채소들을 형태적 지리적 근원을 찾아 대표 형태형을 나타내는 수집단을 분류하는 Core Collection 연구가 이루어지고 있다. 배추과 채소들은 대부분 Heterogeneous 하고, Heterozygous 하기 때문에 본 실험실에서는 와게닝건 대학으로부터 배추과 채소 중 8개의 형태형을 나타내는 19계통 (Chinese Cabbage 3계통, Chinese Turnip Cabbage 2계통, Pak Choi 3계통, Turnip 5계통, Broccolieto 3계통, Mizuna 1계통, Komatsuna 1계통, Turnip green 1계통)을 분양 받아서 소포자배양을 진행 하였다. 소포자배양을 진행한 결과, 8 가지 종들 중, Komatsuna 와 Turnip Green을 제외한 6종에서 모두 배의 발생을 유도 할 수 있었고, 유도된 배들은 식물체로의 재생을 위해 MS배지에 옮겨졌고, 토양순화, 저온처리 의 과정을 거쳤다. 이들 6종들 중 Broccolieto를 제외한 5종에서 채종이 가능하였다. 배추과 채소의 Core Collection을 위한 19계통의 소포자배양 결과, 10계통에서 배가 유도되었으며, 발생된 배의 개체 수에는 차이가 크게 나타났으나, MS 배지로 옮겨진 배들은 10계통 모두에서 정상적인 뿌리를 형성한 Adventitious shoot가 재생되었고, 토양에 4주 이상 적응한 식물체를 획득할 수 있었다. 10 계통 중 2계통을 제외한 8계통이 4주 동안 저온처리의 과정에 적응하였고, 이들 중 7계통에서 채종과정을 거쳐 종자생산에 성공하였다.

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PC-73

강낭콩 유전자원의 종피 색에 따른 항산화 활성 비교

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경상남도 밀양시 내이동 국립식량과학원 기능성작물부 두류유지작물과

본 연구는 강낭콩(*Phaseolus vulgaris*, PV)의 종피 색에 따른 항산화 활성 차이를 알아보고자 수행하였다. 유전자원에 따른 16가지의 강낭콩을 적색 3종, 황색 1종, 적색얼룩무늬 3종, 흰색 얼룩무늬 1종, 회갈색얼룩무늬 2종, 흰색 2종, 회갈색 2종, 흑색 2종으로 총 8가지 색으로 나누어 진행하였다. 연구결과를 요약하면 16가지 강낭콩을 콩 전체, 콩 종피 그리고 종피를 제외한 콩으로 분리하여 각각 80% 메탄올에 48시간 추출하였다. 추출 후 원액을 필터하여 실험에 사용하였다. 강낭콩에서 종피가 차지하는 비율은 6.93 ~ 10.20%이었으며, 총 폴리페놀 함량은 종피에서 7.05~180.33mg GAE/mL, 콩 전체에서 17.96~61.23mg GAE/mL, 그리고 콩 알맹이 16.58 ~ 22.24mg GAE/mL이었다. 종피 추출물에서 PV-151(적색얼룩무늬)이 180.33mg/mL로 가장 높은 폴리페놀 함량을 보였고, PV-132(회갈색)에서 164.67mg/mL, PV-78(회갈색얼룩무늬)에서 158.36mg/mL, PV-133(회갈색얼룩무늬)에서 158.19mg/mL, PV-126(적색)에서 147.93mg/mL, PV-343(흑색)에서 121.49mg/mL으로 나타났다. 흰색 강낭콩은 폴리페놀 함량이 미비하였다. DPPH 라디칼 소거능은 종피 추출물 2.5배 희석 하였을 때, PV-151(적색얼룩무늬), PV-343(흑색), PV-78(회갈색얼룩무늬), PV-132(회갈색)에서 90%이상 소거능을 보였으며 농도 의존적으로 활성이 감소하는 것을 확인하였다. ABTS 라디칼 소거능은 종피 추출물을 10배 희석 하였을 때, PV-78(회갈색얼룩무늬)가 88.16%, PV-132(회갈색)가 81.29%, PV-151(적색얼룩무늬)가 95.26%, PV-343(흑색)이 80.11%의 소거능을 보였다. 이상의 결과로 보아 색이 다른 강낭콩 종피마다 가지고 있는 폴리페놀 함량이 다르며 각각 다른 항산화 활성을 나타냈다. 적색얼룩무늬, 회갈색얼룩무늬, 회갈색 그리고 흑색처럼 강낭콩 종피의 색이 진할수록 총 폴리페놀 함량과 더불어 항산화 활성이 높은 것으로 나타났다.

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PC-74

Development of molecular markers for selection of green rice leafhopper (*Grh1*)-resistant rice varietySoo-Kwon Park^{1*}, Woon-Ha Hwang¹, Dong-Jin Shin¹, Yeon-Jae Hur¹, Tae-Heon Kim¹, Sang-Ik Han¹, Jun-Hyun Cho¹, Jong-Hee Lee², Ji-Yoon Lee¹, Min-Hee Nam¹ and Dong-Soo Park¹¹Department of Functional Crop, NICS, Miryang, 627-803, Republic of Korea²Research Policy Bureau, RDA, Suwon, 441-707, Republic of Korea

Green rice leafhopper(GRH), *Nephotettix cincticeps* Uhler, is one of the major insect pests of rice (*Oryza sativa* L.) in the temperate growing region of East Asia. GRH sucks sap from both xylem and phloem of susceptible rice varieties, and increased GRH populations cause sooty mold disease on the ears of rice after heading stage. In addition to direct plant destruction, GRH also causes damage to rice plants by transmitting rice dwarf viruses causing rice dwarf viruses disease which could decrease the yield of rice. Development of GRH resistant rice varieties for reducing yield loss is an important objective in current breeding programs. In this study, we developed three SSR markers(RM18166, RM516, RM18171) and one Indel marker(Indel15040) which could select *Grh1*-resistant varieties using population derived from cross lines between *Grh1*-resistant variety 'Singwang' which contains *Grh1* gene and susceptible variety 'Ilpum'. PCR products of RM18166 which was one of the developed markers were easily detected in agarose gel. These markers will be useful for development of the *Grh1*-resistant varieties through marker-assisted selection(MAS) without bio-examination in rice breeding.

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PC-75

Characterization and expression profiling of MADS-box genes related to organ development and stress resistance in *Brassica rapa*

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MADS-box transcription factor (TF), primarily involved in the floral organ specification with other several aspects of plant growth and development. Whole genome survey of *B. rapa* revealed 167 MADS-box genes and categorized into MIKC^c, MIKC^{*}, M α , M β and M γ groups based on phylogeny, protein motif structure and exon-intron organizations. MIKC^c group belongs 89 genes, which is the highest in number than in any other crops till date. The MIKC^c group has further classified into 13 sub-families. In case of chromosomal localization, remarkably 57 MIKC^c type MADS-box genes were found in the duplicated segments of *B. rapa* genome, whereas only 4 M-type genes have resulted from tandem duplications. Besides floral and vegetative tissue expression we also identified MADS-box genes with their male and female gametophyte specific expression in different stages of flower bud development. Furthermore, from a low temperature treated whole genome microarray data set 19 BrMADS genes were found to show variable transcript abundance in two contrasting double haploid lines of *B. rapa*. Subsequently, the responsive genes were investigated under three abiotic stresses where they showed differential and corresponsive expression patterns. An extensive annotation and transcriptome profiling undertaken in this study might be useful for understanding the involvement of MADS-box genes in stress resistance besides their growth and developmental functions, which ultimately will provide the basis for functional characterization and exploitation of the candidate genes in the genetic engineering study of *B. rapa*.

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PC-76

Functional characterization of *GmWRKY* (*Glycine max WRKY*) genes induced during abiotic stress conditions

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Comparative time-course expression analyses were carried out to analyze the expression levels of 60 soybean WRKY genes during abiotic stress in order to search for the stress-inducible WRKY genes. Five *GmWRKY*(*Glycine max WRKY*) genes having the significant differential expression in response to the drought stress and abscisic acid(ABA) hormone application were further investigated for their expression profiles with various stresses such as drought, high salinity, cold and with ABA treatments by the quantitative real-time PCR analyses. In this research, the full-length cDNAs of five *GmWRKY* were isolated for the further studies. Five *GmWRKY* proteins were tested for their transcription activation in the yeast assay system. *GmWRKY3* proteins showed the very high transcriptional activities and the other two *GmWRKY* proteins displayed moderate levels of transactivation while the remaining two *GmWRKY* proteins lacked transactivation in yeast. Subcellular localization of five *GmWRKY* proteins was analyzed via the green fluorescent protein-*GmWRKY* fusion protein in tobacco plant cell and all of *GmWRKY* proteins were targeted to the nucleus. In order to analyze the function of *GmWRKY* genes in plant, *35S:GmWRKY* overexpression(OE) transgenic *Arabidopsis* were generated. Root growth and germination rates in transgenic OE plants were investigated in the media supplemented with mannitol, NaCl or ABA compared with that of wild-type(WT) plants. The *35S:GmWRKY42* transgenic *Arabidopsis* displayed reduced tolerance to drought stress compared to the WT. The results of this systematic analysis of the *GmWRKY* family responsive to abiotic stress will provide novel tools and resources for the development of improved drought tolerant transgenic soybean cultivars.

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PC-77

Molecular cloning and characterization of soybean (*Glycine max*) NAC transcription factor genes induced by abiotic stress

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The plant-specific NAC (NAM, ATAF, and CUC)-domain proteins play important roles in plant development and stress responses. Comparative time-course expression analyses were carried out to analyze the expression levels of 62 soybean NAC genes during drought stress in order to search for the stress-inducible NAC genes. Ten *GmSNAC* (*Glycine max* stress-inducible NAC) genes having the significant differential expression in response to the drought stress and abscisic acid (ABA) hormone application were further investigated for their expression profiles with various stresses such as drought, high salinity, cold and with ABA treatments by the quantitative real-time PCR analyses. In this research, the full-length cDNAs of eight *GmSNAC* were isolated for the further studies. Eight GmSNAC proteins were tested for their transcription activation in the yeast assay system. Two GmSNAC proteins showed the very high transcriptional activities and the other two GmSNAC proteins displayed moderate levels of transactivation while the remaining four GmSNAC proteins lacked transactivation in yeast. Subcellular localization of eight GmSNAC proteins was analyzed via the green fluorescent protein-GmSNAC fusion protein in tobacco plant cell. Three GmSNAC proteins with the C-terminal transmembrane domain were localized to the nucleus and cytoplasmic fractions. The other five GmSNAC proteins were targeted to the nucleus. The function of *GmSNAC49* gene was further investigated using the overexpression transgenic *Arabidopsis*. Germination rate in transgenic plants over-expressing *GmSNAC49* was delayed in the media supplemented with mannitol or ABA compared with that of wild-type (WT) plants. The 35S:*GmSNAC49* transgenic *Arabidopsis* displayed improved tolerance to drought stress compared to the WT. The results of this systematic analysis of the *GmSNAC* family responsive to abiotic stress will provide novel tools and resources for the development of improved drought tolerant transgenic soybean cultivars.

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PC-78

Molecular characterization of heat shock transcription factor gene family in *Glycine max*

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Heat shock transcription factors(HSFs) are the major heat shock factors regulating the heat stress response. They participate in regulating the expression of heat shock proteins (HSPs), which are critical in the protection against stress damage and many other important biological processes. In this study, a genome-wide analysis was carried out to identify all HSFs soybean genes. Twenty six nonredundant HSF genes(*GmHsf*) were identified in the latest soybean genome sequence. Chromosomal location, protein domain and motif organization of *GmHsf*s were analyzed in soybean genome. The phylogenetic relationships, gene duplications and expression profiles of *GmHsf* genes were also presented in this study. According to their structural features, the predicted members were divided into the previously defined classes A-C, as described in Arabidopsis. Using RT-PCR, the expression patterns of 26 *GmHsf* genes were investigated under heat stress. The data revealed that these genes presented different expression levels in response to heat stress conditions. Real-time (q)RT-PCR was performed to investigate transcript levels of five *GmHsf*s in response to multiple abiotic stresses. Differential expression of five *GmHsf*s implies their role during abiotic stresses. Subcellular localization using GFP-fusion protein demonstrated that *GmHsf12* and *GmHsf34* were restricted to the nucleus and *GmHsf28* was localized in the nucleus and cytoplasm in plant. The results provide a fundamental clue for understanding of the complexity of the soybean *HSF* gene family and cloning specific function genes in further studies and applications.

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PC-79

국내 밀 품종의 수발아 저항성관 관련 표지인자의 상관관계 분석

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국내 밀 품종의 수발아 특성을 2009년부터 2013년까지 5년간 조사하였으며, 이러한 특성을 관련 표지인자 (*TaVp-1A*, *TaSdr-B1a*와 *TaPHS1*)와 상관관계를 분석하였다. 이러한 결과를 토대로 국내 밀 육종 프로그램에서 수발아 저항성 밀 계통 선발에 이용하고자 하였다. 국내 밀 품종의 수발아 특성은 모래물이법으로 측정하였으며, 수발아 특성은 품종 및 년차간 변이와 이들간의 상호작용에 영향을 받는 것으로 나타났다. 국내 밀 품종의 수발아율은 1.57%에서 84.38%으로 나타났으며, 적립계 밀 품종의 수발아율은 11.39%로 백립계 밀 품종 (62.24%)보다 낮게 나타났다. 국내 밀 품종의 *TaVp-1A* allele는 5 종류가 나타났지만 이들의 변이는 수발아율과 상관성이 없는 것으로 나타났다. 국내 밀 품종의 *TaSdr-B1a* 와 *TaSdr-B1b* allele 발현 빈도는 각각 79.2% 와 20.8%로 나타났으며, *TaSdr-B1a* allele를 지닌 품종의 수발아율은 16.50%로 *TaSdr-B1b* allele를 지닌 품종 (52.99%) 보다 낮아서 저항성이 있는 것으로 생각된다. 국내 밀 품종의 *TaPHS1* allele 변이는 2개의 haplotype (I 과 II)이 나타났으며, haplotype III는 국내 밀 품종에서 나타나지 않았다. haplotype I 과 II의 수발아율은 각각 27.19% 와 20.45%로 품종 간에 차이가 나타나지 않았다.

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PC-80

국내 밀 품종의 수발아 저항성 증진을 위한 종실 무게 및 관련 표지인자의 상관관계 분석

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본 연구에서는 국내 밀 품종의 수발아 저항성 증진을 위하여 germination index와 종실 특성(종실 길이, 폭, 두께, roundness, 리터중과 천립중)을 2010년부터 2013년 까지 4년간 조사하였다. 또한, 종실 무게와 상관이 있는 것으로 알려진 표지인자인 *TaSus2-2B*, *TaGW2-6A*와 *TaCwi-1*의 유전변이 분석을 실시하였다. 이를 통하여 종실 특성이 국내산 밀 품종에 있어서 수발아 저항성과 상관관계를 분석하였으며, 이어한 결과를 통하여 국내 밀 육종 프로그램에 있어서 수발아 저항성 밀 계통 선발의 지표로 이용하고자 하였다. 종실 길이, 폭, 두께, roundness, 리터중과 천립중 및 germination index는 품종, 년차간 변이 및 이들의 상호작용에 영향을 받는 것으로 나타났으며, germination index는 천립중, 종실 길이, 폭과 두께와 정의 상관을 보였다. 특히, 수발아에 취약한 백립계 품종은 적립계 품종에 비하여 종실의 길이, 폭과 두께 및 천립중이 높은 것으로 나타났다. *TaSus2-2B*의 *Hap-L* haplotype을 지닌 품종의 germination index는 0.61로 *TaSus2-2B*의 *Hap-H* haplotype을 지닌 품종의 germination index (0.18) 보다 높아서 수발아에 취약한 것으로 나타났다. *TaGW2-6A-G* haplotype을 지닌 품종의 천립중은 44.62 g으로 *TaGW2-6A-A* haplotype을 지닌 품종의 천립중 (39.75 g)보다 높게 나타났지만, 이러한 결과는 germination index와는 상관이 없는 것으로 나타났다. *TaCwi-1a* allele를 지닌 적립계 밀 품종은 *TaCwi-1b* allele를 지닌 품종 보다 리터중이 높은 것으로 나타났으며, *TaCwi-1a* allele를 지닌 백립계 품종은 *TaCwi-1b* allele를 지닌 품종에 비하여 종실의 길이와 두께 및 천립중이 높게 나타났다.

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PC-81

The complete chloroplast genome sequence of *Solanum nigrum* and comparative analyses with other four solanaceous genomes

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Solanum nigrum is one of useful sources for improving resistance to several diseases in potato (*S. tuberosum*). For enhancing late blight resistance, introgression of late blight resistance from *S. nigrum* was attempted into the cultivated potatoes using somatic hybridization due to their sexual incompatibility. Therefore, we sequenced the chloroplast genome of *S. nigrum* and compared it with those of *Nicotiana tabacum*, *S. bulbocastanum*, *S. tuberosum* and *S. lycopersicum*. The complete sequence of the chloroplast genome of *S. nigrum* consists of 155,432 bp in length including a pair of inverted repeat regions (Ira, Irb) of 25,589 bp each, a small single copy region of 18,402 bp and a large single copy region of 85,852 bp. The genome contains 107 genes. A comparison of chloroplast genome of five solanaceous species revealed that the gene contents and their relative positions of *S. nigrum* are similar to the other four species. Detailed comparison identified 35 indels, including 22 insertion and 13 deletion, in the intergenic and intragenic regions. The phylogenetic tree of chloroplast sequences of five solanaceous species shows that *S. nigrum* is located at a same node with *N. tabacum* and is secondly close to *S. lycopersicum*. A sister clade with *S. bulbocastanum* and *S. tuberosum* is the farthest. The results obtained in this study will facilitate the development of PCR-based markers to select somatic fusion products.

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PC-82

Two Dimensional Code System Using Genome-wide InDel Markers for Rice Cultivar Identification

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Sequence diversity was accumulated through evolution and breeding process. A set of 595 PCR-based novel insertion/deletion (InDel) markers was designed in order to widen the genetic basis for national rice breeding programs. The markers were generated by analyzing of 40 Korean cultivars and published genome sequences of rice (*Oryza sativa* L. spp *japonica*). We selected 112 markers spread across all rice chromosomes among the 595 InDel markers, and they showed polymorphic between rice cultivars, which are 284 Korean japonica and Tongil varieties. Due to their simplicity in design and robustness in genotyping, these InDel markers have been routinely used in quantitative trait loci (QTL) mapping studies and marker assisted selection programs for rice. Moreover, the PCR amplification type of InDel markers was converged to digital code, 0 or 1 and then finally represented as one- and two dimensional bar-code system, which could easily differentiate genetically highly homologous japonica rice cultivars. The developed InDel markers uniquely discriminated among each of the Korean cultivars. Therefore, the systems we developed may be valuable tools in discrimination from cultivars.

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PC-83

애기장대 화분 표현형 분석 및 화분 발달에 관련된 변이체 유전자의 탐색

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비동형분열을 포함한 식물화분 발달과정에 관여하는 유전자를 탐색하기 위하여, Activation tagging vector를 이용하여 조성된 3,500여개의 애기장대 T1세대 약 3,500개의 형질전환체 집단으로부터 4종의 화분 변이형을 보이는 돌연변이체를 선발하였다. 4종의 변이체들은 20-40% 빈도의 성숙화분 변이표현형을 보였다. 변이체에서는 정상적인 화분으로 발달하지 않은 aborted pollen type, 한 개의 핵만이 관찰되는 tio type, 비정상적으로 분열된 gemini type 등 다양한 변이표현형들이 관찰되었다. TAIL-PCR을 통하여 T-DNA의 삽입부위의 염색체 부위를 동정하여, co-segregation 분석을 수행한 결과, 4종 모두 T-DNA 삽입과 무관한 자연발생적 돌연변이로 밝혀졌으며, 현재 map-based cloning 방법에 의해 변이유발 유전자를 탐색중이다. 이들 유전자들은 향후 식물의 화분발달에 핵심적인 역할을 하는 유전자를 발굴하고 이를 이용한 기작을 이해하는데 매우 유용한 정보를 제공할 것으로 판단된다.

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PC-84

Identification of the partial silk protein gene from the spider *Araneus Ventricosus* in rice.

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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. 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)_n, (GA)_n, and (GGX)_n, were conserved in the repetitive region of AvMaSp. Phylogenetic analysis further confirmed that AvMaSp belongs to the spider major ampullate spidroin family of proteins. The AvMaSp-R cDNA, which encodes the 240 amino acid repetitive domain, was expressed as a soluble 22 kDa polypeptide in baculovirus-infected insect cells. To produce transgenic rice plant with high contents of glycine and alanine, the prolamin promoter-driven AvDrag was introduced into rice plant via agrobacterium tumefaciens-mediated gene transformation. The introduction and copy number of the AvDrag gene in transgenic rice plants were determined by PCR and Southern blot analysis. AvDrag expression in transgenic rice seeds was examined by Northern blot and Western blot analysis. Immunofluorescence staining with the AvDrag antiserum revealed that the recombinant AvDrag protein were localized in transgenic rice seed. Furthermore, the amino acid content analysis showed that transgenic rice seeds were greatly increased in glycine and alanine as compared to controls.

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PC-85

Identification and characterization of *osgasd* gene in rice

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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 GeneBank. The *osgasd* mutant was sensitive to exogenous 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 sult 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 such as CPS, KO, KAO, GA 20 ox and GA 2 ox, 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. These results indicated that *OsGASD* gene is involved in GA biosynthesis factors, not only in the internodes, but also leaf length at the developing stage.

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PC-86

Overexpression of MYB4p enhance phosphate acquisition and increase Pi content in riceKi-Deuk Bae¹, Doh-Hoon Kim^{1*}¹Department of Genetic engineering, Dong-a University, Busan 604-714, Republic of Korea

The molecular processing of upstream regulation of Pi response genes during Pi starvation remains inadequately understood. R2R3 MYB transcription factors play regulatory roles in plant responses to various environmental stresses and nutrient deficiency. In this study, we isolated and designated OsMYB4P, an R2R3 MYB transcription factor, from rice under low-phosphate conditions. 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. To investigate the function of OsMYB4P in Pi-starvation signaling, we developed transgenic rice plants overexpressing OsMYB4P for analysis of Pi signaling and uptake. 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 lead to Pi accumulation and acts as a Pi-dependent regulator in controlling the expression of Pi transporters.

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PC-87

Development of salt-tolerant transgenic rice using *OsCBF4* cDNASo-Hyeon Baek^{1*}, Eun-Mi Lee¹, Man-Kee Baek¹, Woo-Jae Kim¹, Jong-Ho Park¹, Ki-Yong Ha¹, Hyun-Soon Kim¹, Young-Chan Cho¹, Jeom-Ho Lee¹¹National Institute of Crop Science, RDA, Iksan 570-080, Korea

This study was conducted to isolate a salt tolerant gene and to develop salt tolerant rice for reclaimed-saline areas through genetic transformation. A rice c/DRE binding factor 4(*OsCBF4*) cDNA was isolated from rice using RT-PCR. The full-length cDNA of the *CBF4* gene consists of 1,429 nucleotides and 274 amino acid residues. In order to develop salt tolerant rice, transgenic rice plants containing the *OsCBF4* gene were obtained via *Agrobacterium*-mediated transformation. The stable incorporation of the *OsCBF4* gene into rice genome was confirmed by PCR and Southern analysis. The stable expression of introduced gene was also validated by RT-PCR analysis in T₂ plants. Biological assay of T₃ progeny of the transgenic plants in Yoshida solution containing 120mM NaCl for 2weeks, confirmed that the *OsCBF4* confers salt tolerance to transgenic rice plants. *OsCBF4* transgene in the transgenic line CBF4-10 was markedly expressed up to over three-fold in the leaf by 120 mM NaCl treatment. Real-time PCR analysis revealed that the levels of the transgene expression were markedly increased under salt treatment. The transgenic line CBF4-10 which showed highest ability to recover from the saline stress could be used as a potential source for salt tolerance in rice breeding programs.

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PC-88

A sheep serotonin *N*-acetyltransferase was expressed in cytoplasm regardless of an addition of chloroplast transit sequence in transgenic rice plants

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Ectopic overexpression of melatonin biosynthetic genes of animal origin has been used to generate melatonin-rich transgenic plants to examine the functional roles of melatonin in plants. However, the subcellular localization of these proteins expressed in the transgenic plants remains unknown. We studied the localization of sheep (*Ovis aries*) serotonin *N*-acetyltransferase (OaSNAT) and a translational fusion of a rice SNAT transit peptide to OaSNAT (TS:OaSNAT) in plants. Laser confocal microscopy analysis revealed that both OaSNAT and TS:OaSNAT proteins were localized to the cytoplasm even with the addition of the transit sequence to OaSNAT. Transgenic rice plants overexpressing the *TS:OaSNAT* fusion transgene exhibited high SNAT enzyme activity relative to untransformed wild-type plants, but lower activity than transgenic rice plants expressing the wild-type *OaSNAT* gene. Melatonin levels in both types of transgenic rice plant corresponded well with SNAT enzyme activity levels. The *TS:OaSNAT* transgenic lines exhibited increased seminal root growth relative to wild-type plants, but less than in the *OaSNAT* transgenic lines, confirming that melatonin promotes root growth. Seed-specific *OaSNAT* expression under the control of a rice prolamin promoter did not confer high levels of melatonin production in transgenic rice seeds compared to seeds from transgenic plants expressing *OaSNAT* under the control of the constitutive maize ubiquitin promoter.

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PC-89

Development of a SNP genotyping set for rice genetic analysis and molecular breeding using the Fluidigm platform

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Single nucleotide polymorphisms (SNPs) are the most abundant variation in plant genomes. As DNA markers, SNPs are rapidly replacing simple sequence repeats (SSRs) and sequence tagged sites (STSs) markers, because SNPs are more abundant, stable, easy to automation, efficient, and increasingly cost-effective. We developed a 96-plex indica/japonica SNP genotyping set for genetic analysis and molecular breeding in rice using Fluidigm platform. Informative SNPs for indica/japonica populations were selected from 1536 Illumina SNPs and 44K Affymetrix SNP chip data of Rice Diversity and our resequencing data sets. Selected SNPs were evenly distributed across 12 chromosomes and average physical distance between adjacent SNP markers was 4.38Mb. We conducted genetic diversity analysis of 49 Bangladesh germplasm and check varieties to test a 96-plex indica/japonica SNP genotyping set we developed. High-throughput Fluidigm SNP genotyping system will serve a more efficient and valuable tool for genetic diversity analysis, DNA fingerprinting, quantitative trait locus (QTL) mapping and background selection for crosses between indica and japonica in rice. This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008125), Rural Development Administration, Republic of Korea.

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PC-90

향기유전자를 이용한 호접란 형질전환빈철구¹, 강선빈¹, 김진기¹, 이병정¹, 신현열¹, 김강권¹¹경남농업기술원 화훼연구소

호접란에서 향기 발현에 관여하는 유전자를 분석하고 정보를 얻기 위해 향기가 있는 호접란 계통 “VIO-6” 과 향기가 없지만 짙은 흑색에 가까운 화색을 가진 “Black Jack” 호접란 품종을 선택하여 각각 꽃의 mRNA를 분리하고 cDNA를 만든 뒤, cDNA fragment를 염기해독 하는 NGS 분석을 시도하였다. 그 중 향기성분 생합성 경로에 관여하는 enzyme을 coding하는 유전자와 유사성이 있는 contig 및 unigene을 따로 분류하였으며 특히 난류 향기성분 발현에 주요 성분으로 사료되는 geraniol과 linalool 합성에 관여하며 enzyme을 coding하는 유전자들의 염기서열 정보를 얻었다. 이를 이용하여 여러 식물 중에서 유사한 유전자를 찾은 결과, Linanool synthase(LIS), Farnesol kinase로 추정되는 유전자 단편을 얻으며, 이를 호접란의 각 조직별, 시기별로 발현정도를 비교해 본 결과, LIS는 꽃이 만개한 시기에 모든 꽃기관에서에서 고르게 발현됨을 알았고 Farnesol kinase는 꽃봉우리시기부터 만개시기까지 고르게 발현된다는 점을 확인할 수 있었다. 이를 바탕으로 우리는 전체 유전자의 염기서열을 분석코자 PCR 또는 RACE방법을 이용해 full length cDNA를 분리하였고 이들 향기유전자를 향기없는 호접란에 형질전환하기 위한 형질전환 벡터를 작성하였다. 이렇게 확보된 벡터는 호접란 내 유전자의 삽입 유무를 확인하기 위해서 phosphinothricin(PPT) 저항성 유전자(BAR)와 향기유전자를 가진 발현벡터로 구축되었으며, 이 발현벡터를 호접란의 PLB조직을 이용하여 아그로박테리움 형질전환을 시도하였다. 아그로박테리움의 접종후 2.5mg/L PPT가 함유된 배지에서 조직을 치상하여 형질전환체 유도를 진행하였고 그 중 PPT 저항성을 보이는 유식물체를 20개체 정도 얻을 수 있었다. 이들의 잎에서 genomic DNA를 분리 한 뒤 PCR을 통해 BAR 유전자의 발현 여부를 확인하였다.

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PC-91

Transcriptome-wide identification and profiling of novel miRNAs involved in cold stress in *Brassica oleracea*

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Cabbage (*Brassica oleracea*) is one of the most important vegetable crops in the world. Yet, its sensitivity to cold stress, especially at the seedling stage, could limit the production. Until now, only, few studies about heritably durable cold tolerance were carried out in cabbage. Hence this study was done to characterize the transcriptome profiles of two cabbage genotypes with contrasting responses to cold stress using Illumina Hiseq short read (paired-end) sequencing technology. MicroRNAs (miRNAs) represent a class of short, non-coding, endogenous RNAs which play important roles in post-transcriptional regulation of gene expression. This study, we sought to provide a more comprehensive prediction of *B. oleracea* cold responsive miRNAs based on high throughput sequencing using two contrasting genotypes. The raw sequences were processed for removal of poor-quality and adaptor sequences. Then, the high quality unigenes (58,094) reads were applied for length filtering. Then, unigenes reads were used in a BLASTN search against of Rfam database and known miRNA database (miRBase 18.0) to removal of non-coding RNA's and identifies conserved miRNA's in *B. oleracea*. Further, novel reads were searched against *B. oleracea* genome. Their flanking sequences in the genome were used to predict their secondary structures, target prediction, and functional analysis. This is first report to identify novel miRNAs for cold stress through high throughput techniques. Our findings will provide an overview of potential miRNAs involved in cold stress, which may provide important clues on the function of miRNAs in from *B. oleracea* and other closely related *Brassica* species.

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Genome-wide identification of AP2/ERF transcription factors and profiling of *CBFs* genes in abiotic stresses in *Brassica oleracea*

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Cabbage (*Brassica oleracea*) is one of the most important leaf vegetables grown worldwide. The entire cabbage genome sequence and more than fifty thousand proteins have been obtained to date. Transcription factors (TFs) are important regulators involved in plant development and physiological processes and the AP2/ERF protein family contains TFs that also plays a crucial role as well and response to biotic and abiotic stress conditions in plants. However, no detailed expression profile of AP2/ERF-like genes is available for *B. oleracea*. In the present study, 226 AP2/ERF TFs were identified from *B. oleracea* based on the available genome sequence. Based on sequence similarity, the AP2/ERF superfamily was classified into five groups (DREB, ERF, AP2, RAV and Soloist) and 15 subgroups. The identification, classification, phylogenetic construction, conserved motifs, chromosome distribution, functional annotation, expression patterns and interaction network were then predicted and analyzed. AP2/ERF TFs expression levels exhibited differences in response to varying abiotic stresses based on expressed sequence tags (ESTs). *BoCBF1a*, *1b*, *2*, *3* and *4*, which were highly conserved in *Arabidopsis* and *B. rapa* *CBF/DREB* genes families were well characterized. Expression analysis enabled elucidation of the molecular and genetic level expression patterns of cold tolerance (CT) and susceptible lines (CS) of cabbage and indicated that all *BoCBF* genes responded to abiotic stresses. Comprehensive analysis of the physiological functions and biological roles of AP2/ERF superfamily genes and *BoCBF* family genes in *B. oleracea* is required to elucidate AP2/ERF, which will provide rich resources and opportunities to understand abiotic stress tolerance in crops.

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배추 글루코시놀레이트 생합성 관련 BrMYB 전사조절 인자의 발현 분석

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글루코시놀레이트는 십자화과 채소에 다량으로 함유되어 있으며 병해충 저항성 및 항균 기능을 가지는 식물의 이차대사산물 중 하나이다. 최근에는 글루코시놀레이트가 가지는 항암 기능이 알려지면서 기능성 물질로써 주목을 모으고 있다. 식물에서 글루코시놀레이트 생합성 조절을 위한 분자생물학적 연구는 애기장대를 중심으로 진행되었고, 그 결과 글루코시놀레이트 생합성과 관련된 MYB 전사 조절 인자의 기능이 확인된 바 있다. 본 연구에서는 십자화과 채소인 배추에서 글루코시놀레이트 생합성에 관련된 MYB 전사 조절 인자를 탐색하고, 유전자의 발현을 분석함으로써 글루코시놀레이트 생합성과 관련된 MYB 전사 조절 인자의 발현 기작을 규명하고자 하였다. 배추 유전체 연구를 통해 밝혀진 정보를 바탕으로 글루코시놀레이트 생합성에 관여하는 것으로 알려진 BrMYB 유전자 13종이 확인되었다. 전사 조절 인자 13종의 microarray 데이터를 분석한 결과, 식물의 생육 단계별로 다양한 발현 양상이 관찰되었고, 몇몇 전사 조절 인자의 경우 abiotic stress 처리에서 강한 유전자 발현이 관찰되었다. 다양한 표현형을 가진 배추 유전자원 35 계통을 대상으로 각 전사조절 인자의 발현을 Real-time PCR 방법으로 분석한 결과, 전사 조절 인자 간 유전자 발현양에 유의한 상관관계가 확인되었다. 또한 HPLC 분석을 통하여 확인된 배추 유전자원 35계통의 글루코시놀레이트 성분 분석 결과와 유전자 발현 간에 상관관계를 분석한 결과, 각 전사 조절 인자와 글루코시놀레이트 성분 간 유의한 상관관계가 관찰되었다. 본 실험의 결과 배추의 글루코시놀레이트 생합성에 관여하는 BrMYB 전사 조절 인자의 발현 분석을 통해 글루코시놀레이트 함량에 관여할 것으로 추정되는 주요 BrMYB 전사 조절 인자를 확인할 수 있었다.

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PC-94

Sumoylation regulates the amounts of Arabidopsis seed nutrient reservoirs

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Arabidopsis E3 SUMO ligase controls vegetative growth and development including responses to nutrient deficiency and environment stresses. Here, we analyzed seed proteins of its mutant *siz1-2*. Proteomic analysis showed that the amount of three major nutrient reservoir proteins were decreased in *siz1-2* mutants. However, quantitative real-time RT-PCR showed that their transcript levels were significantly high in *siz1-2* mutants compared to wild-type plants, which means that these proteins are stabilized by E3 SUMO ligase. In addition, yeast two hybrid assay showed that they interact with E3 SUMO ligase, suggesting that they must be sumoylated by E3 SUMO ligase. Furthermore, 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 carried out with the support of “Cooperative Research Program for Agriculture Science & Technology Development (Project title: Study of rice seed development by post-translational modification, Project No. PJ008123)” Rural Development Administration, Republic of Korea. and also supported by National Research Foundation of Korea Grant funded by the Korean Government (No. 2012-002541).

PC-95**Introduction to agricultural bio-information new resources in NABIC**

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NABIC(National Agricultural Biotechnology Information Center) established integrated management system of agricultural omics information to achieve and analyze a agricultural bio-information resources in Korea. The amount of bio-information is enormously increasing due to emergence of NGS(Next Generation Sequencing) technology. We are building, maintaining and providing agricultural bio-information databases and information services. Various data type for submission is available such as genome, proteome, transcriptome, metabolome, molecular marker, etc. We issue the submission confirmation which is available for research achievement. Currently, the amount of data submitted on our system is 30Tb. We are also providing various analysis pipelines such as NGS analysis(denovo, rna-seq, reference assembly), Gene annotation, GWAS, marker analysis for breeding, Microbial community analysis and differential expression profiling analysis using submitted data through web. We have a plan to provide bioinformatics education portal in this year.

NABIC System is available through web site(<http://nabic.rda.kr/>).

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PC-96**Development of Molecular Marker for Korean Wheat Cultivar Identification using AFLP Technique**

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Amplified fragment length polymorphism (AFLP) is one of molecular marker technique based on DNA and is extremely useful in detection of high polymorphism between closely related genotypes like Korean wheat cultivars. Six Korean wheat cultivar specific marker sets have been developed from inter simple sequence repeat (ISSR) analysis and we can identify the 13 Korean wheat cultivars from other cultivars using six that (Son et al., 2013). We used four combinations of primer sets in our AFLP analysis for developing additional cultivar specific markers in Korean wheat. Twenty-one of the AFLP bands were isolated from ACG/M-CAC primer combination and 19 bands were isolated from E-AGC/M-CTG primer combination, respectively. We used forty bands to design sequence characterized amplified region (SCAR) primer pairs for Korean wheat cultivar identification. Only one of 40 amplified primer pairs, C2, were able to use for wheat cultivar identification. The DNA band of 215bp length was amplified by C2 primer pairs in ten cultivars, Eunpa, Olgeuru, Gobun, Saeol, Milsung, Sinmichal, Jokyung, Sugang, Goso, and Joah. Then C2 primer was applied to these primer sets as newly SCAR marker, six cultivars are identifying from other cultivars, additionally. Finally, to use the C2 and six primer sets, 19 Korean wheat cultivars are identified.

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Improving ginsenoside content in Korean wild ginseng by *Agrobacterium*-mediated transformation with a squalene synthase gene

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With the purpose of improving ginsenoside production in Korean wild ginseng (*Panax ginseng* Meyer) mutant adventitious root lines, a synthetic gene encoding squalene synthase (*PgSS2*) was placed under the control of 35S promoter and transferred to *Panax ginseng*. Embryogenic callus obtained from ginseng adventitious root lines were transformed by infection with *A. tumefaciens* strain EHA105 containing the *PgSS2* gene. Ten phosphinothricin-resistant plants were generated on selection medium, and the transgene integration and expression in these plants were confirmed by PAT test strip, RT-PCR and Southern hybridization. Ginsenoside analysis by HPLC revealed that the total contents of the 8 ginsenoside types (Rg1, Re, Rf, Rh1, Rb1, Rc, Rb2, Rd) in transgenic adventitious root lines were about 1.6-fold higher than that of the mutant control line (MCL1). This transformation method may facilitate the improvement of *Panax ginseng* in terms of the accumulation levels of ginsenoside.

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노화지연 GM 들잔디 (*Zoysia japonica* Steud.)의 제조

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들잔디(*Zoysia japonica* Steud.)는 난지형 잔디로 우리나라를 포함한 동아시아 지역에 자생하고 있다. 내한성이 강해 국내에서는 전국 어디서나 잔디밭으로 쉽게 조성할 수 있으며, 더불어 내건성, 내서성도 강해 일반 정원용으로 사용되는 경우 자연강우만으로도 생육이 가능하다. 또한 내담압성 뿐만 아니라 심근성이어서 묘소, 공원, 골프장, 경사면 녹화 등 여러 가지 목적으로 이용되고 있다. 최근에는 잔디의 이용범위가 확대되면서 한계점이 있는 전통 육종법 대신 분자육종에 의한 신품종 개발이 활발하게 진행되고 있다. 이 분자육종법을 이용하여 신품종 잔디를 개발하기 위해서 먼저 배양이 쉬운 성숙종자 유래의 캘러스를 유도하고, 이 중 재분화 효율이 높은 캘러스 라인만을 선발하여 *Agrobacterium*을 이용한 형질전환을 수행하였다. 본 연구에서는 형질전환 효율을 높일 수 있는 몇 가지 요인들을 조사하여 노화지연 GM 들잔디를 제조하였다. 들잔디의 완숙종자에서 유도/증식하여 선발한 재분화 효율이 높은 배발생 캘러스를 노화지연의 표현형적 특징을 나타내는 애기장대 유래의 AT-hook 유전자들 (*ATPG3*, *ATPG4*)을 도입한 *Agrobacterium* (OD₆₀₀=0.1)에 24시간 동안 감염하고, 3일간 공동배양, 신초유도 및 선발, 뿌리유도 및 선발 과정을 거쳐 증식하여 각각 약 20개체씩의 형질전환 식물체를 생산하였다. 확보한 *ATPG3*, *ATPG4* 유전자도 도입된 형질전환식물은 순화/증식하여 분자생물학적 특성 분석, 표현형적 특성 분석, 기능분석 등을 수행하고 있다.

사사: 농촌진흥청 차세대 바이오그린21사업(PJ009499032014); 한국연구재단 기초연구사업(2009-0094059)

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교배육종기술을 이용한 제초제 저항성 왜성 잔디(탐라그린) 개발송인자¹, 배태웅³, 정옥철¹, 선현진¹, 권용익¹, 강홍규¹, 고석민¹, 이효연^{1,2*}¹제주대학교 아열대원예산업연구소²제주대학교 생명공학부³국립산림품종관리센터

잔디는 우리 생활에 없어서는 안 될 매우 중요한 유전자원 중의 하나로 최근 급격한 수요 증가와 더불어 잔디와 관련된 사업규모가 확대되고 있다. 지금까지 잔디는 전통적인 육종방법을 이용하여 개발되어 왔으며, 전통적 육종 기술로 개발할 수 없는 형질들은 분자생물학적 방법을 이용하여 신품종 잔디를 개발하고 있다. 본 연구에서는 소비자의 요구에 맞는 잔디 신품종을 개발하기 위하여 분자생물학적기법을 이용하여 개발된 제초제저항성 잔디에 전통적 교배육종 기술을 도입하여 잔디 육종기술의 한계점을 극복하고자 하였다. 제초제저항성 들잔디(JG21)의 경우 포복경의 생장 및 증식이 빠르고, 토양활착 능력이 우수할 뿐만 아니라 제초제저항성 기능이 있기 때문에 도로의 법사면 및 경사지에 적합하다. 그러나 공원 및 정원 등의 조경용으로 사용하기 위해서는 보다 키가 작고 밀도가 높은 잔디형질이 요구된다. 그러므로 본 연구에서는 JG21의 단점을 보완하기 위해서 금잔디와 교배육종을 수행함으로써 초고 및 초장이 짧고, 잔디 직립경의 생육밀도가 높은 계통을 선발하였으며, 그 중 가장 우수한 계통은 탐라그린3으로 명명하여 특허출원하였다(국내출원번호 10-2014-0025262). 탐라그린3은 공원 및 정원 등에 사용하여 잔디 재배시 문제가 되고 있는 예초 및 잡초방제에 따른 노동력을 절감할 수 있으며, 농약의 과다사용으로 인한 환경오염 문제를 해소할 수 있는 고부가가치 경제작물이 될 것이다.

사사: 산림과학기술개발사업(S111012L020110), 한국연구재단기초연구사업(2009-0094059, 2011-0014959)

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PC-100

Agrobacterium법을 이용한 고온건조스트레스 저항성 잔디의 개발송인자¹, 홍민지², 박미영¹, 선현진¹, 김우남², 신현숙², 권용익¹, 고석민¹, 강홍규¹, 이효연^{1,2*}¹제주대학교 아열대원예산업연구소²제주대학교 생명공학부

잔디는 전 세계적으로 재배되고 있는 중요한 단자엽 식물중의 하나이며, 세계 4대 작물 중 하나인 옥수수 다음으로 큰 시장을 보유하고 있다 (Lee, 1996). 잔디는 도로, 하천, 비행장의 토양 침식 방지에서부터 주택, 공원, 정원, 골프장, 스포츠 경기장 등으로 널리 이용되고 있어 매년 잔디조성 면적이 전 세계적으로 증가되고 있는 추세이다. 이러한 잔디는 주로 전통적인 육종방법에 의하여 신품종이 개발되어져 왔으나 현대의 다양한 소비자의 요구를 완전히 충족시키지 못하고 있다. 그러므로 최근 유전자조작기술을 이용하여 소비자 요구에 맞는 다양한 신품종 개발이 시도되고 있다. 특히 급격한 기후변화로 인한 작물의 생리장해를 극복하기 위하여 다양한 유전자(내염성, 내건성, 내한성, 녹기연장, 음지내성 등)를 이용한 biotic 및 abiotic 스트레스 저항성을 갖는 기능성 형질전환잔디 개발에 많은 투자를 하고 있다. 본 연구에서는 환경스트레스에 관여하는 유전자 중 벼 유래의 *OsWRKY11* 유전자를 크리핑 벤트그라스와 들잔디에 도입함으로써 고온 및 건조스트레스에 저항성이 있는 잔디를 개발하고자 하였다. 들잔디와 크리핑 벤트그라스의 완숙종자로부터 배발생 callus를 유도 및 증식하여 *OsWRKY11* 유전자가 도입된 *Agrobacterium*에 24시간 감염 하였다. 그 후 공동배양, shoot 유도 및 선발, root 유도 및 선발 과정을 거쳐 형질전환 식물체를 생산하였으며, 확보된 형질전환 식물체는 분자생물학적 검증을 수행하였다.

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PC-101

Development of EST SSR-Markers to study genetic diversity in Foxtail Millet (*Setaria italica*)

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Foxtail millet (*Setaria italica* L.) is the second most widely cultivated species of millet, especially in East Asia and is a tractable experimental model crop for studying functional genomics of millets. However, insufficient researches had been conducted about the foxtail millet germplasm and is significantly impeding its genetic improvement. We attempted to develop EST-derived-SSR (eSSR) markers and utilize them in genetic comparison of germplasm and transferability. A total of 66,027 foxtail millet EST sequences and 42,754 genomic sequence were deduced transcriptom. Approximately 42,000 single tone contigs were generated using DNASTAR 5.0 software for redundancy minimization. Nearly 33% of the 14,012 unigenes contained SSRs, but primers were designed for a total of 314 microsatellites concentrating with more than 24 bp of repeats. A total of 314 primers were successfully designed with more than 24 bp of repeats. From these microsatellites, 56 primer pairs were showed polymorphism with over than 15 bp differences among 96 accessions collected from different countries. Polymorphic information content (PIC) value ranged from 0.020 to 0.700 with an average of 0.381 indicating moderate level of informativeness within these EST-SSRs markers. The EST-SSR markers developed in this study will serve as a useful source for genetic studies, such as genetic variability, transferability, association mapping, and molecular breeding.

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PC-102

Microsatellite marker development for onion genetic purity test

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Bulb onion (*Allium cepa*), which belongs to the family *Amaryllidaceae*, is one of the oldest vegetative crops known to humans. Despite its high economic value, only a few reports are available on the use of molecular markers in genetic diversity analysis of *Allium cepa* for its improvement. Molecular genetic markers have been widely used as powerful tools for analyzing the plant genome. In particular, Microsatellites or simple sequence repeats (SSRs) markers are tandem repeats of one to six bp in length and have been proven to be the most powerful polymerase chain reaction (PCR)-based DNA markers in plant diversity analysis. In this study, the genomic DNA was isolated from different *Allium cepa* lines. The ESTs and gDNA sequences of onion were collected from National Center for Biotechnology information. The SSRs with two to five motifs over a length of 12 bp, were identified using SSRIT (Gramene) software. The PCR products of 100 to 350 bp in length containing SSRs, primers was designed using Primer3 with lengths of 20 to 24 bp and a melting temperature of 60°C. The SSR markers with high polymorphism-information content (PIC) levels was useful for collecting progeny with high genetic homogeneity for onion breeding, and to obtain representative marker sets for genetic tests. The SSR Finder program and the developed SSR markers could be a useful resource for genetic diversity and purity testing in onion.

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PC-103**Optimization of leaf water loss rate assay for rapid and stable drought tolerance screening in rice**

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The global rice reduction due to drought averages 18 Mt, especially, 23 Mha of rice fields in Asia are drought-prone. However, rice breeding programs focusing on drought resistance have made little progress to date. Because proper screening approaches with large scale were not developed to evaluate the drought tolerant degree. In here, we have developed of leaf water loss rate with plastic ware in dark conditions for large screening. Through this bioassay system, we examined drought phenotype degrees of 650 rice varieties. To validate whether this optimized bioassay system is correlated with drought phenotype, we chose 14 varieties having the lowest or highest of the water loss rate. We observed the visual drought phenotype and agricultural traits in green house and field conditions. Apo and Samgang having the lowest of leaf water loss rate showed drought tolerance phenotype, whereas Yeolbaeg and Milyang254 having the highest of leaf water loss rate showed drought sensitive phenotype. Apo displayed proper root length trait and Samgang showed good root dry trait in the greenhouse conditions. These results suggest that a simple screening procedure with water lose rate of leaves is effective to perform large scale screening for drought phenotype in rice.

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PC-104**Analysis of QTLs for vegetative stage drought tolerance using DH population in rice**

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Drought is a one of the most serious abiotic stresses limiting rice production. However, little progress has been made in the genetic analysis of drought tolerance, because it is a complex trait controlled by a number of genes and affected by various environmental factors. The most efficient method for drought tolerance breeding is using drought tolerance genetic resources. We used a doubled-haploid (DH) population consist of 101 lines derived from a cross the drought tolerant cultivar ‘Samgang’ and the drought sensitive cultivar ‘Nagdong’ for QTL analysis. Drought stress was treated by withholding water for 6 weeks, and then rewatered for 7 days. After rewatering visual phenotype was observed according to the standard evaluation system for rice, IRRI. Drought sensitive parent ‘Nagdong’ was almost died, while tolerant parent ‘Samgang’ showed slightly leaf tip dring phenotype. The *qdr11* detected on chromosome 11 with flanking markers RM26755-RM287 and accounted for 19% phenotype variation with a LOD score of 3.7.

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PC-105

Natural occurrence of Fusarium mycotoxins in Korean 32 wheat cultivars harvested in 2011 and 2012

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Fusarium head blight (FHB) is a major disease problem on wheat and barley around the world. *F. graminearum* produces trichothecenes mycotoxins such as nivalenol (NIV), deoxynivalenol (DON), and zearalenone (ZEA). The objectives of this study were to survey the natural occurrence of FHB and mycotoxins of 32 Korean wheat cultivars grown in 2011-2012 seasons at the National institute of crop science, Iksan, Korea. There was great deal of rainfall and high humidity during flowering time in May 2011. FHB incidence was counted by Fusarium infected spikes per square meter. The samples of 32 wheat cultivar were collected. The grain and flour samples were to analysis for DON and NIV by gas chromatography and ZEA by high performance liquid chromatography. The result showed that the average of FHB incidence(%) per square meter in 2011 and 2012 were 4.2%, 0.5% respectively. There were significant cultivar differences for FHB incidence ranged from 0% to 24% in 2011. All of 32 wheat cultivars contained 9-2088 ng/g for NIV and ten wheat cultivars contained 5.7-8.5 ng/g for ZEA. In addition, DON concentration of Tapdong, Shinmichall, and Hanbaek were 217, 35 and 683 ng/g respectively. However, the grain and flour sample harvested in 2012 showed that lower FHB incidence and NIV concentration. These results showed that the 32 wheat cultivars harvested in 2011 were heavily contaminated with Fusarium mycotoxins (NIV, DON, ZEA).

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PC-106

Identification of novel drought stress-regulated coding and noncoding transcripts from *Oryza sativa* L.

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Abiotic environmental stresses cause serious economic losses in agriculture. These stresses include temperature extremes, high salinity and drought. We identified several drought stress-related novel/function unknown coding transcripts (transcription factors and functional genes) and non-coding transcripts (small noncoding transcripts such as microRNA and long noncoding transcripts) using the next generation sequencing method from rice (*Oryza sativa* L.), and have constructed databases of drought stress-related coding and noncoding transcripts. We used novel gene prediction programs for the selections. The expression level of the each gene was analyzed by real-time PCR. The results ended up the selection of 29 transcription factors, 6 microRNAs and 10 long noncoding RNAs. Currently, we are further characterizing these transcripts. We expect that this study could provide functional information of the drought stress-regulated novel genes, and relationships among novel coding and noncoding transcripts.

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PC-107**DNA sequence variations between UVB-sensitive and tolerant soybean genotypes**Sangrea Shim¹, Moon Young Kim^{1,2}, Suk-Ha Lee^{1,2}¹Department of Plant Science and Research Institute of Agriculture and life Sciences, Seoul National University, Korea²Plant Genomic and Breeding Research Institute, Seoul National University, Korea

UVB radiation which causes dermatosis, cancrroid, and necrosis in living organisms is mostly absorbed by ozone layer, resulting in transmission of only small UVB proportion to earth surface. Recently, however, rapid increases of pollutants like CFCs have accelerated depletion of stratospheric ozone layer. Increased UVB irradiation alters affects biomolecule interinity such as DNA, RNA and protein. To understand DNA mutation spectra in response to UVB, in the present study, we used two soybean cultivars, Buseok and Cheongja 3, which were screened as the most UVB tolerant and sensitive genotypes among 140 soybean germplasms, respectively. Whole genomes of Buseok and Cheongja were sequenced at low-coverage depth by illumina Hiseq2000, and we also sequenced 6 hr UVB irradiated genomes of two cultivars. Raw sequence reads were aligned to the soybean reference sequences (cv. Williams 82) by BWA aligner software. To identify DNA mutations induced by UV-B irradiation, multiple comparisons between non-irradiated and irradiated genomes in these two soybean genotypes were conducted using samtools and GenomeAnalyzerTK packages and homebrew python codes. A total, 13,992 and 17,078 single nucleotide polymorphisms (SNPs) were indentified between non-irradiated and irradiated genomes of Buseok and Cheongja 3, respectively. In addition, Buseok and Cheongja 3 have 423 and 465 insertions/deletions induced by UVB, respectively. Approximately 58% of the identified SNPs were C to T or CC to TT transversions, consistent with the previous studies. Chromosomal distributions of the SNPs likely showed differences in UV-B mutation positions depending on the soybean genotype.

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PC-108

Association mapping for novel resistance loci against bacterial spot using genome-wide SNPs in tomato

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Bacterial spot of tomato (*Solanum lycopersicum* L.) is caused by at least four species of *Xanthomonas* with multiple physiological races. In this study, we developed a mapping population for association analysis of bacterial spot resistance. For this population, six advanced breeding lines with distinct sources of resistance were first crossed in all combinations and their F₁ hybrids were intercrossed. The 1,100 segregating progeny from these crosses were evaluated in the field against T1 strains. Based on this individual evaluation, we selected 5% of the most resistant and 5% of the most susceptible progeny for evaluation as plots in two subsequent replicate field trials inoculated with T1 and T3 strains. A total of 461 markers across 12 chromosomes were used for genotyping these selections. Of these markers, an optimized subset of 384 SNPs was derived from the 7,720 SNP Infinium array developed by the Solanaceae Coordinated Agricultural Project (SolCAP). For association analysis to detect known resistance loci and additional novel loci, we used the mixed models with correction for population structure, and found that accounting for kinship appeared to be sufficient. Detection of known loci was not improved by adding a correction for structure using either a Q matrix from model-based clustering or covariate matrix from Principal Component Analysis. Both single-point and haplotype analyses identified strong associations in the region of the genome known to carry Rx-3 (chromosome 5) and Rx-4/Xv3 (chromosome 11). Additional QTL associated with resistance were detected on chromosomes 1, 3, 4, 6 and 7 for T1 resistance and chromosomes 2, 4, and 6 for T3 resistance. Haplotype analysis improved our ability to trace the origin of positive alleles. These results demonstrate that both known and novel associations can be identified using complex breeding populations that have experienced directional selection.

PC-109

Bioinformatics databases for rice research

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Functional identification of rice on a whole genome scale is required to significantly improve the quality of rice, rice yield, and stress tolerance in response to changing climate. In addition to conventional approaches, new methodologies are required for identification of key genes associated with new agronomical traits. Systems biology is an upcoming trend in the field of functional genomics. Recently, there has been a significant improvement in the resources for systems biology in *Oryza sativa* (rice), a model crop. These resources include whole genome sequencing/re-sequencing data, transcriptomes, protein-protein interactomes, reactomes, functional gene network tools, and gene indexed mutant populations. The integration of diverse omics data can lead to greater understanding of the functional genomics of rice. Here, we address the development and current progress of the resources available for systems biology in rice: Genome browsers and databases for the orthology identification, transcriptome analysis, protein-protein interaction network and functional gene network analyses, co-expression network, metabolic pathway analysis for promoter analysis, and gene indexed mutants.

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PC-110

Marker Assisted Breeding for Tolerant Pepper

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Next-generation sequencing (NGS) technology and fast improvement in plant genetics have elevated to massive development of molecular genetic markers through fast analysis of huge molecular biological data. Furthermore, in domestic commercial breeding of horticultural crops, the application of marker assisted breeding (MAB) has been introduced recently. For effective improvement of cultivar breeding, in this research, transcriptome analysis and single nucleotide polymorphism (SNP) comparison with high density pepper map in UC-DAVIS were performed using four lines of *Capsicum annuum* and *C. chinense*. For rapid analysis of MAB of tolerant pepper lines, 412 Fluidigm probes were newly designed in this study. These designed probes and SSR and COSII markers were applied for background selection through the MAB program. In addition, powdery mildew (PM), tomato spot wilt virus (TSWV) resistance related markers were subjected to foreground selection of BC1, BC2, and BC3 progenies. The MAB system using Fluidigm probes, and trait-related and common markers was introduced into domestic pepper breeding, which will rapidly approach to a new elite line and a commercial tolerant cultivar.

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PC-111

Transcriptome Analysis of *Capsicum annuum* varieties Mandarin and Blackcluster: Assembly, Annotation and Molecular Marker Discovery

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Next generation sequencing technologies have proven to be a rapid and cost-effective means to assemble and characterize gene content and identify molecular markers in various organisms. Pepper (*Capsicum annuum* L., *Solanaceae*), is a major staple vegetable crop, which is economically important and has worldwide distribution. High-throughput transcriptome profiling of two pepper cultivars, Mandarin and Blackcluster using 454 GS-FLX pyrosequencing yielded 279,221 and 316,357 sequenced reads with a total 120.44 and 142.54 Mb of sequence data (average read length of 431 and 450 nucleotides). These reads resulted from 17,525 and 16,341 'isogroups' and were assembled into 19,388 and 18,057 isotigs, and 22,217 and 13,153 singletons for both the cultivars, respectively. Assembled sequences were annotated functionally based on homology to genes in multiple public databases. Detailed sequence variants analysis identified a total of 9,701 and 12,741 potential SNPs for both cultivars, which eventually resulted in 1,025 and 1,059 genotype specific SNPs, for both the varieties, respectively. These markers for pepper will be highly valuable for marker-assisted breeding and other genetic studies.

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PC-112

조생계 양배추의 고효율 소포자 배양법

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경기도 이천시 장호원을 아시아종묘 생명공학육종연구소

양배추는 세계적으로 가장 많이 재배되고 있는 채소작물로 잠재적 부가가치가 높다. 양배추의 소포자 배양기술이 확립되면 반수체 유래 이배체의 계통을 조기에 획득 할 수 있으므로 품종육성 연한 단축이 가능하다. 본 연구를 통해 조생계 양배추의 품종육성의 효율을 높이고자 고효율의 소포자 배양조건을 조사하였다. 실험재료로는 조생계의 내병성 도입품종 BN606, 640, 2414.의 3품종을 사용하였다. 배지는 NLN을 기본으로 호르몬 NAA와 BA를 이용하여 조성을 달리한 8종류의 배지를 사용하였으며 배지별로 동량의 Activated charcoal을 넣어 60x15mm의 petri dish에 분주하여 밀봉 후 고온처리하고 25℃(暗)에서 배 발생을 관찰한다. 20일 후 육안으로 배의 형태가 관찰되면 빛은 차단된 상태로 70rpm에서 배양하다가 3일 뒤 배의 크기가 커지고 초록빛이 돌기 시작하면 50rpm에서 명배양하였다. 전처리는 30℃ 2일, 31℃ 1일, 32.5℃ 1일의 조건에서 비교하였고 30℃ 2일 처리구가 가장 높은 배 발생률을 보였다. 발생배 일부는 안토시안이 축적되어 자줏빛이 나타나기도 했으나 식물체로 분화에는 영향은 없었다. 품종 간 배 발생률은 상이하였으나 BN640에서 화퇴 당 12개의 배가 발생하여 배 발생률이 가장 높았으며 배의 분화가 빠르고 정상적인 형태의 발생을 보여 식물체 유기율이 높을 것으로 사료된다. 봄작기 양배추의 소포자 배양으로부터 1683개의 배를 획득하였고 이후 식물체로 분화시켜 가을 교배의 육종소재로 활용할 예정이다.(본 연구는 농림수산식품부 Golden Seed프로젝트(213003-04-1-SB310)의 지원에 의해 이루어진 것임).

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PC-113

소포자 배양을 통한 팍쇼이의 반수체 식물 대량생산

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팍쇼이의 국내시장은 일본 품종들이 우점하고 있으나 2007년 이후에는 국내종묘회사에서 개발한 국산품종들이 수입 대체 되고 있는 추세로서 높은 경제가치가 기대되는 작물이다. 특히 유럽 및 미주로의 종자수출이 매년 증가하고 있어 시장맞춤형 품종 육성이 요구된다. 수출용 품종 육성에 유용한 형질의 반수체 식물 생산을 통해 단기간에 다양한 육종소재를 제공하고자 본 연구를 실시하였다. 실험재료는 우수형질의 도입품종 BN8074품종을 대상으로 실시하였다. 소포자 배양 효율을 조사하기 위해 배지조성, 전처리 온도 및 시간에 따른 배 발생을 조사하였다. 배지조성은 1/2NLN에 13% sucrose와 NAA와 BA의 혼합처리에서 가장 높은 배 발생 효율을 보였다. 전처리는 30℃, 31℃, 32.5℃에서 1일과 2일처리 하였다. 전처리는 31℃ 1일 처리에서 배 발생이 가장 높았으나 식물체로의 유기율이 현저히 떨어졌다. 그에 반해 32.5℃ 1일 처리에서 발생한 배로부터 정상 식물체로의 유기율이 높고 생장도 좋았다. 배양결과 화퇴 1개당 약 7개의 배를 발생시켰으나 발생배의 식물체 분화율이 5%로 현저히 낮았다. 이는 dish당 발생배의 수가 과도할 경우 배의 초기분화가 정상적으로 일어나지 못하여 정상 식물체로 유기되지 못한 것으로 생각되었다. 소포자 배양을 통해 대량 획득한 7625개 발생배를 배양병에서 6주간 배양하여 발근을 유도한 후 정상 식물체를 선발하여 토양 순화하였다. 소포자 배양으로부터 유기된 식물체는 가을 교배기에 육종소재로써 활용하기 위해 저온처리를 실시하였다.

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PC-114**Identification of various complete circle form of mitochondrial genome sequences using WGS in *Brassica oleracea***Kiwoung Yang¹, Nasar Uddin Ahmed¹, Jonghoon Lee², Junki Lee², Ill-Sup Nou^{1*} and Tae-Jin Yang^{2*}¹Department of Horticulture, Suncheon National University, Suncheon, Republic of Korea²Department 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, Korea

Mitochondria are essential organelles of eukaryotic cells and plant cells contain varying numbers of mitochondrial genome sequences. Sizes and shapes of mitochondria differ within a tissue or in the same cells. Previously sequenced complete mitochondrial genome (NC_016118) of *Brassica oleracea* size was 360,271 bp, where segmental duplication (repeat block) was 141,800 bp. In this study, we resequenced this whole mitochondrial genome by using WGS (whole genome sequencing) and assembled organelles genome method (unpublished). Newly sequenced mitochondrial genome length was 219,975 bp and circle form. A new sequence segment of approximately 4,800 bp was obtained compared to the previous genome sequence without any large repeat block. Newly obtained mitochondria genome sequence was compared with recently reported mitochondria genome sequences of various species (*B. oleracea*, *B. juncea*, *B. rapa*, *B. napus* and *B. carinata*) and subspecies (cabbage, cauliflower, brussels sprouts, kohlrabi, broccoli and kale) by PCR using primers specifying different region of genome sequences. PCR analysis results have also confirmed the variation between previous and newly sequenced mitochondrial genome circles form. Thus, the results suggest new *B. oleracea* mitotype, including evolutionary events such as inheritance, rearrangement, genome compaction, and diversity.

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PC-115**Molecular biological characteristics and biosafety assessment for drought-tolerant transgenic rice (Agb0103)**

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Genetically modified (GM) crops have been developed worldwide through the recombinant DNA technology and commercialized by various agricultural biotechnology companies. Commercialization of GM crops will be required the assessment of risk associated with the release of GM crops. The purpose of this research is a molecular characterization of introduced T-DNA in transgenic rice T4 ~ T6 generation lines harboring a pepper *MsrB2* gene under the control of stress inducible *Rab21* promoter, as a part of biosafety evaluation for drought-tolerant transgenic rice (Agb0103). We identified the structure and sequence of transformation vector of T-DNA and analyzed insertion sites, flanking sequences, and generational stability of inserted T-DNA in transgenic rice lines. The transformation vector was consisted of right border, a drought-tolerant CaMsrB2 gene unit (*Rab21* promoter::*CaMsrB2*::*PinII* terminator), a selectable marker herbicide resistance unit (*CaMV 35S* promoter::*bar*::*Nos* terminator), and left border in sequential order. Based on the adaptor-ligation PCR and whole genome sequence database, we confirmed that T-DNA was introduced 2 copies (head to head type) at the position of 2,471,957 ~ 2,472,049 bp of chromosome No. 8. From the generational stability study, T-DNAs were stably inherited through the T4 to T6 generations, and also stable expression of *bar* gene from T-DNA was confirmed. It was also confirmed that the backbone DNA of transformation vector containing antibacterial gene (*aadA*) was not present in Agb0103 rice genome. These results will be filed to biosafety assessment document of Agb0103.

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PC-116

Development of PCR-based molecular markers by transcriptome sequencing in *Platycodon grandiflorum*

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Platycodon grandiflorum, which is the only species in the genus *Platycodon* of the family Campanulaceae, is an herbaceous flowering perennial. *P. grandiflorum* is generally known as bellflower or balloon flower indicating its ornamental uses. It has also been traditionally used as a medicinal crop in East Asia, which is widely employed as an antiphlogistic, antitussive, and expectorant. However, marker-assisted selection and molecular breeding in *P. grandiflorum* has lagged behind other plants such as pepper and tomato because of the lack of genetic information and effective molecular markers. Transcriptome sequencing provides an effective way to obtain large amount of sequence data when there is no available genome sequence. In this study, we performed a transcriptome analysis in platycodons, which has not been attempted previously. We analyzed simple sequence repeats (SSRs) using RNA-seq data. Di-nucleotide motifs were the most abundant repeats (39% ~ 40%) followed by mono- (26% ~ 32%), tri- (25% ~ 31%), tetra- (1.5% ~ 1.9 %), penta- (0.3% ~ 1%) in three platycodon accessions. Based on the SNP information obtained from RNA-seq analysis, we developed 12 PCR-based markers in *Platycodon*. The number of alleles ranged from two to seven with the average PIC value of 0.373. These 12 markers were applied to 21 platycodon accessions and a phylogenetic tree was constructed. The markers developed in this study could be introduced in molecular breeding program of platycodons. The SSR information obtained from RNA-seq analysis could be further utilized for developing genic-SSR markers in platycodons. Since platycodon is considered as an orphan crop, which has not been actively deployed for genetic study, the sequence information obtained from this study will contribute to further genetic improvements, genomic information and gene discovery in platycodon.

PC-117

Development of high-throughput SNP markers from ‘Whangkeumbae’ and ‘Minibae’ pears using next generation sequencing

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Single nucleotide polymorphisms (SNPs) are the most frequent type among variations found in genomic regions and are valuable markers for genetic mapping, genetic diversity studies and association mapping in plants. There are three basic species known as Korean native which are *Pyrus ussuriensis*, *P. pyrifolia*, and *P. fauriei*. Genetic relationship among Korean pear cultivars compared with their parents was identified that they are closely related *P. pyrifolia*, *P. ussuriensis* and/or hybrids between two species. Lack of genetic resources, including molecular markers to study pears are very severe. Recently developed next generation sequencing (NGS) platforms offer opportunities for high-throughput and inexpensive genome sequencing and rapid marker development. The objective of this study was to develop polymorphic SNP markers in ‘Whangkeumbae’ and ‘Minibae’, which were chosen as the representative cultivars of *P. pyrifolia* and *P. ussuriensis* × *pyrifolia* in each among Korean pears, using genomic sequences generated by NGS technology. In this study, more than 18.6 Gbp and 15.8 Gbp sequences were obtained from NGS of ‘Whangkeumbae’ and ‘Minibae’, respectively. ‘Whangkeumbae’ and ‘Minibae’ contained 2,712,288 and 2,747,224 SNPs, respectively. In SNPs validations between ‘Whangkeumbae’ and ‘Minibae’, the number of polymorphic SNPs were 2,516,438 and non-polymorphic SNPs were 1,179,391. For HRM primer design, 2,125,479 HRM candidate primers were obtained from polymorphic SNPs and 343,731 SNP primers were developed. This study shows that the utility of NGS technology to discover efficiently a large number of SNPs and SNP primers can provide valuable information in the genome study of *Pyrus* spp.

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PC-118

High-throughput InDel marker development based on next generation sequencing in 'Whangkeumbae' and 'Minibae' pears

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Currently, the type of short insertions and deletions (InDels) polymorphisms are increasingly focused in genomic research. InDels have been known as a source of genetic markers that are widely spread across the genome. Genetic relationship among Korean pear cultivars compared with their parents was also identified that they are closely related *P. pyrifolia*, *P. ussuriensis* and/or hybrids between two species. Lack of genetic resources including molecular markers has made it difficult to study pears severely. Recently developed next generation sequencing (NGS) platforms offer opportunities for high-throughput and inexpensive genome sequencing and rapid marker development. The main goal of this study was to develop polymorphic InDel markers in 'Whangkeumbae' and 'Minibae', which were chosen as the representative cultivars of *P. pyrifolia* and *P. ussuriensis* × *pyrifolia* in each among Korean pears using genomic sequences generated by NGS technology. In this study, more than 18.6 Gbp and 15.8 Gbp sequences were obtained from NGS of 'Whangkeumbae' and 'Minibae', respectively. 'Whangkeumbae' contained 197,210 InDels and 197,272 InDels in 'Minibae'. In InDels validations between 'Whangkeumbae' and 'Minibae', the number of polymorphic InDels were 149,338 and non-polymorphic InDels were 122,572. For InDel primer set designing, 11,308 of primers were designed from polymorphic InDels and 10,919 of InDel primers were recommended. The study shows that the utility of NGS technology to design amount of efficient InDels and the developed InDel primers will be used for genetic mapping, breeding by marker assisted selection (MAS) and QTL mapping of Korea native pear as well as further genetic studies.

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PC-119

Availability of Novel Pear SSR Markers delivered from ‘Golden Delicious’ Apple Genomic Sequences

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Korea is a origin of three basic species, *P. ussuriensis*, *P. pyrifolia* and *P. fauriei*. Genetic relationship among Korean pear cultivars compared with their parents were also identified that they are closely related *P. pyrifolia*, *P. ussuriensis* and/or hybrid between two species. SSRs or Microsatellites are co-dominant and typically neutral inheritance showing high degree of polymorphism, large number of alleles per locus, abundance in genomes, and suitability for automation. SSR markers were developed in apple and pear where they were used for construction of genetic linkage maps, evaluation of the genetic diversity, cultivar identification, genotype identification, and in the determination of genetic relatedness. Many apple (*Malus × domestica* Borkh.) SSRs would be useful for genetic mapping in European and Asian pears in previous experiments and cross-species amplification was observed between apple and pear. The objectives of this study were to develop polymorphic SSR markers in ‘Wangkeumbae’ and ‘Minibae’, which were chosen as the representative cultivars of *P. pyrifolia* and *P. ussuriensis* in each among Korean pears, from ‘Golden Delicious’ genomic sequences generated by next generation sequencing technology and to evaluate the utility of the SSR markers based on ‘Golden Delicious’ sequences. Of 51 SSR markers, 18 were polymorphic in ‘Wangkeumbae’ and ‘Minibae’. The cross-species transportability of primers designed in ‘Golden Delicious’ sequences makes SSR markers more useful, given the current high level of investment in mapping the genomes of related Rosaceae.

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PC-120

‘거대 1호’ 억새 화기 분화조직으로부터 캘러스 유도 및 재분화 조건 확립

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억새(*Miscanthus* spp.)는 화본과에 속하는 다년생 C₄ 식물로 국내에 자생하는 대표적인 바이오에너지 원료작물이다. 농촌진흥청에서 개발한 ‘거대 1호’는 4배체 물억새로 초장 및 경태 등이 일반 억새의 두 배 크기로 탁월한 건물 생산성을 보여 유망한 바이오매스 자원으로 여겨지고 있다. 본 연구에서는 ‘거대 1호’의 미성숙 화기를 이용한 안정적인 캘러스 유도 및 식물체 재분화 조건을 확립하여 대량증식 및 분자육종을 위한 기초자료를 확보하고자 하였다. 재료는 억새의 2mm 이하인 미성숙화기를 사용하였으며, 수집한 재료는 70% EtOH로 2분, 0.45% NaOCl로 20 분간 표면살균 후 미성숙화기의 정단부위를 실체현미경 하에서 적출 후 사용하였다. MS배지에 2,4-D(Auxin)와 BA(Cytokinin)를 각 농도 별로 첨가하여 캘러스 유도율을 조사한 결과, 2,4-D 5 mg/L와 BA 0.1 mg/L를 혼합 처리한 배지에서 가장 높은 캘러스 유도율을 나타내었다. 유도된 캘러스로부터 신초 재분화를 위해 MS 배지에 NAA와 BA, 2,4-D와 BA 등을 농도별로 첨가하여 배양한 결과, NAA 1mg/L와 BA 1mg/L이 첨가된 MS 배지와 5 mg/L BA와 0.1 mg/L NAA가 첨가된 배지에서 각각 15.4, 15.2 %의 신초 재생율을 보였다.

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PC-121

콩에서 180k Axiom[®] Soybean SNP Genotyping Array를 이용한 고밀도 유전자 지도 작성

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콩에서 유전자지도 작성은 마커간의 상대적인 위치를 설정하여 금후 genome 상에 목표 유전자 위치를 확보하고 이를 표지화하는데 매우 요긴한 수단으로 활용된다. 최근 많은 연구자들이 콩에서 고밀도의 유전자지도 작성을 위해 노력하였고, 현재 soybean consensus map이 soybase(www.soybase.org)에 공유되고 있다. 본 연구에서는 고밀도의 콩 유전자 지도 작성을 위해 genotyping은 한국과 중국의 콩 genome resequencing결과 얻어진 약 4백만 개의 SNP중에서 선정된 약 180만개의 SNP로 만들어진 180k Axiom SoyaSNP array를 이용하였고, 실험집단은 큰올콩/신팔달콩 및 큰올콩/익산10호의 교배후대로 작성된 F₁₂ RIL 집단을 활용하였다. 유전자지도 작성결과 큰올콩/신팔달콩 집단에서 사용된 166,279개의 SNP 중 27,308개의 SNP가 다형성을 보였고 이중 6,535개의 SNP가 유전자지도상에 표기되어 지도의 총 거리는(total coverage)는 약 3,313cM을 나타내었다. 한편 큰올콩/익산10호 집단에서는 사용된 166,279개의 SNP 중 23,581개의 SNP가 다형성을 보였고 이중 6,597개의 SNP가 유전자지도상에 표기되어 지도의 총 거리는(total coverage)는 약 5,017cM을 나타내었다. 본 연구를 통해 작성된 유전자지도에서 마커간 평균거리는 큰올콩/신팔달콩 0.51cM, 큰올콩/익산10호 0.76cM으로 나타나 매우 고밀도의 유전자 지도가 작성되었음을 나타내었다.

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PC-122

Natural Variation of the *FLOWERING BHLH1* Contributes to Flowering Time Divergence in RiceMin-Young Yoon¹, Aye Aye Khaing¹, Win Htet Oo¹, Tae-Sung Kim¹, Yong-Jin Park^{1,2,*}¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340-702, Republic of Korea²Legume 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. The floral transition from vegetative to reproductive development is a very important step in the life cycle of a flowering plant. Although the genetic pathway for short-day flowering in rice is relatively well understood, the naturally occurring molecular mechanisms underlying flowering time diversity of the cultivated rice are still not clear. Resequencing of 295 rice accessions including 137 HS and 158 KB rice accessions, was recently finished with an average of approximately 10x depth and > 90% coverage. A wide range of variation in flowering time was observed within a diversity research set of 295 accessions ranging from 28 to 72 days. GWAS was performed using the resequencing data to investigate the candidate genes associated with flowering time in rice. Our GWAS result suggests that two SNPs in the promoter or 3' UTR of the 'Arabidopsis CO' homolog FBH1 are potentially associated with early flowering. The new SNPs found in the FBH1 locus would be useful in developing markers to screen the varieties with early flowering time in the future molecular breeding.

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PC-123

Expression analysis of UV-B signaling genes in soybean [*Glycine max* (L.) Merr.].Yoon, M.Y.^{1*}, Shim, S.R.¹, Kim, M.Y.^{1,2}, Kim, K.D.¹, Lee, Y.H.¹, and Lee, S.H.^{1,2}

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Due to depletion of the stratospheric ozone layer throughout most of this century, increased UV-B radiation has affected seriously to plant growth and development as one of nature mutagens. We surveyed differential expressed genes (DEGs) under UV-B irradiation in UV-B tolerant Buseok compared to UV-B sensitive Cheongja 3 through RNA seq analysis using six RNA samples of Buseok and Cheongja 3 with 0.5 hr and 6 hr UV-B irradiation or without irradiation. After excluding 1003 DEGs due to genetic background difference of two genotypes, a total of 872 DEGs orthologous to UV-related Arabidopsis genes were identified. BINGO analysis of the DEGs by 0.5 hr UV-B irradiation showed overrepresentation in signaling and cell morphogenesis. Genes related with apoptosis and immune response were overrepresented in 6 hr irradiated Buseok. In addition, KEGG pathway database was used to identify mTOR signaling and phosphatidylinositol signaling pathways. Based on GO and KEGG results, specific focus was given to a serial of genes involved in UV-B defense signaling, besides photomorphogenesis and oxidation reduction-related genes. Several genes playing a role in phosphatidylinositol signaling, such as diacylglycerol kinase, phosphatidylinositol-4-phosphate 5-kinase family protein, were highly expressed in UV-B tolerant Buseok by 0.5 hr irradiation. Mitogen-activated protein kinase (MAPK) 19 and 20 were highly expressed in Buseok under 6 hr irradiation. Furthermore, 51 nucleotide binding site leucine rich repeats (NBS-LRRs) genes were up-regulated in Buseok under 0.5 hr irradiation.

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PC-124

HRM 기술을 이용한 인도수출용 조생계 양배추 종자순도검정 마커개발

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양배추(*Brassica oleracea*)는 전 세계적으로 가장 많이 키우는 작물 중 하나이며 2,084천ha에 달하는 재배면적을 차지하고 있으며 생산량은 58백만 톤으로 경제적 가치가 높은 작물이다. 특히 인도 및 서남아시아의 경제성장과 함께 양배추 생산량이 증가하고 있으며 특히 교배종의 종자수요가 크게 늘고 있다. 인도 및 서남아시아 시장 맞춤형 양배추 품종육성과 함께 고순도의 종자를 안정적으로 공급하기 위해서는 분자마커를 활용한 순도검정 시스템 구축이 필요하다. F1의 순도검정에는 포장검정을 통한 재배시험 방법이 있으나 이는 시간과 비용, 노력이 많이 소비되기 때문에 어려움이 많다. 분자마커를 이용한 유전형 검정을 통한 순도검정을 실시함으로써 환경에 대한 영향을 최대한 줄이고 신속하고 정확하게 결과를 얻을 수 있다. 본 연구에서는 인도수출용 조생계 10품종에 대한 순도검정용 분자마커를 개발하고 생산종자에 대한 검정을 실시하였다. 분자마커의 정보는 배추 및 양배추의 데이터베이스와 문헌조사를 통해 다형성 지수(PIC)가 0.3~0.8이상인 SSR과 SNP 마커를 추출하여 적용을 실시하였다. HRM(High resolution melting) 분석을 실시한 결과, 1차적으로 양배추 품종의 모, 부계와 F1의 다형성 마커를 32개 선발하였고 30세트 이상의 모, 부계로 마커의 실효성을 2차 검정하여 22개의 마커를 선발하였다. 22개의 선발된 마커 중 HRM 해리곡선이 뚜렷한 마커 10개를 재선발하여 각 품종의 종자순도검정을 실시하였다. 각 품종별 채종 방식에 따라 생산 Lot당 검정주를 200~300립으로 조정하여 검정하였다. 양배추 10품종의 분자마커를 활용한 유전형 검정을 통해 95.8% 이상의 유전적으로 안정된 고순도의 종자가 생산되는 것을 확인하였다.

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PC-125

중국수출용 극조생계 양배추 종자순도검정 마커개발

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중국 주요 채소 중 양배추는 소매가 기준으로 6억 RMB로 전체 작물 중 4위의 작물로 매우 중요한 작물이다. 재배 면적은 전 세계 재배면적의 50%인 70-100만ha(한국의 200배)로 재배규모로는 가장 큰 국가이다. 향후, 유럽 및 미국 국가의 가공용 양배추의 재배 및 가공기지로의 성장 가능성이 매우 높은 국가이다. 중국 양배추 시장의 교배종 점유율은 계속해서 증가하는 추세로 고순도의 F1 종자를 안정적으로 공급하기 위해서는 순도검정이 반드시 필요하다. 종자의 순도검정은 생산된 종자를 직접 파종 재배하여 품종특성을 평가하는 포장순도 검정이 있지만 이는 시간과 비용, 노력이 많이 소비되기 때문에 어려움이 많다. 그러나 분자마커를 이용한 순도검정법을 실시한다면 환경에 대한 영향을 최대한 줄이고 신속하고 정확하게 결과를 얻을 수 있으며, 유전적으로 고순도의 종자를 공급할 수 있다. 본 연구에서는 중국 수출용 극조생계 11 품종에 대한 순도검정용 분자마커를 개발하고 생산종자에 대한 검정을 실시하였다. 다량의 샘플을 경제적으로 검정가능한 HRM(High resolution melting) 분석방법을 이용하였다. 이를 위하여 순도검정 마커를 배추과 작물의 데이터베이스를 조사하여 다형성이 높은 마커 SSR과 SNP를 추출하였고 또한 배추과 작물 및 양배추의 문헌을 조사하여 다형성 지수(PIC)가 0.3~0.8인 마커를 추출하여 이용하였다. HRM 분석을 실시한 결과, 1차적으로 양배추 품종의 양친과 F1의 다형성 마커 38개를 선발하였고 30세트 이상의 양친으로 마커의 실효성을 2차 검정하여 25개의 마커를 선발하였다. 선발된 마커 중 HRM 해리곡선이 뚜렷한 마커 11개를 최종 선발하여 각 품종의 종자순도검정을 Lot당 200립 종자를 대상으로 실시하였다. 양배추 11품종의 분자마커를 활용한 유전형 검정을 통해 97.8% 이상의 유전적으로 안정된 고순도의 종자가 생산된 것을 확인하였다.

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PC-126

Characterization of soybean transgenic events harboring Insect resistant genes

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Insect resistant genes encode insecticidal δ -endotoxins that are widely used for the development of insect-resistant crops. Common soybean is a crop of economic and nutritious importance in many parts of the world. Korean soybean variety Kwangan was transformed with Insect resistant genes. These genes were transformed into Kwangan using highly efficient soybean transformation system. Transgenic plants harboring Insect resistant genes were confirmed for gene introduction and their expression using PCR, real-time PCR and RT-PCR. The confirmation of stable gene introduction with Insect resistant genes was also performing by Southern blot analysis. In addition, Flanking sequence analysis and agronomic characters were also investigated.

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PC-127

Anthocyanin accumulation and biological change of purple-colored wheat by chronic gamma-irradiation

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Chronic gamma irradiation can be used an alternative mutation breeding methods for induction of many useful mutants. Seedlings of purple-colored wheat plants were irradiated with wide range doses of chronic gamma-rays (20, 25, 30, 40, 50, 70, 100, 125, 150, 200, 250, 300 Gy) during 6 weeks at gamma-phytotron in the Korea Atomic Energy Research Institute, respectively. To identify the biological responses purple-colored wheat, we examined the plant height, chlorophyll, carotenoid and total anthocyanin contents in leaf. Plant growth, chlorophyll and carotenoid contents in leaf were decreased when the dose rate increased. Anthocyanin contents were increased with the increase of the radiation dose until 50 Gy treatment. To confirm the real contents of anthocyanin, we also investigated cyanidin-3-glucoside in purple-colored wheat leaf by using UPLC analysis. These results indicate that anthocyanin accumulation was observed under chronic gamma irradiation.

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PC-128

Transgenic rice plants expressing double insecticidal genes using anther culture

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Rice is one of the most important cereal crops in the world and a model plant for functional genomics of monocotyledon. Recently, rice crop loss is estimated to be approximately 30% of the total yield due to herbivorous pests, mainly insects. Cry1Ac toxin is a protein produced by the bacterium *Bacillus thuringiensis* and has insecticidal properties. CryBP1 toxin also is an insecticidal protein produced by the bacterium *Bacillus popilliae*. These two toxic genes derived bacteria, which were inserted into a binary vector, have been introduced into rice plants by *Agrobacterium tumefaciens* mediated transformation in order to enhance resistance to insects. Here, we utilized anthers to regenerate transgenic rice plants when it has been plated on the callus induction media as a callus-inducing material. Anther culture has a benefit in terms of being apt to produce doubled haploids in short term in plants breeding compared to seed culture. However, anther culture method in generating transgenic rice still has low productivity of plant regeneration in some genotypes of Japonica rice. Therefore, we examined the efficiency of callus induction and transformation with three different cultivars of Japonica rice, Haiami, Ungwang and Dongjin. In this study, our results showed that Haiami is the best genotype among three cultivars of Japonica rice as callus inducing material in anther culture to produce transgenic rice plants conferring resistance to insects.

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PC-129

Characterization of Anthocyanidin Synthase (ANS) Genes Correlating with Cold and Freezing Stress in *Brassica rapa*

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Flavonoids are divided into several structural classes, including anthocyanins, which provide flower and leaf colors and other derivatives with diverse roles in plant development and interactions with the environment. This study characterized four Anthocyanidin Synthase (*ANS*) genes of *Brassica rapa*, a structural gene of anthocyanin biosynthetic pathway, and investigated their association with cold and freezing tolerance in *B. rapa*. Sequences of these genes were analyzed and compared with similar types of gene sequences of other species and found a high degree of homology with their respective functions. In the organ specific expression analysis, these genes showed expression only in the colored portion of leaves of different lines of *B. rapa*. On the other hand, *BrANS* genes also showed differential expression with certain time course of cold stress treatment in *B. rapa*. Thus, the above results suggest probable association of these genes with anthocyanin biosynthesis and cold and freezing tolerance and might be useful resources for developing cold resistant *Brassica* crops with desirable colors as well. The present work may help explore the molecular mechanism that regulates anthocyanin biosynthesis and its response to abiotic stress at the transcriptional level in plants.

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PC-130

Effects of herbicide tolerance rice on microbial community in paddy soil

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Rice (*Oryza sativa*) is the most important staple food of over half the world's population. This study was conducted to evaluate the possible impact of transgenic rice cultivation on the soil microbial community. Microorganisms were isolated from the rhizosphere of GM and non-GM rice cultivation soils. Microbial community was identified based on the culture-dependent and molecular biology methods. The total numbers of bacteria, fungi, and actinomycete in the rhizosphere soils cultivated with GM and non-GM rice were similar to each other, and there was no significant difference between GM and non-GM rice. Dominant bacterial phyla in the rhizosphere soils cultivated with GM and non-GM rice were *Actinobacteria*, *Firmicutes*, and *Proteobacteria*. The microbial communities in GM and non-GM rice cultivated soils were characterized using the denaturing gradient gel electrophoresis (DGGE). The DGGE profiles showed similar patterns, but didn't show significant difference to each other. DNAs were isolated from soils cultivating GM and non-GM rice and analyzed for persistence of inserted gene in the soil by using PCR. The PCR analysis revealed that there were no amplified protox gene in soil DNA. These data suggest that transgenic rice does not have a significant impact on soil microbial communities, although continued research may be necessary.

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PC-131

Sound wave improves drought and salt tolerance in rice plant in wavelength specific manner

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We investigated whether sound waves could improve salt tolerance in rice seedling. The rice seedlings were sound treated with 800 Hz for 1hr, and then treated with 0, 75, 150, and 225mM NaCl for 3 days to observe changes in physiological and morphological aspects. Sound treatment seedlings resulted in enhanced salt stress tolerance, mainly demonstrated by the sound treated seedlings exhibiting of increased root relative water contents (RWC), root length and weight, photochemical efficiency (ratio of variable to maximum fluorescence, F_v/F_m), and germination rate under salt stress condition. This demonstrates that a specific sound wave might be used, not only to alter gene expression in plant, but also to improve salt stress tolerance. In order to test the sound's effect on plant and its contribution in drought tolerance, plants were subjected to various sound frequencies for an hrs. After 24-hrs sound treatment, plants were exposed to drought for next five days. During the experiment it was observed that sound initiated physiological changes showing tolerance in plant. Sound frequency with ≥ 0.8 kHz enhanced relative water content, stomatal conductance and quantum yield of PSII (F_v/F_m ratio) in drought stress environment. Hydrogen peroxide (H_2O_2) production in sound treated plant was declined compared to control. *ThermaCAM* (Infra-red camera) a software which was used to analyze the plant images temperature showed that sound treated plant and leaf had less temperature (heat) compared to control. The physiological mechanism of sound frequencies induce tolerance in rice plants are discussed.

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PC-132

Assessment of gene flow from disease resistant rice to its weedy rice

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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 quantified the amount determined the frequency of pollen mediated gene flow from disease resistant GM rice to weedy rice (R55). A total of 164,604 seeds were collected from weedy rice, which were planted around GM rice. Resistance of the hybrids was determined by repeated spraying of herbicide and DNA analysis using specific primer to confirm hybrids. Though weedy rice has 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.

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PC-133

Whole genome sequencing of *Brachypodium* mutant induced by gamma radiation.

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Brachypodium distachyon has been well known as a model plant for monocot plants. *Brachypodium* has many advantages such as small plant size, small genome, short life cycle, self-fertility, and etc. Moreover, *Brachypodium* standard line Bd21 had already been sequenced and the data of which now have been available to the public. The development of next-generation sequencing technologies has allowed the discovery of large numbers of genome-wide DNA polymorphisms. *Brachypodium* standard line Bd21 was exposed to chronic gamma radiation. M₂ 1376-1 line was less stained with phloroglucinol compared to wild-type, which indicated reduced lignin content. Also, its filial generations showed dwarf phenotype. Genomic DNA was extracted from the M₃ plant and was used to construct a whole-genome re-sequencing library for using Illumina HiSeq2500. The trimmed reads were aligned to the *Brachypodium* reference genome sequence (<http://www.phytozome.net>). SICKLE, BWA, and Picard were used for accurate variant detection. More than 110 M reads were generated and 96.53% of them were mapped. This represents ~35 fold coverage. As a result, mutant specific SNVs, Insert/Deletions, and non-synonymous mutations were obtained. Moreover, non-synonymous mutations were identified from 5 lignin biosynthesis genes (*Bradi1g31320*, *Bradi3g52350*, *Bradi5g21550*, *Bradi3g22980*, *Bradi5g14720*). The obtained results will be incorporated in development of biofuel crops.

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들깨 유전체 해석용 자원의 특성 및 유전지도작성용 집단 육성

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경상남도 밀양시 점필재로 20 국립식량과학원 두류유지작물과

들깨는 꿀풀과 1년생 식물로 우리나라 주요 유지작물 중 하나이다. 재배종인 *Perilla frutescens* var. *frutescens*(들깨)와 *Perilla frutescens* var. *crispa*(차조기)는 서로 변종의 관계로서 염색체가 $2n = 40$ 이며, 야생종으로는 *Perilla citriodora*, *P. hirtella*, *P. setoyensis*가 있으며 모두 $2n = 20$ 의 염색체를 가진다. 들깨의 표준유전체 해석을 위한 재료로서 *P. citriodora*(YCPL450)를 선정하였다. YCPL450은 2005년 제주도에서 수집한 들깨 야생종으로 *P. citriodora*로 분류되며, 염색체수는 들깨 재배종($2n=40$)의 반인 $2n=20$ 으로 유전체 해석에 효율을 높이고자 선정하였다. 유전지도작성용 집단을 육성하기 위해 표준 유전체 재료인 *P. citriodora*와 *P. hirtella*를 교배하여 F1을 양성하였으며, SCAR marker를 이용하여 교배유무를 확인하였다. 표준유전체 및 비교유전체 분석을 위하여 재료의 순계화 양성 및 특성검정을 수행할 예정이며, 향기성분 및 진화론적 분류 탐색을 위한 집단을 양성할 것이다.

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토마토 TYLCV 검정을 위한 SNP 마커 개발 및 계통검정

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토마토(*Solanum lycopersicum* L.)는 전 세계적으로 생산량이 연간 146백만 톤이며 재배면적은 4,339천ha에 달하는 채소작물로 경제적 가치가 매우 높다. 최근 국내 및 미국, 남미, 유럽, 동남아시아, 일본, 중국 등지로 토마토황화잎마름바이러스 (Tomato yellow leaf curl virus; TYLCV)가 급격히 확산되고 있어 토마토 생산량과 농가소득 감소 등의 심각한 피해를 입히고 있다. 토마토의 TYLCV 저항성 유전자는 야생종에서 *Ty-1*, *Ty-2*, *Ty-3*, *Ty-4*, *Ty-5* 등이 보고되고 있으며 이들 유전자원을 활용한 계통 및 품종 육성이 활발하게 이루어지고 있다. 자사에서 TYLCV의 피해를 최소화할 수 있는 저항성 품종 육성을 주요 목표로 하여 품종 육성을 활발하게 진행하고 있다. 최근에는 내병계 품종 육성에 분자마커를 활용함으로써 신품종 개발기간을 단축시키고자 하는 노력이 많이 이루어지고 있다. *Ty-1*, *Ty-2*, *Ty-3*에 대한 CAPS 또는 SCAR 마커 개발이 보고되고 있으나(Hoogstraten *et al.*, 2005; Garcia *et al.*, 2007; Ji *et al.*, 2007), gel-based 마커로 검정에 많은 시간과 노력이 필요하다. 본 연구에서 TYLCV 내병계 육성을 위해 보다 신속하고 효율적인 분자마커 검정을 실시하고자 *Ty-1*과 *Ty-3*의 SNP마커를 개발하였다. 기 개발 마커를 활용하여 내병계 계통 및 도입품종 20개의 *Ty-1*과 *Ty-3*의 염기서열을 분석하여 20개의 프라이머 셋트를 제작하였다. *Ty-1* SNP2와 *Ty-3* hrm3 마커를 선발하고 계통 및 품종으로 HRM (high resolution melting)분석을 통해 실효성을 판단하였다. 또한 자사의 시판 이병계와 내병계 종자를 대상으로 검정을 실시하여 *Ty-1* SNP2와 *Ty-3* hrm3 마커의 실효성을 확인하였다. 개발된 마커를 활용하여 2014년 봄작기 파종 F2 분리세대 50 계통과 도입품종 21 품종에 대한 검정을 실시하여 품종육성을 위한 자료로 활용하였다.

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PC-136

멜론의 고효율 배주배양법

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멜론은 세계 10대 주요채소로 대표적 글로벌 작물이며, 박과작물에서 가장 큰 비중을 차지하는 주요 작물이다. 멜론은 주로 교배와 선발에 의하여 품종육성이 이루어지고 있어 육종소재 육성에 많은 노력과 시간이 소요되고 있다. 따라서 단기간에 고정계통을 얻을 수 있는 반수체 배양법을 품종 육성에 적용할 필요가 절실히 요구되고 있다. 박과작물은 약배양 및 소포자 배양 효율이 낮아 극히 제한적으로 이용되고 있으며 일반적으로 자성 발생을 이용한 위수정배 배양 및 배주배양법을 이용하고 있다. 본 연구에서는 내병성 및 환경 적응성이 높은 5품종의 F1 (BN143, 145, 150, 152, 153)의 배주를 재료로 하여 배주배양을 실시하여 반수체 식물체를 유기하여 다양한 육종소재를 확보하고자 하였다. 재료는 개화 24시간, 12시간, 6시간, 개화 직후의 샘플을 채취하여 씨방을 1mm로 슬라이스하여 배지조성 (MS와 NLM), 호르몬 조성(TDZ, BAP, NAA, Kinetin), sucrose 농도, 전처리 온도와 기간별로 식물체 유기율을 조사하였다. 품종간의 식물체 유기율은 상이하였으나 BN143, BN145, BN150은 개화 6시간 전의 시료에서 TDZ 0.02mg/L에 10일간 치상 후 BA와 NAA 혼합배지로 계대배양한 절편에서 식물체 유기율이 높았다. BN152와 BN153에서는 배주의 일부가 캘러스화 되기는 했으나 식물체는 유기되지 않았다. 품종별 식물체 유기율이 상이하므로 품종에 맞는 조건설정과 고효율의 배양계 구축이 필요할 것으로 사료된다. (본 연구는 농림수산식품부 수출전략기술개발사업(312065-05-2-HD020)의 지원에 의해 이루어진 것임.)

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PC-137

제조저항성 들잔디의 환경방출 모니터링

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유전자변형(genetically modified, GM)작물 도입 유전자의 이동은 안전성평가 및 안전관리에 있어 매우 중요한 요소이며, 환경 모니터링 연구는 이러한 유전자이동성 확인을 위한 연구 중 하나로 많이 사용된다. 본 연구는 제조저항성 들잔디(zoysiagrass)의 야외환경 모니터링을 수행을 통한 환경모니터링 시스템 기반 구축을 위해 수행되었다. 연구에 사용된 GM들잔디는 제조저항 형질의 JG21과 JG21에 방사능처리로 옹성불임을 유도한 JG21-MS 등 2개의 이벤트를 이용하였다. 환경모니터링은 충남 성환, 충북 오창, 제주대 및 제주 남원읍 등 4개 격리포장 주변에서 2011년부터 2013년까지 3년간 총 265개 지점, 1,634개체에 대해 화분에 의한 유전자이동 및 종자, 영양번식체에 의한 산포 조사를 통해 수행되었다. 모니터링 수행 결과 3개 지역에서 유전자이동 및 산포가 발견되지 않았으나, 2012년 제주 남원읍 지역 조사에서 격리포장 주변 2m 부근에서 JG21 1개체의 유출이 발견되어 보고 및 안전관리 조치를 수행하였다. 또한 RAPD (random amplified polymorphic DNA)법을 이용한 JG21과 JG21-MS의 구분판별법을 개발하여 GM들잔디의 환경방출실험 및 상업화 후 사후 안전관리에 활용될 수 있게 하였다.

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PC-138

Identification of genes associated with leaf-morphology in *Brassica rapa* L. using Br135K microarray

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Chinese cabbage is one of most important vegetable crop in Eastern Asian countries including Korea. Because Chinese cabbage is a leafy vegetable, genetic research with respect to the leaf morphology is important. In this research, we have used two inbred lines of Chinese cabbages (Kenshin and RCBr) and generated recombinant lines having various leaf morphology. In F2 population of Kenshin X RCBr, leaf shape showed very dramatic variations with normal distribution in terms of leaf size, petiole length, leaf margin and *etc.* Microarray with a 135K DNA chip (version 3) integrated 2 sets of total Chinese cabbage genes. Biological process of candidate genes was classified into transcription factor, genes encoding kinase activity protein, protein folding related genes, oxidation-reduction process genes. Putative leaf-morphology-related genes were 142 that are involved in phytohormone pathway genes, cell proliferation & cell elongation related genes and genes controlling leaf morphogenesis *etc.* These genes are further classified to phytohormone signaling-associated genes (*SAUR44*, *PIN2*, *CPK6*, *RDUF2*), leaf development regulating genes (*DWF4*, *CUC2*, *TCP15*, *BLH4*, *NGA4*), and cell division and cell growth related genes (*ILP1*, *TCTP*, *EMB1027*).

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PC-139

형질전환 벼 고세대 계통의 농업형질 평가

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고세대 형질전환 벼 계통인 가뭄저항성 벼(CaMsrb2), 레스베라트롤 합성벼(RS), 인산 이용성 증진 벼(OsPT7) 3계통과 모품종인 일미벼와 동진벼, 그리고 비교 품종으로 화성벼와 남평벼를 이용하여 수원, 익산과 밀양의 3개 지역 GMO 격리 포장에서 표준재배 시험으로 농업형질을 평가하였다. 가뭄저항성 벼 계통(CaMsrb2)은 익산에서 출수기가 모품종 대비 1일 정도 늦었으며 라스베라트롤 합성벼(RS)는 수원, 익산, 밀양에서 모품종과 비교하여 4~5일 늦고, 인산 이용성 증진 벼(OsPT7) 계통은 익산지역에서 모품종 대비 1일정도 늦게 출수되었다. 형질전환 3계통의 수량성은 3개 지역에서 모품종 대비 수량지수가 88~102 였으며 수원과 익산에서 3계통은 모품종과 수량차이가 없었으나 밀양에서 가뭄저항성 벼 계통과 인산이용성 증진 벼 계통은 모품종 보다 수량이 낮은 것으로 나타났다. 형질전환 3계통은 모품종과 생육비교에서 출수기, 등숙비율, 천립중, 수량성과 지역 적응성에 차이가 있는 것으로 평가 되었다.

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PC-140

GBS analysis of *Camelina* germplasms

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Camelina is a promising energy crop for the biodiesel industry, especially for production of airplane fuel. In addition, its distinctive fatty acid profile and high protein contents satisfy the nutraceutical and animal feed uses. About 200 accession collected from all of the world were selected and evaluated during 2012, 2013 and 2014. The important agricultural traits were detemined by field and greenhouse conditions. In addition, genetic diversity was assessed by GBS approach. a total of 20 *Camelina* spp. (mostly *C. sativa*) accessions collected in different locations in Europe and showed different agronomic traits are sequenced. In this section, detail GBS analysis of camelina will be presented.

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PC-141

GBS-based QTL mapping of cucumber downy mildew resistance

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Downy mildew, caused by *P. cubensis*, is one of the most devastating diseases in cucumber (*Cucumis sativus*) worldwide. Due to the variation and mutation of the races of *P. cubensis*, host resistance in cucumber has been lost in recent years, so the identification of new sources of resistance is one of the most important targets in cucumber breeding programs. Moderate levels of resistance against downy mildew has been identified in different cucumber varieties. In this study, we identified new downy mildew resistance QTLs in cucumber using F2 mapping populations originated from the hybridization between breeding lines of cucumber. We used both classical QTL mapping based on SSR markers and GBS (genotyping based sequencing) based QTL mapping. In this presentation, detailed information about downy mildew resistance related QTL will be presented

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PC-142

Programed cell death was induced by infection of *P. cubensis* Effectors

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식물이 병원체의 침입을 받으면 식물체내로 단백질을 전달한다. 병원체가 식물체내로 분비하는 단백질 중에서 cell death를 일으키는 단백질들에 대해 관심을 가졌다. 먼저 *Pseudoperonospora cubensis* 에 감염된 오이 잎에서 발현되어 병원체 유래의 단백질을 기존에 알려진 RLXR 도메인을 가진 염기서열에서 프라이머를 디자인 하여 PCR 반응을 통해 cloning 하였다. 이중에서 *P. cubensis* 접종시 발현이 증가하는 단백질들을 중심으로 *Nicotiana benthamiana*에 Infection 시켰다 그 결과 Infection된 Effector 들 중에서 2개의 Effector에서 visible한 cell death를 관찰할 수 있었다. 상세한 결과가 포스트를 통해서 발표될 것이다.

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PC-143

Safety Assessments of CaMsrb2 Protein for Drought-Tolerant Rice

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The aim of the study was to assess the safety of methionine sulfoxide reductase B2(CaMsrb2) protein as toxicity, allergenicity and identity of inserted gene product that transformed rice. Through bioinformatical research of CaMsrb2, amino acid sequence of CaMsrb2 did not share overall homology with any known or suspected to be allergen or toxin protein. For the biochemical research, CaMsrb2 protein was expressed and purified. Using purified protein, we made a specific antibody. Purified protein was sequenced by Edman degradation methods and confirmed sequence identify.. The amino acid sequences of purified protein were the same as deduced amino acid sequences exclude N-terminal Histidine. And for the internal sequences of CaMsrb2, we performed MALDI-TOF Mass. The results of MALDI-TOF MS was compared Mascot Database and confirmed the sequence coverage was 56%. These results mean bacterially produced CaMsrb2 was the same with inserted gene product. With these purified and identified CaMsrb2 protein, we performed acute toxicity test. Following the OECD guideline 423, 2,000mg/Kg body weight protein were injected as oral administration. After 2 weeks, there did not shown any death and special symptoms.

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PC-144

Characterization of soybean transgenic events harboring ORE7 gene

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ORE7 gene incorporated into 3 different promoters including pCKLSL-35S, pCKLSL-TP and pCSENIIF was transformed to Korean soybean variety Kwangan using highly efficient soybean transformation system. The gene is known to exhibit a delayed leaf senescence phenotype in Arabidopsis. Fourteen, Fifteen and nine transgenic plants were produced from pCKLSL-35S::ORE7, pCKLSL-TP::ORE7 and pCSENIIF::ORE7, respectively. Moreover, transgenic plants were confirmed for gene introduction and their expression using PCR, qRT-PCR and RT-PCR. To identify the transgene insertion events, the analysis of flanking sequence was determined. As a results, T-DNA was integrated intergenically in transgenic line 1 of pCKLSL-35S::ORE7 and line 1 of pCSENIIF::ORE7. Currently, flanking sequence analysis with pCKLSL-35S::ORE7, pCKLSL-TP::ORE7 and pCSENIIF::ORE7 is carrying out to investigate the stable T-DNA insertions.

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PC-145

레스베라트롤 생합성 벼(I526)의 이용확대를 위한 레스베라트롤 및 피세이드 함량 증진 조건 확립

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레스베라트롤(3, 5, 4'-trihydroxytibence)은 포도, 와인, 땅콩 등에서 발견되는 항산화 물질로 과일에서 레스베라트롤과 3-β-mono-D-glucoside가 결합된 피세이드 형태로 발견되며, 항암, 고지혈증, 항혈전작용 등 다양한 약리효과를 가지는 것으로 밝혀졌다. 익산 526호를 25°C와 30°C 암조건에서 1, 3, 5일간 수분 95% 이상 유지하여 발아시켰다. 발아처리 전과 비교하였을 때, 25°C에서 발아처리 후 레스베라트롤 생합성 유전자의 발현은 1.7~2.5배 증가하였으며, 레스베라트롤 및 피세이드 함량은 각각 1.1~1.6배, 1.1~3.8배 증가하였다. 또한, 30°C에서 레스베라트롤 생합성 유전자의 발현은 2.7~14.0배 증가하였으며, 레스베라트롤 및 피세이드 함량은 각각 1.2~2.3배, 2.0~10.5배 증가하였다. 30°C에서 5일간 발아시켰을 때, 레스베라트롤 생합성 유전자의 발현수준이 가장 높았으며, 레스베라트롤 및 피세이드 함량 또한 가장 높은 것으로 나타났다. 발아과정을 통한 레스베라트롤 생합성 유전자 발현 증가는 레스베라트롤 및 피세이드 함량 증가와 밀접한 상관관계가 있는 것으로 생각된다. 따라서 발아처리는 익산 526호의 이용확대를 위한 레스베라트롤 및 피세이드 함량 증진을 위해 효과적인 방법이라고 생각된다.

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PC-146

Search for allopolyploid genome donor of *Vigna reflexo-pilosa*Jayern Lee^{1*}, Suk-Ha Lee^{1,2}¹Department of Plant Science and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul, 151-921, Korea²Plant Genomics and Breeding Institute, Seoul National University, Seoul, 151-921, Korea

Vigna is a genus of flowering plants in the legume family, and about 100 species belong to this genus, including azuki bean, blackgram and mungbean which are well-known in Asia. Among the species in *Vigna* genus, *Vigna reflexo-pilosa* has its own unique characteristic form as allotetraploid ($2n=4x=44$), whereas other *Vigna* species exist as a diploid form ($2n=2x=22$). In this study, we *de novo* assembled *V. reflexo-pilosa* genome and 22 accessions of 18 *Vigna* species' transcriptome using NGS platform and calculated the Ks values of synteny blocks within *V. reflexo-pilosa* to determine the whole-genome duplication event existence. Two WGD events had occurred on *V. reflexo-pilosa* unlike *V. radiata* which only occurred once. Also, we tried to find out which progenitor had contributed to formation of *V. reflexo-pilosa* using transcriptome assemble results of 22 *Vigna* accessions. Ks value calculation between the transcriptome assemble results and predicted gene sets of *V. reflexo-pilosa* has been executed. *V. trinervia* showed 2 peaks (0.0075, 0.0495) on its Ks value bin distribution and confirmed as A-type genome donor. Based on the peak value, we considered the predicted genes of *V. reflexo-pilosa* in Ks value range from 0.033 to 0.072 as B-type genes, inherited from other progenitor. Re-calculating the Ks values of 4,796 predicted genes in B-type with the transcriptome assemble results of 22 *Vigna* accessions, we were able to find 6 *Vigna* species, *V. umbellata*(CIAT34386), *V. umbellata*(2004T2), *V. nakashimae*, *V. nepalensis*, *V. riukiensis*, *V. minima* as candidate B-type genome donor.

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PC-147

Genotyping of apple (*Malus × domestica* Borkh.) using MdACS1 and MdACO1 functional markers

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Apple is a typical climacteric fruit, whose loss of firmness during storage is associated with internal levels of ethylene. MdACS1 (1-aminocyclopropane-1-carboxylate synthase) and MdACO1 (1-aminocyclopropane-1-carboxylate oxidase) genes are characterized well as functional markers for the ethylene production of ripening apple fruit. Presence of two alleles for each gene are commonly reported in cultivated apples. MdACS1-1/1, 1-1/2 and 1-2/2 generally induce high, medium, and low ethylene production, respectively. Homozygosity of MdACO1-1 resulted in low levels of ethylene production than MdACO1-1/2 and 1-2/2. It was reported that cultivars homozygous for MdACS1-2 and MdACO1-1 had superior shelf-life with lowest ethylene production. In this study, genotypes of 42 apple cultivars including Korean-developed ones at MdACS1 and MdACO1 loci were determined. Polymorphisms were detected by PCR and were separated by electrophoresis in a 2.0% agarose gel. Of PCR products of MdACS1, the fragment of 490 bp was corresponded to the MdACS1-1 allele and 640 bp corresponded to the MdACS1-2 allele. ACO1-1 and ACO1-2 alleles had the fragment size of 525 and 587 bp, respectively. The 42 cultivars could be grouped into three classes to each gene, MdACS1-1/1, MdACS1-1/2 and MdACS1-2/2; MdACO1-1/1, MdACO1-1/2 and MdACO1-2/2.

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PC-148

Effects of eukaryotic translation elongation factor 1B (eEF1B) on *Potato virus X* (PVX) infection in plants

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In plants, eukaryotic translation elongation factor 1B (eEF1B) is composed of three subunits, eEF1B α , eEF1B β and eEF1B γ . Two subunits are nucleotide exchange subunits (eEF1B α and eEF1B β) and one is a structural protein (eEF1B γ). In the previous study, eEF1B was identified as a common host factor for several RNA viruses. To test which subunit of eEF1B is essential for *Potato virus X* (PVX) replication, the virus-induced gene silencing (VIGS) for eEF1B α , β or γ was performed in *Nicotiana benthamiana* and green fluorescent protein (GFP)-tagged PVX was inoculated. PVX-GFP accumulation was decreased when eEF1B β or γ subunit was silenced, whereas eEF1B α had no effect on PVX-GFP accumulation in inoculated leaves. Targeting induced local lesions in genome (TILLING) was performed using a *Capsicum annuum* EMS population to test whether mutations in eEF1B β subunit affect virus infection in pepper. We obtained 81 eEF1B β mutant lines consisted of 16,759 individuals. These mutant lines are being tested to validate the function of eEF1B β in PVX replication.

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PC-149

Complete chloroplast genome assembly of *Brassica* species from Next Generation Sequencing-based whole genome resequencing data and comparative analysis

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Chloroplasts are plant-specific organelles, which have their own genome. Most of the plant chloroplast genomes (CP genome) are highly conserved in terms of its gene contents and genome structures, and they exist in cells with abundant copy numbers. Because of numerous copy numbers, the complete chloroplast sequence assembly pipeline with small amount of whole genome resequencing data, produced by NGS technique, was established in our laboratory. From 14 accessions of cabbage (*Brassica oleracea* L.) resequencing data produced by Illumina Hi-seq 2000, CP genomes were assembled and compared to each other. 18 sequence variance regions were detected, and 6 HRM(High Resolution Melting curves) markers were developed. Approximately 1 Gb of whole genome sequencing data of 10 *Brassica rapa* and 2 *Brassica napus* were also obtained from Institute of Vegetables and Flowers, Chinese Academy of Agricultural Science. With these resequencing data, all CP genomes from these accessions were assembled. Total 27 complete CP genomes of *B.oleracea*, *B.rapa*, *B.napus*, and brassico-raphanus which is a novel allotetraploid species between *B.rapa* and *Raphanus sativus*, were compared in sequence level. Phylogenetic analysis based on the comparison revealed that *B.rapa* could be the maternal species when rapeseeds and brassico-raphanus became allotetraploid species. Additionally, CP genome of *B.napus* cv.M083 is closer to *B.rapa* accessions than the other *B.napus* accessions, thus *B.napus* could have several different origins.

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PC-150

SSR 분자마커를 이용한 색소 및 비색소 옥수수 자식계통들에 대한 유전적 다양성, 집단구조 및 association 분석

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본 연구는 강원도농업기술원 옥수수연구소에서 새로운 기능성 색소옥수수 품종을 개발하기 위해 육성한 총 12개의 색소옥수수 계통들과 찰옥수수 및 일반옥수수 계통들에 대하여 SSR 분자마커를 이용하여 유전적 다양성, 집단구조 및 association mapping 분석을 실시하였다. 그 결과 분석에 이용된 300개의 SSR primer들은 12개의 옥수수 자식계통들에서 총 1,331개의 대립단편을 나타내었으며, 각 SSR primer 당 증폭된 대립단편의 수는 2개(umc1515, umc2249, umc1158, umc1659, phi102228, umc2262, umc1058, nc004, phi092, umc2308, umc1314, umc1178, umc1352a, umc2092, phi057, umc1139, umc1473, umc2338, umc2093, umc1107, umc1054)에서 10개(mmc0111)의 범위로 나타났으며, 평균 대립단편 수는 4.44개였다. 집단구조 분석결과, 12개의 옥수수 자식계통들은 groups I, II, III, admixed group으로 구분되었다. 2개의 자식계통(10S4015, 10S4026)은 group I에 포함되었고, Group II는 총 4개의 자식계통(Mo17, B14A, HW7, HW3)이 포함되었다. 그리고 4개의 자식계통(11CS4117, 11CS4124, 11CS7014, HW9)은 Group III에 포함되었으며, 2개의 자식계통(10S4032, KW7)은 admixed group에 포함되었다. 더욱이 본 연구에서는 색소 및 비색소옥수수 자식계통들에서 분석에 이용된 300개 SSR 마커와 4개의 양적 형질(간장, 착수고, 간경, 수숯길이)과의 연관성을 분석하기 위해서 population structure(Q) 값을 이용하여 Q GLM 분석을 실시하였다. 0.01의 유의수준에서, Q GLM 분석을 이용하여 총 17개의 SSR 마커가 4개의 형질과 association을 확인하였다. 본 연구에서 12개의 색소 및 비색소옥수수 자식계통들에 대한 유전적 다양성, 집단구조 및 association mapping 분석의 결과는 앞으로 강원도농업기술원 옥수수연구소에서 기능성 색소옥수수 품종개발을 위한 계통 육성 및 교배조합 구성 등에 유용한 정보를 제공할 것으로 기대한다.

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PC-151**Cytokinin-dependent secondary growth of the radish root (*Raphanus sativus* L.)**Geupil Jang¹, Jung-Hun Lee¹, Soo-Hyung Park², Ji-Young Lee^{1*}¹School of Biological Sciences, College of Natural Science, Seoul National University, Seoul, Korea 151-747²National Institute of Horticulture and Herbal Science, Suwon, Korea 440-706

A root serves as an essential organ in plant growth by up-taking nutrients and water from soil and supporting the rest of a plant body. Root apical growth and system architecture have been extensively studied because they strongly affect overall plant growth and yields. Some plant species also utilize roots as storage organs. Many of them, including sweet potatoes (*Ipomoea batatas*), cassava (*Manihot esculenta*), and radish (*Raphanus sativus*) are important crops, however their root development has remained elusive. In this study, we characterized radial root growth in the radish and found that it is very similar to the secondary growth in stems. We identified well established cambium zones in the actively growing radish roots. Cell proliferation activities in the cambium zones positively correlated with root growth rates and final yields. Through a comparative analysis with Arabidopsis root expression data, we selected some putative transcription factors whose expression is highly enriched in the cambium and validated their expression in various stages of radish roots. By comparing their expression in two inbred lines with distinctive radial root growth, we identified transcription factors that are involved in morphological differences. More importantly, our investigation suggests that the differences in the root growth of two radish inbred lines are from changes in cytokinin responses. These findings together highlight that radish could serve as an excellent system for studying root crops and that transcriptional regulation and cytokinin signaling are indispensable for the secondary root growth.

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PC-152**Analysis of junction site between T-DNA and plant genome in RWW resistance GM rice**

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Four transgenic rice lines harboring insect-resistant gene *cry3A* showed ideal field performances characterized by high considerable resistance to rice water weevil (*Lissorhoptus oryzaophilus* Kuschel). In this study, we estimated the insert number of foreign genes, and analyzed the flanking sequences of T-DNA in rice genome. As a result, The T-DNA of Btt12R 3-1-1-1 line was inserted in exon region of rice chromosome 10 and Btt12R 6-1-1-1 line was inserted in two copies of foreign gene. Btt12R 9-1-1-1 line was analyzed at only left border flanking sequence. The T-DNA of Btt12R 13-1-1-1 line was inserted one copy of foreign gene between position 24,516,607~24,516,636 of rice chromosome 5 and 30bp known genomic sequences were deleted. The Btt12R 13-1-1-1 line confirmed to be inserted in intergenic region having not any expressed gene and no any deletion/addition of T-DNA sequence. From these results, we demonstrated that the molecular data of rice water weevil resistant Bt rice could be acceptable to conduct the biosafety and environment risk assessment for GM crop commercialization

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PC-153

Gene expression profiling study of grapevine in response to the Pierce's disease and drought stress

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Susceptible *Vitis vinifera* responds to *Xylella* infection with a massive redirection of gene transcription. This transcriptional response is characterized by increased transcripts for phenylpropanoid and flavonoid biosynthesis, ethylene production, adaptation to oxidative stress, and homologs of pathogenesis related (PR) proteins, and decreased transcripts for genes related to photosynthesis. In addition, the results suggest that susceptible genotypes respond to *Xylella* infection by induction of limited, but inadequate, defense response. We also compared the transcriptional and physiological response of plants treated by pathogen infection, low or moderate water deficit, or a combination of pathogen infection and water deficit. Although the transcriptional response of plants to *Xylella* infection was distinct from the response of healthy plants to moderate water stress, we observed synergy between water stress and disease, such that water stressed plants exhibit a stronger transcriptional response to the pathogen. This interaction was mirrored at the physiological level for aspects of water relations and photosynthesis, and in terms of the severity of disease symptoms and pathogen colonization, providing a molecular correlation of the classical concept with the disease triangle.

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PC-154

Development of interactive comparative analysis platform for the legume translational genomics

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Comparative analysis is a typically useful tool for translating genomic information from one species to another. However, currently available softwares are relatively difficult to directly use for researchers that are not familiar with use of bioinformatic tools. Therefore, we intended to develop a new platforms and/or interface through which one can use in more comfortable way, based on the concept of interactive comparative analysis. Towards this direction, we, firstly, constructed relational database to store the information on abiotic stress genes identified from multiple plant species using various resources, such as the TAIR (<http://www.arabidopsis.org>), gene expression profiles and relevant literatures, and linked with comparative analysis interface. For purposes of comparative analysis and identification of synteny blocks, cross-species orthologous genes were determined using a combination of tBlastX and BlastP homology searches. We adapted and developed a Circos-like format to present resulting comparative maps. Users can readily choose analysis parameters, for example individual genes and specific chromosomes for chosen species, in the pane of analysis DB, which is useful feature to avoid complexity of comparative genomic analysis. This DB-associated comparative analysis tool, developed in this study, will be able to provide customer-friendly interface for comparative analysis and extend its utility across a broader range of plant genomes.

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PC-155

Integration of comparative genetic maps for ten legume species using gene-based cross-species markersChaeyoung Lee¹, Daejin Hyung², Jinhyun Kim¹, Yejin Jo³, Jusuk Park³, Dongwoon Yu³, and Hongkyu Choi^{3*}¹Department of Medical Bioscience, Dong-A University, Busan, Republic of Korea²Department of Computer Science, Dong-A University, Busan, Republic of Korea³Department of Genetic Engineering, Dong-A University, Busan, Republic of Korea

The legume family is the third largest group, including approximately 650 genera and 18,000 species, in the flowering plants and the second important crops to the Poaceae in the agricultural economy. Comparative analysis is a useful tool to understand cross-species genomic structure and alterations during organism's evolutionary history. In this study, we constructed a composite comparative map of ten legume species, including *Medicago truncatula*, *Medicago sativa*, *Lens culinaris*, *Pisum sativum*, *Lotus japonicus*, *Cicer arietinum*, *Vicia faba* L, *Vigna radiata*, *Phaseolus vulgaris* and *Glycine max*. Of these species, *M. truncatula*, which is a representative model system, played a central role to develop the cross-genome amplifiable PCR gene markers for the purpose of transferring them to other related legume species. A total of 140 cross-species core markers were employed to analyze genomic colinearity across this broad array of legume species. The comparative map demonstrates a diverse array of evolutionary events, such as duplications, inversions and reciprocal translocations. It is anticipated that resulting maps would provide a broader insights into the lineage-specific genomic organization of these glalegoid/phaseoloid legumes, which are two clades containing almost all crop legumes of economic importance, and can further used for the molecular breeding through translating genomic information into other orphan legumes.

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PC-156

Mapping and candidate genes associated with mesocotyl elongation in *Oryza sativa*Hyun-Sook Lee¹, Ju-Won Kang¹, Dong-Min Kim¹ and Sang-Nag Ahn^{1*}¹College of Agriculture and Life Sciences, Chungnam National University, Daejeon 305-764, South Korea

Rice mesocotyl is the region between the coleoptile node and point of union of the culm with the root. The mesocotyl is one of the important factor contributing to rice seedling emergence from soil in direct seedling. Several quantitative trait loci (QTLs) for mesocotyl elongation of rice had been reported in few studies. However, association mapping of mesocotyl elongation QTL was not conducted. For that reason, we detected QTLs for mesocotyl elongation in agar and soil conditions and confirmed the potentials of QTLs using chromosome substitution lines (CSSLs). Backcross inbred line (BILs) and chromosome segment substitution lines (CSSLs) derived from a cross between Kasalath and Nipponbare were employed to detect QTLs for mesocotyl elongation in rice. A total of 12 QTLs for mesocotyl elongation were detected on chromosome 1, 3, 6, 7, 9 and 12 using 98 BILs in agar and soil conditions. Two QTLs, *qMel-1* and *qMel-3* were consistently detected in both conditions. For substitution mapping of *qMel-1* and *qMel-3*, across was made between 2 CSSLs, CSSL-6 and CSSL-15. Our results showed that the *qMel-1* was located between two markers RM5448 and RM5310 on chromosome 1 and the *qMel-3* was located between RM15859-RM15974 on chromosome 3. To understand factors controlling mesocotyl elongation, cell expansion and division of rice mesocotyl were investigated. Moreover, microarray analysis was conducted to select candidate genes using near-isogenic lines for two QTLs. 194 genes were up- and down regulated in rice mesocotyl.

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PC-157

Prediction of structural variations between *G. soja* and *G. max* using novel prediction methods

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With the advent of next generation sequencers (NGS) that provide sequencing at a substantially lower cost, the development SNPs at the level of whole genomes can be done in a single laboratory. However, genome structural variation including large insertions and deletions, and chromosomal reciprocal translocations has not yet been focused due to the limitation of re-sequencing methods as genome structures rely to that of a known reference genome. For an improved detection of the structural variations after deep re-sequencing of the *Glycine soja* accession CS-14, we *de novo* assembled the whole paired-end reads (W-contigs). After the *de novo* assembly, the paired-end reads that did not match the reference genome of Williams 82 were retrieved and *de novo* assembled them (U-contigs). We then predicted structural variation candidates. For predicting the function of the structural variation candidates, we compared those structural variation candidates with SwissProt DB using BLASTX. Most of them were matched with transposable element related proteins or stress tolerance related proteins (Table 1). We designed 24 primers for all candidates and tested in CS-14 and Williams 82 for validation. As a result, the DNA polymorphism was observed between CS-14 and Williams 82 in the three primer sets, CS14IC10, CS14IC12 and CS14IC15, with the expected size of the PCR product. For further validation, we sequenced the DNA band amplified by CS14IC15, and its sequences were aligned well against the Williams 82 and CS-14 contig. Especially, IC15R-CS14 was aligned in the predicted insertion region, consequently, this sequenced region would indicate structural variation. The other primer sets did not amplified either because they were designed for an amplifying long genomic region or because of the fragmented template DNA.

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PC-158

Melatonin plays a signal molecule to trigger defense response against pathogen attack in Arabidopsis and tobacco

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Melatonin plays pleiotropic roles in both animals and plants. Among them, the possible role of melatonin in the innate immune response in plants was emerging recently. As an initial study, we employed Arabidopsis to see whether melatonin is involved in the defense system against a virulent bacterial pathogen *Pseudomonas syringae* DC3000. It was obviously observed that melatonin application of 10 µm concentration onto Arabidopsis and tobacco leaves induced various pathogenesis-related (PR) genes as well as a series of defense genes activated by salicylic acid (SA) and ethylene (ET), two key factors involved in the plant defense response compared to the mock-treated Arabidopsis and tobacco leaves, respectively. The induction of these defense-related genes in the melatonin treated Arabidopsis was well matched with an increase in resistance against pathogenic bacterium by suppressing its multiplication with about 10 fold relative over the mock-treated Arabidopsis. Furthermore, melatonin induced PR genes were almost completely or partially suppressed in npr1, ein2, and mpk6 Arabidopsis mutants indicative of SA and ET dependency of melatonin in plant defense signaling. These results suggest that melatonin may play a novel defense signaling molecule in plant-pathogen interaction.

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PC-159**Characterization and genetic analysis of a *plastochron 1-6* mutant in rice.**Hyerim Lee¹, Jin Zhuo¹ and Hee-Jong Koh^{1*}

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Plastochron and phyllotaxy are important traits to determine plant architecture. A *plastochron 1-6* mutant was derived from japonica rice cultivar Koshihikari treated with ethylmethane sulfonate (EMS). The *plastochron 1-6* mutant showed reduced plant height, shorter internode length, smaller and more leaves than Koshihikari, its wild type. In addition, the mutant has abnormal panicle, abnormal seed and upper node tillers. The F1 plants between mutant and Koshihikari were normal. In F2 population, segregation ratio between the wild type and mutant was fitted to 3:1. This genetic analysis indicated that *plastochron 1-6* is controlled by a single recessive gene. Bulked segregant analysis revealed that the gene was located on chromosome 10. Through sequencing analysis, we found that *plastochron 1-6* mutant had a single nucleotide transition occurred in the first exon of LOC_Os10g26340 (encoding P450 *CYP78A11*). This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No. PJ008125), Rural Development Administration, Republic of Korea.

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PC-160**Screening of suitable reference genes for real-time PCR analysis in *Citrullus lanatus* under diverse stress conditions.**

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Watermelon (*Citrullus lanatus*) is one of the most economically important cucurbitaceous crop over the world. Screening of proper reference genes was needed to reverse transcription quantitative real-time PCR (qRT-PCR), and it is basic step of many researches including gene expression analysis. However, the reference genes on watermelon has not yet been reported systematically. Therefore, eight candidates of reference genes were selected with reference to Arabidopsis or cucumber papers. They are β -Actin, elongation factor 1- α , glyceraldehy-3-phosphate-dehydrogenase, NADP-isocitrate dehydrogenase, leunig, polypyrimidine tract-binding protein1, ubiquitin-conjugating enzyme E2, and 18S ribosomal RNA. The expression levels of genes were evaluated by qRT-PCR under biotic stress (*Colletotrichum orbiculare* treatment), plant hormone treatment (100 μ M ABA), and abiotic stresses such as drought, cold (4°C), salt (250 mM NaCl) stresses. We founded appropriate reference genes which did not induce or reduce gene expression levels under broad spectrum of stresses by qRT-PCR analysis. These results may provide proper information for the use of appropriate reference genes for gene expression studies in watermelon qRT-PCR analysis.

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PC-161

Screening and analysis of the pathogenesis-related genes expression by RT-PCR after inoculation of *Colletotrichum orbiculare* in *Citrullus lanatus*.

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Watermelon (*Citrullus lanatus*) is one of the most economically important cucurbitaceous crop over the world. Anthracnose disease caused by *Colletotrichum orbiculare*, result to severe damage to cucurbits worldwide. Anthracnose is a typical plant disease which significantly affecting the yield of cucurbit crop. Pathogenesis-related (PR) proteins are well-known plant defense proteins against pathogens. Therefore, we observed PR genes expression patterns when watermelon got anthracnose disease. We did RT-PCR experiment to evaluate differences of PR genes expression pattern among Au-Producer(R), one of the representative of resistance watermelon varieties against anthracnose, and 920533(S), one of the representative of susceptible watermelon varieties against anthracnose. As a result, there were differences of the expression of several PR genes between the R and S watermelon. Analysis of the function of these genes is expected to perform in the future.

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PC-162

Molecular analysis of T-DNA insertion mutant population for transgenic rice plants

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We have generated 383 independent transgenic lines for genetically modified (GM) rice that contained *GPD*, *UtrCSP*, *BrTSR15* and *BrTSR53* genes overexpression constructs under the control of the constitutive *CaMV 35S* promoter. TaqMan copy number assay was determined inserted T-DNA copy number. Also 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 95 FSTs, among which 37 (38.9%) were integrated into genic regions and 58 (61.1%) into intergenic regions. About 27 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 than WT plants. These results may be useful for producing of large-scale transgenic plants or T-DNA inserted mutants in rice.

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PC-163

Genome-wide analysis of structural variation in citrus two varieties related to citrus canker

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Citrus canker caused by *Xanthomonas citri* pv. *citri* is one of economically important diseases in the citrus industry. The devastating bacterial disease results in unattractive quality and a significant reduction in fruit production. Citrus growers and industry in Korea has been struggling with the serious disease causing the prohibition of export market. Korea also became the top import market for oranges. The development of markers linked to citrus canker resistance is strongly needed. In this study, we investigated molecular markers between ‘Kiyomi’ (*Citrus unshiu* × *C. sinensis*), a resistant cultivar, and Natsudaikai (*C. natsudaikai*), a susceptible cultivar. To develop markers, we focused on structural variation (copy number variation, CNV, and presence/absence variation, PAV). It has been well documented that CNV and PAV of defense-related genes are associated with resistant cultivars. Using a read depth approach following next-generation sequencing, we performed genome-wide analysis of CNV and PAV in two varieties. As a result, 633 genes showing at least two times difference between the mapping reads from two varieties and 61 genes showing presence of the mapping reads in only either one of them were screened. Visual inspection using the Integrative Genomics Viewer (IGV) was performed and experimental validation is being investigated. Interestingly, one of PAV candidates showed polymorphism in ‘Kiyomi’ and ‘Natsudaikai’ as well as other resistant and susceptible cultivars. Our results suggest a necessity for the detection of structural variation and indicate that the candidates may be useful for molecular breeding for citrus canker resistance and understanding disease resistance mechanism.

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PC-164

Recent Progress of PepMoV Resistant GM Pepper

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The PepMoV has been considered the most frequently detected potyvirus. When it co-infects with CMV or PMMoV, it gives severe impact to total pepper harvest in Korea. Since F1 hybrid that resistant to PepMoV has not been developed, we have developed transgenic peppers using *Agrobacterium*-mediated transformation with a Hc-Pro gene of the PepMoV. A large number of GM peppers were tested for resistance to the PepMoV, and after consequent self-crossing up to T4 generation, a highly tolerant pepper to PepMoV called T20 was selected. So far, BC4F1 lines have been selected by back-crossing with 4 elite lines through a breeding program. Very recently, based on molecular analysis, we have selected another event, #10-2, which is also resistant to PepMoV. Horticultural difference was investigated for both GM lines, #T20 and 10-2, and no significance was found comparing to non-GM lines.

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PC-165

The *gemini pollen 3* gene is required for nuclear division of pollen meiosis and mitosis in *Arabidopsis*

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The correct development of male gametophytes (pollen grains) in flowering plants is essential for proliferate in gamete production. Here we have taken a map-based cloning approach using *Arabidopsis* male gametophytic mutant, named *gemini pollen3* (*gem3*) to identify and characterize key gene that is expressed gametophytically for the completion of microgametogenesis focusing on genes which control cell division and cell fate determination. Previously reported *gem1* and *gem2* mutants with similar characteristics to *gem3* that are disturbed at asymmetric division and cytokinesis at pollen mitosis I (PMI) in *Arabidopsis*. However, *gem3* was mapped to a different genetic locus, and pollen developmental analysis revealed that *gem3* exert an effect at meiosis and mitosis causing complete sterility. We also discovered that *gem3* homozygous lines produce aberrant pollen grains, arising from incomplete cytokinesis during male meiosis with sporophytic phenotypes of twisted-shape leaves, large flowers. This mutation shows reduced genetic transmission of *gem3* allele through male gametophyte. In previous results, the *gem3* locus was confirmed by mapping to the region located on chromosome 5. To further confirm strong candidate gene, we performed sequencing and genetic complementation analysis. Currently, we are performing functional studies of the *gem3* gene for the better understanding of molecular mechanisms that control asymmetric division at meiosis and mitosis during pollen development.

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PC-166

New Breeding Technology: Development of Carrot Germplasm by Protoplast FusionMin Jung¹, Da-Hae Son¹, Da-Som Park¹, Ji-Young Hyun¹, Young-Woo Liu², Sih Woo Lee², Chee Hark Harn^{1*}¹Biotechnology Institute; ²Breeding Institute, Nongwoo Bio Co. Yeosu, Gyeonggi, Korea

The most important factor in breeding program is to obtain the value-added genetic line. Generally, breeders develop genetic sources using several methods such as segregation-breeding, cross-breeding, backcross-breeding, mutation induction, tissue culture and so on. Here, we present one classical way but very valuable method called cell fusion or protoplast fusion to create genetic sources for the breeding practice. The method we developed was the asymmetric somatic-hybridization of protoplast isolated from carrots. This is rather to transfer the nucleus from the high quality F1 hybrid to other mediocre line to produce a new carrot line. Since the breeding a carrot line for higher quality and purity takes a long time, therefore this nuclear transfer technology is very beneficial to generate a new line that could be useful to breed elite varieties. We had obtained around 200 fused carrots (cybrids), 12 cybrids were self pollinated and produced seeds. Selected progenies (C3) have been evaluated for horticultural characteristics and we have found new genetic lines that show better phenotypes.

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PC-167

Identification and Characterization Heterosis Associated Genes in *Brassica oleracea*

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Heterosis is very important for breeding hybrid cultivars and is intensively used to increase the productivity of crop plants. But the molecular basis of heterosis is still unrevealed to the scientists. This study selected 51 heterosis associated genes of Arabidopsis of different family on the basis of their high differential expression in a hybrid compared to its midparent value and identified their orthologues in *Brassica oleracea*. Then the selected *B. oleracea* genes were characterized based on their structural properties, recognized functions and expression patterns in a cabbage hybrid progeny (Cabbage-36) of crosses between Cabbage-34 and Cabbage-35 accessions. Among these genes, a good number were found to express highly in the hybrid then the midparent value and better parent in some cases. Moreover, these highly expressed genes are mostly related to the yield contributing characters. Cotyledon and young leaf sizes of these three genotypes also well correlated with gene expression. Thus, it can be said that, the identified genes might be associated with the mechanism of heterosis of *B. oleracea* hybrid and provide a foundation for the exploration of gene regulatory networks associated with the specification of the phenomenon heterosis in the plant life cycle. Subsequently, these genes would be useful resources for molecular hybrid breeding in Brassica crops as well.

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PC-168

A Large Axiom Soybean SNP Genotyping Array: Development, Validation, and Genetic Mapping

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An important worldwide plant source of dietary protein and oil, modern breeding and improvement of soybean is suffered from a narrow cultivated germplasm relative to other crop species likely because of underuse of wild soybeans as breeding resources. SNP genotyping array is regarded as a promising tool for dissecting wild and cultivated germplasms to find important adaptive genes by high-density genetic mapping and genome-wide association studies (GWAS). Here, we present the establishment of a large soybean SNP array and its use for diversity analysis and high density linkage mapping. More than 4 million high-quality SNPs identified from 16 high-depth and 31 low-depth soybean genome resequencing data were used to select 180,961 SNPs for the Axiom[®] SoyaSNP array. Our validation analysis for a set of 222 diverse soybean lines showed that a total of 171,161 markers were of good quality for genotyping. Of the converted SNPs, 82.6% SNPs had a marker spacing of less than 9 kb and 17.4% SNPs greater than 9 kb with the 297 inter-SNP spacings of >100 kb and with 812 kb of the largest spacing, thereby suggesting that our array is likely suitable for GWAS of soybean germplasm. This array is being used to construct high-density genetic map in populations generated from intermatings of two cultivated and two wild soybeans, with an objective to confirm large structural variations of chromosomes using the ultra-high-density maps.

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PC-169

토마토 과색 및 병저항성 판별용 분자표지 개발

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최근 흑토마토는 기능성 토마토로써 소비자에게 각광을 받고 있으며 다양한 품종이 개발되고 있다. 흑토마토 형질 결정 유전자를 기반으로 흑토마토 판별용 분자표지 셋트를 개발하였으며, 이를 국내 시판 토마토 품종에 적용시켜본 결과, 대부분의 흑토마토를 정확하게 판별해 낼 수 있음을 확인할 수 있었다. 토마토 반신위조병 (*Verticillium wilt*)은 *Verticillium dahliae*와 *Verticillium albo-atrum*에 의한 곰팡이병으로 전형적인 토양전염성 병해이다. 토마토 황화 잎말림 바이러스(TYLCV; *Tomato yellow leaf curl virus*)는 담배가루이를 매개로 전염되며, 최근 기후난민화와 더불어 미국, 남미, 유럽, 동남아시아, 일본, 중국 등지로 확산되고 있어 다양한 TYLCV에 대한 안정적 저항성을 지닌 품종의 육성이 요구된다. 토마토 반신위조병에 대한 저항성 유전자인 *Ve1*은 extracellular leucine-rich repeat (eLRR) receptor-like protein으로써 cell surface receptor를, TYLCV 저항성 *Ty-1*은 RNA-dependent RNA polymerase 를 각기 암호화하고 있음이 기존에 확인된 바 있다. *Ve1*와 *Ty-1*에 대한 연관 분자표지는 각기 개발되어 분자유종에 적극 활용 중에 있으나, 본 연구에서는 유전자 염기서열 내의 다형성에 기반을 둔 functional marker의 개발을 진행하였다. 저항성 *Ve1*과 이병성 *ve1*의 염기서열 상의 다형성 중, 이병성 *ve1*에서 premature stop codon을형성하여 저항성 여부를 직접적으로 결정하는 다형성을 기반으로 cleaved amplified polymorphic sequence (CAPS) 분자표지를 개발하였다. 저항성 *Ty-1*과 이병성 *ty-1*의 염기서열 상의 7개의 SNP를 비교분석하여, 단백질 서열 상의 차이를 유도하는 다형성을 기반으로 CAPS 분자표지로 제작하였다. TYLCV 저항성 중 열성유전양상을 보인다고 알려져 있는 *ty5*저항성에 대해서도 유전자 기반 분자표지를 제작하였다. 본 연구에서 개발된 흑토마토, *Ve1*, *Ty-1*, *ty5*에 대한 기능성 분자표지는 과색판별 및 병저항성 육종의 효율 및 정확도 향상에 크게 기여할 것으로 기대된다.

PC-170

Transferability of microsatellite marker developed from *Vicia sativa* L. across its related species

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The genus *Vicia* comprises 166 annual or perennial species distributed mainly in Europe, Asia, and North America, also extending to the temperate regions of South America and tropical. However, utilization of SSR markers have not been investigated extensively in *Vicia* species as compared to other crop species. Here, we have assessed the potential for transferability (cross-species amplification) of cDNA microsatellites markers developed from common vetch (*Vicia sativa* subsp. *sativa*). In total, 226 alleles were detected in 36 microsatellite loci. The number of alleles per marker ranged from one to 20, with an average of 6.3. The gene diversity and polymorphism information content value averaged 0.540 and 0.503, with a range of 0-0.85 and 0-0.84 respectively. For transferability of the SSRs, amplification was carried out with selected from two to 8 accessions of 22 different *Vicia* species. For individual species, the successful amplification rate ranged from 32.6% in *V. ervilia* to 81.9% in *V. sativa* subsp. *nigra*, with average of 48.8%. As the rate of successful amplification of microsatellite markers generally correlates with genetic distance, these SSR markers are potentially useful in the analysis of genetic relationships between or within *Vicia* species.

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PC-171

Identification of Korean sorghum varieties using a multiplexed fingerprinting platform of SSR markers

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Sorghum (*Sorghum bicolor* (L.) Moench) has been cultivated for cereal grain which has been traditionally used for steaming with rice in Korea. Various Korean sorghum varieties have been developed and distributed for farmers and consumers to meet their needs. Korean sorghum grains have been mostly sold at higher price in the market than sorghum grains imported from abroad. However, no varietal identification method was established to support fair trade in the cereal market. The objective of this study is to develop the identification method of Korean sorghum varieties using a multiplexed fingerprinting platform of SSR markers. One marker for the waxy allele and nine SSR markers were carefully selected based on their product sizes for the multiplexing. A robust multiplexed combination was revealed from serially designed experiments for the optimization of multiplex PCR. Five varieties and two elite breeding lines could be separated with their unique fingerprinting pattern from other sorghum individuals collected over the world. The platform separated most of individuals tested in this study, remaining three genotypes contained two or three identical individuals. The technique may be applied to detect closely-related individuals including full sibling progeny.

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PC-172

Molecular breeding of a pepper cultivar (*Capsicum annuum*) containing high capsinoids

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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 *p-aminotransferase* (*p-AMT*) gene. In the previous study, SNU11-001 (*C. chinense*) containing high levels of capsinoids was found in germplasm collections of Seoul National University. We found that this collection has a unique mutation in the *p-AMT* gene. In order to develop a cultivar containing high capsinoids contents, marker-assisted foreground and background selection were performed in this study. Backcrossing is an effective breeding method for introducing useful traits to an elite cultivar. Compared to conventional backcrossing, marker-assisted backcrossing (MABC) is extremely useful for recovery of a recurrent parent's genetic background. To obtain background selection markers, a total of 412 single nucleotide polymorphism (SNP) markers was screened to obtain polymorphic SNP markers between 'Takanotsume (*C. annuum*)' and 'SNU11-001'. Of the 412 SNP markers, 96 polymorphic SNP markers evenly distributed in pepper genome were finally selected. Plants carrying the *pAmt/pamt* genotype were selected from a BC₁F₁ population using SCAR markers derived from the unique *p-AMT* mutation of SNU11-001. BC₁F₁ plants carrying the *pAmt/pamt* genotype were subjected to background selection. Multiple genotype analysis was done using Fluidigm platform (BioMark). Once we obtain plants carrying most similar genetic background to recurrent parent, capsinoids contents will be measured and another round of MABC be done to obtain plants containing high levels of capsinoids.

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PC-173

Identification and expression analysis of *Alfin-like* transcription factors in response to biotic and multiple abiotic stresses in *Brassica rapa*Md. Abdul Kayum, Hee-Jeong Jung, Jong-In Park, Ill-Sup Nou *

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The Alfin-like transcription factor family is one of the important gene families in eukaryotic plants. They are involved in many biological processes, such as lignocellulosic wall biosynthesis, meristem development, metabolite transport, and responses to biotic and abiotic stresses. But the regulatory mechanism of these genes involved in stresses responses is still unrevealed. In this study, we identified a total of 16 *Alfin-like* genes from *Brassica rapa* database. The 16 putative Alfin-like proteins were divided into four groups (group I-IV) based on structural and phylogenetic analyses. Accordingly, this study analyzed stress resistance-related functions of all *B. rapa Alfin-like (BrAL)* genes through a homology study with existing biotic and abiotic stress resistance-related *Alfin-like* genes of other plant species and found a high degree of similarity with them. Subsequently, these genes were further investigated by real-time quantitative PCR under cold, salt and drought stresses and after infection with *Fusarium oxysporum* f. sp. *conglutinans* in *B. rapa*. These genes showed an organ specific expression and all genes differentially expressed in *Chiifu* compared to *Kenshin* under cold stress. Ten and seven *BrALs* responded highly in *Kenshin* compared to *Chiifu* under salt and drought stresses respectively. In addition, six *BrAL* genes showed responsive expression after *Fusarium oxysporum* f. sp. *conglutinans* infection in *B. rapa*. Interestingly, four *BrAL* genes showed responses against both biotic and abiotic stress factors. Thus, our result provides a useful reference data set as the basis for functional analysis and utilization in the resistance molecular breeding of *B. rapa*.

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PC-174

Evaluation of biological effects of ion beam irradiation in pepper (*Capsicum annuum* L.)Sang Hoon Kim¹, Yeong Deuk Jo^{1*}, Hyo-Jeong Lee¹, Yu-Mi Lee¹, Si-Yong Kang¹¹Radiation Breeding Team, Advanced Radiation Technology Institute, Korea Atomic Energy Research Institute, Jeongeup, Korea

Radiation technologies have been widely used in mutation breeding of crops. Although gamma-radiation has been predominantly applied in radiation breeding, ion beam irradiation is recently emerging as a methodology highly effective in induction of mutations that are useful for plant breeding. Therefore, we investigated the biological effects caused by irradiation of two types of ion beams, which were proton and carbon beams, respectively, in pepper. In the evaluation of survival rate, LD₅₀ values were between 300 and 350 Gy, 30 and 40 Gy in irradiation of proton and carbon beams, respectively, while LD₅₀ for gamma-ray was determined to be between 50 and 100 Gy. Growth traits including shoot length, root length, and root width were also examined in pepper seedlings according to doses of proton and carbon ion beams to estimate biological effectiveness of each radiation. The result was applied in the construction of pepper mutant population which will be used to develop pepper breeding materials containing novel characteristics.

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PC-175

Drought stress induced expression of key genes for glycoalkaloid accumulation in potato

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Steroidal glycoalkaloids which serve the plant defense, are toxic secondary metabolites present in the plants of solanaceae family. The upper safe limit of glycoalkaloids for human consumption is 20mg/KG FW, excess of which may cause severe health disorders. Several factors like drought, high temperature, light exposure, and wounding increase tuber glycoalkaloid content. Among these, drought is an important factor which causes a rapid increase in potato glycoalkaloid content. Glycoalkaloid biosynthetic genes and their expression pattern need to be characterized to regulate the glycoalkaloid accumulation. Three key genes SGT1, SGT2 and SGT3 are demonstrated to be directly participated in the biosynthetic pathway for glycoalkaloid formation. Present study was focused on the study of expression pattern of key genes in GA pathway under drought stress in two different potato cultivars Atlantic and Haryoung which are low and high glycoalkaloid accumulating respectively. Drought stress was imposed by withholding water to the plants grown in pots and control plants kept irrigated. Expression analysis of SGT1, SGT2 and SGT3 was done from the leaf and tuber sample of three time intervals i.e 5, 10 and 20 days after imposing stress. Variation in the expression level of genes was observed in leaf and tuber where the fold increase in expression over control was higher in tuber sample compared to leaf. Expression levels also varied in leaf and tuber among two cultivars. However, expression of SGT1, SGT2 and SGT3 is significant indicating the involvement of these genes in glycoalkaloid accumulation under drought stress.

Keywords: *Solanum tuberosum*, drought stress, glycoalkaloids.

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PC-176

Physiological mechanism of drought tolerance in CaMsrb2-expressing transgenic rice plants

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The *MethioninesulfoxidereductaseB2* (*MsrB2*) gene catalyzes the reduction of free and protein-bound methionine sulfoxide to methionine and is known to provide tolerance to biotic and abiotic environmental stresses. There have yet to be any reports that *MsrB2* enhances drought tolerance. Two drought-tolerant transgenic rice lines, L-8 (single copy) and L-23 (two copy), expressing the *Capsicum annuum* *MsrB2* (*CaMsrb2*) gene were selected for stress tolerance phenotyping under drought stress conditions. *CaMsrb2* enhanced relative water content (RWC), maintained substantial quantum yield (*Fv/Fm* ratio), and subsequently improved photosynthetic pigments. Interestingly, L-23, carrying two-copy T-DNA insertion, showed greater drought tolerance through more effective stomatal regulation, carotenoid concentration, and osmotic potential than the wild type. High-tech infrared technology (FLIR SC620) was used for the selection of stress-tolerant phenotypes. Later, the IR results were correlated with other tested physiological parameters. The IR images, average plant temperature, and physiological parameters of the treated plants were discussed in detail.

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PC-177

Complete chloroplast genome sequence with NGS (Next Generation Sequencing) in tartari buckwheat (*Fagopyrum tartaricum*)Kwang-Soo Cho^{1*}, Bong-Kyoung Yun¹, Hong-sik Won¹, Young-Ho Yoon², Su-Young Hong¹, and Jeong-Ki Jeon¹¹Highland Agriculture Research Center, National Institute of Crop Science, Rural Development Administration, Pyeongchang 232–955, Korea²Functional Cereal Crops Research Div, National Institute of Crop Science, Rural Development Administration, Milyang, 627–803, Korea

Common buckwheat (*F. esculentum*) and tartaryan buckwheat, also called as bitter buckwheat (*F. tartaricum*) grain and leaves (buds) are used in various dietary preparations and as leafy vegetable. The cultivated area of buckwheat is increased based on its nutritional value. Particularly bitter buckwheat is a rich source of rutin compared to common buckwheat which helps in reducing intra-vascular cholesterol, high blood pressure, diabetes and is also reported to have a crucial role in pharmaceutical research. With this functional characteristics of bitter buckwheat, the cultivation is now highly increased. But a few genetic and genomic research of tartari buckwheat are published until now. Here we described the complete full chloroplast genome sequence with NGS. Tartary buckwheat complete chloroplast genome is composed of a total sequence length of 159,272 bp which is 327 bp lesser than common buckwheat genome of 159,599 bp. Large single copy region (LSC) is comprised of 84,398 bp in tartary and 84,888 bp in common buckwheat whereas small single copy region (SSC) is 13,292 bp and 13,343 bp and the size of inverted repeat region (IR) is 61,532 bp and 61,368 bp in tartary and common buckwheat respectively. Total RNA bases were 11942 and 11950 and overall GC-content in tartary and common buckwheat is almost similar which is 37.9% and 38% with a GC skew of -0.016 and 0.02 respectively. Total repeat bases accounted for 1,056 bp and 804 bp with an average repeat length of 48 bp and 45 bp and the length of an average intergenic distance was 495 bp and 502 bp in tartary and common buckwheat respectively. *F. tartaricum* cp genome has a total of 104 genes including 82 protein coding genes, 29 transfer RNA genes and 4 ribosomal RNA genes. Protein coding genes include photosynthesis related genes majorly in addition to transcription and translation related genes. LSC region has 62 protein coding genes and 22 tRNA genes whereas SSC region contains 11 protein coding genes and one tRNA gene. The nucleotide and amino acid sequences of protein coding genes in LSC, SSC and inverted repeat regions in *F. tartaricum* and *F. esculentum* are highly similar with a total average identity of 98.8 and 98.3% respectively.

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PC-178

Discovery of Single Nucleotide Polymorphisms(SNPs) in colored Korean potato cultivars from RNA-Seq data

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The newly developed varieties, Jayoung (violet flesh color) and Hongyoung (red flesh color) that harboring various anthocyanins and flavonoids in flesh colored potato are highly increase their interesting not only for food but also functional characteristics such as anti-inflammatory effects. Up to date, most of the molecular markers developed in potato are linked to disease resistance including late blight and PVY, nematode. A few markers linked to economically important functional materials such as anthocyanin biosynthesis are published. With the low cost and high throughput of NGS (Next Generation Sequencing) technology, numerous molecular markers are highly increased in may crops. Among the molecular markers, SNPs (Single nucleotide Polymorphisms) are most useful markers owing to their large numbers in inter and intra varieties in potato. Here we reported SNPs discovery from transcriptome sequencing data acquired from colored flesh potato cultivars, Jayoung and Hongyoung with white flesh color Atlantic. Total RNA was isolated from shoot in tuber after breaking dormancy about 2cm length. Short read sequence data were obtained form Illumina Hiseq2000 and the raw dat set were trimmed with Q socore over 20. Sequencing data were align to reference genome (*Solanum tuberosum* v4.03, <http://potatogeomics.plantbiolgy.msu.edu>). About 70% of sequence read were mapped int to reference genome. 139,050, 140,976 and 146,429 total SNPs were discovered in Hongyoung, Jayoung and Atlantic, respectively. All SNPs are mapped into the psedomolecules in reference genome by chromosome. SNPs are also analyzed with homozygous and heterozygous SNPs and genic and intergenic region. SNPs are compared with Potato Infinium 8K Chip data. SNPs found in candidate genes of anthocyanin biosynthesis were discovered. These SNPs information of flesh colored potato will be further analyzed for the allele mining for anthocyanin syhthesis and control region.

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PC-179**Production of soybean transgenic events harboring AtRabG3b and CaMsrB2 genes**Hyun Suk Cho¹, Hye Jeong Kim¹, Su Yeong Yun¹, Yoon Jeong Lee¹, Hyun Hee Im¹, Young Soo Chung^{1*}¹Dept. of Genetic Engineering, Dong-A University, Busan, Korea

AtRabG3b and CaMsrB2 genes incorporated into pPZP vector were transformed to Korean soybean cultivar Kwangan using highly efficient transformation system. AtRabG3b gene plays a positive role in xylem development in Arabidopsis and 64 transgenic plants were produced. CaMsrB2 gene is known to confer drought tolerance in rice and 63 transgenic plants were produced. As a result of PPT leaf painting assay, about 20% of transformation efficiency was observed from 2 times of inoculation. These transgenic plants were confirmed for gene introduction using PCR. Currently, the copy number and the gene expression is investigating using qRT-PCR and RT-PCR. Moreover, 62 lines and 53 lines of T₁ seeds from AtRabG3b and CaMsrB2, respectively, were sown in GMO field.

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PC-180**Determination of Fe in Brown Rice of Heuristic set by using ICP-OES**Bu-Woong Choi¹, Win Htet Oo¹, Ji-Hyock Yoo², Min-Young Yoon¹, Tae-Sung Kim¹, Won-il Kim², Yong-Jin Park^{1,3*}¹Department of Plant Resources, College of Industrial Sciences, Kongju National University, Yesan 340-702, Republic of Korea²Department of Crop Life Safety, National Academy of Agricultural Science (NAAS), Rural Development Administration (RDA), Suwon, Republic of Korea³Legume Bio-Resource Center of Green Manure (LBRCGM), Kongju National University, Yesan 340-702, 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. Thus we searched a possible allelic source from Heuristic or core rice set, which is derived from a total 24,368 rice germplasms, to increase the mineral content in rice varieties. The concentration and distribution of Fe in 137 accessions of core set of brown rice grain flour sample were determined by ICP-OES. The range of the concentration and distribution of Fe in 137 core accessions of brown rice grain were wide, from 0.088mg/L to 1.205mg/L, with mean 0.292mg/L. To examine Fe related genes, whole-genome resequencing data of 137 accessions of rice core set were analyzed by Genome Wide Associations Study (GWAS). Our result suggests that Fe determined by ICP-OES facilitates the evaluation of the differences in Fe composition for future rice breeding program.

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PC-181

Development of High Quality SNP Markers Using Improved GBS Approach in *Capsicum*

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Genotyping-by-sequencing (GBS) is a robust and rapid tool to develop SNP markers. Reduced sequencing complexity and multiplex sequencing of GBS has reduced genotyping cost for complex genome. However multiplex sequencing brings low sequencing depth which can lead to reduced number of markers. Therefore to find the appropriate condition for GBS is needed. In this research we demonstrated the use of *ApeKI* and selective primers for GBS of pepper (*Capsicum* spp.). Selective primers which amplify the GBS library with one or two flanking sequences to *ApeKI* site were used to increase sequencing depth. By *in silico* digestion, we developed six different selective primers amplify 4,000-400,000 regions. We made the GBS library with eight pepper accessions in four species using six selective primers and sequenced. Proper selective primers and pooling rate for each species will be determined. This approach will be useful for genotyping *Capsicum* breeding lines or populations by developing high quality SNP markers.

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PC-182

Genetic diversity and population structure by SNP markers in a large germplasm collection in *Capsicum*

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Capsicum diversity is getting lower in modern crops because of the genetic erosion. In *Capsicum*, breeders have been mainly focused on agriculturally important traits such as disease resistances, high yield and pungency. This narrow breeding pool hampered to develop improved cultivars. It has become a hot issue to conservation of genetic diversity and exploitation of wild germplasm in *Capsicum*. However, although a large number of accessions are maintained in *Capsicum* germplasm collections, their use for crop improvement is limited by the scarcity of information on genetic diversity, population structure and proper phenotypic assessment. The identification of representative and manageable subset of accessions would facilitate access to the diversity available in large collections. A genome wide germplasm characterization using molecular markers can offer reliable tools for adjusting the quality and representativeness of core samples.

We investigated patterns of molecular diversity at 48 single nucleotide polymorphisms (SNPs) in 4056 accessions from 11 *Capsicum* species from 89 different countries. Using these genetic variations and 32 different morphological traits, 250 core set was selected in whole *Capsicum* germplasm. The core collection could be a primary source for distributing germplasm to pepper breeders and other national programs as well as for evaluation.

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PC-183

환경위해성 평가를 위한 GM콩과 국내 야생콩/품종들과의 교잡 가능성 측정을 위한 시뮬레이션

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GM콩은 사료용으로 2004년 Monsanto사의 제초제 저항성 콩 승인을 시작으로 11개 이벤트와 3개의 후배교배종들이 Monsanto Korea, Bayer Crop Science, DuPont Korea, BASF 4개의 회사에서 개발되어 국내로 수입되고 있다. 단일 이벤트는 7개의 제초제저항성, 1개의 해충저항성, 3개의 기능성을 강화한 특성들이 있다. 기능성 강화에는 올레산 함량 증가와 SDA 생성하는 특성들이 DuPont사와 Monsanto사에서 개발되었다. 2011년부터는 후대교배종이 신청되어 2가지 특성을 모두 지니고 있는 이벤트들이 수입되고 있다. 이와 같이 GM통이 사료용으로 대량 수입됨에 따라 비의도적 소실로 인한 자연계 방출 가능성을 염두해 두고, 미리 국내에서의 유전자 이동성 평가를 하기 위하여 콩의 화분 특성과 교잡율을 GM콩의 모본으로 사용된 non-GM 모본을 협조 받고, 3개의 국내 야생콩(IT 184230, IT 183042, IT 236804)과 3개의 국내 장러품종(IT 212859, IT 212860, IT 178684)과 함께 개화시기를 맞춰 화분특성과 교잡율을 조사하고자 2014년 전남대학교 60평 격리온실에서 1주인 간격으로 파종하여 재배하고 있다. 개화기간 동안에 화분비산거리, 화분량, 화분형태 및 크기, 화분 발아력, 화분 수명과 교잡율을 조사하여 국내 야생콩과 GM콩 모본과의 교잡 가능성에 대한 기초 자료를 생성하여 향후 GM콩 환경위해성 심사 과정에 참고하고자 연구를 진행하고 있다.

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PC-184

GM속근류의 실질적 동등성 평가를 위한 월동성과 화분 특성에 관한 연구

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Blue GM 카네이션 8품종을 개발한 일본 Florigene사는 미국, 네덜란드를 포함한 10개국에서 상용화하고 있다. 국내에서는 집약적으로 시설내에서 재배되는 화훼류가 유망한 GMO개발 작물이 될 것으로 인식되고 있다. 따라서 저온성 작물인 *Alstroemeria*를 이용한 실질적 동등성 평가 지침서를 개발하고자 식물학적·원예산업적 자료를 조사하였다. *Alstroemeria*의 노지 월동성을 확인하기 위하여 재식 깊이별 생존율을 전남대학교 포장에서 측정하였다. 지표면에서 5cm 이내로 가까이 식재된 경우 모두 고사하였으며, 그 이상의 깊이로 식재된 경우 높은 생존율을 보여, 국내 노지에서의 월동 가능성을 보여주었고 5월부터 개화하여 정원용으로 개발이 가능할 것으로 판단되었다. 화분비산특성을 조사하고자 측정된 1 anther당 화분 수는 대략 25,000-28,000개로 특정되었으며 화분활력은 30-60%로 다양하였다. 화분 발아력 기준을 설정하기 위하여 화분 발아배지 자당의 농도를 10, 15, 20, 25%로 다양하게 처리한 결과 배지 내 자당이 가장 낮은 배지(10%)에서 가장 높은 발아율을 보여 추후 더 낮은 농도의 자당 처리가 필요한 것으로 추정되었다. *Alstroemeria*의 화분 비산 거리를 측정하기 위하여 슬라이드그라스를 이용한 포집 후 측정 방식을 이용하여 측정 중에 있다. 2014년도에는 재배적 측면에서 실질적 동등성 평가기준을 위한 실험을 진행 중에 있다.

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PC-185

유채(*Brassica napus*) 환경위해성평가 가이드라인 개발을 위한 월동성과 결실특성에 관한 연구

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GM 유채는 2013년 국내에서 비의도적으로 방출되어 5곳에서 발견되었다고 추정되고 있다. 봄철 경관용으로 전국 지자체에서 유채를 식재하고 유채 축제 면적이 늘어남에 따라 2013년부터 본연구진은 국내에서의 유채 화분 비산에 관한 연구와 환경위해성 평가 가이드라인 기초DB 준비를 진행 중에 있다. 이에 따라 최근까지의 GM유채의 국제적 상용화 현황과 국내 수입 승인 현황이 조사되었다. 2013년까지의 GMO식물의 국내유출 추정 현황을 조사하고 유채의 유전자 이동 가능성을 제고하기 위하여 식물학적·농업적 특성이 조사되었다. 유채의 표현형 검증에 필요한 비교지표를 설정하고 실험방법에 대한 기준을 제시하였다. 유채의 재식 깊이별 생존 능력을 측정하여, ‘유달’과 ‘영산’ 품종 모두 3cm 깊이에서는 40-65% 정도의 종자 발아율을 보이고, 10cm 깊이에서는 급격히 저하되어 1-17% 정도의 종자 발아율을 보였다. 또한 20cm 깊이부터는 발아가 어려운 것으로 판단되었다. 유채의 결실 특성을 조사하기 위하여 ‘내한’, ‘탐미’, ‘탐라’ 품종들을 대상으로 노지에서의 결실율은 96-98%를 보였으며, 바람과 곤충이 없는 격리온실상에서는 68-78%의 결실율을 보여 격리온실 내에서의 비의도적인 결실 유도 매개를 고려하고 분재배로 생육상태가 노지보다 저조한 상황을 고려하면 대단히 높은 자가 결실율을 보여주고 있다. 비의도적 봄철 종자 비산으로 인한 결실 여부를 확인하기 위하여 ‘유달’, ‘영산’ 품종을 3월 초에 파종한 결과 ‘유달’은 결실이 가능하고 ‘영산’은 결실 불능인 결과가 나와 품종에 따른 차이가 큰 것으로 판단되었다. 이에 따라 유채의 비의도적 유전자 이동과 잡초화 가능성에 관련한 기초자료 수집이 필요한 것으로 보인다.

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PC-186

Relationship of gene in Rice of Heuristic set analyzed (zinc)

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Rice is the staple food for more than half the world's population. It is known that 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. Here, we performed Genome-Wide Association Study(GWAS) with high-resolution density SNPs and InDels to identify natural allelic variation in zinc increase from Heuristic or core rice set, which is derived from a total 24,368 rice germplasm. The range of the concentration and distribution of zinc in 137 core accessions of brown rice grain were wide, from 7.86ppm to 31.76ppm, with mean 18.97ppm. In particular, GWAS result show that the high peak found in Chromosomes (1, 4, 6, 8). The new natural variants identified through haplotyping analysis would be useful to develop new rice varieties with improved storage ability of the valuable mineral through the future molecular breeding.

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PC-187**Comparison of radiosensitivity of wheat plant in response to acute and chronic gamma irradiation**

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Gamma irradiation has been used as a tool for plant mutation breeding to select new cultivar with improved characteristics. Generally, the irradiation of seeds with high doses of gamma rays disturbs the synthesis of protein, hormone balance, and enzyme activity. And also, high dose of gamma rays to reduce plant height, number of tiller, and root length, although the effect of gamma-irradiated plants may depend on the species and cultivar or stress conditions. Biological effects of radiations can be divided into two types according to dose range and periods of exposure. Acute irradiation represents exposure to high-dose of irradiation over short period time, whereas the chronic irradiation is comprised of exposure to low doses of radiation over extended period of time. To compare the effects of acute and chronic exposure to ionizing radiation on two wheat cultivars (K4191 and Geumgangmil), we measured their germination rate, seedling height, and root length. In order to understand the influence of antioxidant-related genes and DNA repair-related genes, we used qRT-PCR methods to identify their expression levels. To study the behavior of a radiation-induced free radical, gamma-irradiated seeds were used for ESR spectroscopy. Plant growth pattern was showed positive correlation with ESR results. This study indicates that low level chronic radiation exposure is even more serious effects than short doses of high level radiation according to different wheat cultivar.

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PC-188**Identification of Chrysanthemum (*Dendranthema grandiflorum* Ramat.) Varieties using SSR Markers**

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Chrysanthemum (*Dendranthema grandiflorum* Ramat.) is a member of the Asteraceae and 588 varieties obtained Plant Variety Protection and 601 varieties were registered to Korea Seed & Variety Service for marketing. Thus, chrysanthemum is one of the important horticultural crop and having a possibility for infringement of Plant Breeder's Rights. We investigated the genetic relationship of 20 chrysanthemum varieties using simple sequence repeat (SSR) markers. A total 335 SSR primer sets were screened for identification of 20 varieties. With 335 SSR primers, seventeen SSR primers showed polymorphism and reproducibility between 20 varieties. A total of 77 polymorphic fragments were identified by 17 SSR markers. Two to eight SSR alleles were detected for each SSR locus with an average of 4.53 alleles per locus. The polymorphism information content values ranged from 0.408 to 0.825 with an average of 0.45. Genetic distance of 20 varieties ranged from 0.36 to 0.73 by unweighted pair-group method with arithmetical average based on Jaccard's distance coefficients. All of twenty varieties were distinguished by 17 marker genotypes. Future work will be investigated to construct DNA profile database for large number of chrysanthemum varieties using DNA sequencer.

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PC-189

Database Construction for Variety Characteristics of Lettuce (*Lactuca sativa* L.) using SSR Markers

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Lettuce (*Lactuca sativa* L.) is a member of the Asteraceae and sixty three lettuce varieties have been registered at the Korea Seed & Variety Service for Plant Variety Protection (PVP). We previously constructed DNA profile database for identifying 159 lettuce varieties using 60 simple sequence repeat (SSR) markers. In this study, we selected optimum markers from previously applied markers and new SSR markers for the standardization of DNA profile database of 65 commercial lettuce varieties containing 18 PVP varieties distributed in Korea. Twenty-eight SSR markers from 60 SSR markers were selected for characterization with 65 commercial lettuce varieties according to the reproducibility, polymorphism, band pattern of marker and easiness of scoring. Out of 156 SSR primers, we additionally selected 11 new SSR primer pairs showed polymorphisms between 8 varieties and repetitive reproducibility on capillary electrophoresis system. Totally 127 polymorphic amplified fragments were obtained using 39 SSR markers. Two to seven SSR alleles were detected for each locus with an average of 3.3 alleles per locus. Average polymorphism information content was 0.517, ranging from 0.281 to 0.771. Genetic distance of clusters ranged from 0.29 to 0.96 by unweighted pair-group method with arithmetical average based on Jaccard's distance coefficients. A total of 65 commercial lettuce varieties were discriminated by 39 SSR marker genotypes. These SSR profile database developed will be continually characterized for the standardization of DNA profiles for lettuce commercial varieties.

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PC-190

Transcriptome analysis and protein dimerization of newly classified bZIP transcription factors of *Brassica rapa* in cold stress response

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Plant bZIP transcription factors play crucial roles in biological processes. In this study, 136 putative bZIP transcription members were identified in *Brassica rapa*. The bZIP family can be divided into nine groups according to the specific amino acid rich domain in *Brassica rapa*. To screen the cold stress responsive *BrbZIP* genes, we evaluated whether the transcription patterns of the *BrbZIP* genes were enhanced by cold treatment in the inbred lines, Chiifu and Kenshin, by microarray data analysis and qRT-PCR. The expression level of six genes increased significantly in Kenshin, but these genes were unchanged in *Chiifu*. Additionally, homo- and hetero-dimerization test between selected bZIP proteins indicated the Bra020735 is a key regulator in cold response. These findings suggest that the six genes that encoded proteins containing N-rich regions might be involved in cold stress response. These results presented herein provide valuable information regarding the molecular basis of the bZIP transcription factors and their potential function in regulation growth and development, particularly in cold stress response.

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PC-191**The effective method to screen high Fe content brown rice**Woon-Ha Hwang^{1*}, Soo-Kwon Park¹, Dongjin Shin¹, Min-Hee Nam¹, In-Jung Lee² and Dong-Soo Park¹¹National Institute of Crop Science (NICS), RDA, Suwon 441-857, Republic of Korea²Department of Genetic Engineering, Kyungpook National University, Daegu, Republic of Korea

Even rice is one of the most important food crops in the world, its micronutrient contents including iron is not enough to solve mineral malnutrition which is a significant public health issue in most developing countries. Iron deficiency is probably the most widespread micronutrient deficiency in humans. Experts estimate that a rice based diet should contain 14.5 ppm iron in endosperm. However, Cesar P et al reported that average iron content in milled rice was 2 ~ 3 ppm, whereas it was 10 ~ 11 ppm in brown rice. Fe content of rice is usually measured by inductively plasma spectrometry (ICP). It takes times and could make error while sample processing. To breed high iron contained rice variety, the effective screen method for select high iron contained elite line is essential. To develop more effective method in screening high Fe contained brown rice, we investigate the relation the leaf chlorophyll content with iron content in brown rice. Result of analyzing leaf chlorophyll content of OsNAS3-OX which contain more Fe than wild-type plant after cultivated on Fe limited MS medium, those of OsNAS3-OX was higher than those of wild-type plant in 0 and 20 % Fe contained MS medium. After measured Fe content in twenty kinds of brown rice, we cultivated those in Fe limited MS medium then investigate the relation of leaf chlorophyll content with Fe content of brown rice. In 0 and 5 % Fe contained MS medium, the leaf chlorophyll content was highly related with Fe content of brown rice as 0.66 and 0.79. Though these result, analyze of leaf chlorophyll content cultivated in 5 % Fe content in MS media was effect on screening high Fe contained.

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PC-192**Primer sets for identifying specific food sources from processed foods**

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Recently, the importance of food safety is increasing due to numerous junk food. Junk food means to violate the law in stage such as production, manufacture, distribution, and sale of food. Many crop plants are processing as foods including bread, noodle, and other foods for supporting nutrition to human. For example, rice is one of the most well-known food crops in the world, and processed rice is being mixed with other processed crops to health food. The object of this study is to detect amount of specific grains, i.e. rice from processed foods mixed with other cereals. This experiment was performed to the following two steps: 1) designed the specific primer sets based on chloroplast DNAs, 2) amplified products using real-time PCR. We designed eleven primer sets within chloroplast DNA of rice, and then the confirmation of primer efficiency was to amplified with rice genomic DNA using real-time PCR. In addition, these primer sets were applied in other crops such as wheat, maize, and adlay to confirm specificity to rice. The rice specific primer sets were determined by the number of amplification and the melting peak through real-time PCR. As a result, five primer sets were confirmed to uniqueness in the rice genome. In conclusion, the specific primer sets would be useful for identifying rice grain from the processed foods to eliminate junk foods and for contribution of food safety.

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PC-193

Triple color FISH karyotypes in two onion cultivars

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Fluorescence in situ hybridization (FISH) is a powerful tool for the detection of DNA sequences in the specific region of the chromosomes. As well as for the integrated physical mapping, FISH karyotype analysis has to be preceded. The detailed karyotypes of two onion cultivars, which are resources for onion genome sequencing project (‘Eumginara’ and ‘Sinsunhwang’), were constructed based on triple color fluorescence in situ hybridization (FISH) using 5S rDNA, 45S rDNA, and tandem repeat sequence. All used our materials showed $2n=2x=16$ with $x=8$ as basic chromosome number. 5S rDNAs were located on 4 loci in one pair of interstitial region of short arm chromosome in both onion cultivars. Two pairs of 45S rDNAs were positioned in distal region of short arm chromosome in ‘Eumginara’. Otherwise 5 loci of 45S rDNAs were located in distal region of two pairs of short arm chromosome in ‘Sinsunhwang’. Among them, two signals of 45S rDNAs were co-localized in distal part of short arm and long arm chromosome, respectively. In case of tandem repeat sequence was detected on telomeric region of 8 pairs of chromosomes except on 45S ribosomal DNA sites. These results will provide a valuable background for physical mapping and help to further more understand the genome sequencing project in *Allium cepa*.

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PC-194

FISH mapping of 5S and 45S ribosomal DNAs in three wild Chrysanthemum species

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Chrysanthemums (Asteraceae) are important ornamental crops in worldwide that are well known as commercial valuable cultivars for cut flowers, potted plants, and garden flowering plants. Genus chrysanthemum consisted of 41 species that are mostly distributed in East Asia. Chrysanthemum has diverse ploidy levels with the basic chromosome number of $x=9$ from $2n=2x=18$ (diploid) to $2n=10x=90$ (decaploid). Fluorescence in situ hybridization (FISH) is a useful tool for studying the distribution of ribosomal DNAs. In this study, we have confirmed ploidy level by chromosome counting method. The somatic metaphase chromosome numbers were observed $2n=2x=18$ in *Chrysanthemum boreale*, and $2n=6x=54$ in *C. indicum* and *C. zawadskii*. More detailed Karyotype was constructed based on FISH method using 5S and 45S rDNA probes. Two (2) loci of 5S rDNA signals were detected in interstitial region of long arm chromosome in *C. boreale* and six (6) loci were in *C. indicum* and *C. zawadskii*. All of 45S rDNAs were located in terminal region of short arm chromosome which were visualize in six (6) loci in *C. boreale* and *C. indicum* and twelve(12) loci in *C. zawadskii*. In this study, it was the main topic to perform physical mapping of the location of 5S and 45S rDNA. Three of wild chrysanthemum showed variations in number of ribosomal DNAs. In the present investigation will help to further study of genome sequencing project in chrysanthemum.

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PC-195

Transcriptome analysis using RNA-seq during early symbiotic signaling in *Medicago truncatula*

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Legume and rhizobia symbiosis plays an important role in conversion of atmospheric dinitrogen to ammonia. On a global scale, this interaction represents a key entry point for reduced nitrogen into the biosphere, and as a consequence this symbiosis is important in both natural and agricultural systems. Symbiotic development of nodule organ is triggered by chito-oligosaccharide signals (Nod factors) from the bacterium which are perceived by the legume root. Understanding the molecular and cellular processes that underlie Nod factor perception is one focus of legume biology. Although forward genetics has proved to be an important tool to identify key players in Nod factor perception, we still know relatively little regarding the functional networks of genes and proteins that connect the earliest steps of Nod factor perception to immediate downstream outcomes. To elucidate genes and proteins that link Nod factor perception to cellular and physiological responses we are taking a discovery-based strategy based on whole transcriptome profiling using RNA-seq analysis in the roots of *Medicago truncatula* in response to *Sinorhizobium meliloti*. Functional characterization of a number of candidate genes is currently in progress to further examine their role in nodulation such as generating transgenic plants.

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PC-196**Strategy for developing a set of vegetable *Brassica rapa* fixed lines for genetic diversity and population structure analysis**Xiaonan Li, Wenxing Pang, Su Ryun Choi, Yong Pyo Lim

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We investigated the genetic diversity and structure of the 239 fixed lines with 47 simple sequence repeat (SSR) and 109 NGS-generated SNP markers evenly distributed in *B. rapa* genome. Phylogenetic analysis classified the vegetable fixed lines to four subgroups, with the three types forming a separate and relatively farther cluster. Population structure analysis identified four sub-populations corresponding to geographic origin and morphological traits, and revealed extensive admixture. The vegetable *B. rapa* fixed lines successfully developed in our study would be valuable materials for multinational *B. rapa* diversity resources establishment. Understanding the genetic diversity and population structure could be useful for utilization of the representing genetic variation and further genetic and genomic analysis.

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PC-197**Assessment of germination ability in segregated population of colored wheat seeds containing various antioxidant chemicals**Oonha Shin, Yong Weon Seo*

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Phytochemical in purple pericarp of wheat seed consist of high phenolic content including ferulic acid, caffeic acid, vanilic acid and anthocyanins which not only perform as source of distinctive red to purple pigmentation but also high antioxidative material. Previous work has demonstrated that certain pigmentation can be generally regarded as good dietary source of food supplement. Yet, its physiological function in other various aspects has been not thoroughly understood. In this study, we organized fundamental experiment which could evaluate germinating ability of different-colored segregated wheat population. Total of five segregated lines were recognized by assist of CIELAB coordinates. After assessing initial content of total phenol, flavonoid, monomeric anthocyanin and ORAC assay for antioxidant activity from each population, germination assay was taken place *in vitro*. From germinating grains, sample was taken every 6 hours for measurement of alpha amylase enzyme activity. Discernible difference in chemical constituent was recognized among population along with disparity in ORAC assay. Alpha amylase activity and germination assay showed that darkening of pericarp was related to inhibition of germination. Pigmentation in wheat is important for its physiological role and commodity value which should be considered as critical factor to be integrated in breeding program.

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골든씨드프로젝트

GSP 채소종자사업단

GSP 원예종자사업단

GSP 식량종자사업단



종자, 식물, 육종과 특허권

이호조

특허청 농림수산식품심사과

2011년 종자산업의 세계시장 규모는 450억 달러이고, 농산물을 이용하는 식품산업의 세계시장 규모는 5조 2천억 달러에 이른다. 이러한 거대 농식품산업의 시작은 종자부터라 할 것이다. 종자의 산업적 가능성을 꿰뚫어 본 미국과 유럽은 종자기업 중심으로 국내시장을 넘어 세계시장의 개척에 주력하여 왔다. 2011년 현재 전체 종자시장의 75%를 장악하고 있는 세계 10대 종자기업의 1~8위가 모두 이들 나라의 기업들이다. 과거 IMF 구제금융 당시, 우리는 이러한 종자의 중요성을 제대로 인식하지 못한 채, 국내 5대 종자기업 중 4개가 외국계 기업에 인수합병되는 것을 그냥 지켜보았다. 그 결과 많은 종자가 외국기업에 넘어가 버렸다. 농촌진흥청에 따르면 외국 품종의 재배로 인해 우리나라가 외국에 지불한 로열티는 2009년 이후 매년 150억원이 넘고 앞으로 국내 대체 품종을 개발하지 못한다면 향후 10년간 로열티가 2900억원에 이를 것으로 추산된다. 지재권이 설정된 종자를 사용하는 대가로 엄청난 로열티가 외국으로 빠져나가고 있는 것이다. 종자산업이 로열티를 창출하고 글로벌 경쟁력을 확보하기 위해서는 개발·개량된 종자를 품종보호권이나 특허권과 같은 지재권으로 보호하는 것이 무엇보다도 중요하다. 몬산토, 신젠타와 같은 다국적 기업들은 국내에서 토마토, 파프리카, 시금치 등 글로벌 작물의 품종은 품종보호로 출원하고, 한편으로 육종소재, 유전자, 육종방법 등은 특허로 출원하고 있다. 이들은 양 제도의 장점을 활용한 지재권 획득 전략을 구사하여 로열티를 창출하고 있다. 2003년부터 2013년까지의 특허출원 동향을 분석한 결과를 살펴보면 생명공학 기술을 활용한 육종기술의 발달과 함께 2009년 이후 식물분야 특허출원이 꾸준히 증가하고 있고, 이 중 60%가 GMO 식물 개발관련 내용이나, 2013년 식물분야 출원은 총 258건으로 전체 특허출원건수 대비로는 0.1%에 불과하다. 이에 종자, 식물, 육종과 관련된 기술을 통해 식물이 갖는 산업적 가치를 높일 수 있는 특허획득 방안과 외국기업의 특허전략, 식물품종보호와 다른 점, 식물관련 특허출원 시 알아야 할 사항 등을 사례를 중심으로 살펴보고자 한다.

Genome-assisted marker development for disease resistance in pepper

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The last decade has witnessed tremendous progress in genome sequencing and explosion of genome sequence information. This remarkable advancement in genomics provides unprecedented opportunities for crop improvement. Pepper (*Capsicum* spp.) is an important vegetable crop worldwide. Pepper production is constantly challenged by various pathogens and developing cultivars harnessing multiple disease resistance genes are ever increasing. Molecular markers linked to disease resistance genes will expedite the gene pyramiding. Here, I introduce genome-assisted development of molecular markers linked to resistance genes, in pepper. *Phytophthora capsici* L. is one of the most destructive pathogens of pepper (*Capsicum* spp.). Resistance of *Capsicum annuum* against *P. capsici* is controlled by quantitative trait loci (QTL), including a major QTL on chromosome 5 that is the predominant contributor to resistance. Here, to maximize the effect of this QTL and study its underlying genes, an F₂ population and recombinant inbred lines were inoculated with *P. capsici* strain JHAI1-7 zoospores at a low concentration (3×10^3 /mL). Resistance phenotype segregation ratios for the populations were close to 3:1 and 1:1 (resistant:susceptible), respectively, consistent with a single dominant gene model. Bulk segregant analysis (BSA) using Affymetrix GeneChips revealed a single position polymorphism (SPP) marker mapping to the major QTL. When this SPP marker (Phyto5SAR) together with other SNP markers located on chromosome 5 were used to confirm the position of the major QTL, Phyto5SAR showed the highest LOD value at the QTL. A scaffold sequence (scaffold194) containing Phyto5SAR was identified from the *C. annuum* genome database. The scaffold contained two putative NBS-LRR genes and one *SAR 8.2A* gene as candidates for contributing to *Phytophthora* resistance. Markers linked to these genes were developed and validated by testing 100 F₁ commercial cultivars. Among the markers, Phyto5NBS1 showed about 90% accuracy in predicting resistance phenotypes to a low-virulence *Phytophthora* isolate. These results suggest that Phyto5NBS1 is a reliable marker for *Phytophthora* resistance and can be used for identification of a gene(s) underlying the major QTL on chromosome 5.

Asymmetry of evolution and selection response of subgenomes in Brassica crops

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Genome polyploidization has provided significant sources of genetic variation for plant adaptive evolution and new species formation. However, the way in which molecular evolution of polyploid genomes builds up genetic architecture underlying speciation is unclear and whether there are any differences in polyploid subgenomes' responses to selection is unknown. *Brassica* is an ideal model to address these questions. Here, we used *Arabidopsis thaliana* as an outgroup to conduct comparative genome analysis of newly sequenced *Brassica oleracea*, *B. rapa* and *B. napus*. We revealed multi-layered modes of asymmetrical interspecific and intraspecific genome evolution. Between parallel species *B. oleracea* and *B. rapa*, these layers include: asymmetrical gene retention rates, asymmetrical TE amplification, asymmetrical tandem duplication of genes and asymmetrically alternative splicing variants between the two sister species; Between subgenomes within species, these layers include: massive and asymmetrical subgenomic gene loss, great variations between paralogs at the DNA sequence level, expression differentiation of triplicated, α -duplicated and tandem duplicated genes across different tissues in the two diploid species, asymmetrical recombination on A and C in *B. napus*. In addition, the predominant mechanism for gene loss is small deletion, rather than asymmetrical cross-over. These patterns provide new insight into genome evolution underlying speciation and trait formation and will underpin research into genetic improvement of these important crops.

Keywords: *Brassica* genomes, comparative analysis, molecular evolution

동남아 주요 국가의 종자수출을 위한 시장 현황 및 동향분석

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본 발표는 GSP 사업의 일환으로 벼, 옥수수, 감자 종자 수출을 위한 수출 주요 예상국의 국가별 정책과 신수요 동향 및 정보분석을 통해 해외마케팅 전략 수립에 관한 내용이다. 분석대상 국가는 중국, 베트남, 캄보디아, 인도네시아의 4개국을 대상으로 하였으며 CPS분석, 산업환경분석, 밸류체인 분석, 시장 전망 분석, 진출 가능성 분석과 진출 전략의 수립을 포함하고 있다. 베트남은 농업이 경제의 큰 비중을 차지하는 국가로 농업 투자를 우대하고 있으며 농업 경쟁력과 생산성 향상을 위한 혜택과 정책을 다수 수립하고 있다. 특히 우리나라 농림축산식품부와 베트남 농업농촌개발부의 교류협력 촉진을 위한 MOU가 체결되어 시장 진입에 강점이 있다. 베트남의 벼 종자시장은 수입 품종에 대한 의존도가 낮고 기후 조건도 양호하여 신품종 수요가 크지 않으며, 옥수수는 수입품종 의존도가 높지만 재배 환경이 열악하여 시장 진입에 어려움이 따른다. 감자 시장 수요의 50% 이상이 (주)오리온이기 때문에 감자 종자 시장의 진입에 유리함이 따를 것으로 보인다. 인도네시아는 최근의 경제 성장과 인구 증가로 식량작물의 수요가 지속적인 상승세를 보이고 있으며 종자의 수요가 매우 높아 매년 외국으로부터 다량의 종자를 수입하고 있다. 특히 인도네시아는 인건비와 토지 이용료가 저렴하여 계약 생산 등의 시스템 도입에 유리한 점이 많고, 기후와 재배 환경이 양호해 다양한 방향의 진출 전략이 가능하다. 중국은 세계 최대의 식량작물 수요국이자 생산국으로 종자 수요 역시 대단히 커서 종자 산업에 대한 정부의 지원과 투자가 적극적으로 이루어지고 있다. 자국기업의 보호를 위해 법적으로 외국 기업에 대한 법적 제약이 많고 차별이 상존하여 시장 진출에는 주의가 요구된다. 캄보디아는 세계 최빈국 중 하나로, 종자의 기술적, 양적 부족이 심각한 상태이다. 따라서 정부에서는 종자 도입에 대해 관대하며, 외국인 투자의 특혜나 시장 친화적 정책을 다수 수립하고 있다. 태국회사인 CP사의 점유율이 매우 높아 독점적 시장을 형성하고 있으며 법적, 제도적 절차가 미흡하여 진출시 권리 보호에 위험이 따를 수 있다. 4개국은 모두 종자의 수요가 높은 반면 자국의 기술 수준이 낮다는 공통점을 가지고 있다. 그러나 베트남을 제외한 3개국의 시장의 진입장벽은 높은 편이며 외국기업에 대한 정책들도 그 강도가 달라 진출 기업의 특성과 해당 시장의 수요에 대한 깊은 이해가 필요할 것이다.

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캄보디아, 베트남 식량종자 수출시장 개척 및 마케팅 전략개발

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본 발표는 베트남, 캄보디아의 기상환경에 적응하는 고품질(高品質) 내병(耐病) 내재해(耐災害) 다수성(多收性) 탈립 및 탈립 저항성(脫粒抵抗性) 품종의 육성 후 수출과 육성 개발품종의 종자상품화를 통한 현지 농가보급 활성화 및 탈립 저항성 품종을 활용한 대면적 재배농가 확대로 재배면적과 생산량 증대 및 국가식량자급도 향상 방안을 알아보고자 하였다. 캄보디아 베트남 현지의 내습성 및 내병성 유전자원 수집과 인공교배로 국내품종의 내습성과 내병성을 보강하고, 동남아 기후 및 재배여건에 적합한 영농기술체계 확립하여야 한다. 캄보디아 베트남에서 생산한 품종의 품질평가를 통하여 고기능성 및 고품산화 품종을 육성, 대 중국 종자시장 소비시장과 세계무역시장 진출 및 국내수입참깨시장에서의 수입대체효과 유발 및 원가절감 방안을 소개한다. 수출 시장개척 및 마케팅 전략으로 우수 육성품종의 종자상품화로 현지 전국의 종자 및 농약사에 우수한 품질의 종자를 농가에게 저렴한 가격으로 보급, 농가의 재배수익성 증대로 생산과 재배면적을 증대시키는 전략이 필요하다. 캄보디아 베트남은 일년의 절반은 건기와 우기로 나뉘어져 한발과 침수가 교차하므로 한발 및 습해저항성 유전자원과 함께 국내에서 무서운 역병, 위조병, 엽고병 등에 강한 유전자원이 풍부히 산재, 수집된 유전자원을 교배모본으로 활용, 국내품종의 재해 및 병해저항성을 강화할 수 있다. 따라서 국내품종의 고품질화를 통해 중국 상류층의 “한류”에 부응, 세계 최고급 농산물 수출시장을 개척하고 캄보디아 베트남 현지농장의 대면적 재배생산 시스템 확립으로 전 세계 세계 무역시장에 진출하는 방안을 모색하여야 한다.

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차세대유전체연구사업단

작물 유전체 육종



Distribution of Single Nucleotide Polymorphism(SNP) in Major Domestic Rice Cultivars compared to Japonica and Indica Reference Genomes

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With the development of next generation sequencing (NGS) technology, the variation of sequences represented as SNP between cultivars becomes available at genome level. The major domestic cultivars with high yield have been developed by breeding of indica and japonica, it is important to localize the region of origin according to the genotype for further characterization of unique features of cultivars. For the localization of SNP at genome level, the paired end sequences of 6 major domestic rice cultivars, Ilmi, Ilpoom, Sulgaeng, Bakjinju, Hwayoung and Woonkwang were compared against Japonica and Indica Rice Genomes as reference genomes. The genomic DNAs were prepared from callus tissues and paired-end of the fragments were sequenced with NGS Sequencer, Illumina HiSeq. About 50x coverage of paired-end sequences were trimmed according to the quality of the sequences, and errors were corrected with statistical analysis of kmers of 15. The trim-corrected sequences were mapped and variants were analyzed against reference genomes. The overall change rate of Ilmi against Nipponbare IRGSP 1.0 and Indica BGI 93-11 reference genomes were 0.92 base/1kb (1/1,079 base) and 8.09 base/1kb (1 base/123 bases), respectively. Among 6 cultivars, overall rate of Bakjinju showed the lowest overall change rate of 0.53 base/1kb, and Hwayoung showed highest frequency of 0.92 base/1kb. Compared to high level in the range of change rate of 7.0-9.3 base/1kb against indica, domestic cultivars showed lower range of change rate 0.2-3.3 base/1kb with unique local high peak against japonica genome depend on the chromosomes. Compared to assembly of genome sequences, the variation of nucleotides compared to reference sequences is much faster and simple to characterize the genotype. The types of variation and the effect on functional categories will be presented.

TGsol : 가지과 유전체 정보 실용화 연계 인터페이스 개발 및 활용

조성환*

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TGsol (Translational Genomics for Solanaceae)은 가지과 작물의 유전체 정보를 육종분야에서 활용할 수 있도록 해석하여 제공하는 특화된 웹 인터페이스이다(<http://tgsol.seeders.co.kr>). 가지과에는 경제적으로 고부가가치 작물인 토마토, 감자, 고추를 포함한 3,000개 이상의 다양한 종을 포함하고 있다. 최근 감자 (Nature, 2011), 토마토 (Nature, 2012) 그리고 고추 (Nature Genetics 2014)의 표준유전체 정보가 발표되었고, 이를 육종에 활용하기 위한 후속 연구가 활발하게 진행 중이거나 계획 중이다. 또한 주요 육종 라인 혹은 중요 유전자원을 중심으로 resequencing이 진행 중에 있어 활용에 대한 기대가 매우 높으나 대규모의 복잡한 유전체 정보를 접근할 수 있는 통로는 매우 제한적이다. 그래서 TGsol은 가지과 작물 표준유전체 그리고 resequencing 정보를 분석하여 분자육종 수요자의 요구에 친화적인 웹 인터페이스로 구축하여 기능적 데이터베이스를 제공하고 있다. 특별히 유전체 정보와 형질관련 유용유전자를 제공함으로써 MAS (maker-assisted selection)와 MAB (marker-assisted backcrossing) 확립에 필요한 다양한 정보를 제공한다. MAS를 위한 목표 형질은 병저항성, 과실발달, 유용 대사산물이다. 또한 토마토, 감자, 고추 사이의 ortholog 정보를 제공함으로써 기존에 연구된 형질관련 유전자를 가지과 내에서 적용할 수 있도록 지원한다. 이러한 결과는 유전체 정보와 육종 간의 상호 소통 및 활용이 원활하도록 지원하는 가교역할을 수행할 수 있도록 발전시켜 나갈 예정이다.

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Development, Validation, and Utilization of Large Axiom[®] Soybean SNP Genotyping Array

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Soybean is an important worldwide crop of dietary protein and oil resources for human foods and animal feeds. However, soybean breeding and improvement has been experienced challenges by a narrow germplasm. SNP genotyping array is regarded as a promising tool for dissecting wild and cultivated germplasm to find important genes by high-density genetic mapping and genome-wide association studies (GWAS). Here, we present the establishment of a large soyaSNP array and its use for diversity analysis and high density linkage mapping. More than 4 million high-quality SNPs identified from 16 high-depth and 31 low-depth soybean genome resequencing data were used to select 180,961 SNPs for the Axiom[®] SoyaSNP array. Our validation analysis for a set of 222 diverse soybean lines showed that a total of 171,161 markers were good quality for genotyping. Of the converted SNPs, 82.6% SNPs had a marker spacing of less than 9 kb and 17.4% SNPs greater than 9 kb, thereby suggesting that our array is likely suitable for GWAS of soybean germplasm. In the GWAS for seed protein content in the wild soybean germplasm with the size of 1,135 accessions, 22 loci on 12 chromosomes showed significant association ($-\log P > 4$). The highest associated peaks were shown at the 28 Mbp region on Gm05 ($-\log P = 5.89$), at 45 Mbp on Gm03 ($-\log P = 5.32$), and at 2.8 Mbp on Gm17 ($-\log P = 5.00$). Of the 22 associations, 8 corresponded with the location of previously reported seed protein QTLs and 14 regions is thought to be new QTLs for seed protein content in wild soybean. This array is being used to construct high-density genetic maps in two recombinant inbred lines and nested-association mapping populations with 30 combinations used Daepung cultivar as hub-parents, with an objective to confirm large structural variations of chromosomes using the ultra-high-density maps.

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GM작물실용화사업단

한·중 벼 육종 및 육종 신기술 공동 심포지움



OG-01**Conventional breeding strategy in China**

Piao Zhong-Ze

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The most noticeable achievement of agriculture in China is that about 7% of the world's arable land feed 23% of the world's population. New varieties of rice breeding and its production play an important role in this great achievement. Rice is one of the most important grain crops in China. More than 60% of the population in China takes rice as the staple food. Rice production accounts for 40% of the total grain output. With the increase of the population, the demand for rice will continue to grow. Therefore, breeding new rice varieties to improve rice production will play a crucial role to ensure food security in 21st century. This paper reviews the development course of rice production and breeding technologies of our country, and the achievements of rice breeding technology as well as the present situation of rice traditional breeding and molecular breeding.

OG-02**Development and utilization of hybrid rice in China**

Luo Zhi-Xiang

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China now has about 69% advantage of the rice yield as compared with the global average. The planting area was 30 million ha and total yield was 180 million ton in China in every year. Now, the breeding strategy of hybrid rice includes the improving ratio of plant morphological and raising heterosis level and using tools of the molecular biology. Some research was fixed on main index of plant type of hybrid Rice, which had the tall erect-leaf canopy and lower panicle position and bigger panicle size. Methods of raising heterosis level were expressed including exploitation and utilization of various male sterility resources, development of male sterile lines with high grain quality and out-crossing capacity, using wide-compatibility (WC) gene to overcome seed-set problem.

Current Status of Rice Breeding in Korea and Action Plan Development against transforming Environment of Rice Industry in terms of Agronomic Trait

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Since green revolution in 1970s, representing by the ‘Tongil type’ rice cultivars, rice breeding has greatly contributed to the Korean society in terms of self-sufficiency in staple food-grains and development of agricultural industry. During last three decades, conventional rice breeding has successfully enhanced rice commercial value in Korea through developing elite cultivars related with high quality, resistant or tolerant against biotic or abiotic stresses, special-purpose, direct seedling, super yielding, and functional rice. In the meantime, breeding technologies has been also improved by adopting and putting to practical use of theories and technologies of plant science such as mutation breeding, cytoplasmic-genetic male sterility, anther culture mediated haploid breeding, marker assisted selection, and transformation. Rice breeding, meanwhile, is an endless procedure of creating desirable haplotype expressing improved performances of agronomic traits. Narrow genetic diversity of Korean commercial rice lines have been a major limit factor not only in developing breeding lines having resistance and tolerance against biotic and abiotic stresses, but also in expanding genetic availability in terms of widening end-use properties. Although introducing novel allele types might be possible via crosses with wild relatives, it demands additional tedious efforts to restore the unique genetic background of the recurrent parents, which determine commercial value in the market. Moreover, due to most conventional breeding programs are prone to depend on phenotypic selections, addressing the driving force to be a superior haplotype would be very difficult in terms of tagging the chromosomal location of the target loci and estimating their genetic effects. Recently, coupling with the decrease of domestic rice consumption, Korean rice industry has being threatened by rapid changes in environmental, social, and even international circumstances, for example climate change, aging population, and opening of the rice market. To maintain the rice industry as a stable and sustainable growth engine of Korean economy, it is strongly demanded to develop practical strategies encompassing wide variety of available resources including germplasm, bioscience, and manpower. As the role of R&D party, technology convergence followed by communication among stakeholders of rice research would be essential. To the context, based on the hypothesis of the future of Korean rice industry, major schemes related with the issues of 1) High Quality, 2) Cost Reduction, 3) Stable Production, and 4) Consumption Boost would be discussed along with the projections over the achievements and shortcomings of Korean rice cultivars in terms of agronomic traits.

세계종자시장 현황과 생명공학작물 재배 및 연구현황

박희영

신젠타코리아

기하급수적인 인구증가와 한정된 경작지로 인한 미래 식량수요에 대한 우려가 커지고 있다. 2005년 현재 전세계 65억인구를 위해 헥타당 4명정도분의 식량공급으로 이를 극복하였지만 2030년 세계인구가 80억이상이 되면 헥타당 5명이상을 위한 식량을 공급하여야 한다. 이를 위해서는 지속가능한 방식으로 전세계 농업생산성을 향상시켜 날로 급증하는 식량 안보를 강화해 나가는 것이 필요하다. 이를 위한 하나의 방법으로 1996년이래 생명공학작물을 통한 농업생산성을 향상시키는 시도가 지속되고 있다. 지난 5년간 종자시장의 CAGR은 약 8.7%로 2013년 현재 394억달러의 시장가치를 지니며 이중 생명공학작물종자는 CAGR 17%, 시장가치 201억달러로서 일반종자의 CAGR 2.8, 시장가치 193억달러에 비해 급속한 성장을 이루었다. 2013년 현재 전세계 27개국, 1800만 농민들이 1억 7520만 헥타에서 GM작물을 재배하고 있다.

- 1) 옥수수 ; 미국 전체 옥수수 재배면적 3억4천4백만 헥타의 96%이상이 생명공학 옥수수이며 이중 67%가 삼중 후대교배종 이상의 품종이다. 브라질의 경우, 2009년이래, 생명공학 옥수수 재배면적은 급격히 증가하여 2012년에는 전체면적의 85%에 도달하였으며, 이 중 68%이상이 이중후대교배종이었다. 새로운 생명공학 옥수수개발은 Refuge 경감대책을 위해 작용기작이 다른 해충저항성 및 새로운 제초제 저항성, 가뭄 저항성 /Water-optimaization, 생산성 향상, 질소 이용 효율 증진 등이 주요 타겟이다.
- 2) 대두 ; 2011년 현재 콩 종자시장 규모는 2011년 현재 약 55억\$ 정도이며 이 중 생명공학 대두 종자는 21.8% (12억 달러)를 차지하고 있다. 2012년 현재는 전체 미국 대두재배면적의 98% (3157만 헥터)를 생명공학 대두가 차지하고 있다. 1%정도가 LibertyLink[®] 이고, 나머지는 모두 Roundup Ready[®] 저항성 대두이다. 새로운 생명공학 대두는 새로운 제초제저항성, 새로운 해충저항성, 선충 저항성, 수확량 향상, 영양성분 강화 (High oleic acid, Omega 3, High oil, High stearate 등)등이 주요 타겟이다.

전 세계 채소종자시장의 가치도 계속 성장하고 있는 중이다. 상업채소종자시장의 규모는 46억 \$(2011)에서 매년 7~8%의 연평균복합성장률(CAGR)을 반영하여 2025년에는 약 130억 \$ 정도로 증가할 것으로 추정되고 있다. 인도, 중국과 같은 많은 개발도상국에서 자가채종 종자에서 상업종자, 특히 교배종 종자로의 전환이 급증하고 있다. 인도에서는 급격한 도시화로 인해 도시근교의 주요 채소재배면적은 감소하고 있으며 중국내 채소재배는 고품질의 종자가 필요한 고품질의 농산물 수출이 증가하는 따라 영향을 받아 증가하고 있다. 서구 국가의 경우, 새롭고, 구별되고, 건강에 좋으며, 색다른 채소에 대한 수요가 증가하고 있어 이에 따라 종자 가격과 산물 가격이 상승되는 것이 받아들여지고 있다. 신선한 가공채소 트렌드는 어린 상추 잎과 시금치 잎 재배면적을 증가시키고 있다. Spring mix lettuce 파종 비율은 일반적인 상추 파종비율에 비해 20배 이상 증가하였다. 전체적으로 교배종 종자의 가격은 매년 5~8%정도 증가하고 있으며, 고정종(OP) 종자의 경우 매년 2~6%정도 가격이 상승하고 있다.

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2014년 한국육종학회상



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○ 시상내용

1. 경산육종학회상

- 수상자 : 서학수 (영남대학교 명예교수)
- 선정사유 : 야생벼 유전자원 수집과 기능성 벼 품종 개발에 헌신하고 후학 양성에 힘써 우리나라 육종학의 학문적 발전에 크게 공헌

2. 연구상(연구부문)

- (1) 박현수 (농촌진흥청 국립식량과학원 벼맥류부 벼육종재배과)
- 논문제목 : 벼흰잎마름병균에 대한 인디카와 자포니카 벼의 단일 저항성 유전자 반응과 이들의 집적 효과 (Reaction of Single Resistance Genes and Their Pyramiding Effects in Indica and Japonica Rice Against *Xanthomonas oryzae* pv. *oryzae* in Korea)
 - 한국육종학회지 Korean J. Breed. Sci. 45(2):119-129(2013. 6)

3. 연구상(품종부문)

- 이명희(국립식량과학원 기능성작물부 두류유지작물과)
- 품종명 : 품종보호 제05-0002-40호
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(韓育誌(Kor. J. Breed. Sci.) 43(6) : 616~619 (2011))

4. 공로상

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