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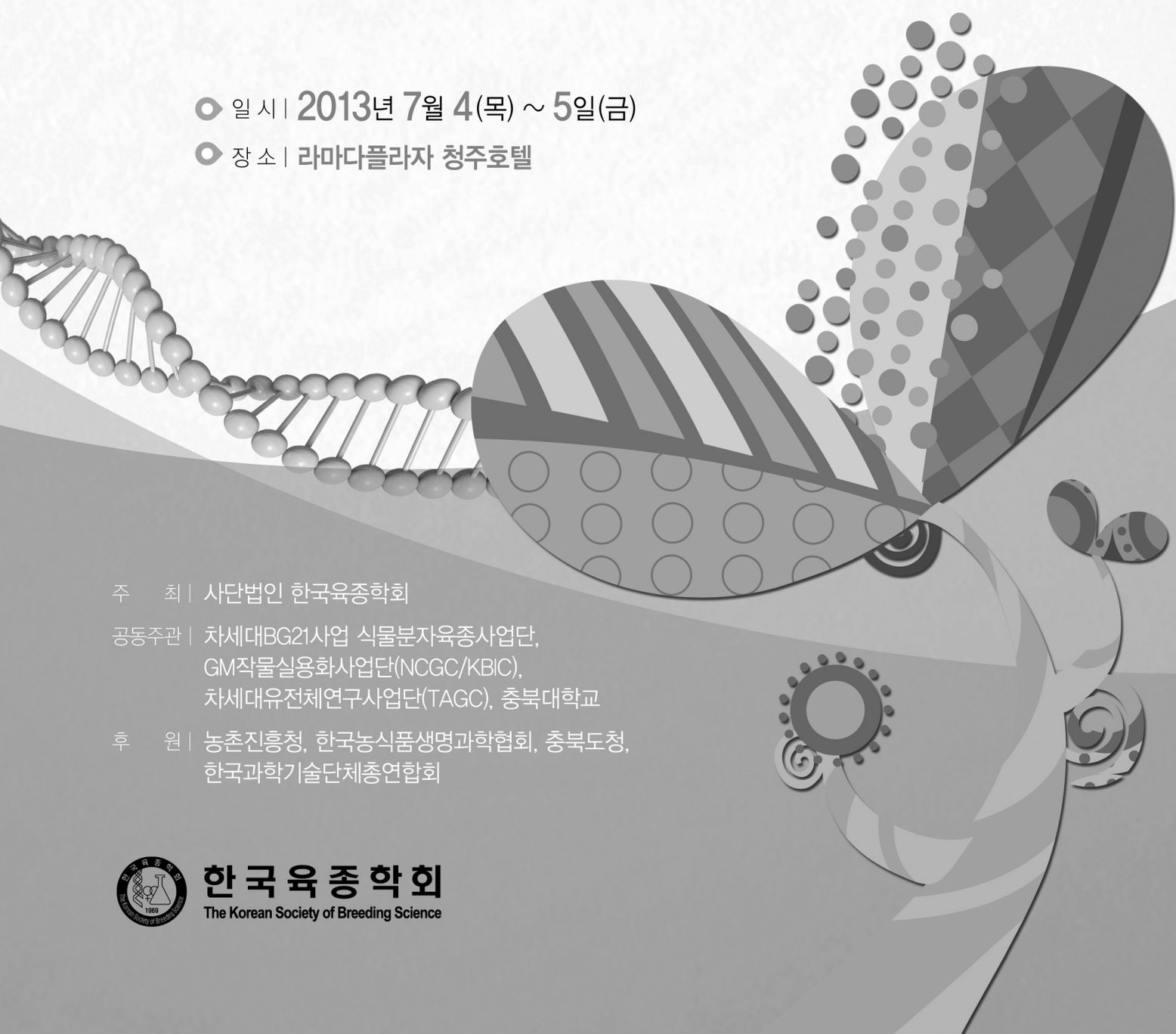
공동 심포지엄

유전체 육종과 종자 생명산업 전략
Strategies on Genomics-assisted breeding and Seed biotechnology



- 일 시 | 2013년 7월 4(목) ~ 5일(금)
- 장 소 | 라마다플라자 청주호텔

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The Korean Society of Breeding Science

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Program

2013 한국육종학회-차세대BG21사업단 공동 심포지엄 (유전체 육종과 종자 생명산업 전략)
Strategies on Genomics-assisted Breeding and Seed Biotechnology

1일째 [2013. 7. 4. 목]

12:00~13:00	등록 및 포스터 부착 (장소: 로비 & 주성홀)		
13:00~13:10	개회식 (장소: 그랜드볼룸) 한국육종학회장 인사		
제1부 학술강연			
Genome assisted breeding (유전체 육종)			좌장 : 고희종 (서울대학교)
13:10~13:50	· 고추 유전체 정보와 농업형질 개발을 위한 응용 최도일 (서울대학교)		
13:50~14:30	· 유전체 육종을 위한 전장유전체 정보의 활용 Qifa Zhang (화중농업대학, 중국)		
14:30~15:10	· 병저항성 벼 개발을 위한 유전체 육종 Shiping Wang (화중농업대학, 중국)		
15:10~15:30	휴 식		
	좌장 : 박범석 (국립농업과학원)		
15:30~16:10	· Sequencing the Norway spruce genome reveals a unique history of repeat expansion Nathaniel Street (우메오 대학교, 스웨덴)		
Epigenetics (후생유전체학)			
16:10~16:50	· Active DNA demethylation during gametogenesis regulates gene imprinting and transposon silencing in Arabidopsis Tzung-Fu Hsieh (노스캐롤리나 주립대학, 미국)		
16:50~17:30	· 크로마틴 리모델링 요소의 수량성과 개화시기 조절 기능 안진흥 (경희대학교)		
17:30~17:40	휴 식		
제2부 수출용 종자개발 사업단 & 분과별 발표			
17:40~18:10	**골든씨드프로젝트**		
	채소종자사업단 소개 및 추진계획 ▸임용표 (충남대학교) (장소: 우암홀)	식량종자사업단 소개 및 추진계획 ▸최임수 (국립식량과학원) (장소: 직지홀A)	원예종자사업단 소개 및 추진계획 ▸노일섭 (순천대학교) (장소: 직지홀B)
	분과별 포스터 발표 (장소: 주성홀)		
18:10~18:45	정기총회 & 학회상(연구상) 시상		(장소 직지홀)
19:00~20:00	리 셉 션 & 경산육종학회상 시상		(장소: 그랜드볼룸)

2일째 [2013. 7. 5. 금]

제3부 분과별 구두발표 및 사업단 워크샵

분과별 구두발표

08:30~10:30	수량 및 저항성육종 ▸좌장 : 박용진 (공주대학교) 강병철 (서울대학교) (장소: 우암홀)	분자육종 및 유전공학 ▸좌장 : 조용구 (충북대학교) 임기병 (경북대학교) (장소: 직지홀B)

차세대바이오그린21 사업단 발표

Plant epigenomics for breeding **(차세대유전체연구사업단)**

▸좌장 : 최상봉 (명지대학교) (장소: 그랜드볼룸A)

08:30~09:00	· Arabidopsis RNA metabolism by the pre-mRNA processing factor 6 homolog 이병하 (서강대학교)
09:00~09:30	· Development of stress-tolerant transgenic plants via RNA metabolism control 강훈승 (전남대학교)
09:30~10:00	· Epigenetic repression of floral genes by long non-coding RNAs in Arabidopsis 허재복 (동아대학교)
10:00~10:30	· Role of a histone-modifying enzyme in plant immunity and tomato small RNAome 정호원 (동아대학교)

GM작물실용화사업단

▸좌장 : 이강섭 (국립농업과학원) (장소: 그랜드볼룸B)

08:30~09:00	**· 글로벌 시장 진출을 위한 GM 작물 개발 전략** 김주곤 (서울대학교)
09:00~09:30	**· 쌀 육종기술의 현황과 전망** 원용재 (국립식량과학원)
09:30~10:00	**· 중국의 GM 벼 개발과 Hybrid 육종** Piao Zhong Ze (상해시 농업과학원)
10:00~10:30	· 종합토의
10:30~10:40	휴 식

제4부 학술강연

Advanced technology for development of GM crops **(최신 GM작물 개발 동향)**

▸좌장 : 박수철 (국립농업과학원)

10:40~11:20	**· 생명공학 기법 활용 선충저항성 콩 개발** Benjamin Matthews (미국농업청, 미국)
11:20~12:00	**· 글로벌 농업생명공학 기업의 GM작물 연구개발 동향** Hangsik Moon (신젠타, 미국)
12:00~12:30	시상식 및 폐회

Symposium Program

Strategies on Genomics-assisted Breeding and Seed Biotechnology
Date and Place (2013. 7. 4 ~ 5)

July 4 (Thursday)	
12:00~13:00	Registration and poster mounting
13:00~13:10	Opening ceremony
Session 1. Plenary lecture	
Genomics assisted breeding	Chair : Hee-Jong Koh (Seoul National University)
13:10~13:50	· Genome sequence of hot pepper (*Capsicum annuum* L.) and its application for agronomic trait development Do-Il Choi (Seoul National University, Korea)
13:50~14:30	· Rice genetic improvement in the post genomics era Qifa Zhang (Huazhong Agricultural University, China)
14:30~15:10	· Exploring broad-spectrum and durable disease resistance genes for rice improvement Shiping Wang (Huazhong Agricultural University, China)
15:10~15:30	Coffee Break
	Chair : Beom Seok Park (National Academy of Agricultural Science)
15:30~16:10	· Sequencing the Norway spruce genome reveals a unique history of repeat expansion Nathaniel Street (Umea University, Sweden)
Epigenetics	
16:10~16:50	· Active DNA demethylation during gametogenesis regulates gene imprinting and transposon silencing in Arabidopsis Tzung-Fu Hsieh (North carolina State University, USA)
16:50~17:30	· Chromatin remodelling factors OsVIL2 and OsVIL4 control flowering time and yield in rice Gynheung An (Kyung Hee University, Korea)
17:30~17:40	Coffee Break
Session 2. Golden seed project workshop & poster presentation	
17:40~18:10	**Golden seed project workshop**
	· Vegetable seed project (chinese cabbage, radish, watermelon, pepper, paprika) Yong Pyo Lim (Chungnam National University)
	· Horticultural seed project (cabbage, tomato, onion, tangerine, lily, mushroom) Ill-Sup Noua (Sunchon National University)
	· Crop seed project (rice, potato, corn) Im-Soo Choi (National Institute of Crop Science)
	Poster presentation
18:10~18:45	Regular general meeting
19:00~20:00	Dinner

July 5 (Friday)	
Session 3. Oral presentation & poster presentation	
08:30~10:30	· Breeding for yield increase and resistant variety Chair : Yong-Jin Park (Gongju National University) Byoung-Cheorl Kang (Seoul National University)
	· Molecular breeding and biotechnology Chair : Yong-Gu Cho (Chungbuk National University) Ki-Byung Lim (Kyungpook National University)
	· Plant epigenomics for breeding (TAGC, NextGeneration BioGreen21) Chair : Sang-Bong Choi (Myongji University)
	· Workshop for National Center for GM crops (NextGeneration BioGreen21) Chair : Kang-Seop Lee (National Academy of Agricultural Science)
10:30~10:40	Coffee Break
Session 4. Plenary lecture	
Advanced technology for development of GM Crops Chair : Soo-Chul Park (National Academy of Agricultural Science)	
10:40~11:20	· Development of cyst nematode resistant soybean through biotechnology Benjamin Matthews (USDA, Agricultural Research Service, USA)
11:20~12:00	· Research & development of GM crops in global ag-biotechnology industry Hangsik Moon (Syngenta Biotechnology, USA)
12:00~12:30	Awards ceremony & closing remark

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분자육종 및 유전공학

GM작물실용화사업단

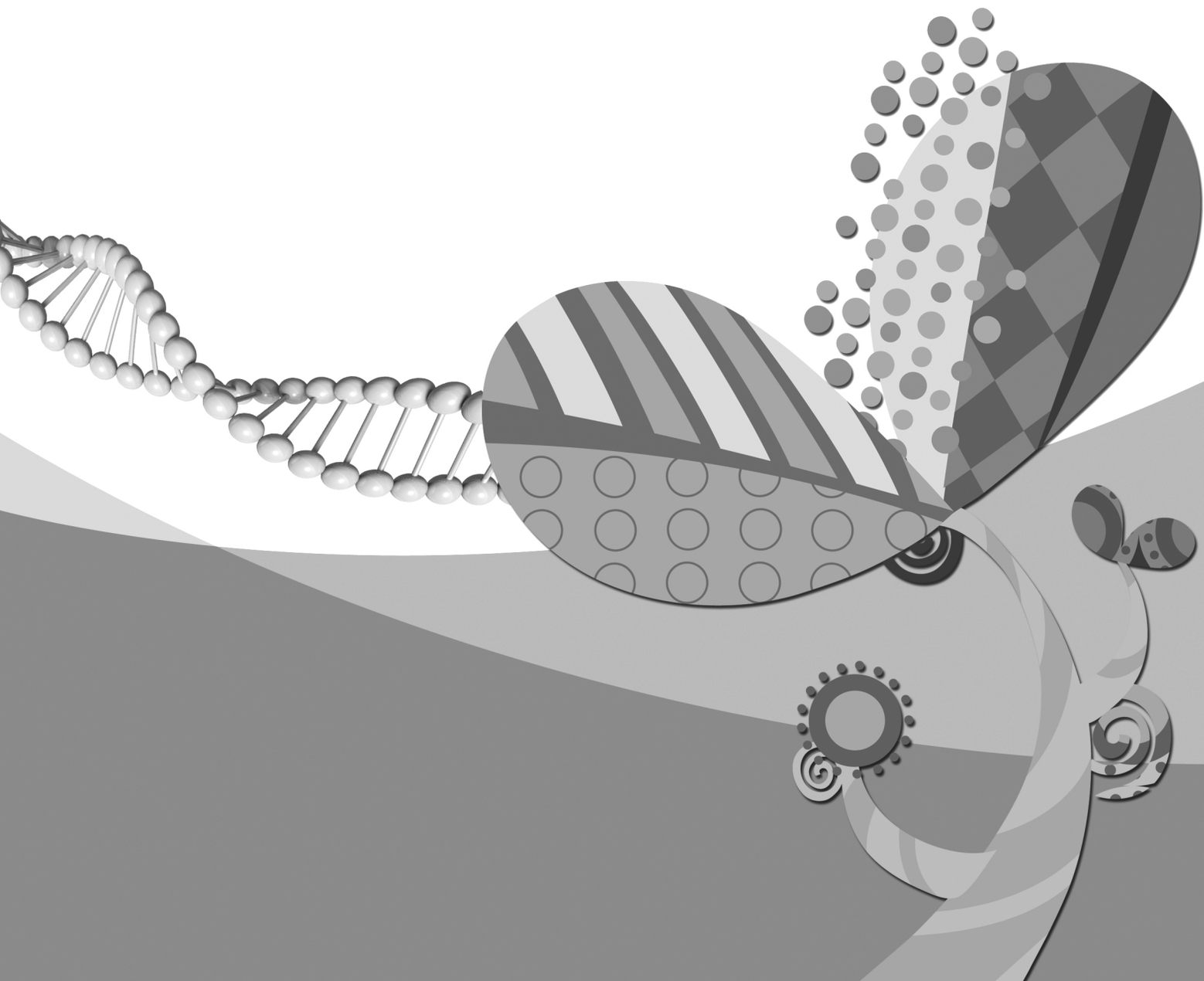
차세대유전체연구사업단 (TAGC)

Plant Epigenomics for Breeding

GM작물실용화사업단 (NCGC/KBIC)

2013 한국육종학회-차세대BG21사업단 공동 심포지엄

연사발표



SY-01

Genome sequence of hot pepper (*Capsicum annuum* L.) and its application for agronomic trait development

Doil Choi

Department of Plant Science and Plant Genomics and Breeding Institute,
Seoul National University, Seoul 151–921, Republic of Korea

Chili pepper (*Capsicum annuum*) is one of the most important vegetable crop for human being as a rich source of nutritions and spicy condiments. To make reference genome sequence of pepper, we sequenced the whole genome of *Capsicum annuum*, CM334 using Illumina/Solexa Genome Analyzer GA2. The genome size of CM334 is estimated as 3.5 Gb. A total of 716 Gb (205.96x coverages of the whole genome) of raw sequences were generated. After filtering out the low quality sequences, a total of 233 Gb (66.7x) of the raw sequences were used for assembly. Total assembled contig length and number were 2.93 Gb and 295,502, respectively. N50 and average length were 25.72 kb and 6,5 kb, respectively. By sequencial scaffolding with mate-pair sequences of 2 kb - 20 kb sizes, a total of 3.04 Gb of scaffold which is approximately 90% of the whole genome was assembled. The total number of scaffolds was 33,876 with N50 length of 1,605 kb. For annotation of the pepper genome, a total of 46 Gb of transcriptome sequences were generated from 12 different tissues using Illumina GA2 and Hi-seq 2000. We are under way of analyzing the characteristic traits of pepper using transcriptome data. The progress of pepper genome sequencing project including gene annotation, gene family analysis, comparative genomics studies on evolution of hot taste, genome expansion and fruit development will be presented in the meeting.

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SY-02

Rice genetic improvement in the post genomics era

Qifa Zhang

National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan 430070, China

In the past half century, production of major food crops in the world has kept pace with the population increase. The yields of major cereals such as maize, rice and wheat have been more than doubled in most parts of the world and even tripled in certain countries. However, food production is facing even greater challenges in the next half century because of high demands in both quantity and quality, and ever increasing pressures on resources and environments. At the same time, advances in genomics, biotechnology and genetic studies have brought about unprecedented opportunities for crop genetic improvement. Rice is a major food crop feeding approximately half of the world's population, and has provided a model system for cereal research. In my presentation, I will describe the demands for increased production for future needs, address the main issues that we have encountered as challenges, present current progress in rice functional genomics research, and provide prospect on how the advance in research can be translated into technologies and activities for rice genetic improvement.

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SY-03

Exploring broad-spectrum and durable disease resistance genes for rice improvement

Shiping Wang

National Key Laboratory of Crop Genetic Improvement, National Center of Plant Gene Research (Wuhan), Huazhong Agricultural University, Wuhan 430070, China

Fungal blast caused *Magnaporthe oryzae*, bacterial blight caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), bacterial streak caused by *Xanthomonas oryzae* pv. *oryzicola* (*Xoc*) are devastating diseases of rice worldwide. Application of host resistance to these pathogens is the most economical and environment-friendly approach to solve this problem. Some major disease resistance (*MR*) genes controlling qualitative resistance and quantitative trait loci (QTLs) controlling quantitative resistance are valuable sources for broad-spectrum and durable disease resistance. We have characterized a number of rice *MR* genes and resistance QTL genes that confer a broad-spectrum or durable resistance to *M. oryzae, Xoo,* and *Xoc.* How to efficiently use these genes for rice improvement will be discussed.

SY-04

Evolutionary insights into gymnosperm genomes resulting from the Norway spruce genome project

Nathaniel Street

Umea University, Sweden

Conifers have been the dominant tree species of many forests for more than 200 million years and are currently ecologically and economically extremely important species. Despite their importance there has, to date, been no gymnosperm genome sequence available. We produced a draft assembly of the 20 Gbp Norway spruce (*Picea abies*) genome. *Ab initio* gene prediction identified 28,354 well-supported genes representing a gene number similar to the >100 times smaller genome of Arabidopsis thaliana. Analysis of synonymous substitutions per synonymous site (Ks) identified no evidence of a recent whole-genome duplication suggesting that genome expansion resulted from other mechanisms. Repeat analysis showed that the large genome resulted from the slow and steady accumulation of a diverse set of LTR TEs that were not subsequently removed by unequal recombination, as evidenced by a high abundance of complete LTRs with few solo LTRs being identified. We performed low coverage sequencing of *Pinus sylvestris*, *Abies sibirica*, *Juniperus communis*, *Taxus baccata* and *Gnetum gnemon* to enable comparative analyses, revealing that the TE diversity is shared among extant conifers. Profiling of 24nt sRNAs, which are known to silence TEs via methylation, was highly tissue-specific and much lower than in other plants. We further identified numerous long (>10,000 bp) introns that arose due to TE insertions and that seem to be shared across gymnosperm species in addition to the genome containing numerous gene-like fragments, most likely representing pseudogenes. We additionally identified 13,031 spruce-specific and 9,686 conserved long non-coding RNAs, 2,719 miRNA candidates and show that the 21nt sRNA population is highly diverse, as reported previously for other conifer species. The availability of a conifer genome will enable further advances in conifer forestry and breeding as well as enabling evolutionary analysis including this previously missing group of land plants.

SY-05

Active DNA demethylation during gametogenesis regulates gene imprinting and transposon silencing in Arabidopsis

Tzung-Fu Hsieh

Plants for Human Health Institute and Department of Plant Biology, North Carolina State University, Kannapolis, NC 28081, US

The companion cells of the Arabidopsis thaliana egg and sperm, the central and vegetative cells, undergo active DNA demethylation prior to fertilization. However, its biological significance, extent of conservation, and targeting preferences are not yet clear. We recently showed that localized demethylation of interspersed, small transposable elements is a common feature of A. thaliana companion cells. The DEMETER DNA glycosylase encodes active DNA demethylase activity and is required for seed production. DME-mediated DNA demethylation in the central cell is required to establish imprinted gene expression in the endosperm, and is considered a master regulator for plant gene imprinting. However, the similarity among DME targets in the central and vegetative cells, despite their different functions and developmental fates, suggests that establishment of genomic imprinting may not be the basal function of DME. Lack of DEMETER in vegetative cells causes reduced methylation of transposons in sperm. Our observation suggests that the primary function of companion cell demethylation is to reinforce transposon silencing in plant gametes.

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SY-06

Chromatin remodelling factors OsVIL2 and OsVIL4 control flowering time and yield in rice

Gynheung An

Kyung Hee University

Flowering is exquisitely regulated by both promotive and inhibitory factors. Molecular genetic studies with Arabidopsis have verified several epigenetic repressors that regulate flowering time. However, the roles of chromatin remodeling factors in developmental processes have not been well explored in rice. We identified a chromatin remodeling factor OsVIL2 (*O. sativa* VIN3-LIKE 2) that promotes flowering. OsVIL2 contains a plant homeodomain (PHD) finger, which is a conserved motif of histone binding proteins. Insertion mutations in OsVIL2 caused late flowering under both long and short days. In osvil2 mutants OsLFL1 expression was increased, but that of Ehd1, Hd3a and RFT1 was reduced. We demonstrated that OsVIL2 is bound to native histone H3 in vitro. Chromatin immunoprecipitation analyses showed that OsVIL2 was directly associated with OsLFL1 chromatin. We also observed that H3K27me3 was significantly enriched by OsLFL1 chromatin in the wild type, but that this enrichment was diminished in the osvil2 mutants. These results indicated that OsVIL2 epigenetically represses OsLFL1 expression. We showed that OsVIL2 physically interacts with OsEMF2b, a component of polycomb repression complex 2. As observed from osvil2, a null mutation of OsEMF2b caused late flowering by increasing OsLFL1 expression and decreasing Ehd1 expression. Thus, we conclude that OsVIL2 functions together with PRC2 to induce flowering by repressing OsLFL1. Transgenic plants over-expressing OsVIL2 flowered early. In addition, they were taller and ticker due to increased in cell number, resulting in yield increase. The same phenotypes were observed from OsVIL4 knockout mutants. These indicate that OsVIL4 represses OsVIL2 function by directly binding to the protein.

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SY-07

Development of cyst nematode resistant soybean through biotechnology

Benjamin F. Matthews

United States Department of Agriculture, Agricultural Research Service, Soybean Genomics and Improvement Laboratory, Beltsville, MD 20705

During pathogen attack, the host plant induces genes to ward off the pathogen while the pathogen often induces host genes that increase susceptibility to the pathogen. Gene expression studies identified many soybean genes altered in expression in resistant and susceptible plant roots over time during infection by soybean cyst nematode (*Heterodera glycines*; SCN). However, it is difficult to assess the role and impact of these genes on resistance and susceptibility by using gene expression patterns alone, because the nematode injects proteins into the host. These nematode effector proteins interfere with and subvert the normal molecular mechanisms of the host cell. Therefore, we cloned >110 soybean genes from gene expression experiments using microarrays and RNA-Seq deep sequencing. The genes were overexpressed in soybean roots of composite plants to determine their impact on SCN development. Several overexpressed genes decreased the number of mature SCN females more than 50% at 32-35 days after inoculation; numerous other genes increased the number of mature females by more than 150%. Genes that reduced the number of mature females per plant by more than 50% when overexpressed, included genes encoding a β -glucanase, two lipases, calmodulin, a possible transcription factor, as well as proteins of unknown function. Four genes increased the number of mature SCN females more than 200%, while eleven more genes increased the number of mature SCN females more than 150%. Genes enhancing susceptibility included several transporters, pectate lyase, a Ca-dependent kinase and ACC oxidase. Our data support a role for auxin and ethylene in susceptibility of soybean to SCN. These studies highlight the contrasting gene sets induced by host and nematode during infection and provide new insights into the interactions between host and pathogen at the molecular level. Some genes that conferred resistance to SCN were also tested against the root-knot nematode (RKN), *Meloidogyne incognita*. Many of the genes that conferred resistance to SCN also conferred resistance to RKN. This demonstrated that the genes conferred resistance across genera and provides new strategies for developing broad resistance in plants to parasitic nematodes.

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SY-08

Research & development of GM crops in global ag-biotechnology industry

Hangsik Moon

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In 2012, the world population exceeded 7 billion and the need to address food security has never been greater. Achieving food security won't be easy considering the megatrends of growing population, greater affluence, and increasing urbanization. Not only are more people demanding more food, but they want greater variety, including meat, dairy, fruits and vegetables. While demand for food is growing, farmers' ability to increase productivity is facing unprecedented challenges. Scarcity of water, energy, and land is expected to define food production in the coming decades. Agricultural practices will also need to protect biodiversity through increasing productivity without expanding into natural ecosystems. Further exacerbating the situation is a changing climate that has led to higher temperatures and erratic weather patterns in some areas. Each day farmers face the challenge of growing more from less - increasing yields while protecting the environment by using less water, land, and energy. Global Agricultural Biotechnology companies like Syngenta have addressed these challenges through innovation in research and development by looking at the grower's challenges holistically, including land, technology, and the community. The presentation will cover general R&D activities in an agricultural biotechnology company, which may differ from those in academic research institutes. Product safety and environmental considerations are integral to industry's R&D work. To make earlier and better-informed decisions on which active ingredients or traits to move forward, normally companies begin safety trials early in the development process, facilitating timely engagement with regulators and other key stakeholders. Also to complement in-house expertise and bring in novel technologies which may or may not be used in agribusiness, companies are actively seeking value-adding partnerships and collaborations to bring exciting new offers to the grower. Development of a GM crop through all those activities mentioned above is quite a costly and lengthy process. My presentation will describe a typical process required for developing a GM crop in an agricultural biotechnology company from early discovery to commercialization to the market, which may give you a different perspective from academic point of view.

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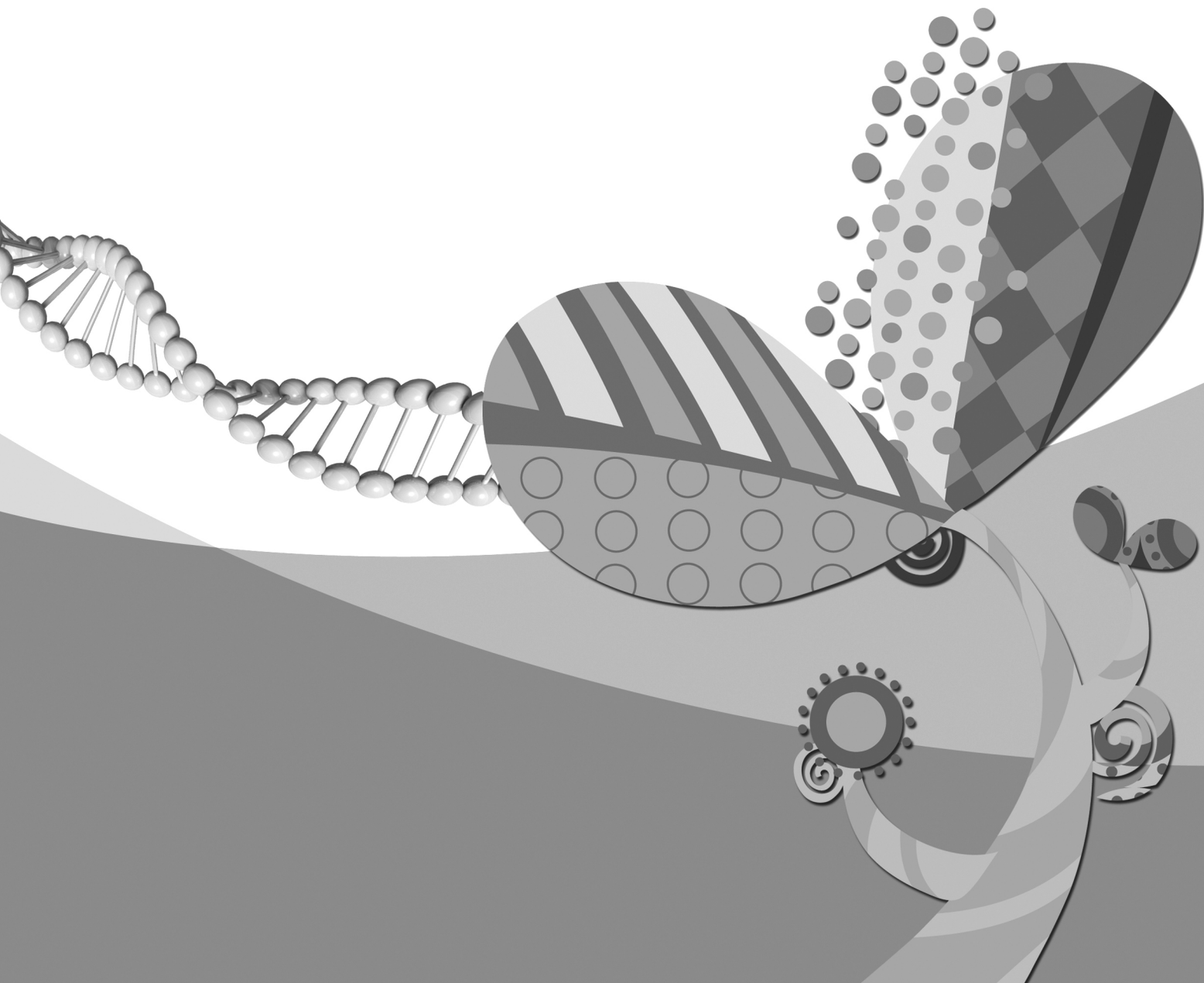
구두발표

1. 수량 및 저항성육종
2. 분자육종 및 유전공학



OA-01

인삼의 고온장해 내성 품종 '선일' 육성

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한국인삼공사 중앙연구원

인삼은 음지성 작물인데 7~8월 고온기에 강광과 고온하에서 잎의 가장자리부터 피해를 받아 결국 고사하게 되는 고온장해(엽소)가 발생한다. 엽소 피해를 받은 인삼은 근중의 감소, 뿌리 조직의 스폰지화로 인해 홍삼제조 시 내공의 발생율이 증가한다. 기존에 육성된 천풍은 지하부 체형과 홍삼품질이 우수하나 엽소에 약하다. 반면 엽소에 강한 연풍은 지하부 체형과 홍삼품질이 불량한 단점이 있다. 이에 따라 엽소에 강하고 홍삼품질이 우수한 인삼 품종의 개발이 시급하다. 본 연구는 엽소에 내성으로 선발된 '선일' 품종의 시기별 고온장해 발생율, 엽록소 형광반응, Fm/Fv 값 변화, 인삼 잎 조직의 큐티클 층의 분포와 두께, 광합성 특성 및 유효성분 분석 결과를 보고 하고자 한다.

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OA-02

Mapping of yield component traits using near isogenic lines from an interspecific cross

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In previous studies, we reported that a QTL for 1000-grain weight (TGW), *qTGW3* was located in the interval between RM60 and RM523 (1.2Mb) on chromosome 3 using advanced backcross lines derived from a cross between *Oryza sativa* ssp. *Indica* cv. Milyang 23 and *O. glaberrima*. The *O. glaberrima* alleles at this locus increased TGW and GL in the Milyang 23 background. To further confirm and narrow down the position of the QTLs on chromosome 3, twenty lines with different *O. glaberrima* segments in the target region were selected. Twenty lines were evaluated for seven agronomic traits including 1,000 grain weight and grain length and also genotyped with ten SSR markers. Sixteen lines(A, B, C groups) with the *O. glaberrima* segment flanked by SSR markers, RM60 and RM7332 displayed significantly higher values than Milyang 23 in TGW and GL whereas four lines(D, E groups) without the *O. glaberrima* segment displayed no difference in TGW and GL. The result indicates that two QTL, *qTGW3* and *qGL3* are located near RM60 and RM7332.

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OA-03

Screening of potato lines tolerant to high temperature through *in vitro* test and field performance

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The high temperature due to climate change may result in the intensification of several drought and heat stress on crops including potato. These abiotic stress affect on potato development staages; sprout development, tuber initiation and maturation. Potatoes need moderate amounts of nitrogen and cool night for good tuber growth. Especially, high temperature in soil will delay tuber initiation and induce malformation. Therefore, to identify quickly heat tolerant lines and breeding potato lines adapt to high temperature in the field are needed. The objectives of this study were as follows; To apply *in vitro* screening method for identifying potato lines adapted to high temperature conditions. To verify these results under field assays carried out under natural high temperature field conditions. We used *in vitro* screening methods with breeding lines from Intranational Potato Center(CIP) under three temperature regime, 18℃, 25℃ and 30℃. All breeding liens had some genotype that produced microtubers at 18℃ and 25℃, with a clear tendency for lower percentage of tuberization at the high temperature. To verify *in vitro* screening methods for heat tolerance lines, we carried out natural high temperature filed evaluation at Tacna, La Molina and Sanramon in Peru. The results of both the *in vitro* test and the field assay showed clear relationship and similar expression of tuberization percentage. This finding supports the use of the *in vitro* assay as a rapid screening methods that represents performance at the field level. But the correlation between performance of the breeding lines under the *in vitro* and field condions was low. This could be due to differential response to breeding lines to characteristics of the field environment, such as soil salinity, drought, which were not represented in the *in vitro* assay.

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OA-04

배가반수체기술과 genomic selection을 이용한 옥수수육종의 새로운 패러다임

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옥수수와 같은 1대교잡종 품종 육성을 위한 타가수정작물의 육종방법은 기본적으로 원종개발과 조합능력검정을 통한 교잡종 육성의 큰 틀에서 pedigree method등과 같은 전통적인 방법이나 분자육종의 최신기술이 이용되고 있다. Golden Seed Project의 시작으로 내수시장에만 머물고 있던 식량작물 육종기술이 해외시장에서 경쟁해야할 상황에 직면하게 되었다. 그 중 옥수수는 소수의 다국적 기업이 선점하고 있는 해외시장에서 수출액 170억원($1,500만USD)을 목표로 종자개발 계획이 작성되고 있다. 현시점에서 소수 다국적 기업의 최신 옥수수 육종기술의 현주소를 파악하여 Golden Seed Project의 목표 달성과 국내 옥수수 육종기술의 질적 향상을 위한 방법을 모색하고자 한다. 인공자가수분을 통한 옥수수 원종 개발은 최소 S6세대까지 진행할 동안 동계온실세대촉진이나 아열대 동계포장을 이용하더라도 최초 교배조합작성으로부터 약 4년의 기간이 소요된다. 현재 파이오니어, 몬산토, 신젠타 뿐만 아니라 CIMMYT과 미국의 주립대학교등에서는 육종년한의 단축과 100% 동형접합체를 확보하기 위하여 배가반수체기술을 도입하여 이를 통한 원종개발을 하고 있다. 이 기술의 핵심은 자연적으로 배수체를 유도하는 옥수수endogenous genes과 반수체의 빠른 식별을 위한 표현형적 표지인자의 gene pyramiding을 통한 반수체 유도계통의 육성이다. 이미 위에서 언급한 회사 및 기관에서 반수체유도율 평균 8%정도의 몇몇의 유도계통들이 개발되어 있다. 이 기술을 통한 원종의 개발은 2년이다. 이 기술을 통해 한해 수천 개의 원종이 개발되는데 이렇게 많이 개발된 원종들에서 우수한 교잡종 생산을 위한 교배조합의 작성이 새로운 문제로 제기되고 있으며 이를 해결하기 위하여 genomic selection을 적극 이용하고 있다. Genomic selection에서는 QTL mapping이나 association mapping과 달리 각 표지인자의 효과에 대한 유의성 검정을 하지 않는다. 비록 각 표지인자의 추정육종가가 미미하더라 그 정보를 그대로 이용하여 양적유전형질 발현에 관련된 모든 polygenes의 효과를 추정함으로써 교잡종상태에서의 형질발현을 예측하고 파종전 genotyping을 통해 예측가가 우수한 교잡종만을 선발하여 파종하고 평가한다.

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OA-05

Development of field corn varieties for adaptation of Primorsky Krai in Russia

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We are importing corn grains more than eight million tons every year, and self-sufficiency rate of corn is less than one percent. It is not easy to increase field corn production in Korea because of limited arable land. For this reason, many companies have been interesting overseas agriculture for corn production. But they don't have enough suitable variety for the target area. Our objective is to develop field corn varieties for adaptation in Primorsky Krai which is the southeasternmost region of Russia. This project has been collaborated with Dr. Huk-Ha Lee in Seoul National Univ. and planted three times in Primorsky Krai since 2011. Planting materials for this project were developed in Maize Research Institute. 74 hybrids in 2011, 76 in 2012, and 80 in 2013 were planted for regional performance test. Primorsky Krai is a colder area and has less frost-free days than Korea. Several hybrids have shown good performance, but lots of materials developed in Korea could not fully ripened in 2011 because of late planting and early frost. In 2012, we mainly selected early flowering materials as well as picked materials from first year. The silking date of our materials was later than local commercial varieties, but some our hybrids had good characteristics and high yield. Among them, we picked two hybrids and planted them in Ussuriysk in Primorsky Krai for field demonstration test. We expect some of the selected hybrids can be candidate varieties for improvement of corn production at overseas agricultural production base.

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OA-06

영양적, 산업적 이용을 위한 콩기름의 지방산 조성 변화

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오일의 산화적 안전성을 높이고 저장기간을 늘리기 위하여 수소를 첨가하여 액체 상태의 오일을 고체상태로 만드는 hydrogenation이란 방법을 마가린이나 쇼트닝을 만드는데 사용해 왔으나 이 과정중에 trans fat 이 생성되는 단점이 있다. 콩의 기름은 약 10% palmitic acid, 4% stearic acid, 17% oleic acid, 55% linoleic acid 와10% linolenic acid으로 구성된다. hydrogenation과정을 회피하여 콩 기름을 마가린 제조에 사용하기 위하여 mangosteen의 steroyl-ACP-thioesterase를 과발현 시킴과 동시에 콩의 palmitoyl-ACP thioesterase 와 delta 12 desaturase의 발현을 억제 함으로서 약 10-20%의 stearic acid 와 70-80%의 oleic acid를 갖는 콩을 생산 했으며. 이러한 지방산 조성은 또한 기후가 온난한 지역에서 바이오디젤의 원료로 사용되어 질수 있다. 어류의 소비는 급속히 증가 되고 있는 반면 재고량은 계속적으로 감소하고 있다. 양식이 어류의 공급을 증대시킬 대체수단으로 여겨져 왔으나 야생 잡어를 양식 어류의 사료로 사용함으로써 먹이사슬 하부에 존재하는 어류의 감소를 초래하여 결과적으로 야생 어류의 재고를 감소시키는 결과를 초래하였다. 따라서 기존의 양식사료를 대체할 새로운 사료의 개발이 절실한 상황이다. 우리는 콩을 이용하여 기존의 양식사료를 대체하려는 연구를 수행중에 있다. 콩이 양식어류의 사료로 사용되기 위한 중요한 요소중의 하나는 콩의 지방산 조성 및 함량으로 어류에 존재하는 지방산과 비슷한 조성 및 함량을 갖아야한다. 4개의 long chain omega 3 fatty acid 합성 관련 유전자와 3개의 astaxanthin 합성 관련 유전자를 집적함으로서 DHA (Docosahexaenoic acid)의 전구물질인 EPA (Eicosapentaenoic acid)를 5% 함유하며 연어의 양식에 사용되는 carotenoid의 일종인astaxanthin을 종자 1g당 25ug 수준으로 생산하는 콩을 개발 했으며 이는 기존의 어류양식에 사용되는 사료를 대체하는데 사용되어 질수있다.

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OC-01

Effectiveness of marker-assisted backcrossing breeding for biotic resistance in rice

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The transfer of a biotic resistance gene from indica rice cultivars into japonica cultivars by conventional breeding methods often difficult due to high sterility of the progenies, poor plant type, and linkage drag. Molecular markers provide opportunities to map resistance genes and accelerate the application of marker-assisted backcross(MAB) breeding through the precise transfer of target genomic regions into the recurrent parent. The basis of MAB breeding is to transfer a specific gene/allele of the donor parent into the recurrent parent genome while selecting against donor introgressions across the rest of the genome. The effectiveness of MAB breeding depends on the availability of closely linked DNA markers for the target locus, the size of the population, the number of backcrosses and the position and number of markers for background selection. We have successfully developed *Bph18* version of the commercially cultivated japonica elite cultivar by using MAB and incorporating the resistance gene *Bph18* that conferred enhanced resistance to BPH. MAB breeding provides a new opportunity for the selective transfer of biotic resistance genes into elite indica rice cultivars devoid of linkage drag. In additon, molecular markers precisely estimate the introgression of chromosome segments from donor parents and can speed up the recipient genome recovery via background selection.

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OC-02

Evolution of the large genome in *Panax ginseng*

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Ginseng (*Panax ginseng* C.A. Meyer) is the most famous medicinal herb in East Asia. Although medicinal components and their functions have been widely investigated, ginseng has been regarded as an underdeveloped crop in genetics and genomics research areas. This study was conducted to elucidate the structure and evolution of the ginseng genome by analyses of expressed sequence tags (ESTs) and bacterial artificial chromosome (BAC) sequences. The EST analysis based on the calculation of synonymous substitutions per synonymous site (Ks) in paralog and ortholog pairs revealed that two rounds of polyploidy events occurred in the common ancestor of ginseng and American ginseng (*P. quinquefolius* L.) and subsequent divergence of the two species. The sequence analysis of repeat-rich BAC clones characterized the major component of the ginseng genome, long terminal repeat retrotransposons (LTR-RTs). The LTR-RTs were classified into five main families, of which three (*PgDel*, *PgTat*, and *PgAthila*) belonged to *Ty3/gypsy* and the other two (*PgTork* and *PgOryco*) to *Ty1/Copia*. High abundance of the LTR-RTs were revealed by whole genome shotgun (WGS) read mapping and fluorescence *in situ* hybridization (FISH) analysis. Particularly, the most abundant *PgDel* family have played major roles in expanding heterochromatic regions as well as remodeling euchromatic regions. Biased intensity of the *PgDel2* FISH signals on half the total chromosomes demonstrates the allopolyploid feature of ginseng genome. Insertion time estimation of each LTR-RT implied that LTR-RTs have proliferated after the recent polyploidization of ginseng. These results suggest that the ginseng genome of the present day has been expanded and evolved by two rounds of polyploidization and accumulation of LTR-RTs.

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OC-03

Fine mapping and candidate gene analysis of a new mutant gene for panicle apical abortion in rice

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The architecture of rice panicle is primarily determined by the arrangement of branches and spikelets, and it directly affects grain yield. We identified a mutant for panicle apical abortion from a japonica cultivar Hwacheongbyeo treated with N-methyl-N-nitrosourea. Under normal growth conditions, the mutant had multiple abnormal phenotypes, such as a slight reduction in plant height, narrow and dark green leaf blades, and small erect panicles with clear panicle apical abortion compared to the wild-type plants. Genetic analysis revealed that the panicle apical abortion was controlled by a single recessive gene, which is tentatively designated as paa. The paa gene was fine mapped at an interval of 71 kb flanked by STS markers aptn3 and S6685-1 at the long arm of chromosome 4. Sequence analysis of the candidate genes within the delimited region showed a single base-pair change corresponding to an amino acid substitution from glycine to glutamic acid. We expect that the paa gene will be a clue to uncover the molecular mechanism of panicle apical abortion and to maintain the panicle identity for grain yield in rice breeding programs. 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.

Keywords: Rice, panicle apical abortion, fine mapping, molecular marker

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OC-04

Gene isolation and characterization of a dominant dwarf mutant, D-h, in rice

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Plant height is an important agronomic trait that affects grain yield. Previously, we reported a novel semi-dominant dwarf mutant, D-h, derived from chemical mutagenesis using N-methyl-N-nitrosourea(MNU) on a japonica rice cultivar, Hwacheongbyeo. In this study, we cloned the gene responsible for the dwarf mutant using the map-based approach. Fine mapping revealed that the mutant gene was located on the short arm of chromosome 1 in a 48 kb region. Sequencing of the candidate genes and rapid amplification of cDNA ends-polymerase chain reaction (RACE-PCR) analyses identified the gene, *d-h*, which encodes a protein of unknown function, but whose sequence is conserved in other cereal crops. Real-time (RT)-PCR analysis and promoter activity assay showed that the *d-h* gene was primarily expressed in the nodes and the panicle. In the D-h mutant plant, the gene was found to carry a 63-bp deletion in the ORF region, which was confirmed to be directly responsible for the mutant's gain of a functional phenotype by subsequent transgenic experiments. Since the mutant plants exhibit a defect in the GA response, but not in the GA synthetic pathway, it appears that the *d-h* gene may be involved in a GA signaling pathway. 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.

Keywords: rice, dominant dwarf, RACE

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OC-05

Genetic engineering of sugarcane for improved biofuel production from lignocellulosic biomass

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Sugarcane is one of the most efficient photosynthesizer in the plant kingdom, able to convert as much as 2% of incident solar energy into biomass. A large amount of lignocellulosic biomass such as leaf litter residues and bagasse are generated during the sugarcane harvest or after the sugar refining process, respectively. Therefore, lignocellulosic biomass from leaf and processing residues will likely become a valuable feedstock for biofuel production. However, higher temperatures and/or acid concentrations result in dehydration of xylose to furfural, and glucose to hydroxymethyl furfural, which act as inhibitors of the fermentation process. New pretreatment protocols are being developed that require the application of xylanases and other enzymes for maximal yields of xylose. Our objectives target the improvement of fermentable sugar yields from hemicellulosic sugarcane residues and enhancing the biosafety of the transgenic plants. We evaluated two transgenic approaches: lignin modification by RNAi suppression of the lignin biosynthetic gene COMT and *in planta* production of a hyperthermostable xylanase. More than 200 transgenic sugarcane plants were generated and lines with suppression or expression of the target genes were selected. RNAi suppression of *COMT* resulted in reduced lignin content and altered lignin composition. *In planta* produced xylanase Xyl10B converted the majority of sugarcane xylan to fermentable xylobiose. Performance and conversion efficiency of transgenic plants grown in replicated field plots under USDA-Aphis notification 11-040-120 will also be presented.

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OC-06

The crosstalk mechanism of Brassinosteroids and ABA in early seedling development

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Seed germination and the establishment of young seedlings are critical phases in the plant's life cycle. To control these processes, plants have evolved diverse hormonal signaling networks in which brassinosteroids (BRs) attenuate abscisic acid (ABA) responses; however, the underlying regulatory mechanism remains elusive. Here, we reveal that epigenetic silencing of the ABA signaling regulator *ABI3* via the BR-related transcription factor BES1 is essential for the inhibitory effect of BRs on ABA signaling during early seedling development. BR-activated BES1 forms a transcriptional repressor complex with TPL via its EAR motif that recruits the histone deacetylase HDA19. This facilitates the histone H3-mediated deacetylation of *ABI3* chromatin, leading to the suppression of *ABI3* and its downstream target *ABI5*, which results in reduced ABA sensitivity. We propose that the BR-activated BES1-TPL-HDA19 repressor complex controls epigenetic silencing of *ABI3* and thereby suppresses the ABA response during early seedling development.

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포스터발표

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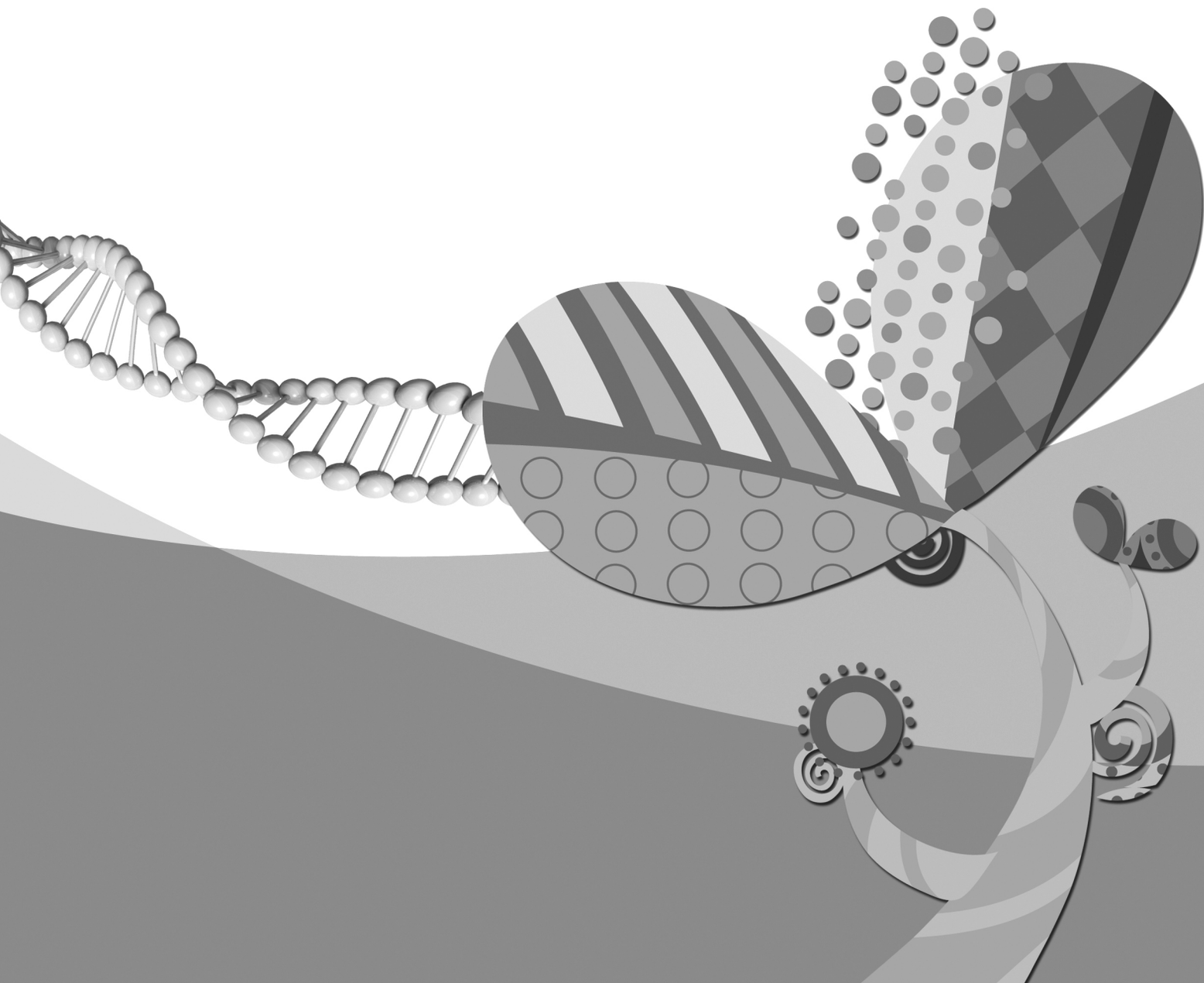

PA-01

강원도 단작지역적응 내재해·고품질 콩 신품종 “강일”

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우리나라 기후 조건은 봄 가뭄에 이은 여름철 강우 및 태풍 등 콩 재배에 불리한 실정이다. 특히 도복에 따른 재배비용 증가 및 수량 감수는 콩 재배 전체에 영향을 미치고 있다. 따라서 강원도 단작 지역에 적응하며 생육중기 집중강우와 태풍 등에 의한 도복에 강하고 수량이 안정적인 품종을 육성하고자 하였다. “강일”콩은 중대립이며 재배형질이 우수한 수원 191호를 모본으로 하고 수원 196호를 부본으로 하여 199년 인공교배 후 ’01~’03년도에 F2 - F5세대를 계통육종법으로 선발한 HS982-3SSD-10-1-1계통이다. ’04~’05년도에 실시한 생산력 검정시험에서는 생육특성이 우수하고 다수성이며 내병성 및 내도복성이 우수하여 “강원 109호”의 계통명을 부여한 후 ’06~’07년도에 강원지역 4개소와 경기지역 1개소에서 지역적응성검정시험을 실시하였다. “강일”콩은 꽃은 자색, 엽모양은 능형이며 백립중 23.3g의 중대립으로 콩의 품질특성이 우수하고 특히 성숙기가 태광콩 대비 9일 빠른 조숙이며 내도복성 품종으로 강원도 북부지역 및 고령지 적응성 품종이다. 2009년 신품종 등록 되었으며 강원도농업기술원 종자보급체계를 통하여 농업인에게 보급종을 생산·보급하고 있다.

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PA-02

기계수확이 가능한 콩나물용 콩 품종 ‘해품’ 육성

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나물용 콩은 콩나물수율을 높이기 위해 소립을 선호하고 있으며, 립크기가 상대적으로 작아지는 경남과 전남의 남부지역과 제주에서 주로 생산되어 왔으며, 최근에는 남부지방에서의 재배면적이 줄어들면서 제주도가 전체 재배면적의 82%를 점유하고 있다. 콩을 기계로 수확하기 위해서는 내도복성과 내탈립성, 협·줄기 동시성숙성 등의 특성과 함께 최저착협고(가장 낮게 맺히는 꼬투리의 높이)가 높아야 한다. 그러나, 영양생장기간이 짧고 바람이 많은 제주에서는 경장이 짧아짐에 따라 착협부위가 낮아 수확기계를 적용하기 어려운 실정이다. ‘해품’은 지역적응시험 4개소에서의 평균 경장이 61cm로 풍산나물콩보다 6cm 길며, 최저착협고 또한 15cm로 풍산나물콩보다 6cm 더 높다. 특히, 제주에서의 3년간 평균을 보면 경장이 49cm로서 풍산나물콩보다 8cm 더 클 뿐 아니라 풍산나물콩이 최저착협고가 6cm로서 기계예취가 불가능한 반면, 해품은 14cm로서 콤바인을 이용한 예취가 가능하다. 해품은 풍산나물콩에 비하여 성숙기가 5일 빠르며 콩나물수율과 아스파라긴 함량이 높다. 100립중은 10.4g으로 소립이며 수량은 3.01MT/ha로 풍산나물콩 대비 10% 증수한다. 탈립과 도복에도 강한 ‘해품’은 주산지인 제주에서 재배확대가 기대된다.

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PA-03

내냉성 벼 품종육성을 위한 중국 운남성에서 국내 계통의 작물학적 특성

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중국 운남성은 북위 20º8'39"N에서 29º15'8"N로 중국의 남방지역이지만 해발 76.4m에서 6,740m의 지대의 범위가 다양하며 벼 재배가능 지역은 고지대(1,600～2,200m)까지 가능하다. 이런 다양한 지대의 운남성은 재배벼의 기원지로 다양한 유전자원의 보고로 특히 고지대의 벼 품종들은 저온에 대한 자연적인 내냉성 선발로 저온에 강한 품종들로 일본 북해도의 논 개간은 일본의 식량부족시대의 대표적 산물로서 내냉성 유전자의 중국으로 부터의 도입이 있었기에 가능하였다.
지구온난화 등 기후 변화에 대응 우리 품종의 다양성을 위한 중국 남방 고산지역 벼 유전자원 수집 및 특성평가와 수집 유전자원 활용 국내 품종의 미질 및 내냉성의 안정성 증진을 하고자 내냉성 고품질 중간모본 육성을 위하여 국내에서 2010년 약배양한 계통 중 수량성 및 농업적 형질이 우수한 3조합 11계통을 공시재료로 이용하였다. 중국현지에서의 내랭성 정도와 현지적응성 및 수량을 평가하기 위하여 실시하였다. 공시재료는 중국 운남성 송밍(1,900m)지역과 추숑(1,775m)지역에 각각 3월20일과 3월17일에 파종하였고, 이앙은 5월22일과 5월25일에 주당 1본씩 각각 주간과 조간을 10×20㎝ 간격으로 이앙하였다. 출수기, 작물학적 특성 및 내냉성 등을 조사하였다.
시험계통의 출수기는 송밍 지역에서 7월23일～8월 2일 사이에 분포하였으며 진부벼와 출수기와 비교할 때 13일에서 24일 정도 늦은 편이었다. 시험계통에 따른 간장은 츄숑 60～72cm, 송밍 50～62cm로 송밍지역이 츄숑지역보다 간장이 작았으며 송밍은 츄숑에 비해 시험계통에 따라 8.5%～19.3%의 간장 단축률을 보였다. 계통별 평균 이삭길이는 송밍은 18～21cm, 츄숑은 20～22cm의 분포를 보엿다. 주당수수의 경우 송밍이 평균 7.6개. 츄숑이 평균8.6개로 고도가 높은 송밍지역이 츄숑지역 보다 간장. 수장, 수수가 감소하는 경향을 보였다.

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PA-04

내병성 고추 육성을 위한 marker assisted breeding

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전통육종과 marker assisted selection(MAS)를 함께 활용하는 방법이 최근 국내 상업육종에서 활발히 사용되고 있다. 식물 유전학의 빠른 발달과 차세대 유전체 염기서열 분석(NGS) 기술이 발전함에 따라, 대량 분자표지를 저렴한 가격에 확보할 수 있는 시대가 되었기 때문이다. 본 연구에서는 고추의 전사체 정보를 이용하여 SNP를 분석하고 Fluidign probe를 자동으로 디자인할 수 있는 파이프라인을 작성하였다. 또한 SNP를 calling하기 위해 총 6개의 accession(5개의 *C. annuum*과 1개의 *C. chinense*)의 전사체 염기서열을 Illumina 플랫폼으로 분석하였고, reference 염기서열은 고추 EST DB를 사용하였다. 분석한 SNP의 유전적 위치를 알기 위하여, UC-DAVIS의 고밀도 고추 유전자 지도와 연계하였다. Fluidigm probe를 design할 수 있는 조건으로 SNP를 filtering한 결과, short read의 depth가 10 이상을 기준으로 총 567개의 SNP를 분석하였고, 총 412개의 probe를 디자인하였다. 제작한 412개의 porbe와 논문에 공개된 SSRs, COSII 분자표지들, 2개의 고추 내병성 형질을 이용하여, 현재 내병성 고추 품종을 육성하기 위한 marker assistant breeding(MAB)을 진행 중에 있다.

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PA-05

내병성, 고품질 참깨품종 “유미” 육성

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“유미” 참깨는 내병성 다수성 품종육성을 목적으로 모본 “양백깨”와 부본 “SIG950480-6-3-1”을 2001년 인공교배하여 계통육종법으로 육성한 품종이다.
“유미”의 주요 형태적 특성을 보면 초형은 소분지형이고 꼬투리는 3과성 2실 4방형이며 화색은 백색이다. “유미” 의 개화기는 7월 5일로 표준품종인 “양백깨”와 같으나 성숙기는 8월 22일로 1일이 빨랐다. 경장은 149cm로 “양백깨”보다 17cm 컸으며 착삭부위장도 컸고, 주당삭수는 82개로 3개가 많은 경향이다. “유미”의 종실수량은 106kg/10a으로 “양백깨” 98kg/10a보다 8% 증수하였다. 또한 “유미”는 표준품종인 “양백깨”보다 역병, 도복에 강한 특성을 나타냈다.
“유미”의 품질 특성을 보면 조지방함량은 49.7%로 높았고, 올레익산 함량이 45.3%로 많았으며, 인체의 노화억제와 항암 효과가 있는 기능성 리그난성분인 세사민 함량은 2.8mg/g으로서 표준품종 “양백깨”보다 0.6mg/g 많은 품종이다.

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PA-06

내재해 안전 다수성 메조 ‘조황메’ 육성

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웰빙 트랜드에 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. ‘조황메’는 안동지역에서 수집된 재래조를 기본집단으로 하여 분리육종법을 통해 2012년 육성된 신품종이다. 출수기는 대비품종인 ‘황금조’보다 보통기에서 12일, 이모작재배시 13일 늦고, 생육일수는 보통기 116일로 ‘황금조’보다 11일 늦은 중생종이다. 간장과 수장은 ‘황금조’에 비하여 큰 편이며, 조곡 천립중은 ‘황금조’와 비슷하다. 배유특성은 메성이며 조단백질 함량은 14.7%로 ‘황금조’와 비슷하다. ‘조황메’는 도복, 불임내성 및 조 도열병에 ‘황금조’보다 강하여 내재해 및 내병성이 우수하였다. 수량성은 지역적응시험 보통기 재배에서 ‘황금조’에 비해 27%, 이모작 재배에서 7% 각각 증수되었기에 적기에 파종하면 높은 수량을 얻을 수 있다.

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PA-07

다수성 종실용 옥수수 신품종 '신광옥'의 생육특성 및 수량성

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우리나라 사료곡물 자급률을 높이기 위한 방안은 다수성 종실 사료용 옥수수를 육성하고 다수확 재배기술을 개발하여 옥수수 생산량을 늘리는 것이다. 새로 개발된 옥수수 품종 신광옥은 다수성 사료용 옥수수 품종 개발을 목표로 2012년에 농촌진흥청 국립식량과학원에서 자식계통 KS172과 KS173을 교잡하여 육성한 다수성 단교잡종이다. 신광옥의 종피색은 황오렌지색이며 입질은 중간종이다. 2008~2009년까지 생산력검정시험을 거쳐 2010~2012년까지 3지역에서 지역적응시험을 실시하였다. 그 결과 우수성이 인정되어 2012 농작물 직무육성 신품종으로 결정되었고 신광옥으로 명명하였다. 신광옥의 출사일수는 대비품종인 장다옥보다 3일 빠르다. 간장은 장다옥과 비슷하나 착수고율은 장다옥보다 낮고 도복은 장다옥과 비슷한 정도로 강하다. 100주당 이삭은 장다옥보다 17개 더 많고 이삭길이는 장다옥과 비슷하며, 100립중은 장다옥보다 무겁다. 깨씨무늬병 저항성은 중강이며, 그을음무늬병에는 강한 편이다. 검은줄오갈병, 이삭썩음병 및 조명나방 저항성은 중정도이다. 신광옥의 종실수량은 7.8톤/ha로 장다옥과 비슷하다. 4 : 1(모본 : 부본) 재식비율로 동시 파종하여 채종 시험한 결과 종자친(모본) 출사기와 화분친(부본) 화분비산기간이 일치하였으며 채종수량은 3.84톤/ha이었다. 신광옥은 전국적으로 재배가 가능하다.

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PA-08

다수성, 갈색 참깨 품종 "갈미" 육성

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"갈미" 참깨는 다수성, 갈색 참깨품종 육성을 목적으로 모본 "HS331-M-3-5-4-1"과 부본 "HS1392"를 2001년 인공교배하여 계통육종법으로 육성한 품종이다. 주요 형태적 특성을 보면 초형은 소분지형이고 꼬투리는 3과성 2실 4방형이고 화색은 분홍색이며 종피는 갈색이다.
"갈미"의 개화기는 7월 5일로 표준품종인 "강흑"과 같았으나 성숙기는 8월 23일로 "강흑"보다 1일 느렸다. 또한 경장은 143cm로 "강흑"보다 4cm 작았으나 주당삭수는 80개로 "강흑"보다 6개 많았다. "갈미"의 천립중은 2.6g으로 "강흑"과 같았으며 "갈미"의 종실수량은 94kg/10a으로 "강흑" 81kg/10a보다 16% 많았다. 또한 "갈미"는 표준품종인 "강흑"보다 역병에 강한 특성을 나타냈다.
"갈미"의 품질 특성을 보면 조지방함량은 43.9%로 "강흑"의 39.9%보다 많았으며 그 중 올레익산 함량이 42.4%로 가장 높았고 "갈미"의 리그난 함량은 291mg/100g을 나타냈다.
재배상 유의점은 적응지역 내 고지대의 일조시간이 적고 온도가 낮거나 물빠짐이 불량한 지대에서는 재배를 피해야하고 병해충의 적기방제에 유의하며 예방위주의 방제를 하여야 한다.

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PA-09

도복 및 이삭곰팡이병에 강한 찰수수 '남풍찰' 육성

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경남 밀양시 점필재로 20 국립식량과학원 잡곡과

대부분의 농가에서 재배되고 있는 재래종 수수는 수량성이 낮고, 일부지역에 보급되고 있는 황금찰수수는 도복에 약해 환경재해에 취약한 실정이어서 국립식량과학원에서는 2012년 도복 및 내재해성이 강하고 기계화재배가 용이한 찰수수인 '남풍찰'을 육성하였다. '남풍찰'은 2009년 경남 남해지역에서 수집한 재래수수를 기본집단으로 하여 순계분리육종법을 통해 육성된 품종이다. '남풍찰'은 파종 후 출수까지 평균 68일, 수확까지는 평균 113일인 중생종이다. 키가 약 165cm이고 이삭의 형태는 밀수형이지만 밀도가 '황금찰'에 비해 조밀하지 않기 때문에 이삭곰팡이병 발생이 적은편이다. 줄기 굵기가 20.2mm로 굵어 15.0mm인 '황금찰'에 비해 쓰러짐에 잘 견디고 수량성은 228kg/10a로 안정생산이 가능하다. 주당 이삭수는 1개이며 현곡천립중은 22.8g, 주당이삭중은 26.6g으로 무겁다. '남풍찰'은 찰수수로 혼반용으로 이용 가능하고 재래 찰수수 종자를 대체하여 농가 생산성 향상을 기대할 수 있다.

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PA-10

벼 극조생 내랭성 중간모본 '중모1022호' 육성

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벼 재해저항성이 강화된 품종육성을 위해서 특정 외래 저항성 유전자원의 활용은 동반하는 불량 인자로 인하여 저항성 유전형의 선발과 고정에 어려움이 있다. 벼 품종육성에 일정한 수준의 농업형질과 목표로 하는 재해저항성을 보유한 중간모본의 활용이 이루어진다면 보다 효율적인 재해저항성 품종육성이 이루어질 수 있다.
조생종 내랭성 강화를 위해 내랭성 우량계통인 진부31호와 내랭성 유전자원 교동 23호를 인공교배하여 계통육종법으로 저온 발아성 및 생식생장기 내랭성이 우수한 벼 중간모본 '중모1022호'를 개발하였다. '중모1022호'의 출수기는 중북부 중산간지 및 고랭지의 보통기 보비재배에서 7월 23일로 진부벼보다 4일 빠르다. 간장은 67cm로 진부벼와 약간 작고, 주당수수는 14개로 적으나 수당립수가 많은 수중형이다. 등숙율을 90%로 진부벼와 비슷하고 현미 천립중은 21.5g으로 진부벼보다 가벼운 중립종이다. 단백질 함량은 5.9%로 낮고 아밀로스 함량은 21%, 밥맛의 관능검정에서 식미는 -0.1로 낮은편이다. 보통기 재배 수량성은 중부북 고랭지에서 3개년 평균 561kg/10a로 진부벼 대비 2% 증수하였다.
13℃, 15일간 처리한 저온발아율은이 96%로 진부벼 대비 17% 증가하고, 감수분열기의 내랭성은 진부벼와 비슷하고 출수기에 17℃, 10일의 냉온처리에 의한 임실율은 64%로 진부벼 보다 내랭성이 우수하였다.

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PA-11

벼 중생 최고품질 내병 내도복 다수성 신품종 “대보”육성

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국립식량과학원 영덕출장소에서 2002년 하계에 YR21247-68-1를 모본으로하고 밥맛이 우수한 영덕35호”를 부본으로 인공교배하여 2002/2003년 동계에 국립식량과학원 기능성작물부 온실에서 26개체의 F_1 식물체를 양성하여 YR23940의 교배번호를 부여하였다. 2003년 하계포장에 F_2 집단을 공시하면서 선발하여 2004년 하계에 F_3세대를 육성하고 57계통을 F_4 계통으로 전개 후 계통육종법으로 선발하여 2007년 생예, 2008년 생본시험을 실시한 후 쌀 품위가 좋으면서 밥맛이 우수하고 재배 안정성이 높은 YR23940-B-17-1-2 을 선발하여 “영덕51호”로 명명하였다. 2009년～2011년까지 3년간 지역적응시험을 실시한 결과 중생종이면서 쌀알이 아주 둥근 단원형 이면서 품위가 좋고 밥맛이 뛰어나며 내병성과 내도복성을 갖춘 것으로 평가되어 2011년 12월 농작물 직무육성 신품종 선정위원회에서 국가품종목록으로 등재 할 것을 결정하고 “대보”로 명명하여 적응지역인 동남부해안지, 중부 및 남부 평야, 남부중산간지에 보급하게 되었다. 출수기는 8월 14일로 “화성벼”보다 1일 늦은 중생종이며 직립 초형이고 탈립은 잘되지 않고 이삭추출은 양호 하고 까락이 거의 없다. 수당립수는 “화성벼”보다 많고 현미천립중도 22.8g으로 “화성벼”보다 약간 더 무겁다. 도정특성이 양호하면서 쌀알 모양이 아주 둥근 단원형이며 맑고 투명하며 밥맛은 “화성벼”보다 우수하다. 불시출수는 안되는 편이고, 위조현상에 강하고 성숙기 엽노화가 느린 편이며 내냉성은 “화성벼”와 같은 수준이다. 잎도열병은 중도저항성을 보였고 줄무늬잎마름병과 흰잎마름병(K_1, K_2, K_3)에는 강하나 오갈병 및 검은줄오갈병에 약하고 벼멸구 등 충해에는 감수성이다. 쌀 수량성은 보통기재배 시 5.93MT/ha로 “화성벼” 보다 11% 증수되었고, 이모작재배에서는 5.23MT/ha로 14%, 만식재배에서는 4.63MT/ha로 21% 증수 하였다. “대보”의 적응지역은 동해안냉조풍지, 중부 및 남부평야지, 남부중산간지이다.

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PA-12

벼흰잎마름병균에 대한 인디카와 자포니카 벼의 단일 저항성 유전자 반응과 이들의 집적 효과

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본 연구는 우리나라 벼흰잎마름병 균주에 대한 인디카형과 자포니카형의 단일 저항성 유전자의 반응과 이들의 집적 효과를 비교 분석하고 자포니카형의 유망 조합을 제시하여 향후 우리나라 환경 여건에 효과적인 저항성 품종을 육성하고자 수행하였다. 단일 저항성 유전자 계통중 *Xa1*, *Xa3*, *Xa21*은 생태형 간에 차이가 없었으나 *Xa4*와 *xa5*는 자포니카에 비해 인디카형에서 저항성이 강하였다. 인디카형과 자포니카형에서 모두 저항성 유전자가 집적되었을 경우에 단일 또는 두 개의 저항성 유전자에 비해 저항성이 정도가 증가하거나, 저항성 수준이 높은 유전자가 저항성 수준이 낮거나 균계 특이적 이병성을 나타내는 저항성 유전자를 보완하는 효과를 나타냈다. 자포니카형에서 새롭게 확인된 저항성 유전자 집적 조합인 *Xa3*+*Xa21, xa5*+*Xa21*과 *Xa3*+*xa5*+*Xa21*은 우리나라 우점 균주와 16개 균주에 대해서 저항성이었으며 현재 우리나라 벼흰잎마름병 저항성 육종에서 주력 저항성 조합으로 이용되고 있는 *Xa3*+*xa5* 보다 높은 수준의 저항성을 나타냈다. 이들 저항성 유전자 집적 조합은 균계 분화 등에 따른 저항성 붕괴에 안정적으로 대응할 수 있고 저항성을 효과적으로 강화할 수 있는 유망 조합으로 생각되어 자포니카 벼흰잎마름병 저항성 증진을 위한 목표 조합으로 설정하여 육종사업을 수행하겠다.

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PA-13

사일리지 및 종실용 옥수수 신품종 '양안옥'의 생육특성 및 수량성

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국내 옥수수 안정생산 기반을 확립하기 위해 사료 품질이 우수하고 수량이 많은 신품종 '양안옥'을 육성하였다. 양안옥은 다수성 사료용 옥수수 품종 개발을 목표로 2012년에 농촌진흥청 국립식량과학원에서 자식계통 KS164과 KS163을 교잡하여 육성한 다수성 단교잡종이다. 양안옥의 종피색은 황오렌지색이며 입질은 중간종이다. 2007~2008년까지 생산력검정시험을 거쳐, 2010년을 제외한 2009~2012년까지 4지역에서 지역적응시험을 실시하였다. 그 결과 우수성이 인정되어 2012 농작물 직무육성 신품종으로 결정되었고 양안옥으로 명명하였다. 양안옥의 출사일수는 대비품종인 광평옥보다 2일 빠르다. 간장은 광평옥과 비슷하나 착수고율은 광평옥보다 높고 도복은 광평옥과 비슷한 정도로 강하며 후기녹체성과 이삭비율도 광평옥과 비슷하다. 깨씨무늬병에는 중강의 저항성을 보이며, 그을음무늬병에는 강한 편이다. 검은줄오갈병, 이삭썩음병 및 조명나방에는 중 정도의 저항성을 보인다. 양안옥의 건물수량은 17.45톤/ha이며, TDN수량은 11.96톤/ha로 광평옥과 비슷한 수준이다. 양안옥의 종실수량은 8.32톤/ha로 장다옥과 비슷하다. 4 : 1(모본 : 부본) 재식비율로 동시 파종하여 채종 시험한 결과 종자친(모본)의 출사기와 화분친(부본)의 화분비산기간이 일치하였으며 채종수량은 1.79톤/ha이었다. 양안옥은 전국적으로 재배가 가능하다.

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PA-14

수량이 높고 병해에 강한 가래떡용 '희망찬' 개발

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가래떡은 그동안 품종특성 구별 없이 보통쌀로 제조되어 왔다. 더구나 원가절감을 위하여 값싼 원료미를 이용하여 제조하기 때문에 품질 면에서 특성이 일정하지 못하고 제조업체마다 맛에서 큰 차이를 나타낸다. 가래떡은 떡국이나 떡볶이를 만드는데 직접 사용되기 때문에 설날뿐 아니라 평소에도 우리국민이 즐겨먹는 음식이다. 최근에는 한식 세계화와 더불어 품질관리가 더욱더 중요하게 되었다. 하지만 지금까지는 가래떡 제조에 적합한 품종도 없을뿐더러 맛에 대한 체계적인 연구도 거의 없는 실정이다. 이에 가래떡 제조에 가공적성이 좋은 '희망찬'을 개발하게 되었다.
'희망찬'은 기존 품종보다 수량이 많고 흰잎마름병과 줄무늬잎마름병에 강한 품종으로 국립식량과학원 벼맥류부에서 2000년 하계에 밀양165호에 '신동진'을 인공교배하여 계통육종법에 따라 우량계통을 선발 고정시켜 2011년에 내병 다수성인 벼품종을 개발하였는데 특히 가래떡 제조에 좋은 적성을 가지고 있다. '희망찬'은 중만생으로 수량이 많고 도열병과 줄무늬잎마름병에 저항성이며 출수기는 8월17일로 '한마음'보다 3일정도 늦고 간장은 큰 편으로 수당립수가 많고 등숙비율이 높다. 수량은 '한마음'보다 보통기다비 재배에서 4% 증수되며 적응지역은 충남이남 평야 1모작지이다.

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PA-15

수량이 높고 병해에 강한 향기 좋은 검정쌀 '흑수정' 개발

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흑미는 대부분 쌀에 있는 안토시아닌 색소가 항산화 작용을 하여 우리 몸의 노화를 느리게 하고 동맥경화 예방에 효과가 있다고 알려지면서 혼반용으로 밥에 섞어 먹어왔다. 한편 수요가 늘어남에 따라 재배면적이 늘어나면서 농가소득 향상에 기여 하여왔는데 농가에서 재배하고 있는 흑미는 수량성이 낮고 병해에 약한 단점이 있다.
'흑수정'은 기존 품종보다 수량이 많고 흰잎마름병과 줄무늬잎마름병에 강한 품종으로 국립식량과학원 벼맥류부에서 2001년 하계에 '흑향'벼에 HR14834-11-4-3-4호를 인공교배하여 계통육종법에 따라 우량계통을 선발 고정시켜 2012년에 내병 다수성 흑향미를 개발하였다. '흑수정'은 중만생으로 색깔이 검고 향기가 있으며 도열병과 줄무늬잎마름병에 저항성이다. 출수기는 8월14일로 '흑남벼'와 비슷하며 간장은 약간 큰 편으로 수당립수가 많고 등숙비율이 높다. 수량은 '흑남벼'보다 보통기보비 재배에서 8% 증수되며, 밥을 지을 때 퍼짐성이 좋다. 적응지역은 충남이남 평야지 및 서남부 해안지이다.

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PA-16

숙기 및 용도별 벼 품종의 묘소질 변이

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최근 육성한 벼 품종을 대상으로 숙기 및 용도별 벼 품종의 묘소질에 대한 차이를 알아보고자 본 연구를 수행하였다. 종자 파종은 국립식량과학원 벼 재배 시험포장 신흥통(사앙토)에서 4월 26일에 하였으며, 파종량은 상자당 150g을 하였다. 묘소질 조사는 30일 성묘를 대상으로 묘초장, 엽수, 생체중, 지상부 건물중 등을 조사하였다. 시험결과 숙기별 묘소질에서는 중생골드, 대보 등 중생종의 묘초장이 20㎝로 가장 컸으며, 엽수는 산호미, 화왕 등 조생종에서 3.7개로 가장 많았다. 지상부 묘건물중을 초장으로 나눈 묘충실도는 조생종이 0.15로 가장 양호하였다. 또한 용도별 벼 품종에서는 현품, 수광 등 최고품질 벼 품종의 묘초장이 17.9㎝로 가장 컸으며, 유색미(17.1㎝) > 가공적성(16.3㎝) >기능성(14.4㎝) 순이었다. 엽수는 가공적성이 3.6개로 가장 많았다. 이들 품종의 묘충실도는 최고품질(0.17) > 찰벼(0.13) > 가공적성(0.11) 순으로 양호하였다. 묘충실도가 양호하고 초기 신장성이 우수한 품종들은 벼 무논점파용 품종으로 적응성이 높을 것으로 사료된다.

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PA-17

약배양 이용 벼멸구, 흰잎마름병 및 줄무늬잎마름병 저항성 벼 계통 육성

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복합내병충성 품종을 조기에 육성하고자 줄무늬잎마름병(RSV)과 흰잎마름병(BB)에 저항성인 우량 계통 HR26234-12-1-1과 줄무늬잎마름병, 흰잎마름병 및 벼멸구(BPH)에 저항성인 SR30071-3-7-23-6-2-1-1 계통을 인공교배한 F_1을 약배양하여 총 213개 계통을 육성하였다. 목표 유전자와 연관된 DNA 분자표지를 이용하여 저항성유전자를 확인하였다. HR26234는 *Stvb-i*, *Xa3*+*xa5*을,, SR30071은 *Stvb-i*, *Xa4(?)*, *Bph18*을 가지고 있는 것으로 나타났다. 이들 유래 계통들은 모두 *Stvb-i*를 가지고 있었고. *Bph18*을 가지고 있는 계통은 42계통이었다. 흰잎마름병 저항성 유전자의 작성 가능한 조합 중에서 *xa5* 단독 계통은 발생하지 않는 등 segregation distortion이 나타났다. BPH(*Bph18*), BB(*Xa4*+*xa5*)와 RSV(*Stvb-i)*의 저항성 유전자 집적 7 계통을 선발하여 2012년에 생산력과 병해충에 대한 저항성을 검정하였다. 이들 계통들의 농업적 특성들 중 출수일수는 96일로 진백(110), 남평벼(106일), 안미(102)보다 빠른 중생종이었고, 간장은 66～71 cm로 진백(71 cm), 남평벼(78), 안미(77)보다 짧으며, 수당립수는 102～119개로 안미(119개)와 비슷한 수준이었다. 등숙률과 수량성은 대조품종인 남평벼, 진백, 안미보다 낮았다. 유묘 및 성체에서 벼멸구에 강한 저항성을 나타냈으며 흰잎마름병 K1,K2,K3,K3a 균계에 저항성이고 줄무늬잎마름병에 강하였다. K3a 균계 접종 후 수량 및 등숙률의 감소율이 이병성인 남평벼와 안미에 비해 낮았다. 약배양을 통해 단기간에 복합내병충성 계통을 확보할 수 있었으나 계통 선발시 파악되지 않았던 일부 수층의 불균형과 불임립 발생, 단간임에도 도복에 안정적이지 못하는 등 열악형질이 발견되었다. 약배양을 통해 조기에 육종목표를 달성하고자 할 경우에 segregation distortion이 발생하여 편의된 변이가 발생할 수 있고 파악되지 못한 형질 특성이 나타날 수 있음을 고려하여 신중하게 목표에 접근하여야 할 것으로 생각한다.

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PA-18

오대벼 대체 고품질 중립 조생종 벼 품종 '새오대'

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강원도는 우리나라 벼 조생종 재배지역으로 벼 조생지대에서는 매년 오대벼 품종이 약 2만ha 정도가 재배되고 있는 실정이다. 강원도 지역에서 오대벼는 '철원오대쌀'이라는 단일미 품종명 브랜드가 성공하고 유지되고 있는데 오대벼가 다른 품종에 비해 쌀알이 25g으로 뚜렷이 굵어 다른 품종과 구별이 된다. 그러나 오대벼의 쌀 외관이 다소 떨어지는 문제점이 있어 이 단점을 해결하기 위하여 쌀 굵기가 오대벼의 중립종 크기의 쌀 외관이 맑은 조생종 품종 개발이 필요하다.
벼 품종 '새오대'는 중북부중간지에 적응하는 오대벼 품종을 대체할 목적으로 2001년 하계에 조생종이면서 단기성인 품종 그루벼와 중립종인 수원472호(남일벼)와 인공교배하여 계통육종법에 의해 선발하면서 주요 병해충 및 미질검정을 병행하였다. 선발된 우량계통에 대해 2008～2009년 2년간 생산력검정시험을 실시한 결과 조생종이면서 쌀 외관이 양호한 중립종인 SR27376-2-2-1-3 계통을 철원81호 계통명을 부여하였다. 2010～2012년 3년간 지역적응시험 실시한 결과 그 우수성이 인정되어 2012년 12월 품종으로 선정되었다.
'새오대'벼는 출수기가 보통기 보비재배에서 출수기는 7월27일로 오대벼 보다 4일 정도 빠르고 쌀알의 크기는 현미 천립중이 오대벼와 같이 중립종인 26g으로 쌀의 외관이 깨끗한 조생종 품종이다. 벼의 키는 오대벼보다 약간 작아 쓰러짐에 강하고 쌀수량은 오대벼보다 약간 증수된 5.26톤/ha으로 적응지역은 중북부 중간지·중산간지에 적합하다. '새오대'벼는 기존 오대벼의 단점인 쌀 외관을 개선 오대벼 재배 2만ha를 대체하여 쌀 품위등급을 향상 쌀 품질고급화 및 재배안전성을 통하여 농가 소득증대가 기대된다.

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월동형 시설 풋고추 야간 온도 차이에 따른 품종별 특성

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에너지 절감형 시설 풋고추 전용 품종 개발을 위한 예비실험으로서, 저온 신장성이 좋고 수량 및 품질이 우수한 풋고추 품종을 선발하기 위하여 야간 온도 조절을 통한 품종별 특성의 차이를 조사하였다. 시험은 경남농업기술원 3연동 비닐하우스에서 지난 2년간 수행되었으며, 현재 시판되고 있거나 최근 고추와 육종에서 개발한 품종들을 대상으로 열풍기 야간온도를 13도와 17도로 처리하였고 시험구 배치는 처리별로 난괴법 3반복으로 하였으며 시기별 생육 및 수량을 비교 분석 하였다. 1년차 시험(2011~2012) 결과, 초장은 일반적인 '녹광' 품종의 농가 야간 최저 온도인 17도 처리에서 일반적으로 컸으며, 정경은 반대로 13도 처리에서 전체적으로 굵었다. 수량에 있어서는 일반 품종인 '녹광'의 경우 13도와 17도 처리에서 각각 상품과가 1,500(kg/10a)과 1,900이었고 대과종 풋고추인 '순한길상'은 각각 2,400과 2,600이었고 '롱그린 맛고추'는 각각 3,000과 2,300으로 오히려 저온인 13도 처리구에서 수량이 증가되었다. 고추와 육종의 'PNBG6' 품종도 저온 처리구에서 오히려 수량이 증가하는 결과를 얻었으며 저온처리에 따른 난방비 절감효과는 LNG 사용시 10a당 약 560만원에 달했다. 2년차 시험(2012~2013)에서는 1년차와 동일한 조건에서 저온처리에 대한 수량증대 효과는 없었으나 난방비 절감효과는 10a당 약 890만원으로 저온에서의 수량 손실분을 제하더라도 추가적인 이익을 얻을 수 있었다. 본 연구를 기초로 선발된 품종들과 저온신장성이 좋은 유전자원 유래의 분리집단을 사용한다면 저온신장성에 대한 유전 연구는 물론 에너지 절감형 풋고추 전용 품종개발이 가능할 것으로 판단되며 이는 종자 산업에서의 저탄소 녹색기술의 표본이 될 것이다.

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재배가 안정적이고 다수성인 장류·두부용 콩 신품종 '진풍'

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우리나라의 콩 재배면적은 꾸준히 감소하여 8만 ha정도에서 정체되어 있고, 식용콩 자급률도 30%정도로 낮은 상황이다. 정부에서는 최근 이상 기후로 인한 세계 곡물 가격의 급등과 식량 안보 대책으로 식용 콩의 자급률을 50 %까지 올리기 위해 노력 중이다. 2002년에 육성된 '대풍'은 3.05MT/ha의 수량성을 보였으나 콩 종자의 배꼽색이 갈색이라는 단점이 있어 농가의 확대 보급에 실패하였다. 대풍콩의 단점을 개선하기 위하여 단경이며 다수성인 대풍콩과 배꼽색이 황색이며 대립인 SS01211을 2002년에 교배 후 계통육종법을 이용하여 2009년에 '밀양216호'의 계통명을 부여하였다. '10～'12년 3개년간 지역적응시험 후 종자 품위가 양호하고 내병성 등을 갖춘 것으로 평가되어 2012년 12월 직무육성신품종선정위원회에서 '진풍'으로 명명하였다. 진풍은 대원콩에 비하여 성숙기가 10월 17일로 3일 늦다. 경장은 61cm로 작아 도복에 강하고, 탈립도 잘 안 되는 특성을 지니고 있다. 뿐만 아니라 불마름병과 SMV에 저항성이다. '10～'12년 3개년간 실시한 지역적응시험에서 충북 이남 남부이모작지대에서 3.37MT/ha로 대원콩 대비 23% 증수하였다. 이러한 특성을 지닌 진풍은 안정적 재배가 가능하여 농가소득향상 및 우리나라 콩 자급률 향상에 기여할 것이다.

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저농도액비 처리에 의한 포플러 단벌기 맹아림의 바이오매스 생산

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본 연구는 가축분뇨 해양배출 금지에 따른 처리방안의 일환으로써 포플러류 목재에너지림에 SCB액비를 처리하였을 때 바이오매스 생산량이 우수한 클론을 선발하고자 실시하였다. 아울러 단벌기 집약재배를 실시하는 목재에너지림에서 SCB액비의 화학비료 대체효과 및 바이오매스 생산 증진량을 구명하고자 수행하였다. 경기도 수원시 권선구 호매실동 소재의 연구림에 포플러류 5개 수종, 총 8개 클론을 대상으로 반복당 5본씩 3반복으로 시험림을 조성하였으며, 식재간격은 1m×1m이었다. SCB액비는 2008년에 본당 115L를 처리하였으며, 2009년도 및 2010년도에는 본당 130L씩 처리하였다. 처리 후 클론별 가지 발생량, 엽면적 및 지상부 바이오매스 생산량을 조사하였다. 평균 줄기 발생수는 처리구 및 무처리구에서 각각 11.8개와 11.5개로 나타나 큰 차이가 없었다. 평균 엽면적은 처리구가 71.0cm^{2}로 무처리구 52.3cm^2 보다 35% 더 우수하였다. 연평균 지상부 바이오매스 생산량을 조사한 결과, SCB액비 처리구가 ha당 8.5톤으로 나타나 무처리구 5.6톤 대비 51% 우수한 것으로 조사되었다. SCB액비 처리에 따른 클론별 평균 지상부 바이오매스 생산량은 현사시나무가 ha당 13.6톤으로 가장 우수하였으며, 그 다음으로 이태리포플러 9.8톤, 양황철 5.6톤, 미루나무 교잡종 4.6톤 순이었다. 수원포플러는 ha당 3.0톤의 저조한 바이오매스 생산량을 나타내었다. 이상의 연구결과를 종합해 볼 때 농지 근처의 산림지역에 단벌기 맹아림을 조성하여 목질계 바이오매스를 생산하기 위해서는 현사사나무 및 이태리포플러가 적합할 것으로 사료된다.

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중산간지 적응 복합내병성 고품질 조생 산호미

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"산호미"는 국립식량과학원 상주출장소에서 중산간지 재배에 알맞은 복합내병성 고품질 벼를 육성하고자 2002년 하계에 모본으로 상미벼와 부본으로 상주24호에 화영벼를 교배한 계통을 인공교배 하였다. F3 이후 계통육종법으로 전개하여 주요 농업형질 조사 및 병해충·미질검정을 실시하였고 2009～2010년 생산력검정을 실시한 결과 복합내병성을 갖춘 YR24337-53-3-18-3-3 계통을 선발하여 "상주44호"로 계통명을 부여하였다. 2010～2012년 지역적응성시험을 실시한 결과 대조품종에 비해 도열병, 흰잎마름병, 줄무늬잎마름병에 강하며 외관품위가 매우 우수하여 2012년 농작물 직무육성 신품종 선정심의회에서 신품종으로 선정하여 "산호미"라 명명하였다. 산호미는 출수기가 7월 26일로 오대벼보다 2일 빠른 조생종이며 오대벼보다 저온발아성은 14%, 수당수수는 1개, 등숙비율은 5.2% 많고 현미천립중은 3.5g 가벼우며 심복백이 없이 맑고 깨끗하다. 수량성은 보통기 보비재배 6개소에서 평균 쌀수량이 499kg/10a으로 북부 평야지 및 중산간지, 남부고냉지에 재배에 적합한 품종이다.

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지역특산화를 위한 장류 · 두부용 극대립 콩 신품종 '중모3008호'

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'중모3008호'는 지역특산화를 위한 극대립 콩 품종육성을 목표로 곡립 및 초형이 양호한 황금콩과 대립인 SS01408을 2002년에 교배 후 계통육종법으로 육성하여 '밀양217호'의 계통명을 부여하였다. '10～'12년 3개년간 지역적응시험 후 콩모자이크바이러스병에 저항성이고 극대립으로 품종육성을 위한 중간모본의 특성을 갖춘 것으로 평가되어 2012년 12월 직무육성신품종선정위원회에서 '중모3008호'로 명명하였다. 개화기는 8월 3일로 표준품종인 '대원콩'보다 8일, 성숙기는 10월18일로 4일 늦은 중만생종 품종으로, 신육형은 유한신육형이고, 탈립이 잘 되며, 도복에 약하다. 경장은 70㎝로 대원콩 대비 다소 길고, 개체당 협수는 적고, 주경절수 및 분지수는 비슷하였다. 100립중은 36.5g으로 대원콩 대비 매우 무거운 극대립종이다. 콩모자이크바이러스는 유묘접종 결과 저항성이었으나 불마름병은 포장에서는 강하였으나 인공접종시 대원콩 수준으로 발병하였다. 메주수율은 77%, 청국장 수율은 199%로 대원콩 대비 다소 낮은 경향을 보였다. 수량성은 '10～'12년 3개년간 실시한 지역적응시험에서 서부해안지방을 제외한 내륙지방에서 2.25MT/ha로 대원콩 대비 84% 수준이었다. 수량성 및 내재해성에 약한 단점을 지니고 있지만 고품질 콩 품종육성을 위한 중간모본으로 활용이 가능할 것으로 보인다.

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친환경 재배 적응 복합내병충성 고품질 벼 "친들" 육성

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최근 안전식품에 대한 소비자의 선호도 변화에 따른 고품질 친환경 품종개발이 요구되고 있다. 이에 병해충 피해를 최소화하여 쌀수량을 증대시키고 품질 및 밥맛을 높여 농가소득을 증대 시킬 수 있는 친환경 재배 적응 복합내병충성 고품질 벼 '친들'을 육성하였다. '친들'은 수량이 높고 도열병, 흰잎마름병, 줄무늬잎마름병 뿐만 아니라 벼멸구에도 강한 중만생 고품질 벼 품종이다. 출수기는 보통기 보비재배에서 8월 15일로 남평벼보다 1일 늦다. 간장은 83㎝로 남평벼보다 3㎝ 크며, 현미 천립중은 21.7g으로 남평벼보다 무겁다. 주당 수수, 수당립수, 등숙비율은 남평벼보다 같거나 높다. 위조현상은 나타나지 않았으며 성숙기 하엽노화가 늦고 내수발아성이다. 입형은 현미장폭비가 1.71로 단원형이며 아밀로스와 단백질 함량은 남평벼와 같거나 낮다. '친들'은 평야지를 중심으로 다양한 환경에서 3년 동안 지역적응성 시험결과 쌀수량(561kg/10a)이 남평벼에 비하여 8%가 증수되고 안정성이 높으며 또한 친환경재배 농가보급시 농약사용 절감 등 시장성이 높은 품종이다.

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PA-25

캄보디아 적응 옥수수 품종개발을 위한 자원유래별 농업특성 및 수량 평가

박기진*, 류시환, 박종열, 장은하, 서영호, 용우식, 이상민, 유정훈, 김경희

강원도 홍천군 두촌면 장남길 26 강원도농업기술원 옥수수연구소

농림축산식품부의 해외식량기지 구축을 위한 기반 구축과 동남아시아 지역에 진출한 국내기업이 요구하는 현지 적응 우량 옥수수 품종개발을 위하여 본 연구를 수행하였다. 서울대학교 이석하 교수와 공동으로 수행하는 본 과제는 2011년 8월부터 캄보디아 캄퐁수프 및 캄폿주에서 현지 옥수수 재배기업인 (주)에이퍼플의 현지법인 JNJ Bora의 협조로 년 3회, 현재까지 총 5회를 추진하면서 안정적인 육종시스템을 정착시키고 우량한 후보 품종을 선발하였다. 1차(2011.8.～2011.12.04), 2차(2012.3.25～2012.7.31), 3차(2012.8.1～2012.12.4), 4차(2012.12.5～2013.4.7), 5차(2013.4.8～2013.8월상순)를 걸친 육종을 통하여 국내 육성 또는 도입 고정계통의 특성평가, 현지 평가용 교잡종의 구성 및 평가, 열대 수집자원을 중심으로 한 분리계통의 육성 등을 추진하였다. 고정계통의 평가는 연구소 육종 자식계통과 열대지역에서 육성, 순화된 고정 계통의 균일성, 내병충성, 알곡유형, 립색, 수확 후 저장성 등을 조사하였다. 그 결과 온대기반의 국내 육성 계통은 균일성과 자체 수량성은 높고 마치종(dent)이나 반마치종(semident)의 입질을 가지지만 조명나방(corn borer) 및 깨씨무늬병(southen leaf blight)에 대한 저항성이 상당히 떨어져 현지 품종개발의 직접적인 교배친으로 활용하기 부적절하였으며 태국 및 열대지역에서 육성된 고정계통 및 품종으로부터 분리 육성중인 계통은 자체 수량성은 다소 낮고 알곡의 작으며 립형은 경립종(flint)이나 반경립종(semiflint)이 대부분을 이루었으며 식물체 및 알곡의 충해저항성이 상대적으로 우량한 특성을 보였다. 교잡종의 수량성은 연구소 육종 온대자원은 큰 이삭, 높은 탈립률, 알곡 우량으로 현지 보급 품종보다 높은 수량성을 보였으나 병충해 저항성, 안정성, 가뭄저항성, 알곡의 저장성 등에서 열대 육성 교잡종보다 현저하게 불량하였다. 현지 많은 면적 보급되고 있는 CP, Pioneer 계열의 교잡종은 수량은 다소 낮았으나 광지역 적응성, 안정성, 내재해성에 다소 강하였다. 5회의 육종을 추진하면서 총 256 교잡종을 평가한 결과 온대와 열대자원의 조합으로 다수성과 병충해 및 안정성을 개선한 현지 보급 품종과 비슷하거나 우량한 10교잡종을 선발하여 품종등록에 앞서 현재 기업체와 함께 실증평가를 추진 중에 있다.

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통일형 중생 다수성 '중모1028' 육성

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'중모1028'은 쌀가루를 이용하는 가공식품의 원료곡 사용을 목적으로 개발된 통일형 다수성 품종이다. 2002년 하계에 재배안정성이 우수하고 수량성이 높은 한아름벼를 모본으로, 천립중이 크고 단간 다수성인 다산벼와 YR22841(YR18241-B-B-47-1/YR18241-B-B-210-1)의 F_1을 부본으로 이용하여 인공교배를 실시하였다. 2003년 하계에 F_1을 양성하였고, 2005년도 F_3세대부터 2007년도 F_5세대까지 계통육종법으로 고정된 계통을 육성하여 우량한 YR24232-16-1-1계통을 선발하였다. 이 후 2008년 하계에 예비선발시험, 2009년부터 2010년까지 2년간 생산력 검정시험을 수행한 후 2010년부터 2012년까지 3년간 지역적응시험을 마치고 2012년 신품종선정위원회에서 우수성이 인정되어 '중모1028'로 명명되었다.

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항산화 활성이 높은 건강기능성 메수수 '동안메' 육성

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[2]경기도 수원시 권선구 서호로 34 국립농업과학원 농업유전자원센터

수수는 최근 생활습관병 개선을 위한 곡물로서 각광받고 있어 그 수요가 증가하고 있으나 농가에서 재배하고 있는 수수는 대부분 재래종을 사용하고 있어서 유전적으로 순도가 높지 못하고 수량이 낮아 품종개선이 필요하였다. 이에 따라 국립식량과학원에서는 항산화 활성과 수량성이 높은 건강 기능성 메수수인 '동안메'를 육성하였다. '동안메'는 2009년 국립농업유전자원센터에서 분양받은 'CS-4 LOCAL COLLECTION'을 기본집단으로 하여 분리육종법을 통해 2012년 육성된 품종이다. '동안메'는 파종 후 출수까지 평균 71일, 수확까지는 평균 115일인 중생종이다. 키가 약 160cm이고 이삭의 형태는 밀수형이며 밀도는 조밀하며 받침껍질(영)색과 종실색은 짙은 갈색으로 '황금찰'보다 좀 더 붉은색을 띈다. 한 주당 이삭수는 3～4개로, 각 분얼의 이삭이 동시에 성숙하여 일시에 수확할 수 있다는 장점이 있으며 수량성은 약 310kg/10a로 다수성이다. 폴리페놀, 탄닌, 플라보노이드 등 다양한 기능성 성분을 많이 함유하고 있으며 항산화활성(ABTS)이 42.0mgTE/g으로 '황금찰'에 비해 30%가 높다. 현곡 천립중은 26.8g, 주당 이삭중은 33.6g으로 무거우며, 도복은 '황금찰'보다 강한 편이다. '동안메'는 메수수이므로 점질성이 높은 찰수수보다 빵, 과자, 국수 등 가공식품 원료곡으로 이용하기에 적합하여, 건강기능성이 높지만 단순 혼반용으로만 이용되던 수수의 섭취방법을 가공제품 등으로 다양하고 폭넓게 활용이 가능한 품종이다.

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황색 · 대립의 불임내성 찰기장 '황실찰' 육성

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기장은 주로 밥에 혼반용으로 많이 이용되는 잡곡으로 연간 14,000천톤에 이르는 양이 수입되고 있다. 농가에서 주로 재배되고 있는 기장은 수전기에 강우가 지속될 때 불임이 심하여 이를 개선한 기장의 품종 개발이 필요하다. '황실찰'은 경산지역에서 수집한 재래기장을 기본집단으로 하여 분리육종법을 통해 2012년 육성된 신품종이다. 출수기는 대비품종인 '황금기장'보다 보통기에서 18일, 이모작 재배시 14일 늦고, 생육일수는 보통기 117일, 이모작 101일로 '황금기장'보다 13～19일 늦은 만생종이다. 간장, 수장 모두 '황금기장'에 비하여 큰 편이며, 등숙비율은 '황금기장' 65.9%, '황실찰' 76.7%, 조곡 천립중은 '황실찰' 6.3g, '황금기장' 5.5g으로서 '황실찰'이 등숙비율과 천립중이 높았다. 특히, 수전기 연속 강우에 의해 나타나는 기장의 불임현상에 대해 비교적 내성이 강하여, 강우가 잦았던 2011년 보통기 생산력검정시험에서 수량성은 202kg/10로 '황금기장' 131kg/10a에 비하여 50% 이상 높았다. 전국 3개 지역 2년간 실시한 지역적응시험 평균수량은 보통기 207kg/10a, 이모작 165kg/10a로 '황금기장'에 비해 보통기 재배는 38% 증수되었고 이모작은 비슷한 수량성을 나타내었다.

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후기녹체성 및 복합내병성 총체사료용 벼 중간모본 '중모1029호' 개발

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논 형태를 그대로 유지하면서 쌀 생산 조절 및 조사료 자급률 향상을 위한 방안으로 총체사료벼 연구를 추진하고 있다. 최근의 총체사료벼 품종육성은 기존의 쌀 수량증대를 위한 초다수성 품종 및 계통집단을 활용하여 총체사일리지사료로서 우수한 특성인 경엽다수성, 사료적성, 후기녹체성, 복합내병충성 및 직파적성 등을 가진 품종이 육성되고 있다. 그러나 기존의 다수계 육종재료를 이용하지 않고 사료적성이 우수한 새로운 유전자원을 교배친으로 하여 총체수량성, 후기녹체성 및 복합내병성이 개선된 '중모1029호'를 개발하였다. '중모1029호'는 총체건물수량이 높고 후기녹체성 및 복합내병성이 개선된 품종을 육성할 목적으로 바이오매스가 큰 '길림수집1호'를 모본으로 다수성이며 흰잎마름병 및 줄무늬잎마름병에 강한 '주남'을 부본으로 하여 국립식량과학원 답작과에서 2001년에 인공교배하였다. 계통육종법에 의해 세대를 진전시킨 후 고정세대에서 실시한 지역적응시험에서 총체건물수량이 1.70ton/ha로 '녹양' 1.35ton/ha보다 통계적으로 유의하게 26% 증수하였다. '중모1029호'는 출수기가 8월29일로 '녹양'보다 15일 늦은 만생종이며 초장이 '녹양'(109㎝)보다 큰 131㎝로 바이오매스가 큰 장간 품종이다. 흰잎마름병(K_1～K_3)과 줄무늬잎마름병에는 강한 반응을 잎도열병에는 중정도의 반응을 벼멸구에는 약한 반응을 보였다. 사료가치는 후기녹체성(SPAD; 22.9)이 '녹양'에 비해 높았고 조단백질 6.5%, 산성세제불용섬유소 28.2%, 중성세제불용섬유소 55.0%, 가소화양분총량은 66.6%로 '녹양'과 비슷한 경향을 보였다. 금후 본 품종은 건물수량성이 높고 후기녹체성 및 복합내병성이 강화된 총체사료벼 중간모본으로 활용가치가 높은 것으로 판단된다.

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PA-30

흰앙금 제조가 가능한 팥 신품종 '흰구슬'

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소비자 및 가공업체가 원하는 다양한 색깔의 양갱 및 앙금 제품 개발에 붉은색 팥은 제품 다양화에 한계가 있으므로 '흰구슬'은 흰앙금 제조가 가능한 황백색 종피의 품질이 우수한 팥 품종육성을 목적으로 2001년 하계에 IT144994를 모본으로 하고 Suwon38을 부본으로 인공교배하여 F_3이후부터는 계통육종법에 의하여 육성 선발하였다. 2009～2010년 생산력검정시험에서 내도복성과 가공적성이 우수하여 '밀양12호'로 계통명을 부여하였다. 2010-2012년 3년간 지역적응시험을 실시한 결과, 황백색 종피를 가진 중만생종으로 고품질 내재해성 품종으로 우수성이 인정되었다. 경장은 53㎝로 단간이며 개화기는 빠르지만 성숙기간이 길어 종자가 알차고 협당립수가 많았다. 100립중은 13.6g으로 중대립에 속하고, 수량성은 지역적응 보통기 보비재배에서 평균수량이 2.00MT/ha로 표준품종 대비 7% 증수되는 품종이다. '흰구슬'의 재배적응지역은 강원도 산간고랭지를 제외한 전국 팥 재배지역에서 재배가 가능하다. 흰앙금은 물론 다양한 색상의 앙금 및 양갱생산으로 팥의 신수요 창출 및 소비 확대가 기대된다.

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PA-31

A comparison in physiological responses and photoinhibition tolerance between superior and inferior families of *Pinus densiflora* under drought condition

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This study was conducted to figure out the differences in physiological responses, e.g. growth, photosynthetic activity and water potential, and photoinhibition tolerance in photosystem between superior and inferior families of *Pinus densiflora* under drought condition. Superior which is KW85 and inferior which is KW40 families were selected using progeny test results of height growth. In 2007, seeds were collected from seed orchard. In 2008, seedlings were produced and cultivated, and from April 2009 drought treatment was started with shading treatment and plants were harvested in Sept. 2009. There was no significant difference in height growth between families. In case of leaf water potential, KW85 showed higher water potential under drought condition. But there was no significant difference in drought with shading treatment. There was no difference in photosynthetic rate but stomatal conductance and transpiration rate of KW85 showed lower value than KW40. So water use efficiency of KW85 showed higher value in every treatment. Non-photochemical quenching of KW40 showed higher value in drought treatment, but there was no significant difference in control and drought with shading treatment. Xanthophyll cycle pool size of KW85 showed higher value in drought treatment, but in drought with shading treatment KW40 showed higher value. Selected superior family showed higher drought tolerance according to water use efficiency, and it also has effective non-photochemical quenching ability. In contrast inferior family respond more sensitively in photoinhibition under drought condition.

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PA-32

A large-scale screening analysis for the evaluation of Bakanae disease in rice

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Bakanae disease of rice, caused by *Fusarium moniliforme* Sheldon, the imperfect stage of *Gibberella fujikuroi*, is one of the most important rice diseases worldwide, but no rice variety has been found to be completely resistant to this fungus. Cultivation of resistant cultivars is the most beneficial way of reducing quantitative or qualitative losses to for bakanae disease in rice. To facilitate the study of this disease, accurate and large scale screening methods were developed for the inoculation and evaluation of Bakanae disease. Even and large scale infection was achieved by using *F. moniliforme* spore in tissue embedding cassette and seedling tray. The efficiency of *F. moniliforme* infection with the concentration of 1×10^6 spore/ml caused better distribution (F-value=33.96) than 1×10^2 (F-value=10.69), and 1×10^4 spore/ml (F-value=2.63). We established new criteria of healthy and non-healthy plant, and introduced calculation of proportion of healthy plants to meet fast evaluation of resistance level of each variety. The effect of *F. moniliforme* strains containing different genetic background was also evaluated with rice varieties to figure out the stability of resistance level. GA3 response of rice variety was significantly correlated with bakanae disease, but it did not adequate for direct indicator of bakanae disease resistance. These results indicated that a large scale infection method developed in this study is fast and reproducible, as well as a disease evaluation system provides an accurate measurement of bakanae disease resistance of rice.

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PA-33

A new early maturing and high yielding vegetable peanut "Ami"

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Recently, fresh peanut eaten after boil is popular to korean consumer owing to its sweet taste. A new vegetable peanut variety "Ami"(*Arachis hypogaea* ssp. *fastigiata*.) was developed at the Department of Functional Crop, NICS, in Milyang in 2012. It was developed from the cross between the short stem cultivar "Satonoka" and the large grain cultivar "Milyang 16". "Ami" which is Shipung plant type has 50cm main stem length and 10 branch number per plant. Each pod has two grains with brown testa and long-ellipse shape and dried 100-seed weight was 84g in the regional yield trials(RYT). The Sucrose and tannin content of fresh peanut are 24.9mg/g and 4.9mg/g, respectively. Functional compound content was 3944μg/g of Luteolin in peanut shell, This variety also showed more resistant to stem rot and lodging, compared with check variety, Palkwang. In the regional yield trials "Ami" was outyielded than check variety by 9% with 10.10MT/ha for fresh pod and by 14% with 4.51MT/ha for dried kernel.

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PA-34

A New forage barley (*Hordeum vulgare* L.) awnless spike type with lodging and disease resistance, 'Jungmo2502'

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'Jungmo2502' (*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 2011. It was derived from the cross between 'Samheung/Suwon 300' and 'Milyang 100'. Among the cross made in 2000, a promising line, SB00T2018-B-B-B-B-3, showed good characteristics in potential forage yield in the yield Trial tested at Iksan in 2007 to 2008 designated as Iksan 448. The line in the Regional Yield Trials(RYT) tested in eight locations around Korea for three years from 2009 to 2011, and was released as the name of 'Jungmo2502'. It has the growth habit of group Ⅵ, erect plant type, green leaf and awnless spike. Its average heading and maturing dates were on May 4, and May 30, respectively, with are similar to check cultivar 'Youngyang'. The cultivar had 98cm of culm length, 607 spikes per m^2 and it showed better rate of leaf, winter hardiness, and resistance to BaYMV than those of the check cultivar. The average forage yield of 'Jungmo2502' was about 11.0 ton ha^{-1} in dry matter in paddy field. 'Jungmo2502' also showed 8.7% of crude protein content, 21.9% of ADF (Acid Detergent Fiber), 40.7% of NDF (Neutral Detergent Fiber), and 71.6% of TDN (Total Digestible Nutrients), including higher grade of silage quality for whole crop barley.

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PA-35

A new mid-late maturing japonica rice variety 『Hyeonpum』 with a good grain quality and eating quality

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'Hyeonpum' is a new japonica rice variety developed by a cross breeding between Iksan469 having a good canopy architecture and Sindongjin and Musashino 7 having a good eating-quality with a view to develop a new variety having high quality of grain and palatability by the rice breeding team of Rice Breeding and Cultivation Research Division, Department of Rice and Winter Cereal Crop, NICS, RDA in 2012. The heading date of this variety is August 18 and later than that of check variety, Nampyeongbyeo, by four days. 'Hyeonpum' has 74cm of culm length and 101 spikelets per panicle. This variety showed resistance to bacterial leaf blight and rice stripe virus, but susceptible to leaf blast and planthoppers. The milled rice of this variety exhibits translucent and very clear non-glutinous endosperm. 'Hyeonpum' has much better palatability of cooked rice than that of Nampyeongbyeo. The whole grain rate of milled rice and milled rice recovery of 'Hyeonpum' are slightly higher than those of Nampyeongbyeo as 91.8% and 75.2% respectively. The yield of 'Hyeonpum' is 5.6 MT/ha in milled rice. 'Hyeonpum' could be adaptable to the southern part plain area of Pyeongtaek and southwestern costal areas in Korea.

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PA-36

A new mid-late maturing rice variety 「Subo」 with a good grain quality and for direct seeding

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'Subo' is a new japonica rice variety developed by a cross breeding between HR21124-B-59 and HR19567-B-70-3 having a good Phenotype with a multi-resistance and high yield elite line. The new variety developed for direct seeding by the rice breeding team in Rice Breeding and Cultivation Research Division, Department of Rice and Winter Cereal Crop, NICS, RDA in 2012. The heading date of this variety is August 13 and earlier than that of check variety, Nampyeongbyeo, by two days. 'Subo' has 72cm of culm length and 104 spikelets per panicle in direct seeding cultivation. This variety showed resistance to bacterial leaf blight and rice stripe virus and have germinating ability in sumerged soil conditions. The milled rice of this variety exhibits translucent and very clear non-glutinous endosperm. 'Subo' has much better palatability of cooked rice than that of Nampyeongbyeo. The whole grain rate of milled rice are 86.9% and milled rice recovery of are 74.6%. The yield of 'Subo' in direct seeding cultivation is 5.55MT/ha in milled rice. 'Subo' could be adaptable to the southern part plain area of Pyeongtaek and southwestern in Korea.

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PA-37

A new peanut variety "Sinpalkwang" with large grain and high yeild

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Korean peanut yield by new varieties has marvelously increased since first variety with 1.09 MT/ha was developed in 1960. This means 77.58kg/ha yield increment every year from 1960 to 2012. A new peanut variety "Sinpalkwang"(*Arachis hypogaea* ssp. *hypogaea* L.) showed the highest grain yield, 5.40 MT/ha, of Korean varieties was developed at the Department of Functional Crop, NICS, in Milyang in 2012. This was developed from the cross between cultivar "Palkwang" and crossing line from cultivar "Palkwang" and "PI156649". "Sinpalkwang" which is Virginia plant type has 41cm of main stem length and 25 branch number per plant. 45 pod number per plant, 79% of shelling ratio and 92g of 100-grain weight in the regional yield trials(RYT) greatly contributed to increase the yield potential of this variety. Each pod has two grains with brown testa and ellipse shape. Seed quality showed 45.4% of crude oil and 29.2% of protein content. This variety also showed more resistant to web blotch and stem rot, compared with check variety, Daekwang.
In the regional yield trials "Sinpalkwang" outyielded check variety by 28% with 5.40 MT/ha for kernel.

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PA-38

Biological function of *Brassica rapa* cysteine protease in transgenic rice and *Xanthomonas oryzae* pv. *oryzae* pathosystem

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Bacterial blight is a serious problem of rice in irrigated and rainfed lowlands. It is caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) which is represented by many pathotypes, making it difficult to control. Plant proteases are important players in immunity acting either in the execution of attack, in signaling cascade or in perception of invader. This study demonstrates the response of cysteine protease (CP) upon interaction with the pathogen. The cysteine protease encoding full-length cDNA was identified and characterized using web-based tools. Conserved domain of the gene revealed its affinity to Peptidase_CIA family. The full-length cDNA of *CP* in *Brassica rapa* was then cloned and overexpressed in rice. Insertion of gene was verified in the transformants through PCR assay. Spatiotemporal expression of the gene was performed in transgenic rice. To evaluate the resistance of *CP*-overexpression lines to *Xoo*, transgenic plants were inoculated with two races of *Xoo*. *In planta* analysis of enzymatic activity of *CP* was also performed before and after infection by the pathogen.
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PA-39

Development of molecular marker linked to white rust resistance in chrysanthemum using bulked segregant analysis (BSA)

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For developing molecular markers linked to white rust resistance in chrysanthemum, RAPD and AFLP were carried out in 'Puma White' x 'Dancer' mapping population through Bulked Segregant Analysis (BSA) methods. 10 resistant and 10 susceptible individuals were selected and bulked. And then, these bulks were screened using 280 RAPD primers (10 mer) with two parents. As a result of BSA-RAPD, 25 Dancer/R-bulk specific bands in 21 primers and 22 Puma White/S-bulk specific bands in 18 primers were selected. These resistant or susceptible specific bands were screened in 10 resistant and 10 susceptible individuals. Except OPI-13_{520}, all bands were confirmed as false positive. OPI-13_{520} band presumed as closely linked marker to white rust disease resistance was tested in whole population. Among 187 progenies, just six off-springs did not correspond with phenotypic data. Based on expected phenotypic segregation ratios in the pseudo F1 progenies, it was assumed that a duplex type of white rust resistance in 'Dancer' (RRrrrr) were in combination with a duplex type of OPI-13_{520} marker. As a result of x^2-test of independence between resistance gene and OPI-13_{520} marker, x^2 score is 76.08 and probability is 2.13×10^{-16}. And resistance gene and OPI-13_{520} marker were assumed to be linked in coupling phase. The value of recombination fraction obtained by successive trials and second derivative of log likelihood was 0.03832±0.0271.

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PA-40

Evaluation of Korean wheat cultivars for type I and II resistance to Fusarium head blight in 2013

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Fusarium head blight (FHB), caused by *Fusarium graminearum* is a major disease problem on wheat and barley in Korea. The objectives of this study were to evaluation of korean wheat cultivars for Type I and Type II resistance to FHB. We screened for Type II resistance in the greenhouse using single floret inoculation and for Type I resistance in the field using spray inoculation. Sumai 3 was used the FHB resistant check. Thirty-two korean wheat cultivars were evaluated for resistance to spread of symptoms within spike. The 2013 field screening with wheat cultivar was located in Kimjae-si Joeonbuk Korea. All plots were inoculated twice. Mist-irrigation was applied to facilitate FHB development. FHB severity was assessed visually 21 days after inoculation on 20 arbitrarily selected spikes per plot. FHB severity was determined as the percentage of symptomatic spikelets from the total of all spikelets. For FHB resistance, the average of FHB severity of Type I exhibited ranging from 21.9% to 77.2% and FHB severity of Type II ranging from 20.8% to 100%. Namhae, Milseong, Geuru, Joen, Anbaek and Sukang were the moderately resistant cultivars while Gobun, Alchan, Dajoong, Eunpa, Shinmichal1, Eunpa and Uri were the most susceptible cultivars for Type II resistance.

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PA-41

Evaluation of late-sowing-adaptable soybean cultivar in paddy field

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Soybean self-sufficiency in Korea was 22.5% in year 2011, and as free trade agreement between Korea and US comes into effect, the amount of soybean importation increases. In 2012, paddy field soybean cultivation was over 0.1 million ha and it is expected to increase continuously due to rise in market price of soybean. Moreover, double cropping system including paddy field soybean is widely adopted nationwide, but studies on appropriate cultivar for this environment are insufficient. In this research, the effect of planting date and different cultivars on soybean growth and yield was investigated for three planting dates (June 20, July 5, and July 20) with 15 cultivars. According to ANOVA test, soybean yield was significantly different depending on sowing date and cultivars and interaction between sowing date and cultivars was also detected, meaning each of cultivars resulted different yield depending on sowing date. When planted on July 20, stem length, nod number, branch number and grain weight was decreased because of short growing period, resulting in yield decrease. Percentage of yield obtained from July 20 in contrast to that of June 20 showed that Pungwon, Nampung and Daepung recorded the least yield decrease and the highest yield when planted late. Evaluation of late-sowing-adaptable soybean cultivar in paddy field is now being carried on following last year.

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PA-42

Genome-based fine mapping of the *Tomato spotted wilt virus* resistance gene, *Tsw,* in *Capsicum*

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Tsw, a single dominant resistant gene against *Tomato spotted wilt virus* (TSWV), has been mapped on chromosome 10 in *Capsicum chinense* species. Previously reported molecular markers linked to the *Tsw* gene are not transferable for all pepper breeding materials. To develop additional markers and do genome-based fine mapping of the *Tsw* gene, approaches of mapping comparison, pooled transcriptome analysis, and genome walking were applied. Eleven additional SNP molecular markers tightly linked to the *Tsw* gene were developed using tomato and pepper whole genome sequencing databases. Among them, four SNP markers, SNP7715-1, SNP68-1, SNP17918-1, and SNP1072-1, showed no recombination in two segregating populations of F_2 'Telmo' (210 individuals) and 'SP' (843 individuals). Three scaffold sequences from the *C. annuum* BAC database and two BAC clones from the BAC library of *C. annuum* 'CM334' covering the *Tsw* gene were identified by transcriptome analysis and genome walking. A pepper scaffold sequence covering three pepper scaffold sequences was identified from a final version of the *C. annuum* BAC database. The *Tsw* gene was delimited within 149 kb by alignment analysis of two BAC clone sequences and the pepper scaffold sequence. A total of 22 predicted genes were resided in the target region between SNP7715-1 and SNP1072-1 co-segregating markers. Among them, five predicted genes showing annotations of CC/TIR-NBS-LRR resistance proteins, mRNA-6, mRNA-7, mRNA-11, mRNA-12, and mRNA-13, were identified. The transcriptome analysis and gene expression study showed that the mRNA-13 was expressed in 'PI152225' but was absent in 'Special', demonstrating the mRNA-13 could be a strong candidate gene for the *Tsw* gene. This result will be favorable for cloning the *Tsw* gene and developing cultivars which carry the TSWV-resistance gene.

Keyword: Tomato spotted wilt virus, pepper, virus disease, map-based cloning, and *Tsw*

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PA-43

Genome-wide identification and analysis of *Catharanthus roseus* RLK1-like kinase family in rice

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Drought and salinity are two major environmental factors determining plant productivity that due to their high magnitude of impact and wide distribution. The regulatory circuits include stress sensors, signaling pathways comprising a network of protein-protein reactions, transcription factors and promoters, and finally the output proteins or metabolites. Plant receptor-like kinases (RLKs) are transmembrane proteins family, are predicted to be major components of the signaling pathways that allow plants to respond to diverse environmental and development condition. Subfamily of *Catharanthus roseus* RLK1-like kinases (CrRLK1Ls) is a novel type of RLK, was identified in *Arabidopsis* with 17 members carrying a putative extracellular carbonhydrate-binding malectin-like domain. To study the function of CrRLK1Ls subfamily in rice which is a most widely consumed staple food, we produced the phylogenomic data with the integration of microarray-based anatomical and stress expression profiling data to the context of rice CrRLK1Ls family phylogenic tree. The expression profiling data are based on a large number of public microarray data such as 1150 Affymetrix arrays and 209 Agilent 44K arrays. Chromosomal localization of CrRLK1Ls reveals that three of 16 genes were tandem duplicated. Subsequently, we identified 7 genes that showed circadian regulation pattern and three genes of them simultaneously response to drought stress: two were down-regulated and one was up-regulated. Functional gene network development mediated by these stress responsible genes might be an useful foundation to explain the molecular mechanism of stress response mediated by this gene family.

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PA-44

Introgression of brown planthopper resistance of *O.rufipogon* to japonica rice cultivars

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The Brown planthopper (Bph) is one of the most serious pests of rice affecting rice yield and quality throughout the country. Combining the Bph resistance in the existing quality japonica cultivars is an important breeding target in Korea. Wide crosses using several strains of AA-genome wild rices, *O.rufipogon* have been used to produce the primary germplasm which is highly resistant to Bph. By repeated backcrossing, the resistance gene was introgressed in the background of two japonica cultivars, Ilpum and Hwaseong. Among the advanced backcross progenies, the ten BC_2F_3 lines were identified as the highest resistance in the comparative Bph bioassay with other resistant sources. The 24 polymorphic markers spanning the twelve chromosomes were tested for association with marker genotypes and resistance/susceptibility reaction in the 80 BC_2F_3 lines, RM3748 on the chromosome 7 showed the highest association.

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PA-45

Ion accumulation of five rice cultivars in drought and salt stress environment

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Drought and salinity are the major abiotic stresses which are being continued to hamper the ecosystem and agriculture of the affected region. Plant species have adaptations to enhance their ability to tolerate stresses through physiological adjustment. Therefore, substantial amount of research are ongoing to provide insights about those mechanisms which enlighten the stress tolerance in plant. In this study, several rice cultivars were collected from the different parts of the world and ion accumulation experiments were conducted to select the best stress tolerant cultivar in drought and salt stress environment.

For stress treatment, five rice cultivars were subjected to salt (200 mM NaCl) and drought (200 mM Mannitol) for 72h. Later Na^+, Ca^{++}, K^+ concentrations in shoot and root samples were examined at different time interval. In both drought and salt stress, rice cultivar C201 (collected for uzbekistan) showed the lowest levels of Na^+ ion and Na^+: K^+ ratio compared to other cultivars. It was significant parallel observation with pokkali (known salt tolerant cultivar). In this preliminary study, it was observed the C201 had more stress tolerant in terms of ion accumulation; however detail physiological studies are required to strengthen the idea regarding the best stress tolerant physiotype.

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PA-46

'Jungmo2503', A new forage barley(*Hordeum vulgare* L.) cultivar with hood spike type and non-scatteredness

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'Jungmo2503' (*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 2011. It was derived from the cross between 'Dongsanpi81' and 'Kangbori'. Among the cross made in 1999, a promising line, SB992028-B-B-B-B-B-2, showed good characteristics in potential forage yield in the yield Trial tested at Iksan in 2007 to 2008 designated as Iksan 449. The line in the Regional Yield Trials (RYT) tested in eight locations around Korea for three years from 2009 to 2011, and was released as the name of 'Jungmo2503'. It has the growth habit of group Ⅰ, erect plant type, green leaf and hood spike. Its average heading and maturing dates were on May 2, and May 29, respectively, with are similar to check cultivar 'Yuyeon'. The cultivar had 102cm of culm length, 691 spikes per m^2 and it showed better rate of leaf, winter hardiness, and resistance to BaYMV than those of the check cultivar. The average forage yield of 'Jungmo2503' was about 10.9 ton ha^{-1} in dry matter in paddy field. 'Jungmo2503' also showed 9.4% of crude protein content, 27.3% of ADF (Acid Detergent Fiber), 49.0% of NDF (Neutral Detergent Fiber), and 67.3% of TDN (Total Digestible Nutrients), including higher grade of silage quality for whole crop barley.

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PA-47

Leaf temperature response of soybean (*Glycine max*) to saline stress

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This study was conducted to investigate plant body temperature response of soybean (*Glycine max*) to saline stress. Two-weeks-old seedlings of soybean in V1 growth stage were treated with 0, 10, 20, 40, 80 and 160 mM of NaCl for salt stress. Thermal images acquired using Flir T-420 (US) were obtained at 4 days after treatment. Soybean leaf temperature increased with increasing NaCl concentration, resulting in significant positive correlation between soybean leaf temperature and stress intensity ($P < 0.01$). Leaf temperature of soybean was significantly different at 160 mM of NaCl, where no visual symptom was observed. Therefore, soybean leaf temperature can be used for evaluating the response of soybean to salt stress as a non-destructive and phenomic parameter. Non-destructive diagnosis of soybean leaf temperature may be a key parameter in a high throughput screening (HTS) system in breeding program for salt stress tolerance soybean cultivars.

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PA-48

Mapping and validation of quantitative trait loci for spikelets per panicl and grain weight in rice.

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High grain yield is one of the most important traits for improvement in rice breeding program. Much attention has been given to the genetic bases of spikelets per panicle (SPP) and grain weight (GW) because of their imporftance in rice yield. In this study, IL28, near isogenic line (NIL) developed by introgressing chromosomal segments from Moroberekan into Ilpumbyeo, showed significant increase in number of spikelets per panicle and 1,000 grain weight compare to the recurrent parent Ilpumbyeo. Quantitative trait locus (QTL) analysis in 1150 F2 plants derived from a cross between IL28 and Ilpumbyeo, indicated that both *qspp6* and *qgw6* were located in the interval RM3430 – RM20580. To map the QTL more precisely, substitution mapping of *qspp6* and *qgw6* using F4 lines was conducted. As a result of substitution mapping with fifty F4 lines, *qspp6* was mapped to an 429kb interval between RM20521 and RM20562 while *qgw6* was mapped to a 267kb interval between RM20562 and RM20572 based on the japonica genome sequence. This result seems to indicate that *qspp6* and *qgw6* are two different genes. It is notable that these QTL, *qspp6* and *qgw6* are independence from undesirable height and flowering time. Moreover, there was no negative correlation between *qspp6* and *qgw6* when two genes are pyramided in the genetic background of Ilpumbyeo. SSR markers tightly linked to the *qspp6* and *qgw6* will facilitate cloning of the gene underlying these QTLs as well as marker assisted selection for variation in SPP and TGW in an applied breeding program.

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PA-49

Mapping of SSR markers closely linked to a bean rust resistant gene in common bean following bulked segregant analysis with whole genome SNP genotyping

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Recently whole genome SNP genotyping has been used to do association analysis and to map a gene of interest. Here we report application of bulked segregant analysis(BSA) using Infinium HD assay with 'BARC Bean6K_3', a SNP genotyping beadchip containing 5,399 SNPs for common bean to locate a target gene. We used BSA using Infinium HD assay was performed to find the candidate region of a single dominant rust resistant gene in PI310762, a common bean cultivar. And SSR markers were identified and mapped on the candidate region using F_2 population derived from the cross of susceptible Pinto114 x resistant PI310762. BSA revealed the candidate region of the resistant gene is on chromosome 4 where we developed nine SSR markers. Three SSR markers (beanssr1170, beanssr1168, and beanssr1167) of them appeared closely linked to the resistant gene which is located between beanssr1167 at 0.1cM and beanssr1170 at 0.5cM on chromosome 4. This study showed BSA using high-throughput whole genome SNP genotyping is a very fast and efficient method to locate a gene of interest on chromosome.

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PA-50

Molecular characterization of *BrUGE1* encoding UDP-glucose 4-epimerase from *Brassica rapa* in transgenic rice

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UDP-glucose 4-epimerase catalyzes the reversible conversion of UDP-glucose to UDP-galactose. The gene, named *BrUGE1,* isolated from a Chinese cabbage composes of a total length of 1,328 bp that contains a single open reading frame (ORF) of 1,056 bp which encodes a polypeptide of 351 amino acid residues with a calculated mass of 39.0 kDa. Expression analysis showed that *BrUGE1* is tissue specific and highly expressed in stem of rice plant. Interestingly, *BrUGE1* mRNA was highly accumulated by drought stress with significantly higher amount of soluble sugar. Morphological evaluation showed an increase in yield and yield components compared to the wild type. Moreover, a better growth performance on galactose as well as higher *UGE1* expression was observed in transgenic rice lines than in wild type. In the *Ubi-1*::*BrUGE1* lines, the increase of *UGE1* expression was apparently sufficient to overcome the toxic effects of galactose. Taken together, the *Ubi-1*::*BrGUE1* rice lines increased yield probably by increasing the rate of filled grains. 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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PA-51

Photochemical response analysis for selection of wet tolerant sorghum(*Sorghum bicolor* L. Moench) mutants

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The aim of this study was to select the abiotic tolerant sorghum mutants using chlorophyll a transient OJIP analysis of PS Ⅰ and PS Ⅱ so called Kautsky's effect within 1 second. It was clearly identified that wwt-and drought tolerant sorghum mutants could be classified by wet factor index(WFI). On the basis of WFI, wet tolerant sorghum matants were classified as follows; Ⅰ group, MUT534 bmr/new, MUT525 bmr; Ⅱ group, M2P1207 bmr, 25M2-0404 bmr, MUT371 bmr24, unknown bmr22, 10M2-0775 bmr, MUT135 bmr23; Ⅲ group, M2P0411 bmr, MUT641 bmr, M2P1064 bmr36, MUT855 bmr, 25M2-0137 bmr/new, MUT436 bmr, M2P0929 bmr, 25M2-0026 bmr, 10M2-0387 bmr, 25M2-0173 bmr/new; Ⅳ group, 25M2-0698 bmr. In conclusion, for the selection of wet tolerance, four photochemical parameters such as Electron transport flux until PSI acceptors per PSII(RE1o/RC), Performance index for energy conservation from photons absorbed by PSII antenna, until the reduction of PSI acceptors(PI_total ABS), Driving force on absorption basis(DF_total ABS) and Electron transport flux from Q_A to Q_B per PSII(ETo/RC) were important photochemical parameters deduced from maximum quantum yield and electron transport efficiency.

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PA-52

QTL identification for yield components under low P and water condition from *indica x japonica* RILs

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This study aims to identify major quantitative trait loci (QTL) for yield components under low-input systems in tropical regions in rice. A total of 156 highly advanced recombinant inbred lines (RILs) have been developed from a cross between two temperate rice varieties, Dasanbyeo (Tongil-type *indica*) and TR22183 (*japonica*). Both parental lines and RILs were tested under two different regimes of irrigation and phosphorus (P) application levels. During the wet season of 2012, under mild drought conditions, TR22183 showed more vigorous root growth at 15 days after sowing than Dasanbyeo. The early root establishment of TR22183 may have contributed to the enhanced P uptake from the top soil in the early growth stage. The linkage map for DT-RILs was constructed with 312 single nucleotide polymorphism markers aided by 384-plex platform of BeadXpress high-throughput genotyping system. For the vegetative growth, major QTLs on chromsome 6 for plant height and tiller numbers were identified. For the grain yield related traits, major QTLs on chromsome 2 were closely linked to each other. On the other hand, panicle length QTLs were identified on chromsomes 2 and 9. We are currently analyzing phenotypic data and the experiment is being repeated in dry season and temperate region. This work was supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ009076), RDA.

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PA-53

QTL mapping for grain width using near-isogenic lines from a cross between 'Hwaseongbyeo' and *Oryza rufipogon*

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Grain size is a major determinant of grain yield in rice. In a previous study, a QTL for grain width(GW), *qgw1* was detected on chromosome 1 using 96 BC_3F_8 lines derived from a cross between 'Hwaseongbyeo' as a recurrent parent and '*O. rufipogon*' as a donor parent. At this locus, the *O. rufipogon* allele increased GW. Among the 96 introgression lines, three ILs with the *O. rufipogon qgw1* locus showed significantly increase in grain width compare to the recurrent parent. One of the three lines, CR572 was selected and crossed to 'Hwaseongbyeo'.
A total of 494 $F_{2:3}$ were evaluated for grain width and agronomic traits in the field. QTL analysis in 494 $F_{2:3}$ lines indicated that QTL for grain width was located in the interval RM495-RM5443.
To narrow down the position of *qgw1*, substitution mapping using F_4 lines with different cross-over breakpoints in the region is underway. The result will be discussed.

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PA-54

Study on phenotyping of rice for drought tolerance using hyper-spectral reflectance imagery

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This study was conducted to provide basic data for high-throughput screening (HTS) system construction based on phenomics. Rice (*Oryza sativa* cv. Chucheongbyeo) seedlings in vegetative growth stage were grown in the glass house and treated with 0, 3.75, 7.5, 15, and 30% (w/v) of polyethylene glycol (PEG) to give osmotic stress. Three days after PEG treatment, hyper-spectral reflectance images were obtained and analyzed after removing background image in several steps. The reflectance of rice seedlings treated with 15 and 30% of PEG solutions were significantly different at 680 nm, where differences in the chlorophyll reflectance spectrum and visual symptoms were not observed. These results thus indicate that hyper-spectral reflectance observed at 680 nm can be used to screen drought tolerant rice lines. A HTS system equipped with this hyper-spectral reflectance system may play an important role of future rice breeding program.

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PA-55

Selection of salt-tolerant rice mutant lines from Ac/Ds insertional mutant population

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In order to find new genetic sources of rice salt tolerance, we did screening with about 10,000 rice mutant lines created by Ac/Ds insertional mutagenesis. First, we raised rice seedlings with media soil on 0.7% NaCl solution and selected 71 putative salt tolerant lines and analyzed their Ds insertion sites. We tested their salt tolerance by growing seedlings on MS medium containing, 0 mM, 150 mM, and 250 mM NaCl. Also, their seedling salt tolerance were evaluated by growing on Yoshida nutritional solution containing 0.6% NaCl. Finally, we selected eight mutant lines showing increased seedling salt tolerance compared with wild type variety, Dongjin, repeatedly. We grow them in rice field and investigated their agronomic traits such as heading time, culm length, panicle length, and panicles per hill. Among them two lines which were named Salt10 and Salt23 and showed favorable agronomic characteristics were crossed with Dongjin for further genetic analysis and mapping the causative gene variation.

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PB-01

구기자나무 유전자원의 구기순 관련 형질 특성검정

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구기자나무는 열매, 잎, 뿌리 등 이용부위가 다양한데 지표성분인 베타인이 구기순과 잎에도 존재한다. 중국에서는 열매가 달리지 않고 줄기만 자라는 Ningqi vegetable No. 1을 육성하였고, 각종 요리에 상용하고 있다. 따라서 구기순을 대량생산하기 위해서는 맹아력이 왕성하고 순이 굵으면서 잎이 넓은 계통을 선발할 필요가 있다. 이를 위해 청양구기자시험장에서 보존하고 있는 구기자나무 유전자원 143계통에 대하여 특성검정을 실시하였다. 구기순은 맹아되는 새순을 10cm 길이로 채취하여 분석하였다. 구기순의 엽형지수는 0.37 ± 0.068로 피침형이었고, 베타인 함량은 평균 2.8 ± 0.89%이었으며, 대한약전에서 규정한 0.5%(열매)보다 높았다. 잎 폭은 길이나 두께에 비하여 변이계수가 높았고, 구기순의 건조 무게는 줄기 굵기와 정의 상관관계를 나타내었다. 5월 2일에 채취한 구기순의 베타인 함량과 8월 24일에 채취한 잎의 베타인 함량을 분석한 결과 두 시기 모두 베타인 함량이 높은 계통으로 IT232687, 232711, 232648 등 3계통을 선발하였다. 또한 두시기의 베타인 함량에 대한 단순상관을 분석한 결과 정의 상관관계를 나타내었고, 생육초기에 베타인 함량을 분석하여 그 함량이 낮은 계통을 조기에 도태하는 것으로 육종효율을 높일 수 있을 것으로 판단되었다. 구기순의 건물중이 높고 베타인 함량이 높은 계통으로 IT232589, 232648, 232676, 232679, 232705등 5계통을 선발하였고, 앞으로 구기순 생산 전용품종을 육성하기 위한 육종소재로 이용할 수 있을 것으로 사료되었다.

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PB-02

국내 육성 단옥수수 자식계통 특성평가

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옥수수는 타식성 작물로 잡종강세 육종을 하기 위한 자식계통이 요구되며 육종효율을 높이기 위해서는 반드시 자식계통들의 특성 평가가 선행되어야 한다. 본 시험은 농촌진흥청 국립식량과학원에서 육성한 단옥수수 자식계통들의 특성을 평가하여 육종효율을 높이고 유전체 연구의 자원으로 활용코자 수행하였다. 시험에 사용된 계통들은 국립식량과학원에서 육성한 KSE1 등 sugary enhancer(*se*) 유전자를 가진 단옥수수 자식계통 45점이며 4월 중순에 국립식량과학원 밭작물시험포장(수원)에서 재식거리 60×25㎝(6,600본/10a)로 파종하여 발아율, 식물체특성, 생육특성, 화분 및 종자생산 관련 특성 등을 조사하였다. 발아율은 KSE2가 31%로 가장 취약하였고 수광태세와 관련된 엽신과 줄기사이의 각도는 21~65°로 다양하게 분포하였으며 숙기와 관련된 출사일수는 47~67일로 다양하게 나타났다. 화분의 생산량과 관련된 웅성소수의 밀도는 3~7, 1차 지경수는 5~25개, 웅수의 길이는 19.1~40.7cm 범위였다. 종자생산량과 관련된 이삭의 길이는 7.8~16.2cm, 폭은 3.0~4.5cm, 이삭당 열수는 10~18열 범위였다.

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PB-03

국내 적응 quality protein maize (QPM) 옥수수 종실의 일반성분, 지방산 및 아미노산 함량 비교

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국내 적응 Quality Protein Maize (QPM) 옥수수 교잡종을 육성하려면 효율적인 선발 체계를 확립하는 것이 필요하다. 본 연구는 최근 국립식량과학원에서 육성중인 QPM1 등 4 교잡계 종실의 일반성분, 지방산 조성 및 아미노산 함량을 대비품종인 일반 옥수수 장다옥과 비교 검토하여 QPM 옥수수 신품종 육성을 위한 기초 연구 자료로 활용하고자 실시하였다. QPM 교잡계들의 단백질함량은 10.0∼11.40%로 장다옥의 8.1%보다 모두 많았다. QPM 교잡계들의 지방함량은 3.8∼4.0%이었으며 QPM1을 제외한 QPM 교잡계들은 장다옥과 차이가 없었다. QPM2 교잡계를 제외한 QPM 교잡계들의 회분함량은 장다옥보다 많았다. QPM 교잡계들과 장다옥 모두 linoleic acid의 조성비가 가장 높고 oleic acid, palmitic acid, stearic acid, linolenic acid의 순으로 지방산 조성비가 높은 것으로 나타났다. QPM 교잡계들의 포화지방산 함량은 17.2∼18.4%로 장다옥과 비슷하였다. QPM 교잡계들의 불포화지방산 함량은 81.6∼82.8%로 장다옥과 비슷하였다. QPM 교잡계들과 장다옥간 필수아미노산 중 isoleucine, valine, threonine, 황을 함유한 methionine, cystine 등의 함량 차이는 없었으나, lysine함량은 QPM 교잡계들이 장다옥(3.84g/100g)보다 4.05∼4.69g/100g로 많았으며 그중 QPM1 교잡계가 4.69g/100g으로 가장 많았다. QPM 교잡계들과 장다옥간 산성아미노산인 MMA(monoamino monocarboxylic acid), DMA(diamino monocarboxylic acid), 방향족 아미노산인 AAA(aromatic amino acid) 등의 함량 차이는 없었다. 본 연구에서 육성된 국내 적응 QPM1 교잡계는 옥수수의 경우 필수아미노산 중 가장 문제시 되고 있는 lysine 함량이 보통 옥수수보다 개선되어 식용 및 사료용 옥수수로 활용 가치가 높을 것으로 기대된다.

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PB-04

난지형 마늘 조숙다수성 신품종 “장새미”

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제주특별자치도 서귀포시 중산간서로 제주특별자치도농업기술원 원예연구과

“장새미” 품종은 제주특별자치도농업기술원에서 수집한 유전자원 중 조숙 다수성 계통을 육성하기 위하여 자체 선발하고 있는 유전자원 중 중국 산동지역에서 수집한 모집단 제주-도입-501호 모집단에서 계통분리에 의해 1998년 선발하였고, 그 중 2차 생장 등 환경변이를 일으키는 개체를 제외하고 인편분화가 빠르거나 화경 및 주아가 이상적으로 비대한 개체를 중심으로 2003년 계통분리 육성하였다. 2003년부터 2005년까지 생산력 검정, 2006년부터 2009년까지 지역적응을 거쳐 “장새미”로 명명하였다. 2010년 품종보호 출원하여 2012년 품종보호등록 되었다.
“장새미” 품종의 숙기는 조생종이며 생육적온은 중온이다. 생리적 특성은 잎색은 연녹색이며 인편분화기 1월 중·하순, 화경추대는 완전추대 형이고 구색은 진한 자색을 띤다. 재배적 특성은 제주지역에서 겨울철 지상부 생육이 왕성하게 진행되고 화경을 제거하면 구 비대가 급속히 진행되고 잎 노화도 빠르게 진행된다. 자식체 특성은 화경이 직립형태에서 돼지꼬리 모양과 성숙이 진행되면 직립으로 진행되며 총포내 주아수가 많고 1개 주아무게가 0.2g이하이다. 구 모양은 넓은 편원형이며 저반의 위치는 편편형이고 알리인 13.070mg/kg, 알리신 함량이 189mg/kg이다. 평균 구중은 52.5g이고, 초장은 85㎝, 평균 엽수는 9.1개, 초형은 반개장형이다. 마늘의 수확 시기는 제주지역에서 4월 하순부터 5월 중순까지 수확이 가능하다. 재배상의 주의점은 질소비료를 과용했을 때 병 발생이 많고 특히 무름병이 증가할 수 있으므로 균형시비를 해야 한다. 또한 조숙성이기 때문에 다른 난지형 품종보다 빠른 비배관리가 필요하다.

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PB-05

대륜계통의 분홍색 반겹꽃 절화용 거베라 'Pinkholic' 품종 육성

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거베라 'Pinkholic'은 2007년 수원 국립원예특작과학원에서 자주색 반겹꽃 'A Cappella'와 분홍색 반겹꽃 'Peter'를 교배하여 획득한 종자로부터, 2007년 실생 계통을 양성하여, 화색이 선명하고 화형이 안정된 대륜계통의 분홍색 반겹꽃 거베라 '07B3-2'를 개체 선발하였다. 선발된 계통에 대하여 2008년부터 2011년까지 개체증식 및 1·2차 생육특성검정을 수행하고, 2012년에 '원교B3-49호'로 계통명을 부여하여 3차 특성검정, 안정성·균일성에 대한 연차별 재현성 및 기호도 평가를 수행한 결과, 화색 및 화형에 대한 기호도가 우수하고, 절화수명이 우수한 품종으로 그 우수성이 인정되어, '원교B3-49호'는 2012년 농촌진흥청 직무육성품종심의회를 거쳐 'Pinkholic'으로 명명되고 직무육성품종으로 등록되었다.
'Pinkholic'의 생육 및 개화특성은 화색과 화형이 유사하며 교배모본으로 사용된 'Eta'를 대조품종으로 하여 조사하였다. 'Pinkholic'은 녹색 화심의 RHS color chart RP58C의 분홍색 반겹꽃으로, 대조품종(RHS R52C)보다 밝은 분홍색 품종이다. 평균 화경은 12.0cm로 대조품종보다 0.8cm 큰 대륜계 품종이며, 설상화의 길이와 폭도 각각 5.7cm와 1.2cm로 비교적 길고 넓다. 대조품종의 꽃대 굵기가 꽃목부위 4.0mm, 중간부위 5.5mm인데 반해, 'Pinkholic'은 각각 4.9mm, 6.8mm로 비교적 굵고 둥글어 경할현상이나 꽃목굽음 등의 생리장해 발생이 적고, 절화수명도 평균 10.4일로 길다. 절화장이 평균 55.7cm 정도로 길어 절화 품질이 우수하며, 연간 채화량도 53.9(본/주) 정도로 많은 다수성 품종이다.

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PB-06

백도의 생육환경에 따른 엽색도 반응과 엽색에 관한 유전분석

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우리나라의 벼 품종은 대부분 벼의 엽색이 녹색인데 반해 최근 벼의 새로운 용도 개발을 위해 다양한 엽색의 품종이 개발되고 있으나 이러한 품종들의 재배적 특성이 기존품종보다 열악하여 새로운 색깔의 벼 품종개발에 대한 유전적 검토가 필요하며 우량한 형질이 집적된 벼 품종을 육성하기 위해서는 꾸준한 노력이 필요하다. 벼 품종의 다양화와 기능성 벼 품종을 육성하기 위해 벼 엽색 형질을 품종의 특성으로 고정하고 계통육성을 통하여 중간보본 등을 양성하고 육성 중이다. 본 연구는 2011년 이후 우리나라에서 육성된 품종들과 백색엽 품종의 교배를 통하여 엽색의 유전분석을 실시한 결과이다.
유전분석결과 백색엽인 "F_1 126" 유전자원을 우리나라에서 육성된 자포니카형 녹색엽 품종인 호품, 화영, 진백, 드래찬의 4품종과 2009년 인공교배 후 2010년 F1을 양성하고 2011년에 국립식량과학원 영덕출장소에 F_1, F_2집단 4조합을 재식거리 30×15cm로 1본식 5월 23일 본답 이앙 후 조사 하였다. 기타 재배법은 농촌진흥청 국립식량과학원 표준재배법에 준하였다. F_1에서는 4조합 모두 녹색으로 나타났으며 F_2 집단의 유전분리비는 3:1로 (녹색:백색) 분리비에 적합하여 유전자원 "F_1 126"의 백색은 국내 품종과 교배되었을 때 단순열성의 유전양상으로 나타났다.

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PB-07

벼 중생 가공용 향미 우량계통 육성

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최근 국내 쌀 소비량은 지속적으로 감소하고 있으며 수입량이 꾸준히 증가하여 국내 쌀의 과잉 공급의 문제가 발생하고 있다. 특히 밥쌀용은 해마다 감소하고 있으나, 가공용 쌀의 소비량은 2005년 이후 꾸준히 증가하고 있어 다양한 기능성 품종개발 및 새로운 수요 창출이 요구되고 있다. 본 연구는 가공용 향미 벼 품종육성을 위해 수행되었으며, 다수성 통일계 품종인 다산벼와 향 특성을 갖는 IR841을 교배하여 F_1을 얻었고, F_2를 전개한 후, F_3 이후 다수계이며 향을 갖는 계통을 선발하여 초형과 수량성이 우수한 계통(JS14-12-36-8-5-3-1-1-1)을 육성하였다. 육성계통은 수원지역에서 8월 14일경에 출수하는 중생종으로 간장이 평균 81.5㎝으로 다산벼 보다 다소 크고, 이삭길이는 26.2㎝, 이삭당 벼알수는 평균 128개로 다산벼와 비슷한 수준이다. 현미의 길이는 평균 6.67㎜, 폭은 2.29㎜, 두께는 1.70 수준으로 장폭비 2.9의 장원형이다. 현미의 단백질함량과 아밀로스 함량은 각각 8.4%. 19.4% 수준이었다. 현미의 천립중은 20.8g이며 10a 당 수량은 627kg 수준이다. 도복에 강하고, 도열병에 어느정도 견디는 편이나 멸구 등 해충에는 약하다. 육성 다수성 향미계통은 떡복이용 떡, 볶음밥 등 조리가공용으로 활용이 가능할 것으로 기대된다.

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PB-08

보라색 홑꽃 중형 프리지아 '모브토파즈' 육성

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프리지아 'Mauve Topaz'는 2005년 수원 국립원예특작과학원에서 초세가 강 보라색 홑꽃 중생종인 'Avila'품종과 초세가 강한 보라색 겹꽃 중생종인 'Blue Bayou'품종을 교배하여 획득한 종자로부터 2007년 직립성이 좋고 초세가 강한 연보라색 다화성 겹꽃 프리지아 '07-223' 계통을 개체 선발하였다. 2008년부터 2011년까지 구근 증식 및 1·2차 생육특성검정을 수행하고, 2012년에 '원교C3-51'호로 계통명을 부여하여 3차 특성검정 및 기호도 평가를 수행한 결과, 절화장이 길고 직립성이 강한 홑꽃품종으로 화색 및 화형에 대한 기호도가 좋고, 초세가 강한 계통으로 그 우수성이 인정되어 2012년에 직무육성품종심의회를 거쳐 'Mauve Topaz' 로 명명하고 품종을 출원 중에 있다. 'Mauve Topaz'의 생육 및 개화특성은 국내에서 재배되고 있는 보라색 홑꽃 품종 'Striped Jewel'을 대비품종으로 하여 조사하였다. 'Mauve Topaz'는 RHS color chart V85A의 연보라색 홑꽃 프리지아 품종으로 초장이 109.7cm, 소화수가 13.0개로 대비품종보다 많다. 분지수가 4.3개이며, 개화도 대비품종보다 8일 정도 빠르다. 자구번식력은 4.1배이며 바이러스와 구근 부패병의 자연발생이 적다.

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PB-09

보리호위축병에 강한 고품질 다수성 겉보리 신품종 '혜다'

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겉보리는 대부분 가공용으로 이용되는데 특히 보리차 및 엿기름 등으로 많이 이용되고 있다. 따라서 이에 적합한 품종을 육성하기 위해 2001년에 조숙, 다수성 특성을 가진 계통인 '진미찹쌀보리/부농' 모본으로, 내재해성 특성을 가진 '동보리1호'를 돌연변이 처리한 것을 부본으로 하여 인공교배 하여 계통육종법에 따라 우량계통을 선발 (SB01T1008-B-B-35-2). 보리호위축병 저항성이면서 다수성으로 품질이 우수한 '혜다'를 개발하였다. '혜다"는 6조이며 파성이Ⅱ(춘파형)인 병성 겉보리로 이삭의 형태는 밀수형이며, 까락이 길고 탈망성이 좋다. 출수기는 올보리에 비해 전작에서 5월 6일로 1일 늦었으나, 답리작에서는 4월 29일로 1일 빨랐다. 간장은 78㎝로 올보리보다 3㎝ 짧고, 수장은 4.4㎝로 0.4㎝ 길었으며, ㎡당 수수는 617개로 올보리보다 12개, 1수립수는 54개로 7개 많았다. 천립중(31.9g)은 올보리보다 2.5g 가볍다. 병해저항성 중 보리호위축병 저항성을 나타냈으며, 내한성은 올보리보다 약하고 도복정도는 같았다. '혜다'의 원맥 품질(조곡·정곡) 중 단백질 함량(11.6%)과 효소력가는 올보리보다 다소 높았으며, 수량성은 전작 412㎏/10a, 답리작 440㎏/10a으로 올보리보다 각각 3%, 25% 증수하였다. 엿기름 품질특성 중 효소력가, 발아세, 발아율이 올보리보다 좋아 엿기름용으로 1월 평균기온이 -6℃ 이상인 지역에 보급 될 것으로 기대 된다.

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PB-10

복색 폼폰 화형의 절화용 스프레이국화 '러빙유' 육성

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스프레이국화 '러빙유' 는 2008년 10월에 경남농업기술원 화훼연구소에서 황색 폼폰형에 중심부가 녹색인 'Furore'를 모본, 흰녹병에 강한 녹색 스파이더 화형의 'Green Joy(234213)'를 부본으로 인공교배하여 획득한 506개의 종자로부터 실생 계통을 양성하여 초세가 강하고 화형이 안정되며, 화색이 우수한 폼폰 화형의 복색(녹색/황색) 스프레이국화 'FG09-257'을 개체 선발하였다. 삽목에 의해 개체증식 후 화훼연구소 비닐온실 내에 정식하였으며, 2010년부터 2011년까지 2년간에 걸쳐 1·2차 생육특성검정을 통해 안정성, 균일성과 흰녹병 저항성 등을 조사하였고, 2012년에는 계통번호 '경남CS-31호'를 부여하여 3차 특성검정을 수행해 안정성과 균일성에 대한 연차별 재현성 그리고 주년생산성(자연, 촉성, 억제재배) 및 품평회와 시장출하 등을 통해 생산자와 소비자의 기호성 평가를 받았다. 그 결과 기호성이 좋고, 화색 및 화형 등 품질이 우수하다고 판단되어 2012년 농작물 직무육성신품종심의회 심의를 거쳐 '러빙유'로 명명하고 국립종자원에 품종보호출원 하였다. 국화 '러빙유' 품종의 자연개화기는 11월 상순이며, 선명한 황색(Y8B) 꽃잎 끝 부분에 녹색(YGN144C) 테두리를 두른 복색 폼폰 화형인 스프레이국화로서 착화성이 좋고 생육이 균일하다. 초장이 96.1cm, 줄기 직경 5.9mm로 대조품종 95.9cm, 5.6mm과 비슷한 편이나 꽃 크기가 5.6cm로 약간 큰 편이다. 꽃자루 길이는 14.6cm로 약간 긴 편이고 설상화의 주된 형태는 선단 모양이 둥근 모양이며, 꽃잎수가 305.2개로 밀도가 조밀하다. 평균 착화수는 13.4개로 대조품종 보다 2~3개 많으며, 절화수명은 26.2일로 매우 긴 편이고 휴면에는 약하다. '러빙유' 품종은 디스버드와 스프레이 형태로의 재배가 가능하고 비닐하우스 내에서 연중재배 할 수 있다. 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-11

복합내병성 및 밥맛이 우수한 고품질 중생 벼 신품종 '청운' 개발

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'청운'은 중부지역 적응 중생종 벼 품종의 재배안정성과 다양성을 확대하고 내병성 및 내재해성을 강화하여 이지역에서 재배되고 있는 외래품종을 대체할 목적으로 '수원462호'를 모본으로 하고 '밀양192호'를 부본으로 하여 2002년에 국립식량과학원에서 인공교배 한 후 계통육종법으로 육성하였다. 선발계통에 대해 2008~2009년에 생산력검정시험을 실시하여 중생종으로 밥맛이 우수하고 복합내병성을 가진 SR27931-25-3-2-1계통을 선발하여 '수원537호'로 계통명을 부여하였다. 2010~2012년 3개년 간 지역적응시험을 거쳐 중부평야지 및 중서부해안지에 적응하는 '청운'을 육성하였다. 출수기는 중부평야지 보통기 재배에서 8월13일로 중생종으로 반직립성의 양호한 초형이며 이삭추출도 양호하고 탈립은 잘 되지 않는다. 수발아에 강한 '청운'은 주당 수수는 '화성'과 비슷하나 수당립수가 많다. 또한 쌀이 맑고 투명한 '청운'은 백미완전립율과 완전미 도정수율이 '화성'에 비해 우수하고 단백질 함량이 6.7%, 아밀로스 함량이 19.5%이며 밥맛 관능검정에서 '추청'보다 우수하였다. 벼멸구에는 약하나 잎도열병, 이삭도열병, 흰잎마름병 및 줄무늬잎마름병에 모두 강한 복합내병성을 가지고 있다. 수량성은 3개년 간 실시한 지역적응시험 보통기 보비재배(5개소)에서 498㎏/10a로 '화성'(486㎏/10a)과 비슷하였다. '청운'은 중부지역에 많이 재배되고 있는 외래품종보다 도정특성, 쌀 품위 및 밥맛이 월등히 우수하였다.

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PB-12

선명한 핑크색 반겹꽃 대륜화 절화용 거베라 '써니팜' 육성

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경상남도농업기술원 화훼연구소에서 2012년 화색이 선명한 핑크색 절화용 거베라 '써니팜'을 육성하였다. 교배조합 육성을 위하여 2005년부터 국내 재배농가에서 유전자원 수집 후 특성을 검정하였다. 2007년 3월 교배 후 우수계통을 선발하여 2008년부터 2012년까지 3회의 특성검정을 거친 다음, 화색과 화형이 우수한 경남교G-45호를 선발하였다. 이 계통은 절화특성이 우수하고 화색 등 소비자의 기호도가 높아 2012년 10월 농촌진흥청 농작물 직무육성 신품종 선정 심의회의 심의를 거쳐 '써니팜(Sunny Farm)'으로 명명하였다. '써니팜' 품종의 생육 및 개화특성 조사를 위하여 대조품종으로 교배모본인 '핑크라이트(234254)'을 사용하였다. '써니팜' 품종은 핑크색계의 '핑크라이트'(234254)와 자주색계의 '메피스토'(234275) 와의 교잡에서 육성된 품종으로, 화색이 선명한 핑크색(RHS, 39-B) 반겹꽃으로, 화폭이 11.3cm 정도인 절화용 대륜화이다. 또한 포기당 연간 평균절화수량은 48.3송이 정도이며, 절화수명은 약 12.7일 정도이다. 개화소요일수는 95.5일로 대비품종 '핑크라이트'의 99.2일에 비하여 약 4일 정도 빠르며 이때 개화엽수는 약 8.8매 정도이다. '써니팜' 품종의 설상화의 길이는 5.1cm 정도로 대조품종 '핑크라이트'의 4.9cm에 비하여 길며, 설상화은 1.3cm 정도로 대조품종 '핑크라이트'의 1.2cm와 비슷한 편이다. 화경 직경은 상부는 0.6 cm 정도이고, 하부는 0.8cm 정도로 대조품종 핑크라이트의 상부 0.6cm와 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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PB-13

'설향찰'에서 발견된 웅성불임계통의 특성

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벼에서 웅성불임을 이용한 잡종강세육종은 수량성 한계를 극복하고자 시도 된 이후 중국과 인도를 비롯하여 세계적으로 21.7백만ha에서 재배, 생산되고 있다. 그러나 japonica에서는 잡종강세가 크지 않아 상용화되지 않고, 일대잡종품종의 대부분은 30%정도의 잡종강세를 보이는 indica형이다. 육종체계는 3계통이 필요한 CGMS를 주로 이용하는데, 잡종종자 생산효율을 높이기 위하여 2계통체계인 TGMS가 부분적으로 활용되고 있다. 우리나라에서 TGMS는 지역간 온도차가 크지 않아 어렵지만, 우리 환경에 맞는 불임친을 찾으면 활용도를 높일 수 있을 것이다. 본 시험은 2012년 '설향찰' 포장에서 발견된 정상이삭은 불임이지만 지발분얼은 정상적으로 임실된 계통의 특성을 확인하고자 국립식량과학원 인공기상실에서 수행하였다. 웅성불임계통은 24℃(20～28℃)에서 9～18%, 27℃(23～31℃)에서 1～3%의 임실율을 보여 TGMS 가능성을 보였지만 완전 불임이 아니어서 향후 다른 온도처리를 더 실시할 계획이다.

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PB-14

소화성 단백질함량이 낮은 반찰벼 '건양2호' 육성과 유전분석

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건강 기능성식품은 농업분야에서도 실버세대를 위한 블루오션으로 부각되고 있다. 고령화 될수록 발병율이 높으며, 단백질 습취가 제한되는 만성신부전증 같은 생활습관병 환자의 식이요법용 벼 신품종 '건양2호'가 개발되었다. 건양2호는 출수기가 8월 10일의 중생종 품종이며, 간장 이 75cm로 단간이며 내도복성이 우수한 품종이다. 또한 수당립수는 90개, 등숙율은 82%로 양호한 편이다. '건양2호'쌀의 단백질 조성 중에서 소화성 단백질인 글루테린 함량의 조성비가 낮고, 난소화성 단백질인 플로라민의 함량이 높은 특성을 가지고 있다. 먹어도 소화 흡수되는 단백질이 낮아서 단백질습취가 제한된 생활습관병 환자의 식이요법용을 적합하다. 건양2호는 아밀로스 함량이 11.5%로 일반 멥쌀과 찰벼의 중간정도이며, 중간찰 품종으로서 찰기가 높고 밥이 부드러운 특성을 가지고 있다. 건양2호의 반찰특성에 관한 유전분석을 수행한 결과 1개의 단순열성 유전하는 것으로 밝혀졌으며, 찰벼인 백옥찰벼와 교배한 후대 집단에서 찰, 메, 반찰로 분리되었으며 벼의 찰성을 조절하는 GBSS와는 비대립관계에 있다. 또한 국내육성된 반찰벼 품종인 백진주와 대립성 검정을 수행한 결과 메와 반찰로 분리되었다. 따라서 백진주와도 서로 다른 유전자를 가지고 있음을 확인하였다. 건양2호의 후대 집단을 이용하여 유전자지도 작성 및 SSR마커를 이용하여 연관분석을 수행한 결과 건양2호의 저아밀로스 유전자는 6번 염색체 말단에 존재하는 것을 확인하였다.

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PB-15

쌀 도정도에 따른 식미 및 이화학 특성 변이

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쌀의 도정 정도는 분도나 현백율로 표기하는데 현미에서 쌀겨 층과 배를 제거한 이론적인 현백율은 92%(10분도)이다. 도정도는 쌀이 부족했던 시기에는 쌀의 수율을 높이기 위해 중요시되었으나 최근 쌀의 품질이 중요시 되면서 이론적인 현백율인 92%보다 과도정된 쌀이 유통되고 있는 실정이다. 본 연구는 농촌진흥청 국립식량과학원 시험포장에서 표준재배된 일반형 3개 품종, 통일형 1품종을 대상으로 현백율 80, 85, 90 및 95%로 각각 도정하여 식미관능성적, 이화학적 특성 및 기계적 식미치의 차이를 비교하고자 수행되었다. 이화학적 특성은 도정도가 높을수록 백도와 아밀로스 함량은 증가하는 경향을 보였고, 단백질함량은 유의하게 감소하였다. 호화점도 특성은 도정도가 높을수록 최고점도, 최저점도, 최종점도는 증가하는 경향을, 치반점도는 낮아지는 경향을 보였다. 식미관능검정에서는 현백율 85, 90%에서 다른 80, 95%보다 높은 식미총평을 보였다. 이에 반해 3가지 기계적 식미계의 식미치는 도정이 많이 될수록 높은 값을 나타내었다. 이와 같은 결과에서 육종과정에서 시간과 노력이 많이 소요되는 식미관능검정을 대체하여 사용하고 있는 기계적 식미계는 시료가 현백율 85%보다 과도정 되었을 때에는 활용이 어려울 것으로 판단되었다.

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PB-16

양파 극조생계 웅성불임 중간모본 “제주O-MS-1호”

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[2]전라남도 무안군 청계면 국립식량과학원 바이오에너지작물센터

극조생종 양파 중간모본 웅성불임 계통 “제주O-MS-1호”는 2004년 극조생볼 중간모본에 자식계통 JC11-2S를 교배하여 채종하고 2005년 모구를 선발하였다. 2006년 F1 채종모구로부터 웅성불임을 확인하였으며 2006년부터 2012년에 걸쳐 3세대를 여교배 하였으며 2012년 농작물 직무육성 신품종 선정 심의위원회를 거쳐 “제주O-MS-1호”로 명명하였다. “제주O-MS-1호”는 웅성불임(CMS-S)계통으로 초형은 직립에서 반직립 형태이며 도복기는 4월 15일이다. 초장은 70.2㎝, 엽수 8매, 엽초경은 19.1mm로 지상부 생육이 왕성하며, 구중은 305g, 구형지수는 95인 원형 양파이다. 모구의 채종특성으로 개화기는 4월 26일이며 구당 화경수는 4.5개, 화경장은 106㎝은 10.6㎝이다. 내한성은 중간정도이며 노균병에 강하고 흑색썩음균핵병은 중간정도이다. 재배상의 유의점은 모구정식 적기보다 빠르거나 늦으면 꽃대 출현이 안되고 도복이 이루어질 가능성이 있음

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PB-17

'일품' 내병성 강화 고식미 벼 중간모본 '중모1025호' 개발

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'중모1025호'는 중부지역 적응 품종의 내병성 강화 및 식미 고급화를 위해 '일품'의 품위 및 도열병 등을 보완할 목적으로 '일품'과 도열병 저항성원을 갖고 있는 잡초성벼인 '금릉앵미33'을 1회친으로 이용하여 2003년부터 여교배 육종을 시작하여 도열병 저항성 유전자가 도입된 후대를 계통육종법으로 육성하였다. 2009~2010년에 생산력검정시험을 실시하여 도열병이 강화되고 밥맛이 좋은 SR30058BC_3F_2(52)-1-1계통을 선발하여 '수원545호'로 계통명을 부여하였다. 2010~2012년 3개년 간 지역적응시험을 거쳐 2012년에 직무육성 신품종 선정위원회에서 '중모1025호'로 명명되었다. '중모1025호'의 출수기는 중부평야지 및 중서부해안지 보통기 보비재배에서 8월15일로 '일품'과 비슷한 중만생종이며 초형은 반직립으로 양호하고 '화성' 대비 주당수수는 같고 수당립수는 많으며 등숙비율은 낮았다. 잎도열병 및 이삭도열병은 '일품'과 '화성'에 대비했을 때 강한편이고 흰잎마름병 K_1에는 강하나 K_2, K_3, K_{3a}에는 약하고 줄무늬잎마름병 등 기타 바이러스병과 멸구류에도 약하였다. 단원형인 쌀은 심복백이 약간 있으며 '화성'과 비교하여 단백질 함량(6.6%)은 비슷하고 아밀로스 함량(19.4%)은 낮은 경향으로 식미관능검정치가 매우 우수하였다. 또한 도정율은 '화성'보다 약간 낮으나 백미완전립율이 월등히 높았다. 수량성은 3개년 간 실시한 지역적응시험 보통기 보비재배(5개소)에서 492㎏/10a로 '화성'과 비슷한 수준이나 중부평야지 4개소에서는 4%정도 증수되었다.

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PB-18

잎 생산 전용품종 육성을 위한 구기자 유전자원의 잎 특성검정

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구기자 잎은 열매에 비하여 베타인 함량이 많고, nicotianamine, glutamic acid, 7종의 무기성분 등이 함유되어 있다. 또한 잎 추출물은 고지방 식이(high-fat diet)로 인한 체지방 및 혈장내 leptin 수준 증가 현상을 억제하는 것으로 밝혀졌을 뿐만 아니라 미백 활성이 우수하여 식품과 화장품의 기능성 소재로 개발될 가능성 있다. 이에 잎 생산 전용품종을 육성하기 위하여 청양구기자시험장에 보유하고 있는 유전자원 143계통에 대하여 특성검정을 실시하였다. 보유한 유전자원의 잎 길이는 평균 7.0±0.84cm, 잎 폭 2.5±0.44cm, 잎 두께 0.25±0.057mm이었고, 길이와 폭으로 산출한 엽형지수는 0.22 ~ 0.50 범위로서 유전적 변이가 다양하였다. 변이계수는 잎 두께가 잎 길이와 폭에 비하여 높았고, 잎이 두터운 계통을 선발할 필요가 있었다. 엽면적은 길이 및 폭과 고도의 정의 상관관계를 나타내었는데 이중 잎 폭이 넓은 계통을 선발하는 것이 효율적일 것으로 사료되었다. 구기자 엽면적을 간이로 측정하기 위하여 다중회귀를 구한 결과 엽면적은 (0.28 × 잎 길이) + (3.88 × 잎 너비) - 4.13(R^2 = 0.88**)로 산출될 수 있었다. 구기자 엽면적이 큰 계통으로 IT232288, IT232589, IT232620, IT232709등 4계통을 선발하였다. 지표성분인 베타인 함량은 평균 2.36±0.642%로 열매에 비하여 높은 것으로 분석되었고, 4.0% 이상인 계통으로 IT232593, IT232609, IT232615, IT232648, IT232687 등 5계통을 선발하였다. 앞으로 엽면적이 큰 계통과 베타인 함량이 높은 계통을 육종소재로 이용하여 잎이 크고 두터울 뿐만 아니라 지표성분이 높은 잎 생산 전용품종을 육성할 수 있을 것으로 사료되었다.

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PB-19

자주색 홑꽃 프리지아 '샤이스마일' 육성

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프리지아 'Shiny Smile'은 2006년 수원 국립원예특작과학원에서 초세가 강한 자주색 반겹꽃 중생종인 'Troubadour'품종을 자가교배하여 획득한 종자로부터 2008년 직립성이 좋고 초장 및 분지수가 분화용으로 적절한 자주색 다화성 겹꽃 프리지아 '08-219' 계통을 개체 선발하였다. 2009년부터 2011년까지 구근 증식 및 1·2차 생육특성검정을 수행하고, 2011년에 '원교C3-52'호로 계통명을 부여하여 3차 특성검정 및 기호도 평가를 수행한 결과, 분화용 품종으로 화색 및 화형에 대한 기호도가 좋고, 초세가 강한 계통으로 그 우수성이 인정되어 2012년에 직무육성품종심의회를 거쳐 'Shy Smile'으로 명명하고 품종을 출원 중에 있다. 'Shy Smile'의 생육 및 개화특성은 국내에서 재배되고 있는 자주색 홑꽃 품종 'Opala'를 대비품종으로 하여 조사하였다. 'Shy Smile'은 RHS color chart RP64A의 자주색 홑꽃 프리지아 품종으로 초장이 69.7cm, 소화수가 14개, 분지수가 4.7개로 대조품종보다 우수하며 개화도 대비품종보다 9일 정도 빠르다. 자구번식력은 약 5배 이며 바이러스와 구근 부패병의 자연발생이 적다.

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PB-20

재래종 찰벼를 활용한 고기능성 찰벼 우량계통 육성

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최근 지속적인 쌀 소비량 감소로 쌀 가공식품에 대한 관심이 높아지고 있다. 차별화되는 양질의 가공용 쌀의 개발과 안정적인 원료 공급을 통해 쌀 소비 기반을 확대할 필요가 있다. 또한 전통지식을 바탕으로 하는 전통식품에 대한 관심이 고조되고 있는 바, 국내 토종 유전자원에 대한 육종 소재로서의 활용을 확대할 필요가 있다.
본 연구는 민요, 문헌 등에서 떡으로 가공했을 때 오랫동안 굳지 않는 특성이 있는 것으로 알려진 재래종 찰벼인 '돼지찰벼(돈나)'의 우수한 가공특성을 규명하고, 재배안정성 및 수량성이 개선된 양질의 찰벼 신품종 육성을 위해 수행되었다. 단간 내도복 찰벼 계통 육성을 위해 주남벼에 돼지찰벼를 교배하였고, 복합저항성 찰벼 계통육성을 위해 보석찰벼와 돼지찰벼를 교배하여 F_1을 얻었고, 각각의 F_2를 전개하여 계통육종방법에 의해 우량계통을 선발하였다. 단간내도복 특성의 찰벼 우량계통(JS22-3-24-1-6-2-1-1-1)은 수원지역에서 8월 22일경에 출수하는 중만생종으로 간장이 평균 66.2㎝이고, 이삭길이는 22.5㎝ 이다. 현미의 길이와 폭은 각각 4.5㎜, 2.8㎜로 장폭비가 1.9 정도였고, 현미 천립중이 18.5g 정도로 다소 소립이며, 10a 당 수량은 480kg 정도이다. 육성된 복합저항성 찰벼 우량계통(JS23-4-39-14-4-5-1-1-1)은 수원지역에서 8월 15일경에 출수하였고, 간장이 82.3㎝이고 현미천립중은 21.0g 정도이며, 10a 당 수량은 500kg 내외로 동진찰벼와 비슷한 수준이었다. 포장에서 목도열병, 흰잎마름병, 줄무늬마름병에 대해 저항성을 보였다. 토종 찰벼의 우수 가공특성을 활용한 양질의 찰벼 계통으로 친환경재배용 품종 및 쌀가루 가공용 등으로 활용이 가능할 것으로 기대된다.

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조생 복합내병성 벼 중간모본 '중모1023호' 개발

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조생품종의 용도를 다양화하고 기후변화에 대응한 고온등숙 및 복합내병성이 강화된 품종을 육성하고자 '영덕34호'와 '익산456호'를 2003년에 교배하여 계통육종법으로 육성하였다. 2009~2010년에 생산력검정시험을 실시하여 SR29156-11-2-B-2 계통을 선발하여 '수원534호'로 계통명을 부여한 후 2010~2012년 3개년 간 지역적응시험을 거쳐 2012년에 직무육성 신품종선정심의회에서 조생 복합내병성 중간모본으로 사용하도록 '중모1023호'로 명명되었다. '중모1023호'의 출수기는 중부평야지 및 중서부 해안지 보통기 재배에서는 8월3일, 중북부중산간지나 동북부해안지 보통기 보비재배에서는 8월8일이고 중부평야지 조기재배에서는 8월3일로 조생종이다. 초형은 반직립으로 양호하고 주당수수는 '화성'과 비슷하나 수당립수는 '화성'보다 많고 등숙비율은 높다. 도열병, 흰잎마름병 및 줄무늬잎마름병에는 강하나 벼멸구에는 약한 복합내병성을 가지고 있다. 쌀은 매우 맑고 투명하여 심복백이 적어 외관품위가 우수하고 '화성'과 단백질함량(6.9%)은 비슷하고 아밀로스 함량(18.4%)은 낮은 편이고 식미가 양호하다. 또한 제현율은 '화성'보다 약간 낮으나 백미완전립율은 매우 높다. 수량성은 3개년 간 실시한 지역적응시험 보통기 보비재배(7개소)에서 456㎏/10a로 '화성' 대비 92% 수준이었다. 중부평야지 조기재배(1개소)에서는 499㎏/10a로 '화성'과 비슷한 수준이었다. 금후 조생종 품종 육성 시 복합내병성 교배모본으로 활용될 것으로 기대된다.

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PB-22

중부지역의 맥후작 재배에 적합한 청예사료용 피의 재배적 특성

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중부지역의 맥후작 재배에 적응하는 청예사료용 피 유전자원을 선발하기 위하여 농촌진흥청 농업유전자원센터로부터 유전자원 58종, USDA GRIN으로부터 26종, 외국재배품종 3종, 국내자생종 8종을 수집하였다. 전체 95종의 피 유전자원을 경기도 수원의 시험포장에 20112년 6월5일 침종한 후 육묘하여 7월3일에 열간 40cm, 주간 10cm 간격으로 이식하여 사료용으로의 재배적 특성을 평가하였다. 피 유전자원의 출수기는 8월1일에서 9월17일까지, 초장은 52cm에서 202cm까지, 주당 분얼수는 2개에서 45개까지, 주당 건물중은 8g에서 231g까지로 다양한 변이를 보였다. 그리고 엽폭, 탈립성에서도 많은 변이를 보였다. 주요재배형질간의 상관관계는 출수기가 늦은 만생종일수록 초형이 직립형에 가깝고, 초장이 길며, 주당 분얼수가 많은 경향을 보였다. 그리고 엽폭이 넓은 광엽형이 초장이 길고, 주당 분얼수가 적고, 종실의 탈립이 잘되지 않았다. 주당 건물중은 만생, 장간, 다분얼성과 높은 상관을 보였다. 맥후작으로 재배시 청예사료용으로 적합한 피는 어느정도 생육기간을 확보할 수 있는 9월에 출수하는 만생종과 엽폭이 넓은 광엽종, 분얼수가 10개 내외인 중소얼형이 수량성이 높아 적당할 것으로 사료된다. 그리고 채종을 위해서는 탈립이 잘되지 않는 내탈립성이어야 할 것이다.

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PB-23

한국 재래밀유전자원의 작물학적 특성

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농촌진흥청 농업유전자원센터에서 보유하고 있는 재래밀 유전자원 303점을 대상으로 2011년 10월 16일 국립식량과학원 벼맥류부 익산 전작포장에서 파종재배하여 이삭형태, 수밀도, 망의 형태 및 장단 등의 작물학적 특성을 조사하였고, 출수기에 식물체, 성숙기에 이삭, 수확기에 종실특성의 영상자료를 제작하여 재래밀 유전자원 특성을 조사하였다. 한국 재래종 밀 303점은 이삭의 형태에 따라 추형(52%), 봉형(31%), 방추형(12%), 곤봉형(5%)의 4개 그룹, 이삭의 소밀에 따라 소수형(26%), 중간형(44%), 밀수형(33%)의 3그룹, 망의 유무장단에 따라 장망종(64%), 단망종(26%), 무망종(10%)의 3그룹으로 나눌 수 있었다. 지역별로는 영남지방의 자원이 기호, 중원 및 호남지방의 것보다 수집빈도가 높았다. 유망한 재래밀 유전자원으로는 간장이 60cm 미만으로 단간인 자원은『김제4(IT112968)』,『김제6(IT018723)』,『임실1(IT159750)』,『장수10(IT159763)』,『영일4(IT159778)』등이었다. 한편 성숙기가 5월 하순으로 조숙인 자원은『고창1(IT1010531)』,『고성1(IT104873)』,『경산1(IT118995)』,『경산2(IT118996)』,『상주1(IT119904)』등 이었고, 특히 내한성이 강하면서 단간이고 도복에 강한 자원은『군포1(IT166455)』,『밀양1(IT166468)』,『거제27(IT166469)』,무망이며 단간인 자원은『KLW8631(IT140792)』, 무망이며 장간인 자원은『거제17(IT15048)』이였다. 본 연구에 활용된 다양한 한국재래종 밀 유전자원은 자원주권 확보 및 육종소재로서의 활용도가 높을 것으로 생각된다.

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한국 재래옥수수 유전자원의 작물학적 특성

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농촌진흥청 농업유전자원센터에서 보유하고 있는 재래옥수수 유전자원 940점을 대상으로 2008년에서 2012년의 5개년에 걸쳐 강원도원 홍천옥수수시험 포장에서 재배하여 출사기, 간장, 착수고, 엽형, 주간엽수, 자수열수, 종피색, 1수립중, 백립중 등의 작물학적 특성을 조사하였고, 동시에 이들 자원의 이미지특성을 확보하기 위하여 웅수출현기에 전식물체, 성숙기에 이삭, 수확후에 종실의 영상자료를 제작하였으며, 메찰성 분석은 홍천옥수수시험장에서 증식된 종실자원으로 요드반응을 조사하였다. 재래옥수수 유전자원 940점은 용도별로 메옥수수 48%(453점), 찰옥수수 43%(407점), 사료용옥수수 5%(47점)로 나눌 수 있었으며, 재래옥수수 지역별 분포는 강원도 21%, 충남도 15%, 경남도9% 순으로 분포가 높았다. 용도별 지역별 분포는 메옥수수에서는 지역간 차이가 없었으나, 찰옥수수에서는 강원도가 전체의 17%로 높은 분포를 보이고 있어 용도별 지역특이성이 큰 경향이었다. 또한 간장은 메옥수수에서 장간이나 단간이 많았으며, 숙기는 메옥수수에서는 조생종이, 찰옥수수에서는 만생종의 분포비율이 다소 높아 용도별 특이성도 인정되었다. 수당립중과 백립중은 메옥수수가 찰옥수수 보다 대체로 무거운 경향이었다. 재래옥수수 중 대표적인 유망한 자원은 흰찰옥수수에서는『서천찰 **IT208593**』이 극조생,『고성찰, **IT195284**』이 조생,『홍천찰17, **K 139943**』이 중생,『평창찰11, **IT026524**』이 만생으로 유망하였으며, 검정찰옥수수에서는『금산찰15 **K140119**』이 중생,『성주찰 **IT208576**』이 만생,『미상찰 8 **IT178746**』이 극만생종으로 유망하였다. 본 연구에 활용된 다양한 한국 재래옥수수 유전자원은 자원주권 확보 및 육종소재로서의 활용도가 높을 것으로 생각된다.

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PB-25

한국 재래조 유전자원의 작물학적 특성

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농촌진흥청 농업유전자원센터에서 보유하고 있는 재래조 유전자원 325점을 대상으로 2007년에서 2008년, 2년에 걸쳐 단국대학교 전작과 포장에서 재배하여 출수기, 간장, 수형, 성숙기, 종피색, 1수립수, 천립중 등의 작물학적 특성을 조사하였고, 동시에 이들 자원의 이미지특성을 확보하기 위하여 출수기에 전식물체, 성숙기에 이삭, 수확후에 종실의 영상자료를 제작하였으며, 메찰성 분석은 농업유전자원센터에서 증식된 종실자원으로 요드반응을 조사하였다. 재래조 유전자원 325점은 용도별로 메조 49%(159점), 차조 51%(166점)로 나눌 수 있었으며, 메조, 차조를 합쳐서 강원도 29%, 경북도 25%, 경기도12% 순으로 수집도수분포가 높았다. 용도별 남한지역별 분포는 메조에서는 경북도가 전체의 22%, 차조에서는 강원도가 전체의 17%로 가장 높은 분포를 보이고 있어 용도별 지역특이성이 뚜렷하였다. 이삭모양 분포는 메조, 차조 공히 원통형 42%, 원추형 31% 순으로 가장 높았고, 또한 간장은 메조에서 장간이나 단간이 많았으며, 숙기는 메조에서는 조생종이, 차조에서는 만생종이 수집분포비율이 높아 용도별 특이성도 뚜렷한 경향이었다. 재래조 중 대표적인 자원은 극조생이며 곤봉형인 자원은 삼척메조-2**(IT103288)**, 극조생이며 원통형인 자원은 강화차조-10**(IT209312)**, 극조생이며 방추형인 자원은 강화차조-11**(IT209313)**, 중생이며 선단분지형은 정선차조**(IT104454)**, 중생이며 분지형인 자원은 화성차조-1**(IT103755)**, 극만생이며 원추형인자원은밀양차조**(IT185955)**등 이었다. 본 연구에 활용된 다양한 한국 재래조 유전자원은 자원주권 확보 및 육종소재로서의 활용도가 높을 것으로 생각된다.

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PB-26

한국 재래종 콩의 isoflavone과 saponin 함량 변이

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고품질 콩 품종육성을 위한 기초자료로 활용하기 위하여 한국 재래콩 292점의 isoflvone과 saponin 함량의 변이를 구명한 결과, 총 isoflavone 함량은 평균1390.2μg/g 이었고 420.6～2907.3μg/g의 범위였다. isoflavone 함량의 분포는 1000～1500μg/g 범위에서 가장 많이 분포하였고, 1500～2000μg/g의 범위가 그 다음으로 높았고, 2500μg/g이상은 5점 이었다. isoflavone함량은 genistein, daidzein 및 glycitein 순으로 높았다. 총 isoflavone의 함량은 daidzein 및 genistein과 높은 정의 상관관계 이었고, daidzein 과 genistein 간에도 정의 상관관계이었다. 총 saponin 함량은 평균4347μg/g 이었고 1932～8400μg/g의 범위였다. Group A saponin 함량은 평균529μg/g 이었고 243～1231μg/g의 범위였다. Group B saponin함량은 평균3817μg/g이었고 1584～7598μg/g의 범위였다. Group B saponin이 높은 자원은 IT226841, IT228304, IT228251이었으며, 총 saponin함량이 높은 자원은 IT226841 (8,400μg/g)이었다. 총 saponin 함량과 Group B saponin의 함량 간에는 정의 상관이었다.

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한국 콩 육성품종의 saponin 함량 변이

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국내에서 2009년까지 육성된 콩 120품종들의 saponin 함량 변이를 구명하여 콩 기능성 품종 개발의 기초자료로 활용코자 본 연구를 수행하였다. Saponin 함량은 Group A saponin이 225.6～1,193.3μg/g의 범위였고 평균은 592.5μg/g이었으며, Group B saponin은 2168.6～7270.0μg/g 범위였고 평균은 4318.0μg/g이었다. Group A와 B saponin을 합한 총 saponin 함량은 2431.1～8231.3μg/g의 범위였고 평균은 4910.5μg/g이었다. 콩 saponin 함량은 품종, 육성연대, 용도, 종실크기 및 육성모지 간에 따라서 유의한 차이를 보였다. 각종 생리활성을 나타내는 물질로 인식되는 group B saponin이 높은 5개 품종들은 원황콩, 녹채콩, 부광콩, 장기콩 및 흑미콩 이었다. 육성연대는 2000년도 이후가, 용도는 나물콩이, 종실크기는 소립종이, 육성모지는 익산이 총 saponin 함량이 가장 높았다. 총 saponin 함량과 Group B saponin의 함량 간에는 정의 상관이었다.

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PB-28

헤어리베치(*Vicia villosa* Roth) 백색과 분홍 꽃의 유전분석

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헤어리베치의 분홍색과 백색 화색 유전검정을 위하여 헤어리베치 유전자원 집단에서 파생된 백색 화색 계통을 모본으로 하고 분홍 화색을 지닌 품종(마메초)을 부본으로 하여 2011년에 교배하여 2013년 F_2 후대를 조사하였다.
분홍색과 백색의 잡종(F_1)은 보라색으로 나타났고 후대(F_2) 화색은 백색 1 보라 2, 분홍색 1의 비율로 분리되었다. 따라서 헤어리베치의 분홍색 화색은 보라색에 대한 열성상위 관계에 있는 것으로 추정된다.

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PB-29

황색 흩꽃화형 스프레이국화 '에스미키' 육성

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스프레이국화 '예스미키(Yes Mickey)'는 2008년 예산국화시험장 육종온실내에서 네덜란드에서 육성된 홑꽃화형의 '포워드(Forward)'를 방임수분하여 얻어진 280개의 종자를 2009년에 파종하였고, 이중에서 다화성으로 화색이 선명하고 녹색의 짙은 화심을 갖고 있는 'SP09-182-03'계통을 선발하였다. 이 품종의 주년재배 특성검정을 위하여 2009년부터 2011년까지 1·2차 생육특성 검정을 수행하였고, 2012년 3차 특성검정 및 기호도 평가를 수행한 결과 기호도가 4.08/5.0로 높아 '예산SP-40호'로 명명하였으며 2012년 직무육성 신품종선정위원회를 통과하여 '예스미키(Yes Mickey)'로 명명하고 품종등록 출원하였다. '예스미키(Yes Mickey)'의 생육 및 개화특성은 모본으로 사용된 황색의 '포워드(Forward)'를 대조품종으로 하여 조사하였다. '예스미키'는 황색(7A)의 화심이 진한녹색인 조기개화성 절화용 스프레이국 품종이다. 본당 착화수는 23.7개로 대조품종 17.2개보다 월등히 많았으며 꽃직경이 3.6cm이고 꽃잎수는 31.0매로 대조품종의 2.7cm에 43.0매와 비교하여 볼륨이 크고 녹심이 뚜렷한 산티니계열의 수출용 꽃다발로 적합하였다. 개화소요일수는 자연재배에서 45일로 대조품종보다 5일 빠른 경향을 보였다. 재배상 유의사항은 개화반응기간이 짧아 영양생장기에 비배관리를 철저히 하고 다화성으로 적정 재식거리를 준수하여야 한다.
(본 연구는 국화연구사업단 "화훼품종 육성 및 상품성 향상 기술개발사업"으로 지원받은 과제임)

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PB-30

A new waxy white grain wheat variety, "BaekChal" with pre-harvest sprouting and cold hardiness resistance and good cooking quality

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"Baechal", a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA, Iksan, Korea, during the period from 2006 to 2012. The heading and maturing dates of this variety were May 1 and June 5 in upland, and May 2 and June 8 in paddy field, respectively. It is an It is an awned, semi-dwarf and hard white wheat. Culm and spike length of "Baekchal" were 75cm and 8.7cm. It had lower test weight (794 g/Ⅼ) and 1,000 grain weight (35.7g) than "Keumkang". It showed moderate to pre-harvest sprouting, which lower rate of pre-harvest sprouting (13.7%) than "Keumkang". "Baekchal" had similar ash content (0.47%) and protein content (13.1%) to "Keumkang". It showed lower gluten content (9.6%), SDS-sedimentation volume (38.2㎖) and amylose content (6.5%) than "Keumkang". It showed higher high viscosity (643BU), water absorption (213%), expansibility of cooking (357%). It showed different composition in HMW-GS compositios (2*), PPO18 (876bp), GBSS (waxy type) and Puroindolines composition compared th "Keumkang". Average yield of "Baekchal" in the regional adaptation yield trial test was 4.89 ton/ha in upland and 4.83 ton/ha in paddy field. "Baekchal" would be suitable for the area above −10℃ of daily minimun temperature in January in Korean peninsula

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PB-31

A new wheat variety, "Hojoong" with pre-harvest sprouting resistance, low amylose content and good noodles quality

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"Hojoong", a winter wheat (*Triticum aestivum* L.) cultivar was developed by the National Institute of Crop Science, RDA, Iksan, Korea, during the period from 2006 to 2012. The heading and maturing dates of this variety were May 2 and June 10 in upland, and May 3 and June 7 in paddy field, respectively. It is an It is an awned, semi-dwarf and soft red winter wheat. Culm and spike length of "Hojoong" were 79cm and 9.1cm. It had lower test weight (803 g/L) and 1,000 grain weight (39.5g) than "Keumkang". It showed resistance to pre-harvest sprouting, which lower rate of pre-harvest sprouting (5.5%) than "Keumkang". "Hojoong" had lower flour yield (66.7%) and ash content (0.38%) than "Keumkang". It showed lower protein content (11.3%) and lower SDS-sedimentation volume (34.0㎖) and amylose content (20.5%) than "Keumkang". It showed higher high viscosity (204BU) and lightness of noodle dough sheet (80.63). It showed different composition in HMW-GS compositios (2.2+12), PPO18 (876bp), GBSS B (null type) and Puroindolines composition compared th "Keumkang". Average yield of "Hojoong" in the regional adaptation yield trial test was 5.51 ton/ha in upland and 5.10 ton/ha in paddy field. "Hojoong" would be suitable for the area above -10℃ of daily minimun temperature in January in Korean peninsula

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PB-32

Analysis of seed proteome from wild and mutant lines of sorghum

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Grain sorghum (*Sorghum bicolor*) is a major staple for a large portion of the world. The crop ranks fifth among the cereals world-wide with respect to its importance for food and feed applications. To this end, the grain harvested from sorghum, and the millets provides an important source for dietary calories and protein for approximately one billion people in the semi-arid regions of the world. However, grain sorghum products are known to have relatively poor digestibility, only approximately 50%-70%, in comparison with other grains, such as wheat and maize, which tend to have digestibility percentages over 80% and 70%, respectively. Protein with high digestibility is by definition nutritionally superior owing to the increased availability of amino acids. Digestibility can be impacted by both protein-protein and/or protein-nonprotein interactions. However, with respect to grain sorghum, it is thought that the major factor influencing digestibility is the former because of high protein cross-linking around the protein body. To understand the mechanism of seed storage proteins in the sorghum, the proteomic analysis was carried out between the wild(BTX623) and mutant(M271207) genotypes of sorghum. Proteins were separated from the mature seed using IEF in the first-dimension and SDS-PAGE in the second dimension along with hybrid LTQ-FTICR mass spectrometry. After image analysis using Progenesis SameSpot software, we identified the 62 differential expressed protein spots out of 293 protein spots. Out of total differential expressed spots, 35 differential expressed protein spots (more than2-fold) were analyzed by mass spectrometry. Out of 35 protein spots, we were identified 20 protein spots as up-regulated and 15 protein spots as downregulated, significantly. In our proteomic investigation, the candidate proteins may provide novel clues for better understanding the characteristics of seed proteins in Sorghum.

Keywords: Seed Storage Protein, Sorghum, Wild and Mutant Genotypes, Proteomics

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PB-33

Characterization of an ethyl methane sulfonate (EMS) mutant lines in *C.annuum*.

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Mutant lines induced by ethyl methane sulfonate (EMS) have been used for crop improvement and functional genomics. Since pepper is very recalcitrant to be transformed, EMS mutagenesis could be an alternative method to generate useful mutant lines and to characterize the function of genes. We have developed mutant lines consisting of about 3,938 M_2 mutant lines using Korea local landrace, *C. annuum* 'Yuwolcho'. Yuwolcho has suitable traits for mutagenesis such as early flowering and maturation, large number of seeds per fruit, and susceptibility to various diseases. Up to now, 917 M_2 mutant lines were evaluated to confirm the effect of EMS. M_2 mutant lines have shown variations in plant stature (small size, dwarfism, and early death), leaf development (light color, variegation and morphological change) and flower (inflorescence, morphological change) and fruit (size and color). We observed the largest morphological variation in leaf development. Most of these mutant phenotypes were inherited recessively. In addition, we are applying cel1-based TILLING to identify useful mutant lines. We will apply cel1-based TILLING to identify useful mutant lines. We are expecting that these mutant lines will be very useful to study the function of genes in *C. annuum*.

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PB-34

Differentiation of isoflavones of breeding populations between yellow and black soybean

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Soybean isoflavones include daidzein, genistein and glycitein with their glycosides, and their malonated derivatives are the main polyphenolic compounds that are helpful for human health. Our research objective was to investigate the differentitation of soybean isoflavones contents of breeding populations between yellow and black soybean. Isoflavones contents in soybean are a wide range from 500 to 7000 ㎍/g. In this study, we used Ilmi (Isoflavones content, 3.612 ㎍/g) as male parent and 04GAYT-4 (Isoflavones content, 1,648 ㎍/g) as female parent. From these varieties, we obtained 94 breeding lines (yellow, 48 lines; black, 25 lines; brown, 21 lines) which have isoflavones content range from 1000 to 6000 ㎍/g. Highest isflavone contents of three different breeding lines was yellow seed coated lines (average isoflavone content, yellow 3,046㎍/g, brown 2,935 ㎍/g, black 2,813 ㎍/g).

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PB-35

Evaluation of fruit quality in pepper germplasms(*Capsicum annuum*) introduced from china for high-red pigments breeding.

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Fruit quality traits like heat, color and flavor are unique and important for pepper cuisines and industrial use. Pepper pigments include chlorophyll, carotenoids, anthocyanin and red pigments like capsanthin are unique carotenoids to *capsicum* spp. So developing carotenoids-rich peppers and use of red pigments extraction along with capsaicinoids are one of interest pepper breeding goals in the world.
Horticultural traits of 113 germplasms introduced by international cooperative research with YASS of China were evaluated to select promissing materials for high quality peppers during the past 3 years. All of germplasms including 60 local peppers were belong to *C. annuum* and fruit characteristics were diverse. Especially fruit chemical compositions like ASTA color, capsaicinoids and sugars were evaluated compared with korean commercial peppers. Average contents of ASTA color was 98±37, 55±63mg in capsaicinoids and 12±6% in total sugars. ASTA color which generally means red pigments content was over 120 in 25 germplasms including over 200 in 2 germplasms. Higher ASTA colors were observed in different fruit types. Capsaicinoids content was over 90mg/100g in 24 germplasms including 5 germpalsms over 200mg. Especially higher capsaicinoids were higher in local peppers with round and wrinkled fruit shape. And total sugar content was over 20% in 10 germplasms. Germplasms of different fruit shapes and characteristics will be useful materials for diverse fruit quality breeding.

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PB-36

Evaluation of soluble sugar content in soybean mutant lines derived from gamma-irradiation

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Soluble sugar content in soybean seed is an important quality attribute for soyfood and feed. Usually, soluble sugars comprise 6 to 17% of total dry wt. in mature soybean seeds. In this study, 414 soybean mutant lines induced by gamma-ray were screened by colormetric assay, FACE (Fluorophore-assisted carbohydrate electrophoresis), and GC-MS to identify the change of soluble sugar contents. Among 414 soybean mutant lines, 12 mutant lines derived from three different soybean cultivars (Hwanggum, Paldal, and Bangsa) showed higher level of soluble sugar content compared to their original cultivars. However, 5 mutant lines derived from soybean landrace KAS 636-15 showed lower level in the colormetric assay. In FACE, 17 soybean mutant lines selected by colormetric assay also showed different band intensity compared with their original cultivars. However, there were no different soluble sugar patterns between soybean original cultivars and mutant lines. Finally, the variations of soluble sugar content in 17 soybean mutant lines were confirmed by using GC-MS. These mutant lines will be used for genetic study to find mutations of genes related soluble sugar biosynthesis.

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PB-37

Global genome expression analysis of rice mutant line in response to salt stress

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To determine the expression levels of genes related to the salt stress response in rice, gene expression profiles were investigated through microarray analysis using the rice mutant line Till-II-877. There were no significant changes in physiological response under salt stress of the mutant increased less than that in the WT. The intensity of gene expression was analyzed and compared between the wild type and mutant lines using a microarray. Among the most significantly affected pathways, α-linolenic acid metabolism and linoleic acid metabolism (in lipid metabolism), fructose and mannose metabolism and glycolysis-gluconeogenesis (in carbohydrate metabolism), cysteine and methionine metabolism (in amino acid metabolism), and carbon fixation (in the energy metabolism of photosynthetic organisms) showed changes in gene expression levels under salt stress. These results further our understanding of the effects of salt stress in rice and may aid in the development of salt-tolerant rice cultivars.

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PB-38

Identification of genetic diversity and DNA polymorphisms in Korean rice accessions through resequencing

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With the rapid development of sequencing technologies, next-generation sequencing is widely utilized for molecular breeding in several crops including rice. We performed whole genome resequencing of ten Korean rice accessions including six cultivars and four mutant lines. In total, 2,448 million raw reads were generated with over 58x coverage of Nipponbare genome. We mapped the reads from each of the ten accessions onto genomic sequence of japonica rice cultivar, Nipponbare. We detected 3,144,016 SNPs, which estimated to be one per 2.2kb on average. We found SNPs in genes that have been reported to be involved in rice flowering time regulation and bacterial blight resistance among ten rice accessions. Unmapped region against Nipponbare genome occupied about 1 ~ 2% in each accession. Over 50% of the unmapped region were found in the repeat region. The minimum length of gap in all accessions were 1bp and the maximum length of gap was 45,967bp in Ilpum. We also identified 3,497 possible gene loss events within these unmapped regions. The frequency of gene loss in each chromosome ranged from 33 on chromosome 5 to 913 on chromosome 11. The genetic variations we detected among ten rice accessions will provide invaluable resources for identification of genes associated with diverse traits of agronomical importance for molecular breeding.

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PB-39

In vitro anther culture of Chrysanthemum (*Dendranthema ssp.*)

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This study was set up to get plants from anther culture of Chrysanthemum (*Dendranthema grandiflorum*) gardenmum cultivar "Yes Morning' and potmum cultivar "Peace Pink" for breeding program. The induction of callus was quick and high on MS basal medium supplemented with 1.0 mg/L of 2,4-D + 2.0 mg/L of 6-BA + 4% W/V sucrose. Induction potential was slightly increased by addition of 250 mg/L Casein hydrolysate to the induction medium. Calluses were allowed to differentiate on MS basal medium + 2.0 mg/L of BA + 0.1 mg/L of NAA + 3%W/V sucrose. The rate of callus formation differed little between the cultivars. A pretreatment of anthers at 4℃ for 48h enhanced both the induction and differentiation ratio. Multiple shoots were initiated from most of the calluses and were shifted to MS basal medium + 0.1 mg/L of NAA + 3%W/V sucrose for rooting. Regenerated plantlets were acclimatized and transferred to the soil. Some of the regenerated plants showed slow growth with little morphological difference.

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PB-40

Influence of high temperature during grain filling and seed maturation on the accumulation of storage proteins in rice

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High temperature impediment in developing stages of crops has been occurred due to the impact of global warming. Rice production is notable to be sensitive to increasing environmental temperature and grain filling temperatures are already approaching threatening levels in many countries with rice cultivation. Recent proteomic analyses exposed impulsive changes of metabolisms during rice grain development. Interestingly, proteins involved in glycolysis, citric acid cycle, lipid metabolism, and proteolysis were accumulated at higher levels in mature grain than those of developing stages. High temperature (HT) stress in rice ripening period enhances damaged (chalky) grains which have loosely compacted shape starch granules. We carried out two-dimensional gel electrophoresis to analyze protein profiles during grain filling and different developmental stages of rice seed maturation. Proteins were separated from the fertilized seeds (seeds from 7 days and 21 days after fertilization) and seed maturation stage using IEF in the first-dimension and SDS-PAGE in the second dimension along with MALDI-TOF mass spectrometry. More than 1,000 protein spots were detected on a two-dimensional gel electrophoresis. A total of 120 different protein spots out of 140 protein spots were identified by MALDI-TOF and nano LCQ-TOF mass spectrometer. The identified proteins were categorized into six (6) different groups according to their expression patterns during grain filling and seed maturation. Some proteins were confirmed during seed development stages such as cytoplasmic malate dehydrogenase, whereas others were appeared at a specific stage like putative subtilisin-like protease, germin-like, seed allergenic proteins. Furthermore, the chalking mechanism of rice grain under the HT stress could be discussed in terms of grain starch glycome, transcriptome, and proteome.

Keywords: *Oryza sativa*, High Temperature Stress, Grain filling, Proteomics

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PB-41

Mitochondrial proteome analysis of the seedlings of wheat in roots using LTQ-FTICR-MS/MS

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Sub-cellular proteomics provide insight into the molecular mechanisms of plant cell modulation of protein accumulation in intracellular compartments regarding various perturbations, and thus provides rectified knowledge about signal transduction in organelles. Mitochondria are important organelles for cellular respiration within the eukaryotic cell and serve many important functions including vitamin synthesis, amino acid metabolism and photorespiration for the cell as well. To define the mitochondrial proteome of the roots of wheat seedling, a systematical and targeting analysis were carried out on the mitochondrial proteome from 15 days-old wheat seedling roots material. Mitochondria were isolated by Percoll gradient centrifugation; and extracted proteins were separated and analyzed using Tricine SDS-PAGE along with LTQ-FTICR mass spectrometry. From the isolated mitochondrial proteins, a total of 140 proteins were identified. The identified proteins were functionally classified into 12 classes using ProtFun 2.2 server based on cellular roles, Proteins were shown to be involved in including amino acid biosynthesis (17.1%), biosynthesis of cofactors (6.4%), cell envelope (11.4%), central intermediary metabolism (10%), energy metabolism (20%), fatty acid metabolism (0.7%), purines and pyrimidines (5.7%), regulatory functions (0.7%), replication and transcription (1.4%), translation (22.1%), transport and binding (1.4%), and unknown (2.8%). These results indicated that many of the protein components present and functions of identified proteins are common to other profiles of mitochondrial proteomes performed to date. The data presented here will begin to reveal a better understanding the characteristics of proteins and metabolic activity in mitochondria in wheat roots.

Key words: Mitochondrial proteins, Wheat Roots, SDS-PAGE, LTQ-FTICR, Proteomics

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PB-42

Modification of starch composition using antisense and RNAi vectors by targeting *SSS1* and *GBSS1* genes in rice (*Oryza sativa* L.)

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Amylopectin composition is determined by the relative activity of soluble starch synthase (*SSS*) and granule-bound starch synthase (*GBSS*). Soluble starch synthase and starch branching enzymes are major determinants for the synthesis of amylopectin while *GBSS1* is responsible for amylose synthesis *in vivo*. The formers are made of linear and branched molecules and the latter is composed of highly branched molecules. To increase the palatability of rice, down-regulation of amylose synthesis by antisense and RNA interference (RNAi) could be excellent and powerful tools for controlling the starch composition which is responsible for grain eating quality. The goal of this study is to generate breeding lines with lower amylose content relative to its wild type. This study also reports the results of the two down-regulating technology in lowering the amylose content of rice grain. Furthermore, this study elucidates the effect of using antisense and RNAi for *SSS1* and *GBSS1*.

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PB-43

Palatability and physicochemical properties of rice varieties in the year when yield increased by 10% than usual

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In this study, we examined the palatability and physicochemical properties of rice varieties in the year when there was 10% increase in yield compared to normal year due to daily temperature range and sunshine hours. The results of the analysis of rice yield over the last 20 years (1993-2012) showed 10% difference between the yield in 2000, which was normal, and that in 2001. With regard to the crop weather condition during the ripening period in 2001 compared to 2000, the daily range and sunshine hours were higher, but the mean temperature was similar. The rice yield in 2001 was 9.8% higher than that in 2000 due to the increased number of spikelets per panicles and ratio of ripened grain. In terms of chemical traits, protein, Mg, and K contents decreased in 2001 compared to 2000, but amylose content increased. Trough and final viscosity assessed with a Rapid Visco Analyser were significantly higher in 2001 than 2000. The results suggested that the palatability of cooked rice was good in that year with about 10% increase in rice yield compared to normal year due to daily temperature range and sunshine hours.

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PB-44

Phenotypic variation of *Brachypodium* M_2 population that is chronically irradiated by gamma-ray

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Mutant analysis is one of most optimized genome-wide approach towards acquiring utile phenotypes and defining related genes. Gamma-irradiation, an acknowledged way of mutant-generating method, was applied to gain sets of mutant line in *Brachypodium distachyon. B. distachyon* is a model plant, commonly used in genus of *Gramineae* for the research of structure genomics and functional genomics. *B. distachyon* contribute to rapid and easy analysis because of its small size and quick growth. Mutant population was generated by different doses of gamma-irradiation (0, 50, 100, 150, 200, 250 Gy) in the gamma field phytotron. Distance from the source gives same irradiation duration for each plant. Plant growth parameters such as plant height, tiller number, leaf length & width, internode number & diameter, maturity and yield components (ear number biomass) were scored on M_0 plants. Plant responses to different doses of radiation are evaluated and the effective radiation dosages to generate mutant using gamma-phytotron are suggested. Chronic irradiation using gamma-phytotron is useful tool to generate mutants for genomic variations such as SNP or INDEL as well as suitable for functional study of genes in *Gramineae.*

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PB-45

Selection of genotype with high methionine content in soybean

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Soybean is an excellent source of protein for human and animal feed. But, nutritional quality is compromised by a low content of the sulfur amino acid, methionine. The purpose of this research is to screen the genotype with high methionine content. Forty genotypes including current cultivars, breeding lines, and germplasms were evaluated in the for two years. After harvest, random seeds of each genotypes were used to check methionine content by HPLC method. Methionine contents ranged from 1.9 - 5.0 (mg/g) for first year to 2.4 - 4.3 (mg/g) for second year. At first year, three genotypes [76F7-4(1), 86F8-2(1), and 70F7-1] had high content of methionine. At second year, three genotypes [Jinnon#1, daalkong, 86F8-2(1)] had high content of methionine. Genotype, 86F8-2(1) had high content of methionine at both years. Also, effect of environment on methionine content was observed. However, methionine content is a very different from genotypes.

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PB-46

Selection of strains with high sucrose content in soybean

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Sucrose, raffinose, and stachyose are major soluble sugars in soybean seeds. Sucrose is the major source of energy for fermentation and contributes to the sweetness of soybean foods. The soyfood and animal feed markets prefer soybean cultivars with high sucrose because they provide high levels of energy and better tasting food and feed. The objective of this study is to select soybean lines with high sucrose content. A total of 295 soybean genotypes including 13 current cultivars, 34 germplasms, and 248 breeding lines were planted at the field. After harvesting, sucrose contents for 295 genotypes were measured through HPLC method. Wide variation was detected among the 295 genotypes in sucrose content. The sucrose content ranged from 15.1 to 39.0 g. kg^{-1} in 13 current cultivars. The highest sucrose content was identified in "Dayangkong" (39.0 g. kg^{-1}), whereas was lowest in "Seomoktae" (15.1 g. kg^{-1}). The sucrose content ranged from 9.6 to 47.6 g. kg^{-1} in 34 germplasms. The sucrose content ranged from 0.9 to 46.4 g. kg^{-1} in 248 breeding lines.

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PB-47

se/wx Double mutant 육종 소재 개발

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찰옥수수, 단옥수수, 초당옥수수 등은 종실에 전분이 저장되는 과정에서 돌연변이가 발생하여 전분의 구성에 차이를 일으키며 이들의 유전자들 상호간에는 상위성이 존재한다. 배유의 저장전분에 관여하는 유전자 중에서 *brittle1*(*bt1*), *brittle2*(*bt2*), *shrunken1*(*sh1*), *shrunken2*(*sh2*), *sugary1*(*su1*), *sugary2*(*su2*), *sugary enhancer*(*se*)들은 전분 합성을 억제하고 *amylose extender*(*ae*), *dull*(*du*), *floury*(*fl*), *opaque2*(*o2*), *waxy*(*wx*)들은 배유 내에 전분의 구성 및 구조 등을 변경한다. 전분합성을 억제하는 유전자들은 전분의 구성을 변경하는 유전자에 상위성을 가지며 그들의 작용을 피복한다. 이들의 사실을 기초로 본 시험은 단옥수수(*se*) 유전자와 찰옥수수(*wx*) 유전자를 함께 가지는 자식계통을 만들어 육종 소재로 활용하고자 수행하였다. 2011년에 *se* 유전자를 가진 자식계통과 *wx* 유전자를 가진 자식계통을 상호 교배하여 F_1 종자를 만들고 2012년 이들을 자식(selfing)시켰다. 멘델에 유전법칙에 따라 유전자형은 *Se_Wx_*:*Sesewxwx*:*seseWx_*:*sesewxwx*가 9:3:3:1로 분리되고 표현형 분리비는 이들 유전자 간의 상위성에 따라 일반옥수수, 단옥수수, 찰옥수수가 9:4:3으로 표현된다. 이들 분리1세대(S_1) 종자를 White light transilluminator (LCF-900-470V, Ultra Violet Products)를 이용하여 찰옥수수의 표현형을 나타내는 종자를 골라 2013년 4월 중순에 파종하였다. 앞으로 이들을 자식(selfing)시켜 분리2세대 종자를 수확하고 단옥수수의 형질을 나타내는 것을 분리하면 이들은 찰옥수수(*wx*)와 단옥수수(*se*)의 유전자를 동시에 가지는 double mutant일 것으로 사료되며 분자마커 및 검정교배를 통해 유전자들을 확인할 수 있을 것으로 생각된다.

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PB-48

The genetic architecture of heterostyly and homostyly in buckwheat: the influence of modifiers genes on the stability of self-incompatibility in buckwheat

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Common buckwheat has the sporophytic self-incompatibility mechanism and that's why it has the ability to cross pollinate between two plants with different styles (thepin type and thrum type). The *S* supergene is thought to govern self-incompatibility, flower morphology and pollen size in buckwheat. Already, we have produced self-compatible buckwheat lines by an interspecific hybridization between *Fagopyrum esculentum* and *F. homotropicum* by embryo culture. The pollen size of F_1 plants produced by a cross between a pin type plant and the self-compatible plant was similar to that of the self-compatible lines and segregated together with flower morphology without exception. The pollen tubes of the self-compatible plants were compatible with styles of the pin plants but incompatible with the styles of thrum plants. But, the pollen tubes of thrum flowers were compatible with the styles of self-compatible plants. Also, the pollen tubes of pin flowers were incompatible with the styles of self-compatible plants. Already, from these results, we have reported a tentative genotype for heterostyle and homostyle flower types. Homomorphism was controlled by a single allele S^h, while the pin/thrum-complex gene was governed by a single genetic locus *S*, with two alleles, *S* and *s*, which control *Ss* (thrum-type) as well as the *ss* (pin-type), respectively. Corresponding represents the case of a single locus *S* with three alleles, S^h, *S* and *s*, and the phenotypes, homomorphic, pin and thrum. It can be characterized by relationship of dominance, $S>S^h>s$. Using the two self-fertile lines, one is considered as the long-homostyle flowers and the other is considered as the short homostyle flowers. If the short-homostyle trait had arisen by recombination in the *S* supergene, its genotype would be considered to be $GI^s\ i^p\ a/GI^s\ i^p\ a$. The pollen tubes of the short-homostylous plant should be compatible with the styles of thrum plants. Also, the pollen tubes of short-homostylous plants should be incompatible with the style of long-homostylous plants, and the reciprocal cross also should be incompatible, because the genotype of long homostyle is $gi^s\ I^p\ PA/gi^s\ I^p\ PA$. Furthermore, the flower morphology of F1plants produced by the cross between cross and short homostyle flowers should be thrum or short homostyle and only short-homostylous plants should be produced by the cross between pin and short homostyle flowers. However, the compatibility or incompatibility of short homostyle flower was not clarified. So, we need to clarify the compatibility or incompatibility of the style of short homostyle flowers for the next step.

Key words: Common buckwheat, homo style and heteromorphic flowers, self-incompatibility, modifiers gene

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PB-49

The strategy and potential utilization of temperate germplasm for the improvement of tropical germplasm: genetic diversification program is a GEM (germplasm enhancement of maize) of a resource for(*Zea mays* L.) growers in USA

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In U.S.A. maize breeding, exotic germplasm is considered as high-risk and usually introduced by backcrossing specific traits into elite lines. The U.S.A. maize germplasm base is narrow. Only a few open-pollinated varieties are well represented in current programs. Currently, the barrier in using of exotic germplasm in the U.S.A is less formidable than in the 1980s. The major reason is that U.S.A materials are now used in tropical breeding to accelerate earlier maturity and lodging resistance. These exotic materials, developed with U.S.A germplasm, are being introduced back into the U.S.A.Since1994, the ARS-led Germplasm Enhancement of Maize (GEM) project has sought to help broaden the genetic base of America's corn crop by promising exotic germplasm and crossing it with domestic lines. New hybrids derived from such crosses have provided corn researchers and the producers. These may include improved or alternative native source of resistance to insect pests such as corn rootworms and diseases like northern leaf blight. GEM's aim is to provide source of useful genetic maize diversity to help the producers to reduce risks from new or evolving insect and disease threats or changes in the environment or respond to new marketing opportunities and demand. During the 2009 growing season, the Ames (Iowa) and Raleigh (North Carolina) locations managed or coordinated evaluations on 17,200 nursery plots as well as 14,000 yield trial plots in Ames and 12,000 in Raleigh. A new "allelicdiversity" study is devoted to exploring and capturing the genetic variation represented by over 300 exotic corn races. Since 2001, GEM has released 221 new corn lines to cooperators for further development into elite commercial new hybrids. GEM has already identified about 50%-tropical, 50%-temperate families tracing primarily to tropical hybrids that are competitive with commercial checks. In North Carolina State University program, they have examined the potential of tropical inbredand hybrids for U.S.A. breeding by crossing temperate-adapted, 100%-tropical lines to U.S.A hybrids. There should be favorably unique alleles or genomic regions in temperate germplasm that can be helpful in tropical maize improvement as well as utilization of tropical lines in temperate areas.

Key words: Maize breeding, Tropical inbred, Germplasm, Incorporation.

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PB-50

TILLING analysis using *Brachypodium* mutant induced by gamma irradiation

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Brachypodium has been focused as new model plant for grass species. Like small size, small room requirement, and fast growth, *Brachypodium* shows numerous advantages as a model plant. *Brachypodium* is a typical grass at the genome level, which also exhibits an overall similarity of gene content and gene families when compared with rice (*Oryza sativa*) and sorghum (*Sorghum bicolor*) genomes. *Brachypodium* is an excellent material for structural and functional genomic studies in grass species. Targeting-Induced Local Lesions IN Genomes (TILLING) is a high-throughput technique and an approach for reverse genetics study. Moreover, it has been wildly utilized to find induced mutation. *Bradi3g45515* is orthologue of the cellulose synthase-like *HvCslF8* in barley. For TILLING library construction, 384 M_2 *Brachypodium* mutants induced by chronic-gamma irradiation were used. Single nucleotide polymorphysm (SNP) and small deletion in *Bradi3g45515* were searched through TILLING analysis. Template DNA for PCR reaction were prepared according to two dimensional pooling (eightfold) strategy. Heteroduplex DNA was digested by SURVEYOR nuclease (TRANSGENOMIC) and the DNA fragment was detected using polyacrylamide gel electrophoresis. Positive signal appeared at polyacrylamide gel from more than 4 lines and their *Bradi3g45515* region were sequenced. SNP(s) were identified in 509-2 and 677-3 mutant line. Cellulose content and/or cell wall materials content will be measured using these mutants.

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PB-51

Variation of phosphatidylcholine component in soybean seed

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Soybeans [*Glycine max* (L.) Merr] are an important source of nutrients including protein, oils and various useful secondary metabolites. Phosphatidylcholine (PC) component serves as a nerve cell membrane material and a choline supplier, so it may improve memory function in subjects suffering from memory impairment and dementia. Content of PC component in soybean seed may depend on genotype and environment. Genotype with high PC content is valuable in breeding project. Fifty-seven soybean genotypes were cultivated at first year. After harvesting, PC contents were analyzed. Content (mg/kg) of PC component was from 7.02 to 19.55. At second year, 111 genotypes including 57 genotype used at first year were cultivated. After harvesting, PC contents were analyzed. Content (mg/g) of PC component was from 0.061 to 12.324.

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PB-52

'Youhan', A new whole crop barley cultivar of hooded spike and spring early regenerative type

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'Youhan' (*Hordeum vulgare* L.), a new whole crop barley cultivar, was developed by the breeding team at the Department of Rice and Winter Cereal Crop, National Institute of Crop Science, RDA in 2012. 'Youhan' has the growth habit of III, light green and middle size leaf, hooded and lax-type spikes. The cultivar showed 107 cm of culm length, 641 spikes per m^2. Heading date of 'Youhan' was May 1, one day later than that of check cultivar 'Yuyeon' in upland, and 2 days earlier than that of check in paddy field. Maturing time was similar to check cultivar 'Yuyeon' as June 4 in upland and May 31 in paddy field. 'Youhan' also showed better winter hardiness, the resistance to lodging and disease than those of check cultivar. The average forage dry matter yield in the regional yield trial was about 12.6 and 12.0 ton ha^{-1} in upland and paddy field, respectively, which were 6%, 5% higher than that of the check. It also showed 7.3% of crude protein, 26.8% of ADF(Acid Detergent Fiber), 47.8% of NDF(Neutral Detergent Fiber), and 67.7% of TDN(Total Digestible Nutrients), including higher grade of silage quality for whole crop barley. Fall sowing cropping of 'Youhan' is recommended only in areas where average daily minimum mean temperatures in January are higher than −8°C, and it should not be cultivated in mountain areas of Korea.

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PC-01

고추 탄저병 저항성 QTL mapping을 위한 양친의 NGS re-sequencing을 통한 대량 SNP 탐색

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고추 탄저병은 국내에서 아주 피해가 심한 병 중의 하나로 본 연구팀은 십수 년 동안 탄저병 저항성에 대해 유전분석을 수행하는 동시에 저항성 품종 육성에 노력을 기울여 왔다. 이전에 사용하였던 탄저병 저항성 소재는 *Capsicum baccatum* 종의 PBC81 accession이었는데, 이와 가장 교잡화합성이 높았던 *C. annuum* 종의 SP21 계통을 모친으로 사용하여 종간 교잡을 수행하였고, 이에 대한 BC_1F_1과 BC_1F_2 분리집단에서 QTL mapping을 수행하여 두 가지의 탄저병(*Colletotrichum acutatum*과 *C. capsici*)에 대한 각각의 저항성 주동 QTL을 탐색함과 동시에 연관된 분자표지를 개발하였다. 본 연구에서는 탄저병 저항성 소재로 PBC81이 아닌 PI594137과 AR을 사용하여 NGS re-sequencing을 수행한 후 대량의 SNP를 탐색하고자 하였다. PI594137은 *C. baccatum* 종에 속하며, PBC81보다 좀 더 broad spectrum resistance를 보인다. AR은 AVRDC에서 분양 받은 재료인데, *C. chinense* Jacq. PBC932의 열성 저항성을 *C. annuum*에 도입한 계통이다. 탄저병 저항성 QTL mapping은 Golden aji(*C. baccatum*, 탄저병 이병성)와 PI594137의 F_2 분리집단과 SP211(*C. annuum*, 탄저병 이병성)과 AR의 F_2 분리집단에서 수행할 계획이어서 각각의 양친 사이(Golden aji vs. PI594137과 SP211 vs. AR)에서 SNP를 탐색하였다. NGS re-sequencing을 통해 읽혀진 염기서열 총 길이는 PI594137이 40.5Gbp, Golden aji가 12.1Gbp, AR이 12.8Gbp, SP211이 11.5Gbp였다. 이 염기서열을 사용하여 생물정보학적 분석((주)씨더스에 의뢰)을 수행하였는데, PI594137과 Golden aji 사이에서 333,816개, AR과 SP211 사이에서 1,218,595개의 SNP를 최종적으로 탐색할 수 있었다. 탐색된 SNP는 탄저병 저항성 QTL mapping 분석에 유용하게 사용될 수 있을 것이다.

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PC-02

기 개발된 식미관련 분자표지의 육종적 활용 가능성

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고품질 벼 품종육성과정에서 고식미계통을 저세대에서 선발하는데는 많은 어려움이 있다. 최근에는 식미연관 분자표지들이 개발되고 있는데, 본 시험에서는 이러한 분자표지를 자포니카간 교잡계통에 적용하여 육종적 활용 가능성을 검토고자, 자포니카 4개 조합에서 육성된 F3계통을 관행선발과 분자표지에 의한 선발(MAS)로 나누어 선발하였다. 분자표지는 G4등 SNP마커 13개를 분석하였고, 이들 분자표지에 의한 식미회귀식값을 구하여 고식미계통을 추정하여 선발하였다. 관행선발에 의한 선발비율은 38%, MAS에 의한 선발비율은 34%였다. MAS와 관행선발을 병행하여 선발하였을때는 16%의 계통이 선발되었다. 분자표지 13개로 교배모본들을 군집분석한결과, 2개 군으로 나누어지며, 1군의 교배모본들이 식미회귀식값과 밥의윤기치가 2군보다 높게 나타났다. 분자표지분석에 의한 식미회귀식값은 교배조합별 모본들 간에는 상관관계가 일정한 경향을 보이지는 않았지만, 전체 모본들에 대해서는 유의한 상관관계가 인정되었다. 본 시험에 사용된 분자표지들은 식미관련 밥의윤기치가 높은 계통을 선발할 수 있는 확률이 높을 것으로 기대된다.

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PC-03

배추에서 이원적 전사유도 시스템의 확립

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전 세계적으로 채소 종자시장의 규모가 커짐에 따라 종자 시장 보호를 위한 다양한 전략이 요구되고 있다. 최근 육종 편의성을 높이고 우수한 유전자원을 보호하기 위한 분자생물학적인 방법들이 활발하게 개발되고 있다.
이원적 전사 유도시스템(Binary trans-acitvation system)은 목적 유전자의 발현을 유도하는 프로모터가 전사촉진인자를 가지고 있는 배우체와의 교배를 통해서만 활성화 되는 형질전환 시스템이다. F_1 식물체에서 선택적으로 유전자의 발현시킬 수 있는 이 시스템은 모본과 부본의 교배를 통해 생산되는 작물에서 F_1 선택적으로 불임을 유도는 방법으로 활용되어 유전자원 보호 및 육종 편의성 증대를 위한 재료로 이용될 수 있다.
본 실험에서는 배추 작물에서 이 시스템의 이용 가능성을 신속하게 검정하기 위하여 이원적 전사촉진시스템 카세트가 각각 도입된 T_0 형질전환체를 교배하는 방법을 사용하였다. 이를 위하여 토양미생물(*Agrobacterium tumefaciens*)을 이용하여 전사유도 카세트와 활성화 카세트를 각각 형질전환하여 T_0 형질전환체를 생산한 후 유전자 도입이 확인된 T_0 형질전환체를 모부본으로 F_1을 생산하였다. 또한 모본과 부본의 교배조합 능력을 검정하기 위하여 두 카세트가 모본과 부본, 또는 부본과 모본이 되도록 조합하여 유전자 발현 및 유전적 안정성을 F_1세대에서 검정하였다.

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PC-04

A genetic linkage map of rice using F_1 DH plants with SSR markers

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Quantitative trait locus (QTL) mapping is a highly effective approach for studying genetically complex forms of plant shattering. With QTLs mapping, the shattering loci can be described. SSR marker is based on the imformation of Simple Sequence Repeat and easy to analyze using PCR and has high reproducibility. For analyzing QTLs associated with shattering, we selected 219 SSR markers from 254 SSR markers and used them for implementing Mapmaker(Ver. 3.0) and Mapchart(Ver. 2.2). Mapmaker help to calculate distances between each markers and Mapchart is a program for drawing Genetic map. This Genetic map of rice (*Oryza sativa* L.) covering 2082.4 cM with 9.5 cM between makers in the Kosambi function has been constructed using 120 F_1 DH plants from a single cross between the *indica* variety Chungchung and the *japonica* variety Nagdong.

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PC-05

A new carrot germplasm constructed by protoplast fusion

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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 have been evaluated for horticultural characteristics and we have found new genetic lines that show better phenotypes.

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PC-06

A potential link between miRNA expression and fruit development

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MicroRNAs (miRNAs) are a class of non-coding RNAs of approximately 21-nt which play important roles in regulating gene expression in plants. Although many miRNA studies have focused on a few model plants, the miRNAs and their target genes remain largely unknown in pepper, one of the most important crops cultivated worldwide. Here we employed high-throughput small RNA sequencing to extensively identify miRNAs in pepper from 10 different libraries, including leaf, stem, root, flower, and six developmental stage fruits. Based on bioinformatics pipeline, we successfully identified 29 and 35 families of conserved and novel miRNAs, respectively. We noticed that some miRNAs, whose targets were validated experimentally in this study, exhibited prominent changes in expression levels during fruit development stages. From the qRT-PCR analysis of the target mRNAs, including the SBP-transcription factor and F-box protein, we found that expression of these two target mRNAs gradually decreased in general during fruit development and was negatively correlated with the expression of their corresponding miRNAs. The validation of miRNA-directed cleavage of these target mRNAs, combined with the results of qRT-PCR analysis, likely suggests that some miRNAs in pepper may play a role in fruit development. Conclusively, our study first utilizes high-throughput sequencing to identify and characterize conserved and novel miRNAs and their targets in pepper, providing a basis for understanding the functional roles of miRNAs in pepper. This work is supported by a grant from the Next-Generation BioGreen 21 Program (No. PJ008206), Rural Development Administration, Republic of Korea.

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PC-07

A simple, rapid, and high-throughput DNA extraction method for PCR analysis from rice plants

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Polymerase chain reaction (PCR) is highly utilized for QTL analysis, positional cloning of valuable genes, and molecular breeding in crop science. Usually those experiments handle DNA samples of many genotypes (up to several thousands). However, many DNA extraction protocols require longer time using harmful chemicals such as chloroform, phenol, and liquid nitrogen. Here, we introduce a new DNA extraction method for PCR with agarose/PAGE analysis from a diversity panel of rice genotypes identified with yield enhancing traits. This protocol consists of four steps including injection of extraction buffer (20 mM Tris-HCl pH9.5, 200 mM KCl, 2 mM EDTA) into the tubes containing leaf tissues and steel balls, and crushing tissues using Geno-Grinder without liquid nitrogen, sample incubation at 65°C, and then centrifugation for removing cell debris. After centrifugation the crude extracts directly used as template DNA for PCR. Through this protocol we could complete F_1 hybridity test from approximately 2,100 plants that come from 96 cross combinations with 13 SSR markers. In addition, we tested the DNA quality by PCR amplification of high GC-rich region and large target size (-2kb). From these results our DNA extraction method produces enough DNA quality for PCR and is suitable for large scale molecular analysis from rice plants.

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PC-08

A variant block-based comparative genomics method for the detection of functional loci in soybeans

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Although much effort has been made to find agronomically important loci in the soybean plant, extensive linkage disequilibrium and genome duplication have limited efficient genome-wide linkage analyses that can identify important regulatory genes. In this respect, recombination block-based analysis of cultivated plant genomes is a potential critical step for molecular breeding and target locus screening. We propose a new three-step method of detecting recombination blocks and comparative genomics of bred cultivars. It utilizes typical reshuffling features of their genomes, which have been generated by the recombination processes of breeding ancestral genomes. To begin with, mutations were detected by comparing genomes to a reference genome. Next, sequence blocks were examined for likenesses and difference with respect to the reference genome. The boundaries between the blocks were taken as recombination sites. All recombination sites found in the cultivar set were used to split the genomes, and the resulting sequence fragments were named as core recombination blocks (CRBs). Finally, the genomes were compared at the CRB level, instead of at the sequence level. In the genomes of the five Korean soybean cultivars used, the CRB-based comparative genomics method produced long and distinct CRBs that are as large as 22.9 Mb. We also demonstrated efficiency in detecting functionally useful target loci by using indel markers, each of which represents a CRB. We further showed that the CRB method is generally applicable to both monocot and dicot crops, by analyzing publicly available genomes of 31 soybeans and 23 rice accessions.

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PC-09

An event 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 16 years or so creating a huge GMO industry. One of the notorious pests in brassica crops is diamond backmoth (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 T_0 cabbages were tested for resistance and independent GM cabbages resistant to DBM were selected. Molecular analysis was conducted to find GM cabbage to hold one copy transgene and intergenic insertion. We found two independent GM cabbages as an event and those have been self-crossed for two generation. Also we are working the development of GM cabbage with different vector that contains *bar* gene as a selection marker.

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PC-10

Analysis of chemical changes after WBPH inoculation in the rice leaf

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This experiment conducted to identify the changes of the response when white-back planthopper (WBPH, *Sogatella furcifera),* were inoculated in 10 days rice leaves after germination. We confirmed the difference between inoculated and uninfected plants by in the different time period (1day, 1 week, 2 weeks, and 3 weeks after inoculation). Breeding rice and WBPH maintained at 26～28℃ with 60 % humidity. 3 leaves plants (TN1, Cheongcheong, and Nagdong) were inoculated with 2～3 instars WBPH. Harvested rice plant samples were completely dried in dark condition and then samples were completely immersed in a solution of methanol for 3 days under darkness. Dissolving in water and then de-fatted three times with hexane. 100 ppm samples were applied to HPLC, eluting with acetonitrile and 0.1 % acetic acid by C18 (5ph column Agilant) and detected at 254 nm. We confirmed the difference of peak using LC/MS/MS (API-2000). The results showed that three weeks from the day of inoculation was increased at the molecular weight 118.1, 264.2 and 364.2.

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PC-11

Analysis of transcriptome change in high level of VitE accumulating rice mutant induced by *in vitro* mutagenesis

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VitE (tocotrienols and tocopherols) are micronutrients with antioxidant properties synthesized by photosynthetic bacteria and plants that play important roles in animal and human nutrition. A new mutant line, T1001-1, was isolated from *in vitro* mutagenized population by ionizing radiation and shown to have increased VitE contents. The total VitE content was 26% increased in the T1001-1 mutant seeds compare with cv. Dongan (wild-type). In addition, we showed that the mutant confers retarded seedling growth during the early seedling growth stage in rice. To study the molecular mechanism of VitE biosynthesis, we used the rice microarray to identify genes that are up- or down-regulated in T1001-1 mutant. In addition, we identified differentially regulated pathway using MapMan analysis, which provides deep insight into changes in transcript and metabolites. Our results enhanced the transcription of genes involved in starch and lipid metabolism in T1001-1 mutant. To identify the molecular mechanisms of the events involving transcription factors in tocopherol accumulation, we compared the expression patterns of transcription factors. The AP2-EREBP, WRKY, C2H2 transcription factor were up-regulated, whereas the MYB family was down-regulated in T1001-1 mutant. Our results demonstrate change of important transcript in high level of VitE accumulating rice mutant.

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PC-12

Arabidopsis fused kinase TWO-IN-ONE dominently inhibits male meiotic cytokinesis

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Arabidopsis Fused kinase TWO-IN-ONE (TIO) controls phragmoplast expansion and interacts with the Kinesin-12 subfamily proteins that anchor the plus ends of interdigitating microtubules (MTs) in the phragmoplast midzone. Previous analyses of loss-of-function mutants and RNA interference lines revealed that TIO positively controls both somatic and gametophytic cell cytokinesis, however, knowledge of the full spectrum of TIO functions during plant development remains incomplete. In order to further characterize TIO functions, we expressed TIO and a range of TIO variants under control of its own promoter in wild type Arabidopsis plants. We discovered that TIO-overexpressing transgenic lines produce enlarged pollen grains, arising from incomplete cytokinesis during male meiosis, and showed sporophytic abnormalities indicating polyploidy. These phenotypes arose independently in TIO variants that abolished either gametophytic function or the ability of TIO to interact with Kinesin-12 subfamily proteins. Interaction assays in yeast showed TIO to bind to AtNACK2/TETRASPORE and plants doubly homozygous for *kinesin-12a* and *kinesin-12b* knockout mutations to produce enlarged pollen grains. Our results show that TIO dominantly inhibits male meiotic cytokinesis in a dosage dependent manner that may involve direct binding to acomponent of the canonical NACK-PQR cytokinesis signaling pathway.

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PC-13

Assessment of genetic diversity among Korean sorghum (*Sorghum bicolor* (L.) Moench) resources using SSR markers

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Grain sorghum is the fifth most important crop grown in the world for either a major food crop or animal feed. It is important to identify the genetic diversity of sorghum genetic resources for cultivar development and evaluation of sorghum accessions in Korea. Two hundred thirty six SSR primer sets, which are evely distributed across the sorghum genome, were used to assess the genetic variation of 23 sorghum accessions with a US cultivar, BTx623. Results showed that SSR markers were highly polymorphic among the sorghum collections and the average alleles per locus were 3.15 with the average of 0.436 PIC (polymorphism information content) values. The sorghum accessions in this study were unequally separated and were clustered into 4 groups. The results showed that there was a sufficient SSR polymorphism with SSR primers used among Korean sorghum accessions, and the development of genetic map and marker-assisted selection for cultivated sorghum would be feasible with further studies.

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PC-14

Association analysis of vitamin E and phytosterols content in dehulled rice

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Vitamin E and phytosterols are both valuable nutrients that act as antioxidants in human bodies. Understanding the genetic basis of these traits is necessary for the improvement of nutritional quality by breeding. In this study, 119 rice accessions of diverse origin were genotyped using 232 SSR markers to identify marker-trait associations with Vitamin E and phytosterols in rice. Analysis of population structure revealed four subgroups in the population. Linkage disequilibrium (LD) patterns and distributions are of fundamental importance for genome-wide mapping associations. The mean r2 value for all intra-chromosomal loci pairs was 0.3361. LD between linked markers decreased with distance. Marker-trait associations were investigated using the unified mixed-model approach, considering both population structure (Q) and kinship (K). In total, 81 marker-trait associations were identified using 232 different SSR markers covering 12 chromosomes. The results suggest that association mapping in rice is a viable alternative to quantitative trait loci mapping. The results from this association mapping study will be the basis for improving rice nutritional quality.

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PC-15

At least nine independent natural mutations of the *DFR-A* gene are responsible for appearance of yellow onions (*Allium cepa* L.) from red progenitors

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Inactivation of the gene (*DFR-A*) coding for dihydroflavonol 4-reductase (DFR) involved in the anthocyanin biosynthesis pathway results in a yellow bulb color in onion (*Allium cepa* L.) and three inactive alleles have previously been identified in onion. Additionally, three active and six inactive *DFR-A* alleles were newly identified from extensive analyses of diverse onion germplasm. Presently, a yellow mutant containing a 171-bp deletion in the promoter region was identified and designated *DFR-A*^{PD}. Critically reduced transcription of this mutant allele and perfect co-segregation with color phenotypes in segregating populations were observed. Another yellow mutant (*DFR-A*$^{5'DEL}$) containing a 518-bp deletion covering exons 1 and 2, which played important roles in DFR function, was identified. Meanwhile, both 2-bp and 4-bp insertions in the coding region leading to creation of pre-mature stop codons were also identified and designated *DFR-A*^{GT} and *DFR-A*^{2AT}, respectively. A 1-bp substitution mutation (*DFR-A*^{K48N}) changing a positively charged lysine residue into a neutral asparagine was identified. This lysine residue, a NADPH binding site, was strictly conserved in other species. In addition, insertion of a leucine residue around substrate binding sites and catalytic triad was identified in several yellow accessions and was designated *DFR-A*^{TTA}. Phylogenetic analysis of *DFR-A* alleles showed that all inactive alleles were independently derived from four different active alleles. In addition, the close relatedness and diversity of *DFR-A* mutants implied that all these mutations might have occurred after domestication of onions and had probably been maintained by artificial selection.

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PC-16

Caffeine synthesis by exogenous methyltransferase genes in rice confers a broad-spectrum resistance against biotic stresses

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Plants have evolved a set of protecting mechanisms against pathogens, which include secondary metabolites and induced defense responses to pathogen attack. The biological role of purine alkaloids including caffeine is largely unknown. It has been proposed that caffeine confers a resistance against pathogenic bacteria and herbivores. We, in this study, tested direct effects on the growth of rice pathogenic microbes, *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) causing a bacterial leaf blight and *Magnaporthe grisea* (*M. grisea*) causing a rice blast. Cell growth of *Xoo* and *M. grisea* were significantly retarded in presence of high concentration (2mM) of caffeine. Exogenous caffeine (5mM) induced resistance of wild type rice (cv. Dongjin, susceptible to *Xoo* and *M. grisea*) against those pathogens. These results indicated that caffeine enhanced the basal resistance to infection with *Xoo.* In addition, expression of pathogenesis-related (PR) genes was tested in the caffeine treated rice to elucidate the acquired resistance by caffeine, resulted in induction of PR genes including *OsPR1a* and *OsPrb1*. We have generated a transgenic rice producing caffeine by introduction of three *N- methyltransferase* genes (*CaXMT1*, *CaMXMT1*, *CaDXMT1*) identified from coffee plant. The transgenic rice successfully expressed the three genes, synthesized caffeine up to 5ug/g and showed enhanced resistance to *Xoo*. We also observed that transcripts of PR genes such as the *OsPR1a* and *OsPrb1* encoding PR-1 type pathogenesis-related protein increased in the caffeine-producing rice. These result showed that caffeine is likely to act a powerful factor to increase level of rice defense as a natural and non-harmful metabolite.

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PC-17

Characterization and genetic mapping of the early senescence mutant in rice

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The early senescence mutant was isolated from the *japonica* rice Koshihikari through Ethyl-methane-sulfonate (EMS) mutagenesis. The early senescence phenotype was controlled by a single recessive gene, tentatively symbolized as *es-k*. Using an F_2 population derived from a cross between the mutant and Milyang23 and molecular markers, we mapped the *es-k* locus to the long arm of chromosome 7 between STS markers 147-1 and 147-2 with a physical distance of 66-kb. The symptom of early senescence appeared even before heading, while appeared during ripening in wild-type. Physiological characteristics of the *es-k* mutant before initiation of senescence was similar to the wild-type. However, after heading, *es-k* mutants started to exhibit a significant decrease in chlorophyll and soluble protein content compared to the wild-type. The wild-type leaf color appeared normal irrespective of temperature treatment, while the leaf of *es-k* mutant appeared pale-green at the low temperature and dark-green at the high temperature. During dark-induced senescence, mutant did not show significant differences compared to normal type. The results show that *es-k* is sensitive to temperature but not to light.

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PC-18

Comparison of isoflavones in soybean (*Glycine max* (L.) Merill) germplasms by different origins

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Soybean [*Glycine max* (L.) Merrill] is one of the world's most major crops as not only an important source of oil and protein, but also secondary metabolites. Intake of soybean is associated with decreased risk of cardiovascular disease and osteoporosis, as well as cancer, including breast and colon cancers. Seventy soybeans germplasms collected from 4 different countries, America (6 varieties), China (15 varieties), Japan (16 varieties), and Korea (33 varieties), were distributed by Chungbuk National University (Cheongju, Chungbuk, Korea) and cultivated in Konkuk University farm. This study investigated the isoflavones in seventy soybeans according to 4 different origins (America, China, Japan and Korea). Between 4 different origins, Korea showed highest concentrations of total isoflavones (1292.6 ± 438.6 $\mu g\ g^{-1}$) and China showed the lowest concentrations of total isoflavones (843.8 ± 365.7 $\mu g\ g^{-1}$). The total isoflavone contents in soybean of America and China ranged from 572.3 $\mu g\ g^{-1}$ to 2001.9 $\mu g\ g^{-1}$ and from 275.8 $\mu g\ g^{-1}$ to 1521.8 $\mu g\ g^{-1}$, respectively. And the isoflavone contents of Japan and Korea ranged from 473.3 $\mu g\ g^{-1}$ to 2314.6 $\mu g\ g^{-1}$ and from 419.0 $\mu g\ g^{-1}$ to 3010.7 $\mu g\ g^{-1}$, respectively. Malonylgenistin (356.9 ± 158.8 $\mu g\ g^{-1}$) was the major isoflavones among 12 isoflavones. Specially, glycoside and malonylglycosides constituted 49.2 % and 45.3 % of total isoflavones in soybeans, respectively.

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PC-19

Construction of a microsatellite database for fingerprinting analysis of soybean (*Glycine max*) Varieties in Korea

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Microsatellites are one of the most suitable markers for variety identification as it has great discrimination power for varieties with narrow genetic variation. The polymorphism level between forty microsatellite primer pairs and 148 soybean varieties was investigated through fluorescence based automatic detection system. A set of 16 primer pairs showed highly reproducible and polymorphic in these varieties. A total of 204 alleles were detected by using 16 microsatellite markers. The number of alleles per locus ranged from 6 to 28 with an average of 12.75 alleles per locus. The average polymorphism information content (PIC) was 0.86 ranging from 0.75 to 0.95. Two hundred four microsatellite loci were used to calculate Jaccard's distance coefficients for unweighted pair group method using the arithmetic averages cluster analysis. These varieties were separated into several distinctive groups corresponding to varietal types. All of the varieties were perfectively discriminated by markers genotypes. This information may be useful to compare through genetic relationship analysis between existing and candidate varieties in distinctive tests and protection of plant breeders' intellectual properties rights through variety identification.

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PC-20

Construction of composite comparative genetic maps for ten legume species

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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 108 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-21

Cross-species translation of abiotic stress-responsive genes between *Arabidopsis thaliana* and *Medicago truncatula.*

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Cross-species translation of genomic information may play a crucial role in applying biological knowledge gained from one species to other genomes. To screen and identify a broad range of abiotic stress-responsive genes, we employed a diverse array of resources, including Arabidopsis databases (http://www.arabidopsis.org), expression profiling data and previously reported literatures. As a result, a total of 1,377 genes were identified and classified into 18 different functional criteria based on biological processes of gene ontology. The gene set was translated into M. truncatula, which is a representative model system in the Fabaceae, by identifying orthologous genes between these two genomes with a combination of tBlastx and BlastP analyses. It is shown that approximately 82% of genes were estimated to be translated between the two genomes below the E-value of 10^{-30}. These orthologous loci were used to construct comparative maps by developing a user-friendly analysis platform, resulting in a total of 52 synteny blocks. Furthermore, to discover central genes by which control responses to the abiotic stresses, a combination of AraNet (http://www.functionanet.org) and the Cytoscape program was used for the gene network analysis. The analysis resulted in the identification of 240 potential key genes. We anticipate that these genes may impact molecular breeding programs by discovering trait-associated SNPs followed by marker development.

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PC-22

Detection of copy number variations using array-based comparative genomic hybridization analysis in rice responding to different types of ionizing radiations

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Copy number variations (CNVs) are considered major sources of genetic variation, and CNVs may influence phenotypic variation and gene expression. To detect CNVs, rice seeds were exposed with 100～400 Gy of gamma-ray (GA, ^{60}Co), cosmic-ray (CR) by Russia ISS, and 30 and 40 Gy of ion beam (IB, 220 Mev carbon ion). After the exposed rice seeds were cultured in 1/2 MS medium for 14 days, they were used for array-based Comparative genomic hybridization (CGH) analysis using Agilent's RICE CGH array. As a results, the highest number of CNVs (Gain 808 and Loss 24,080) were detected in the CR treatment, whereas GA100 (100 Gy of GA) was identified the least CNVs. Compared individual chromosome, the chromosome 8 and 11 were identified the highest CNVs, the chromosome 3 had the least CNVs. Most of identified CNVs existed in the range of 10～500kb. In particular, the same CNV locations among different types of ionizing radiation were observed in chromosome 12, and these CNVs contained the commonly 5 amplified genes, containing retrotransposon protein, NADH-ubiquinone oxidoreductase chain 3, heavy metal transport/detoxification protein domain containing protein, and 2 unknown proteins. Other studies were reported that Ty1 (Long Terminal Repeat-retrotransposon family 1) transcription and retrotransposition were induced by different environmental stresses such as ionizing radiation, UV-light exposure, DNA damage and nutrient starvation in *Saccharomyces cerevisiae*. Our results also show that retrotransposon protein (LOC_Os12g34016) was specifically amplified by different types of ionizing radiation.

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PC-23

Development of antifungal transgenic plant by using host induced gene silencing

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Small RNAs including microRNAs (miRNAs) and small interfering RNAs (siRNAs) play crucial roles in post-transcriptional gene silencing (PTGS) in eukaryotes. Small RNAs function cell-autonomously as well as non-cell-autonomously. It has been well characterized that pathogenic fungi secrete some effector molecules, which facilitate their infection into plants. However, it is not clear whether molecules in plant cells are able to move into fungal cells during infection. To test if small RNAs generated from plant cells can also move to fungal cells during infection, we generated transgenic Arabidopsis and rice plants ectopically expressing either double-stranded RNA interference (dsRNAi) or artificial miRNA (amiRNA) constructs targeting *GFP* gene. And then these transgenic plants were inoculated with transgenic rice blast fungus, *Magnaporthe oryzae*, expressing *GFP* transgene. Here, we showed that ectopic expression of both dsRNAi and amiRNA targeting *GFP* gene in transgenic plants significantly suppressed *GFP* expression in rice blast fungi inoculated, indicating that small RNA molecules generated in plant cells can move into infected fungal cells and efficiently degrade fungal *GFP* transcripts. Our results would provide a new small RNA-based strategy for the development of resistant crops against fungal pathogens.

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PC-24

Development of interactive comparative analysis platform for translation of genomic information across different plant species

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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-25

Development of marker-free transgenic rice expressing wheat storage protein, *Glu-Dx5*

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Development of transgenic plant increasing crop yield or disease resistance is good way to solve the world food shortage. However, the persistence of marker genes in crops leads to serious public concerns about the safety of transgenic crops. In the present study, we developed marker-free transgenic rice inserted high molecular-weight glutenin subunit (HMW-GS) gene (D*x5*) from the Korean wheat cultivar 'Jokyeong' using *Agrobacterium*-mediated co-transformation method. The Dx5's own promoter was used for protein expression. Two expression cassettes comprised of separate DNA fragments containing only the D*x5* and hygromycin resistance (*HPTII*) genes were introduced separately into *Agrobacterium tumefaciens* EHA105 strain for co-infection. Each EHA105 strain harboring D*x5* or *HPTII* was infected into rice calli at a 3: 1 ratio of EHA105 with D*x5* gene and EHA105 with *HPTII* gene expressing cassette. Then, among 270 hygromycin-resistant transformants, we obtained 27 transgenic lines inserted with both the D*x5* and *HPTII* genes into the rice genome. We reconfirmed integration of the D*x5* gene into the rice genome by Southern blot analysis. Wheat D*x5* transcripts in T_1 rice seeds were examined with semi-quantitative RT-PCR. Protein expression of the D*x5* was analyzed with Western blot using polyclonal antibody recognising x-type of glutenin subunits in T_1 seeds. It was suggested that the protein-processing system was conserved between rice and wheat. Finally, the marker-free plants containing only the D*x5* gene were successfully screened at the T_1 generation.

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PC-26

Development of new markers to genotype the functional insertion of badh2, a gene responsible for fragrance in aromatic rice

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Aroma development in rice has been reported due to the lack of function of betaine aldehyde dehydrogenase gene (badh2) on rice chromosome 8. A lot of functional markers have been designed based on the InDels, such as 7bp deletion in exon 2, 803bp deletion in exon 4 and 5, 8bp deletion in exon 7, and 3bp insertion in exon 13. Although there were a lot of functional SNPs, other InDels have not been detected by a PCR-based marker. Here we developed a simple, co-dominant, functional cleaved amplified polymorphic sequence (CAPS) marker for fragrance trait based on 1bp insertion in exon 14. The developed marker showed a high efficiency in discriminating that special aromatic rice variety, and displayed perfect co-segregation with the trait of fragrance in the F2 population. This new marker developed in the present study would be useful in molecular breeding of fragrant rice varieties.

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PC-27

Development of rice molecular breeding platform based on DMB(Dense Mutation Block) and construction of rice NAM(Nested Association Mapping) populations

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NGS costs are decreasing rapidly, and beneficial application of the technology to plant genomics seems inevitable. Trying to interpret the agriculturally important traits like yield is actively in progress all across the globe. However, the current stage of bio-informatic technology as applied to the interpretation of agricultural trait appears not yet at a level of maturity to justify widespread plant genome sequencing for user-friendly molecular breeding. It is necessary to construct dense mutation block (DMB) based molecular breeding system for selecting plants with optimal agricultural performance; as well as for identifying useful quantitative trait loci (QTLs).
Firstly, we screened and selected DMBs-specific INDEL markers obtained from SNV density profiles using 42 genome sequences of Korean cultivar and public sequences of 24 japonica rice cultivars. Secondly, we analyzed the genetic similarity between 288 Korean cultivars using 113 DMB-specific INDEL markers, which could differentiate on agarose gel by PCR. And we are going to integrate 360 INDEL markers up to 30 per each chromosome. Finally, we selected 40 founder lines considering the importance of the breeding, the purpose of use, and plant ecotype. To construct rice nested association mapping population we crossed each founder lines with the pollen of Hwayoungbyeo which was most commonly used in korean rice breeding program. F_2 seed multiplication and generation iteration are ongoing.

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PC-28

Development of sequence characterized amplified region markers for cultivar identification in persimmon

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The precise, fast, and cost-effective identification of important fruit crop cultivars is essential for practical breeding and plant breeder's rights. Traditional methods for identification of persimmon cultivars are based on the evaluation of sets of morphological characteristics. However, the identification using only morphological traits is difficult to distinguish among genetically closely related cultivars. This study was conducted to develop more reliable DNA markers for identification of the 32 persimmon cultivars in Korea and Japan. In total, 309 random amplified polymorphic DNA (RAPD) markers were identified using 40 different random primers. The 4 (OPP-08) to 14 (UBD159) polymorphic bands were detected with an average of 7.7. The resulting 57 RAPD fragments were selected, and their sequences were determined for developing sequence-characterized amplified region (SCAR) markers. As a result, 15 of 57 RAPD fragments were successfully converted to SCAR markers. A single polymorphic band of the same size as the RAPD fragments or smaller DNA fragments were amplified depending on primer combinations in the 15 SCAR markers. Among these markers, a combination of eight SCAR markers (PS225_200, PSN05_420, PSF13_523, PSN11_540, PS372_567, PS485_569, PSP08_635, and PS631_735) provided sufficient polymorphisms to identify 32 persimmon cultivars depending on number and size of amplicons. These newly developed markers will be useful as a fast and reliable tool to identify persimmon cultivars.

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PC-29

Differential gene expression in Korean soybean under heat stress condition.

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Soybean is an important crop with useful traits such as the high seed protein and oil contents. Soybean reproduction is sensitive to temperature over 35℃. To obtain database of gene expression profiles, we used soybean cultivars, sensitive and tolerant. RNA sequencing was performed to find differentially expressed genes in two Korean soybean cultivars under heat stress condition. The transcriptomic changes in each cultivar under heat stress. We found 2727 common transcripts in two soybean cultivars under heat stress, and selected 20 transcripts to heat stress response genes. The 20 selected genes were analysed using BLAST2GO and PLANEX. The genes were major factor in co-expression networks. It appears that these 20 genes were mainly attributable to heat stress.

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PC-30

Ectopic expression of mungbean ubiquitin conjugating enzyme E2 enhances resistance to osmotic stress in *Arabidopsis*

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The ubiquitin conjugating enzyme E2 (UBC E2) mediates selective ubiquitination, acting with E1 and E3 enzymes to designate specific proteins for subsequent degradation. In the present study, we characterized the function of the mung bean *VrUBC1* gene (*Vigna radiata UBC 1*). RNA gel-blot analysis showed that *VrUBC1* mRNA expression was induced by either dehydration, high salinity or by the exogenous abscisic acid (ABA), but not by low temperature or wounding. Biochemical studies of VrUBC1 recombinant protein and complementation of yeast *ubc4/5* by *VrUBC1* revealed that *VrUBC1* encodes a functional UBC E2. To understand the function of this gene in development and plant responses to osmotic stresses, we overexpressed *VrUBC1* in Arabidopsis (*Arabidopsis thaliana*). The *VrUBC1*-overexpressing plants displayed highly sensitive responses to ABA and osmotic stress during germination, enhanced ABA- or salt-induced stomatal closing, and increased drought stress tolerance. The expression levels of a number of key ABA signaling genes were increased in *VrUBC1*-overexpressing plants compared to the wild-type plants. Yeast two-hybrid and bimolecular fluorescence complementation demonstrated that VrUBC1 interacts with AtVBP1 (*A. thaliana* VrUBC1 Binding Partner 1), a C3HC4-type RING E3 ligase. Overall, these results demonstrate that *VrUBC1* plays a positive role in osmotic stress tolerance through transcriptional regulation of ABA-related genes and possibly through interaction with a novel RING E3 ligase.

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PC-31

Effects of plant growth regulator combination on embryo formation for haploid production in wheat

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Doubled haploid system is a very effective tool which has been widely applied in wheat breeding programmes. Wide-hybridization, wheat X maize cross, is used for the production of wheat doubled haploids (DH). The introduction of doubled haploid (DH) approach into breeding programs has reduced the times and population sizes required for the production of pure lines. We carried out the experiment for development on effective method of producing haploid in wheat. Emasculated spikelets of wheat were pollinated with maize pollen and cultured in the solution containing 40 g/L sucrose and 2,4-D, ABA and GA_3 24 h after pollination, and then incubated until embryo rescue. twelve to fourteen days after pollination, the embryos are excised and cultured in half-strength MS basal medium supplemented with 20 g/L sucrose and 1 ㎎/L NAA. The type of plant growth regulators was found to be most significant in production of haploid plants. The application of synthetic auxins to pollinated florets, stimulates haploid embryo development to a stage where the embryos can be rescued onto nutrient media. The percentage of embryos formed was significantly affected by 100 ㎎/L 2,4-D plus 50 ㎎/L BAP and 100 ㎎/L 2,4-D plus 50 ㎎/L GA_3. There was varied efficiency in embryo formation from 5.7 to 53%.

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PC-32

Evidence of genome duplication through analysis of EST-SSR in *Panax ginseg* C.A. Meyer

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Genome duplication is an abundance phenomenon and in plant kingdom and consequently formed paralogous region. Korean ginseng (*Panax ginseng* C.A. Meyer) has a possibility of tetraploid by comparing chromosome numbers of relative species. During development of EST-SSR markers in Korean ginseng, most of primer sets have produced multiple bands in gel electrophoresis. In this study, for identifying origin of multiple bands, five EST-SSR markers showing multi-band were selected and two bands around expected size were sequenced. Sequence comparison classified the multiple bands into individual loci. Two bands can be identified by SNP or InDel variation with number of SSR units. Sequencing result represented that paralogous loci with high similarity were existence caused by recent duplication. One clear band were amplified with newly designed locus specific primer picked from SNP variation. SNP and InDel polymorphism between paralgous loci were useful for identifying each locus. This study will provide better understanding of ginseng genome and will be helpful for development of DNA markers.

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PC-33

Expression analysis for selected transcripts during reproductive stage in several rice varieties subjected to heat stress

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Recent global warming and climate change has presented greater challenge to the global agriculture of having to cope with more severe adversaries from various abiotic stress conditions including drought, cold, and heat. As a preliminary step towards developing a heat-tolerant japonica rice variety through molecular breeding, we examined and compared expression of several genes that have been reported being expressed specifically during rice panicle development in different rice varieties after subjecting them heat stress. Although the induction of these transcripts upon heat treatment was invariably observed in all rice varieties tested, the magnitude and kinetics of the induction were found to be different among these varieties, suggesting possible functional implication of these genes in conferring heat tolerant phenotype during reproductive organ development of these plants. General protein synthesis activity as well as pollen viability incurred by the heat stress treatment were also monitored in these plants and the result showed a close correlation overall with the induction dynamic of these transcripts under heat stress. Therefore, these genes, together with the ones involved in the regulatory network for the expression of them, could serve as candidates for useful markers with which molecular breeding of heat tolerant japonica rice can be facilitated. 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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PC-34

Expression and characterization of the major ampullate silk protein gene from the spider *Araneus ventricosus* in transgenic rice.

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In this study, we generated and characterized the transgenic rice plant expressing a spider silk protein. A cDNA coding for the C-terminus of spider silk protein (*AvMaSp*) was cloned from the spider *Araneus ventricosus*. Analysis of the cDNA sequence shows that the C-terminus of *AvMaSp* consists of 165 amino acids of are petitive region and 99 amino acids of a C-terminalnon-repetitive region. The peptide motifs found in spider silk proteins, GGX and A_n, were conserved in the repetitive region of *AvDrag*. The *AvMaSp* cDNA was expressed as a 28kDa polypeptide in baculovirus-infected insect cells. To produce transgenic rice plant with high contents of glycine and alanine, the prolamin promoter-driven *AvMaSp* was introduced into rice plant via *Agrobacteriumtumefaciens*-mediated gene transformation. Because of seeds pecific prolamin promoter, expression of *AvMaSp* protein has been achieved inriceseed. The introduction and copy number of the *AvMaSp* gene in transgenic rice plants were determined by PCR and Southern blot analysis. *AvMaSp* expression in transgenic rice seeds was examined by Northern blot and Western blot analysis. Immuno fluorescence staining with the *AvMaSp*antiserum revealed that the recombinant *AvMaSp* proteins were localized in transgenic rice seeds. Furthermore, the amino acid content analysis showed that transgenic rice seeds were greatly increased in glycine and alanine as compared to controls. The present study is the first to show the expression of spider silk protein in rice seed.

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PC-35

Fine-mapping new gene conferring resistance to bacterial blight isolates (K1, K2, K3, and K3a) in Korea

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Bacterial blight (BB) of rice, caused *by Xanthomonas oryzae* pv. *oryzae* (Xoo), is a significant disease in most rice cultivation areas. The present study was performed to identify new BB R-gene conferring resistance to Korea *Xoo* isolates, derived from IR65482-7-216-1-2 and to construct a physical map of the candidate gene. An F_2 population derived from a cross between 11325 and Anda was used to determine the exact position of the nearest recombination event to the target region. The position of the R-gene was delimited by flanking markers, RM1233 and RM5766, on chromosome 11. Of the 56 markers designed in the flanking region, 20 were selected as anchor markers and the R-gene was mapped to a 295kb region on chromosome 11. To narrow down the interval spanning the R-gene, an additionally SSR marker, 20 STS markers, and CAPS marker between RM27320 and ID55.05-79 were developed using rice reference genome information. From the result the gene was defined by RM27320 and ID55.WA18-5 located in the BAC clone OSJNBa0036K13. The physical distance between these two markers is approximately 80kb. In a further study, gene expression analysis against listed candidate genes was investigated using semi-quantitative transcription PCR. These results will useful for future disease breeding as well as gene function studies regarding resistance genes.

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PC-36

Food Security and the role of plant biotechnology

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Current agriculture encounters several challenges including increase in human population, increased meat consumption from income growth, climate change, and demand for healthier foods. Together this puts a tremendous strain on limited natural resources and on an increasingly fragile ecosystem. Today, 55% percent of habitable land is used for agriculture. Two-thirds (66%) of all annual fresh water withdrawals are used for irrigation. Energy is another vital input for agriculture productivity and experts are predicting increasing global competition for supply sources.
Monsanto Company uses biotechnology, plant breeding, and agronomic solution to meet the increased food demand. In June 2008, we issued a three-fold commitment (produce more, conserve more and improve farmer's lives for agriculture to be sustainable) that we call our Commitment to Sustainable Yield.
Here, we present Monsanto pipeline to fulfill our commitment for sustainable agriculture.

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PC-37

Functional analyses of the novel salt-inducible genes from Korean halophytes

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Salinity stress severely affects plant growth and development causing crop loss worldwide. *Suaeda asparagoides* is a salt-marsh euhalophyte widely distributed in southwestern foreshore of Korea. To isolate salt tolerance genes from *S. asparagoides*, we constructed a cDNA library from leaf tissues of *S. asparagoides* that was treated with 200 mM NaCl. A total of 1,056 clones were randomly selected for EST sequencing, and 932 of them produced readable sequence. By sequence analysis, we identified 538 unigenes and registered each in National Center for Biotechnology Information. The 80 salt stress related genes were selected to study their differential expression. Reverse Transcriptase-PCR and Northern blot analysis revealed that 23 genes were differentially expressed under the high salinity stress conditions in *S. asparagoides*. They are functionally diverse including transport, signal transduction, transcription factor, metabolism and stress associated protein, and unknown function. Among them dehydrin (*SaDhn*) and RNA binding protein (*SaRBP1*) were examined for their abiotic stress tolerance in yeast (*Saccharomyces cerevisiae*). Yeast overexpressing *SaDhn* and *SaRBP1* showed enhanced tolerance to osmotic, freezing and heat shock stresses. This study provides the evidence that *SaRBP1* and *SaDhn* from *S.asparagoides* exert abiotic stress tolerance in yeast. Information of salt stress related genes from *S. asparagoides* will contribute for the accumulating genetic resources to improve osmotic tolerance in plants.

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PC-38

Functional diversification of soybean *FLOWERING LOCUS T* homologs

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FLOWERING LOCUS T (FT) is major determinant of the length of the vegetative phase in plants. To understand the role of FT homologs in flowering time control of soybean, we identified ten soybean *FT* genes and named *GmFTs*. Expression analysis of *GmFT* homologs showed that the transcripts of most FT clade genes are mainly expressed in leaves. The expression of *GmFT2a*, *GmFT2b*, *GmFT5a*, and *GmFT6* strongly induced in response to floral inductive short-day condition, but *GmFT4* and *GmFT6* exhibited opposite expression pattern. To understand the biological function of each *GmFT/TFL1* genes in flowering time control, we ectopically expressed *GmFT* cDNAs in *Arabidopsis* under the control of CaMV 35S promoter. Interestingly, while *35S:GmFT2a* and *35S:GmFT5a* transgenic plant showed extremely early flowering phenotype, overexpression of *GmFT4* delayed flowering. Furthermore we analyzed expression patterns *GmFT* genes in the leaves of Korean soybean landraces showing various flowering time. The results showed that the transcript level of two FT homologs, *GmFT2a* and *GmFT5a,* was high in early flowering landraces, but low in late flowering landraces. In contrast, *GmFT4* exhibited opposite expression pattern to those of *GmFT2a* and *GmFT5a*, suggesting that *GmFT4* may function antagonistically to *GmFT2a* and *GmFT5a* in flowering time control of soybean. These results demonstrated that soybean FT homologs have both unique and conserved functions in the photoperiodic control of flowering compared with those in *Arabidopsis*.

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PC-39

Functional implication of β-carotene hydroxylases in soybean nodulation

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β-carotene hydroxylase (BCH) has been implicated as a key enzyme conferring a stress tolerant mechanism in plants by production of carotenoids, which serve as protectants against photoinhibition and precursor of ABA biosynthesis. We previously cloned a gene encoding a novel cytosolic form of BCH (GmBCH1) from soybean (Glycine max) whose expression increased during nodulation with Bradyrhizobium japonicum. In the present work we extended our study to three GmBCHs as soybean is an allotetraploid, and examined their possible role(s) in nodule development. In situ hybridization revealed the expression of three GmBCHs (GmBCH1, GmBCH2, and GmBCH3) in the infected cells of root nodules, and their enzymatic activities were confirmed by functional assays in E. coli. Localization of GmBCHs by transfecting Arabidopsis protoplasts with GFP fusions and by EM immunogold detection in soybean nodules indicated that GmBCH2 and GmBCH3 were present in plastids while GmBCH1 appeared to be cytosolic. RNAi of the GmBCHs severely impaired nitrogen fixation as well as nodule development. Surprisingly, we failed to detect zeaxanthin, a product of GmBCH, or any other carotenoids, in nodules. We therefore examined the possibility that most of the carotenoids in nodules are converted or cleaved to other compounds. We detected the expression of some carotenoid cleavage dioxygenases (GmCCDs) in wild-type nodules, and also a reduced amount of zeaxanthin in GmCCD8-expressing E. coli, suggesting cleavage of the carotenoid. In view of these findings we propose that carotenoids such as zeaxanthin synthesized in root nodules are cleaved by GmCCDs, and we discuss the possible roles of the carotenoid cleavage products in nodulation. 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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PC-40

Functional screening of plant genes suppressed salt sensitive phenotype of calcineurin deficient mutant through yeast complementation analysis

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Understanding salt tolerance mechanisms is important for the increase of crop yields, and so, several screening approaches were developed to identify plant genes which are involved in salt tolerance of plants. Here, we transformed the *Arabidopsis* cDNA library into a salt-sensitive calcineurin (CaN)-deficient (*cnbD)* yeast mutant and isolated the colonies which can suppress salt-sensitive phenotype of *cnbD* mutant. Through this functional complementation screen, a total of 34 colonies functionally suppressed the salt-sensitive phenotype of *cnbD* yeast cells, and sequencing analysis revealed that these are 9 genes, including *CaS*, *AtSUMO1* and *AtHB-12*. Among these genes, the ectopic expression of *CaS* gene increased salt tolerance in yeast, and *CaS* transcript was up-regulated under high salinity conditions. *CaS*-antisense transgenic plants showed reduced root elongation under 100 mM NaCl treatment compared to the wild type plant, which survived under 150 mM NaCl treatment, whereas *CaS*-antisense transgenic plant leaves turned yellow under 150 mM NaCl treatment. These results indicate that the expression of *CaS* gene is important for stress tolerance in yeast and plants.

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PC-41

Generation of bacterial blight resistance rice with OsNAC58-overexpressing

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Plant specific gene family, NAC (NAM, ATAF, and CUC) transcription factors have been characterized for their roles in plant growth, development, and stress tolerance. In this study, we isolated *OsNAC58* gene from rice and analysed expression level by inoculation of bacterial leaf blight pathogen, *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). NAC transcription factor family can be divided into five groups (I-V). On the basis of phylogenetic analysis, OsNAC58 was fall into group III. 35S::OsNAC58-GFP fusion protein was localized on the nuclei. To investigate its biological function in the rice, we constructed vector for overexpression in rice, and then generated transgenic rices. Gene expression of OsNAC58-overexpressed transgenic rice lines were analyzed by northern blot. Analysis of disease resistance to pathogen *Xoo,* twelve OsNAC58-overexpressed transgenic rice lines showing high expression level of OsNAC58 were shown more resistant than wild type. These results suggest that *OsNAC58* gene may play regulatory role during pathogen infection.

PC-42

Genetic diversity and construction of core 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. However, 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*. Analysis of genetic diversity and construction of core collection is the first step to make efficient use of germplasm. Although there have been several attempts to construct core collections in *Capsicum*, most of these works were limited due to handling small number of samples, relying mainly on the characterization of morphological traits or focusing only *C. annuum* species. To expand understanding of the structure and genetic diversity of germplasm in *Capsicum*, we need to have a highly efficient genotyping tool to handle large number of samples. Toward this end, we are analyzing 3,599 germplasm accessions including other cultivated species and wild species in *Capsicum* with 48 single nucleotide polymorphism (SNP) markers.

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PC-43

Genetic diversity and population structure analysis of Amaranth collected from the Asian region using 14 SSR markers

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Amaranths (*Amaranthus* sp.) are cosmopolitan and include grain, vegetable, ornamental and weed types. Forteen simple sequence repeat (SSR) markers were used to analyze the genetic diversity of 59 accessions of cultivated amaranth from Asian countries. A total of 63 alleles were detected with an average of 4.5 per locus. The averaged values of gene diversity and polymorphism information content (PIC) were 0.35 and 0.33, respectively. Alleles per locus in accessions from South Asia was 4.35, whereas 2.93 and 3.79 alleles per locus were found in Nepal and India, respectively. The mean gene diversity in Central Asia and East Asia was 0.36 and 0.28, respectively, whereas the mean PIC values were 0.27 and 0.22, respectively. The genetic diversity and PIC of the India amaranths were higher than that of other Asian countries. The model-based structure analysis revealed the presence of three subpopulations, which was basically consistent with clustering based on genetic distance. An AMOVA analysis showed that the between-population component of genetic variance was less than 56.16% in contrast to 43.84% for the within-population component. The overall F_{ST} value was 0.56, reflecting genetic differentiation within Asian amaranths. These findings could be used for designing effective breeding programs aimed at broadening the genetic bases of commercially grown varieties.

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PC-44

Genetic diversity and structure analysis of wild soybean (*Glycine soja*) in Korea

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Undomesticated soybeans (*Glycine soja*) are an important source of genetic variation for introducing useful traits to domesticated soybeans (*Glycine max*). Although Korea is known as the origin of the soybean, a little is known about genetic diversity and structure analysis of *G.soja*. The objectives of this study were to investigate the genetic diversity and the structure analysis of wild soybeans, and to construct a core collection of *G. soja* accessions in Korea. To evaluate the genetic diversity and structure analysis of G.soja, we analyzed allelic profiles at 21 SSR loci of 1028 accessions using POWERMARKER V3.25. These markers generated a total of 581 alleles over all loci. The number of alleles per locus ranged from 21 to 40, with a mean of 28 alleles per locus and a mean gene diversity of 0.886 in this accessions tested. Polymorphic information content value ranged from 0.737 to 0.946, with an average of 0.877. Using STRUCTURE V2.34, wild soybean originated from Korea was divided into two distinct populations, largely corresponding to two geographic regions. Population 1 consisted of eight sub-groups corresponds to mountains; population 2 to entire regions in Korea. Based on theses 21 SSR markers, a core collection development was performed by POWERCORE V1.0. A *G. soja* core collection consisted of 148 accessions which were established from 1028 accessions in Korea. Most accessions of the core collection were belonged to population 2 and only four were belonged to population 1. These results of this study would provide valuable information for future breeding programs using the *G. soja* core collection.

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PC-45

Genetic diversity, population structure and association mapping for agronomic traits in waxy/flint maize inbred lines

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Our study is performed to confirm the level of genetic diversity and population structure with 80 maize inbred lines (40 waxy inbred lines and 40 flint inbred lines) and to explain the genetic basis of agronomic traits using an association mapping. The 200 SSR loci are confirmed a total of 1,610 alleles in total 80 maize inbred lines. The average number of alleles per locus was 8.05. The average GD was 0.72. The average PIC value was 0.68. The average MAF was 0.40. Population structure was revealed for K=2. Total 80 maize inbred lines were divided by groups I, II and admixed group. The 14 waxy inbred lines were assigned to group I. The 45 inbred lines include 5 waxy inbred lines and 40 flint inbred lines were contained to group II. The 21 waxy inbred lines were contained in the admixed group with lower than membership threshold 0.8. Association mapping between 200 SSR markers and 10 phenotypic traits of waxy/flint maize inbred lines were performed by Q GLM and Q+K MLM. In significant level at 0.01, 72 SSR markers were associated with 10 phenotypic traits using Q GLM. The 4 marker-trait association were detected in Q+K MLM. The results derived from this study will be used for designing efficient new maize breeding programs.

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PC-46

Genetic transformation experiments applying *MdIAA14 transcription factor* related to self thinning gene for apple

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Abscission is an important developmental process used to shed organs such as leaves, flowers and fruits. Despite the detailed characterization of growth dynamics and hormonal balance during the early steps of fruit development, the molecular aspects remain unclear. Abscission of young fruit occurs by separation of cells in anatomically distinct regions between the pedicel and junction. Differences of gene expression between central pedicel and lateral pedicel were investigated by NGS. Partial cDNAs from 15 clones from both the central pedicel and lateral pedicel were selected for nucleotide sequence determination and homology searches, and 12 clones were subsequently selected for further analysis. In preliminary series of Real Time PCR analysis, 9 genes were confirmed as showing a higher expression level in lateral pedicel than in central pedicel. Many of these genes are expressed in a central or lateral pedicel in specific manner, and the expression profiles of the representative genes were confirmed. To clarify the mechanism of *MdIAA14 transcription factor* gene underlying abscission zone development, we are investigating the expression patterns between central and lateral pedicels in different apple cultivar using real-time PCR and constructing the vector for transformation into apple.

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PC-47

Genome wide survey and 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 GmHsfs 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 *GmHsfs* 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-48

Genome-wide association studies approach and post-GWAS study in rice

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AGenome-wide association studies (GWAS) have proven a useful technique for identifying genetic loci responsible for natural variation in rice. With the fast developed next-generation sequencing technology, it is possible for people to carry out GWAS by phenotyping different traits. However, how to make full use of huge data, abandon unnecessary data, and solve the problem of data application effectively seems still an obstacle for many researchers. Taking the case of whole-genome resequencing of Korean authentic rice core set, here we present a general technological path of GWAS including: 1) a schematic view of sequencing-based GWAS in rice; 2) a user-friendly and interactive web application for GWAS in rice by the aid of experience from Arabidopsis; 3) Haplotype and association analysis of candidate genes in a certain mechanism pathway, giving 10 starch synthesis genes as example; and 4) functional validation by Trans- and Mata-Omics analysis.

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PC-49

Genome-wide identification and analysis of *Catharanthus roseus* RLK1-like kinase family in rice

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Drought and salinity are two major environmental factors determining plant productivity that due to their high magnitude of impact and wide distribution. The regulatory circuits include stress sensors, signaling pathways comprising a network of protein-protein reactions, transcription factors and promoters, and finally the output proteins or metabolites. Plant receptor-like kinases (RLKs) are transmembrane proteins family, are predicted to be major components of the signaling pathways that allow plants to respond to diverse environmental and development condition. Subfamily of *Catharanthus roseus* RLK1-like kinases (CrRLK1Ls) is a novel type of RLK, was identified in *Arabidopsis* with 17 members carrying a putative extracellular carbonhydrate-binding malectin-like domain. To study the function of CrRLK1Ls subfamily in rice which is a most widely consumed staple food, we produced the phylogenomic data with the integration of microarray-based anatomical and stress expression profiling data to the context of rice CrRLK1Ls family phylogenic tree. The expression profiling data are based on a large number of public microarray data such as 1150 Affymetrix arrays and 209 Agilent 44K arrays. Chromosomal localization of CrRLK1Ls reveals that three of 16 genes were tandem duplicated. Subsequently, we identified 7 genes that showed circadian regulation pattern and three genes of them simultaneously response to drought stress: two were down-regulated and one was up-regulated. Functional gene network development mediated by these stress responsible genes might be an useful foundation to explain the molecular mechanism of stress response mediated by this gene family.

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PC-50

Genome-wide SNP database for marker-assisted background selection in tomato

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Backcrossing is a plant breeding method most commonly used to incorporate one or a few genes into an adapted or elite variety. To facilitate MAB (marker-assisted backcrossing) in a practice breeding program, we developed a SNP database and a program for providing selected markers for background selection from genome-wide SNPs of seven tomato accessions downloaded from NCBI-SRA. We identified 425,935 SNPs among 21 parental combinations with data from seven transcriptomes and developed a SNP database. To select the optimized number of markers for background selection, we divided 12 chromosomes according to physical length and genetic length. Initially, each chromosome was equally divided into five blocks according to physical length, and three SNPs were positioned per block. Additionally, we applied the genetic distance calculated from the recombination rate because the frequency of recombination can vary greatly among chromosomal regions. When considering genetic distance, each chromosome was divided into fifteen blocks unequally and one marker composed of EXPEN-2000 was positioned per block. The program for background selection was designed to be simple and easy to use, and it is available at http://tgsol.seeders.co.kr/ index.php/tg/mab. When the user selects the parental combination, the program provides selected markers with primer information. The value of this program for tomato breeding will further increase if more accession numbers are added to the database.

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PC-51

Genotypic variation of embryo dent of rice grains

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As the market demand on functionality rice has been increasing, embryo rice in which embryo residue remains even after milling has come to comsumers' attention because rice embryo contains several functionality components. Consequently, development of rice varieties for higher rate of embryo adhesion to grains after milling has become one of the breeding objectives for quality improvement. In this study, we observed embryo dent of 49 commercial varieties and analyzed the relationship between embryo dent and grain size and shape. Embryo dent of rice grains varied 0.27 (Keunnun)~0.59 (Daerip 1) mm. Varieties Jinbu, Jinbo, Heugseol, Obong, Unkwang, and Cheongnam showed relatively deeper embryo dent, suggesting that they will be applicable in breeding for embryo rice. Embryo dent was correlated positively with grain width (r=0.53**) and grain size(r=0.34*), and negatively with grain width/length ratio (r= -0.38**). Strategies for breeding embryo rice were discussed in relation to embryo dent, grain size and shape.

Keywords: Embryo rice, Embryo dent, Grain shape, Rice

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PC-52

Haplotype analysis of major blast resistance (R) genes in rice; Pi9, Pia, and Pib

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Rice blast disease caused by the fungal pathogen *Magnaporthe oryzae* is one of the most destructive rice diseases worldwide. Resistance to rice blast pathogen mostly shows a quantitative trait controlled by several genes. A total of 13 major blast resistance (R) genes were reported in a number of Korean rice varieties using molecular markers. The Pi-ta gene, which locates near to the centromere of chromosome 12, was haplotyping using 1790 accessions including cultivated and wild varieties in previous research. However, the genetic variations of other R genes in rice still not clear. Three R genes, Pi9, Pia, and Pib on chromosome 6, 11 and 2 respectively, were resequenced among 84 accessions of rice core set. Different types of halotype among the 84 accessions were detected. Some new SNPs and InDels found in exon part of R genes were expected to result into amino acid changes following analysis of the genetic code variations, and the germplam in this rice core set which are resistance to blast were explored. We are expecting to develop the new functional markers and incorporate of resistance genes into existing rice cultivars and finally these apply outcomes in breeding rice resistance to blast diseases.

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PC-53

Haplotype analysis of preharvest sprouting related genes in rice; *OsVP*1, *Osaba1*, *Alpha-amylase3D* and *OsGA20ox1*

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Preharvest sprouting (PHS) not only causes reduction of grain yield, but also affects the quality of grains, resulting into significant economic losses. PHS is governed by multiple genes. Little is known about the large genetic variation of preharvest sprouting in rice. In the present study, genetic variations of four PHS genes, OsVP1, Osaba1, Alpha-amylase3D and OsGA20ox1 were studied by using whole-genome resequencing data of 84 accessions of rice core set. A total of haplotype groups; 27, 29, 6 and 14, for OsVP1, Osaba1, Alpha-amylase3D and OsGA20ox1, respectively, were detected among the 84 accessions. Some new SNPs and InDels were found in exon part of PHS related genes were expected to result in amino acid changes following analysis of the genetic code variations, and the germplasm or varieties which are resistant to preharvest sprouting were explored. Based on this step, phenotyping for PHS is ongoing, and the association mapping of PHS will be conducted by using SNPs resulted from the haplotyping data. The present results will be ultimately useful to the molecular breeding for the development of PHS resistant rice cultivars.

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PC-54

Haplotype variation in *Sub1*, *Sub2* and *Ramy3D* contributing to the anaerobic germination (AG) in rice

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Direct seeding of rice is increasingly being practiced in both rainfed and irrigated areas because of labor shortage for transplanting and opportunities for crop intensification. However, slow seed germination and delayed seedling establishment will become a major problem for rice production in flood-prone lowland areas as sowing method shifts from transplanting to direct seeding. Identification of anoxia-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, genetic structure variability of three AG related genes, Sub1 (Sub1A, Sub1B, Sub1C), Sub2 (OsGAPPH) and Ramy3D were examined by using whole-genome resequencing data of 84 accessions of rice core set. Some new SNPs and InDels found in exon part of anaerobic germination related genes in the present study would be useful in developing markers to identify the submergence resistant varieties in the future molecular breeding.

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PC-55

Identification and interacting partners of OsGRP in rice during gamma-ray irradiation

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Rice is one of the most important food crops in the world, and has been used as model monocots for genetic studies, because of its relatively small genome size. We have previously reported the different functions of several RING (Really Interesting New Gene) proteins to respond the various abiotic stresses. In order to study a regulation of RING proteins in rice under ionizing irradiation such as gamma ray (GA), we have identified the expression patterns of these genes by RT-PCR. We found Gamma-ray induced RING finger protein (OsGRP) gene, which were associated with cytosol by subcellular localization analysis. *in vitro* ubiquitination assay revealed that OsGRP possess E3 ligase activity. Also, we demonstrate that C196A point mutation in the RING finger domain of OsGRP can have a critical effect to the breakdown of structural integrity in RING constructs. To identify the interaction partners for OsGRP in protein-protein interactions, we found the seven genes interacted with OsGRP by Yeast Two Hybrid method. To examine the GA-influence of interaction partners by RT-PCR, two genes were specifically down-regulated in rice during GA treatment. These interaction partners were identified the reliable interactions and subcellular localizations via BiFC method. Interestingly, five genes associated with plastid, while two down-regulated genes associated with cytosol and plastid. These results of OsGRP based on genetic approach might provide a clue to understanding the GA responsive mechanism in rice.

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PC-56

Identification of promoters conferring anther specific expression in rice

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A male gametophyte, or pollen develops in the anther, and its development plays an important male reproductive process in flowering plants. A properly designed transgene construct can help to tailor transgene expression in plants by altering the expression strength, timing, and location. In this process, the promoter plays a pivotal role in controlling transgene expression. In this research, the promoter regions of rice anther/pollen-specific genes, named as OsMSP1 to OsMSP11,were selected from the microarray data sets covering 4 developmental stage of male gametophyte and then used for the construction of vector by Gateway cloning method and transformed into rice and Arabidopsis. All 11 promoters in rice and 9 in Arabidopsis were displayed as anther/pollen-specific/preferential genes by GUS assay and RT-PCR analysis. Three out of 11 promoters showed consistent results with published data. In this study, we demonstrated on eight new anther/pollen-specific or -preferential promoters (OsMSP1, OsMSP2, OsMSP3, OsMSP4, OsMSP5, OsMSP6, OsMSP8, and OsMSP9, which have not been reported before. Although the expression pattern of different genes active in pollen grains is diverse and complex, these experimental results would be helpful to understand the molecular mechanism of regulatory elements in rice microspore/pollen-specific genes.

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PC-57

Identification of rice genes associated with cosmic-ray response via co-expression gene network analysis

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In order to better understand the biological systems that are affected in response to cosmic ray, we conducted the weighted gene co-expression network analysis with module detection method. By using the Pearson's correlation coefficient value, we were evaluated the complex gene-gene functional interactions between 680 CR-response probes from integrated microarray datasets, which included large-scale transcriptional profiling of 918 microarray samples. These probes were divided into 6 distinct modules that contained 20 enriched function such as oxidoreductase activity, response to stimulus and stress, and hydrolase activity. Especially, module 1 and 2 commonly showed the enriched annotation categories such as oxidoreductase activity, including the enriched cis-regulatory elements known as ROS specific regulator. These results suggest in module1 and 2 that ROS-mediated irradiation response pathway are affected by CR. We found the 243 irradiation-dependent probes, which were exhibited the similarities of differentially expressed patterns in various irradiation microarray datasets, and RT-PCR for confirmations of several irradiation-dependent genes were exhibited the similar expressed patterns in rice by CR, gamma ray and Ion beam treatments. Interestingly, these genes were differentially expressed by non-gravity. Moreover, we were identified the co-regulations between several irradiation-dependent genes and functional interacted genes in the CR-responsive network by various GA treatments such as different conditions of dose and treatment time. These results of network-based analysis might provide a clue to understanding the complex biological system of CR.

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PC-58

Increased accumulation of anthocyanins in transgenic alfalfa by overexpressing the sweetpotato R2R3-Type *IbMYB1a* Gene

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Alfalfa (*Medicago sativa* L.) is one of the most important forage crops in the world and it's has been known as the best feed materials for dairy cows and other high valued animals. The new uses of alfalfa are being explored as bio-energy, food, medical and biochemical uses. R2R3-type MYB transcription factors play important roles in transcriptional regulation of anthocyanin biosynthesis. The R2R3-type IbMYB1 is known to be a key regulator of anthocyanin biosynthesis in the storage roots of sweetpotato. We previously showed that the expression of IbMYB1a led to anthocyanin pigmentation in tobacco and Arabidopsis. In this study, we generated transgenic alfalfa plants expressing the IbMYB1a gene under the control of CaMV 35S promoter. Overexpression of IbMYBa in transgenic alfalfa produced strong anthocyanin pigmentation in seedlings and generated a deep purple color in leaves, stems, roots, and even in seeds. High performance liquid chromatography (HPLC) analysis revealed that IbMYB1a expression led to the production of cyanidin as a major core molecule of anthocyanidins in alfalfa, as occurs in the purple leaves of sweetpotato (cv.Sinzami). We also examined expression of several structural genes in the anthocyanin biosynthetic pathway in alfalfa by RT-PCR analysis. In this presentation, we will further present molecular and biochemical characterization in IbMYB1a-overexpression lines. This result shows that the IbMYB1a transcription factor is sufficient to induce anthocyanin accumulation in the forage legume alfalfa plants.

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PC-59

Investigation of genetic factors related to quantitative control of capsiate biosynthesis

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Capsinoids which were found recently in non-pungent pepper show the same biological effects as capsaicinoid including anticancer and anti-obesity. A precursor of capsaicinoids, vanillyl alcohol, is known to be produced by mutations in the p-aminotransferase (*pAMT*) gene. In the previous study, we showed that capsinoid production is also controlled by the capsaicin synthase (*CS*) gene. However correlation between the *CS* gene expression and capsinoids contents has not been fully understood. This study was conducted to elucidate correlation between the expression level of *CS* gene and capsinoids contents. Through germplasm screening, we identified one *C. chinese* pepper cultivar, SNU11-001, which contained capsinoids as much as *C. annuum* 'CH-19 Sweet'. SNU11-001 was crossed with five Capsicum cultivars (ECW, Takanotsume, Yuwolcho, Habanero and Jolokia) containing different levels of capsaicin, 'ECW' is non-pungent pepper line, and 'Takanotsume' and 'Yuwolcho' have mild pungency, and 'Habanero' and 'Jolokia' is known to be included in the most pungent pepper lines. When we analyzed the expression of *CS* and *pAMT* genes using the six Capsicum cultivars, the expression levels of *CS* were higher in pungent Capsicum cultivars. To test whether the expression levels of *CS* also control capsinoids contents, we will analyze several F2 populations derived from crosses between SNU11-001 and Capsicum cultivars containing different levels of capsaicin.

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PC-60

Isolation and characterization of novel gene and microsocopic analysis of a rice mutant with narrow leaves.

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Rice is not only a model plant of monocots but also one of the most important crops all over the world. Despite the importance of leaf shape for achieving effective plant architecture for photosynthesis, little is known about the genetic mechanisms that determine leaf morphological characteristics. Explanation of the genetic basis of the control of leaf shape could be of use in the manipulation of crop traits, leading to increased crop production. Many mutants related to leaf morphology have been identified and classified according to their function in determining leaf morphology. search on the genetics of leaf development has used mutagensis to create loss-of-function mutations that change leaf shape. To understand the molecular mechanism of leaf morphogenesis, we identified a rice mutant gene, which was characterized by a phenotype of narrow leaves. While the mutation resulted in reduced leaf width, no significant morphological changes at the cellular level in leaves were observed, except in bulliform cells. The gene locus guess that it encodes a adenosine kinase, which displays sequence homology with ribokinase pfkB like superfamily. To test function of gene, we cloned gene which have 1140 nucleotides and 379 amino acids. This gene was transcribed in various tissues and was mainly expressed in panicles and leaves. NAL7, NAL1 and SLL1 were found to be downregulated, whereas OsAGO7 and NRL1 were upregulated in the mutant. These findings suggested that there might be a functional association between these genes in regulating leaf development.
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PC-61

Light induced expression of key genes for glycoalkaloid accumulation in potato

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Glycoalkaloids are a family of toxic secondary metabolites present in the plants of solanaceae family, which serve for plant defense. Two major glycoalkaloids present in plants are a-solanine and a-chaconine. The upper safe limit of glycoalkaloids for human consumption is 20mg/KG FW and its excess may cause severe health disorders. Light is the major factor known to increase the glycoalkaloid content in post harvest potato tuber. Glycoalkaloid pathway is not completely understood. Hence, identification and characterization of SGA biosynthetic genes and the genetic factors that control their expression levels assumes significance. Present investigation was focused on the study of expression pattern of key genes in steroidal glycoalkaloidal pathway under various light qualities in potato (Solanum tuberosum L). Two potato cultivars Atlantic and Haryeong which accumulates low and high glycoalkaloids respectively were used to check the levels of gene expression under various light qualities viz., red, blue, white, green, yellow, purple, UV light and in dark at different time intervals. Expression of three genes viz., SGT1, SGT2 and SGT3 which are directly involved and four other genes, HMG1, SQS1, SMT1 and SMT2 in the pathway envisaged to be indirectly involved in the glycoalkaloid formation was quantified by RT PCR. Varietal variation in the expression among the genes was observed in different light qualities. White, red and green light compared to other light qualities majorly contributed for the increased expression of genes for glycoalkaloid accumulation at different time intervals. Importantly, there is no significant transcript accumulation of these genes in dark condition. However, more efforts would be extended for further understanding of glycoalkaloid accumulation under light.

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PC-62

Localization and expression analysis of U-box-containing E3 ligase *OsUPS result from* phosphate deficiency in rice

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Rice is a staple food crop in the world. A number of agronomically important traits including enhancement of stress tolerance, quality improvement, and nutrition value increases have been introduced to rice. In this study, an *Oryza sativa* cDNA containing a U-box motif was cloned; its deduced amino acid sequence was compared to that of other U-box genes and indicated that encodes a U-box-containing E3 ligase. E3 ligases are structurally divided into three groups. We isolated the *OsUPS* gene from rice (*Oryza sativa*). The *OsUPS* protein has domain which is a single ~70-amino acid region of the protein and GKL domain containing conserved Glycine, Lysine/ Araginine residues and leucine-rich feature. A full-length expression of *OsUPS* was up-regulated in the rice plant and in cell culture in the absence of phosphate. To express the *OsUPS* cDNA, it was inserted into the pGEX-2T vector. And the gene was expressed in *E.coli* strain BL21 (DE3). Induced after 3h of IPTG treatment and was isolated by affinity chromatography. Using the GUS reporter genes regulated by the *OsUPS* promoter, we have carried out the analysis of transcriptional and spatial regulation of gene expression. To investigate the function of these genes, the CaMV 35S promoter-driven these genes were introduced into *Arabidopsis* and rice via *Agrobacterium tumefaciens*-mediated gene transformation. We found that full-length expression of OsUPS was up-regulated in both rice plants and cell culture in the absence of inorganic phosphate (Pi). A self-ubiquitination assay indicated that the bacterially expressed *OsUPS* protein had E3 ligase activity, and subcellular localization results showed that *OsUPS* was located in the chloroplast. These results support the notion that *OsUPS* plays an important role in the Pi signaling pathway through the ubiquitin-26S proteasome system.

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PC-63

Mass propagation in cassava(*Manihot esculenta* Crantz) by somatic embryogenesis

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Somatic embryogenesis is a process where a plant or embryo is derived from a single somatic cell or group of somatic cells. Application of this process include: clonal propagation of genetically uniform plant material; elimination of viruses; provision if source tissue for genetic transformation; generation of whole plants from single cells called protoplasts; development of synthetic seed technology. In this study tissue culture was carried out for mass propagation of cassava using somatic embryogenesis. For tissue culture set up, we used cassava variety ("Rayong5", "Rayong7", "Rayong9", "Rayong11") developed in Rayong Field Crop Research Center(RYFCRC). In induction of callus step, the callus formed from each cassava variety. "Rayong 7" showed the highest induction rate of 95%, while induction rate of other varies were ranged from 50% to 85%. In the case of weight of callus "Rayong5" has the highest weight. Results in the present study would be useful in mass propagation of cassava by somatic embryogenesis.

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PC-64

Molecular characterization of a gibberllin-sensitive dawaf mutant gene in rice.

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The utilization of several genetic resources is the most important for developing rice, such as high yield seeds or various stresses. 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 (*Oryzasativa Gibberellin Acid Sensitive Dwarf*). *OsGASD* gene encodes a 344 amino acid polypeptide and nohomology proteins in GeneBank. The *osgasd* mutnat was sensitive to exogenous gibberellic acid (GA) level. We performed experiment to controlled expression the *OsGASD* gene, its role in plant development, a quantitative analysis of endogenous GA content and sensitivity to GA. The *osgasd* mutant includes smaller amount of active GAs than wild-type. *osgasd* mutant plant of GA biosynthesis pathway causes GA deficiency and dwarf plants ,and endogenous GA suppliance can restore the wildtype phenotype in this mutant. The result indicated that *OsGASD* gene regulated the elongation of shoot, stem and plant height. The increased expression of *OsGASD* gene dramatically induces expression of the factors associated with GA biosynthesis such as CPS, KO, KAO, GA20ox and GA2ox, whereas *os*gasd mutant suppression of the factors associated with GA biosynthesis, loading to dwarf phenotypes. That applied GA_3 at the plant development stage to survey the response of *OsGASD* gene to GA_3. We suggest that *OsGASD gene* is related to factors of GA biosynthesis pathway regulating rice internodes development.

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PC-65

Molecular characterization of stress memory using Arabidopsis suspension-cultured cell lines adapted to high salt

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In order to adapt to various environmental stresses, plants have employed diverse regulatory mechanisms of gene expression. Epigenetic changes, such as DNA methylation and histone modifications play an important role in gene expression regulation under stress condition. It has been known that some of epigenetic modifications are stably inherited after mitotic and meiotic cell divisions, which is known as stress memory. To understand molecular mechanisms underlying stress memory mediated by epigenetic modifications, we developed Arabidopsis suspension-cultured cell lines adapted to high salt by stepwise increases in the NaCl concentration up to 120 mM. Adapted cell line to 120 mM NaCl, named A120, exhibited enhanced salt tolerance compared to unadapted control cells (A0). Moreover, the salt tolerance of A120 cell line was stably maintained even in the absence of added NaCl, indicating that the salt tolerance of A120 cell line was memorized even after the stress is relieved. By using salt adapted and stress memorized cell lines, we intend to analyze the changes of DNA methylation, histone modification, transcriptome, and proteome to understand molecular mechanisms underlying stress adaptation as well as stress memory in plants.

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PC-66

Molecular characterization of two *OsSHSP* (*Oryza sativa* Small Heat Shock Protein) genes in rice

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We used a microarray dataset that is deposited in the public database to evaluate plant responses to heat stress and selected two genes, *OsSHSP1* (Os03g16030) and *OsSHSP2* (Os01g04380), that are highly expressed under heat stress in rice. *OsSHSP1* and *OsSHSP2* gene transcripts were highly induced in response to salt and drought. In addition, *OsSHSP1* and *OsSHSP2* gene transcripts were induced under ABA and SA. Subcellular localization of proteins of *35S::OsSHSP1* were associated with the cytosol, whereas those of and *35S::OsSHSP2* were associated with the cytosol and nucleus. Heterogeneous overexpression of both genes exhibited higher germination rates than those of wild-type plants under the salt treatment, but not under heat or drought stress. The network of both genes harboring 9 sHSPs as well as at least 13 other chaperone genes might support the idea of a role for sHSPs in the chaperone network. Our findings might provide clues to shed light on the molecular functions of *OsSHSP1* and *OsSHSP2* in response to abiotic stresses, especially heat stress.

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PC-67

Molecular characterization of type III DnaJ-like proteins from *Arabidopsis*

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Arabidopsis *atDjC53* and *atDjC32* gene DnaJ-like protein homologous to DnaJ-like protein was characterized for the functional analysis of DnaJ-like protein. It was shown that *atDjC53* and *atDjC32* RNA expression is induced by heat shock stress and atDjC53- and atDjC32-GFP was targeted to the nucleus of protoplasts. The *atDjC53* and *atDjC32* promoter (1 kb) was isolated and fused to the GUS reporter gene to investigate gene regulation of *atDjC53* and *atDjC32* specific to heat shock stress or to developmental organ in the transgenic lines. RNAi and overexpression construct was employed to generate *atDjC53* and *atDjC32* knock-out plants for the study of their function. Molecular function of *atDjC53* and *atDjC32* is discussed in relation to heat shock and also developmental stages in Arabidopsis.

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PC-68

Morphological and genetic characterization of Off-type rice plants collected from farm fields in Korea

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Off-type rice plants occurring in farm fields cause yield loss due to competition with cultivated rice, in addition to hindering field management and harvest work. This study aimed to observe the agronomic characteristics and trace the origins of off-type rice plants using molecular markers. A total of 116 rice accessions, comprising 35 off-type plants collected from Korean farm fields, 19 Korean commercial cultivars, 12 Korean land races, and 50 weedy rice collections, were phenotyped and genotyped using selected SSR and Subspecies Specific (SS)-STS markers. The results showed that the plant height, culm length, and leaf length of off-type rice plants were larger than those of cultivated rice, which is the typical phenotype of weedy rice. However, off-type plants were highly sterile, as opposed to weedy rice, which were highly fertile. Genotype analysis with SSR and SS-STS markers revealed that off-type rice plants were heterozygous at most of the tested marker loci, suggesting that the off-type rice plants may have originated from natural outcrossing. The genotypes of off-type rice plants were closely related to both weedy and cultivated rice, and the phylogenetic analysis revealed that the relationship of the clustered group of offtype rice plants is intermediate between Indica type weedy rice and Japonica type commercial varieties. These results suggested that off-type rice plants collected in Korean farm fields might have originated from natural outcrossing between Indica type weedy rice and the cultivated Japonica type commercial varieties. 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.

Keywords: Marker, Off-type rice, Weed rice

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PC-69

Multiplex marker를 활용한 고추 병저항성 마커 스크리닝

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60년대와 70년대의 녹색혁명은 전통적인 육종의 성과이지만, 최근의 육종기술은 유용유전자의 유전자형을 활용한 분자표지 마커를 활용하고 있다. 목적 형질을 갖고 있는 계통을 선발하는 MAS(Marker assisted selection) 마커는 많은 육종가들에 의해 활용되고 있지만, 유전자의 SNP(Single nucleotide polymorphism)을 활용한 MAB(Marker assisted backcross) 마커는 거의 활용되고 있지 않다. SNP 마커는 단 하나의 염기서열의 차이를 구별할 수 있어, 유전적으로 매우 가까운 계통들도 구분할 수 있으며, 자동화 분석이 가능하다는 점에서 활용도가 높다. 솔젠트(주)에서는 내수 및 종자수출에서 차지하는 산업적 비중이 가장 큰 채소작물 중 고추 병저항성 관련 유전자를 활용한 multiplex 고추병 진단 제품을 개발했다. 이 제품에는 오이모자이크바이러스(CMV), 담배 etch 바이러스(TEV), 토마토반점위조바이러스(TSWV), 토바모바이러스(TMV), 세균성점무늬병(BS), Chilli venial mottle virus(ChiVMV), 고추역병에 관련된 저항성 유전자의 SNP을 활용해 개발했으며, 본 제품을 활용해 고추 육종가들이 쉽고 간편하게 육종 소재에 적용해 신품종 육종에 도움을 줄 것으로 기대한다.

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PC-70

Overexpression of *OsCHI* genes increases tolerance to drought, and salt stress in transgenic arabidopsis

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Low temperature is a major factor restrict to growth and limiting productivity of rice crops. We used a cDNA microarray approach to monitor the expression profile of rice (*Oryza sativa*) under chilling stress and identified 20 chilling inducible genes in previously study. Ten such genes encoding bHLH, metal transporter and, zinc finger protein with unknown functions showed a significant change in expression under various abiotic stresses. Among them, *OsCHI1* (Os07g15460), *OsCHI2* (Os02g43660), and *OsCHI3* (Os01g61160), were selected for further study. They have structural features such as metal-binding signature sequences in their protein sequences, and OsCHI genes were expressed in root of rice seedling and induced in chilling and salt or drought. Expression of *OsCHI1*, *OsCHI3* and *OsCHI2* were targeted to membrane and ER when transiently expressed in tobacco cell, respectively. The Arabidopsis (*Arabidopsis thaliana*) transgenic plants overexpressing showed increased tolerance to salt and drought stress in the seed germination and root elongation than that of wild type. This comprehensive study provides insight into the biological function of OsCHIs, which may be useful in understanding how rice plants adapt to unfavorable environmental conditions.

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PC-71

Phenotypic characterization and genetic mapping of an open-hull sterile mutant in rice.

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Rice hulls remain closed throughout the ripening period to maintain internal humidity of the grains. An Open-hull sterile mutant was induced by N-methyl-N-nitrosourea(MNU) treatment on Sinsunchalbyeo rice, a japonica type. This mutant showed open hulls even in the ripening stages and fully mature grains. In addition, several altered characteristics were observed, including of narrowed palea, decreased grain size, partial pollen sterility and erect panicle. Microscopic analysis showed that the palea was positioned slightly inside the lemma, and the size of palea decreased in the mutant. Genetic analysis of F2 and F3 segregation populations derived from the cross between the Open-hull sterile mutant (Oryza sativa ssp. japonica) and Milyang23 (O. sativa ssp. indica) indicated that the Open-hull trait was controlled by a single recessive allele. The fine-mapping with STS (sequence tagged site) markers revealed that the mutant gene was located on the short arm of chromosome 3. We were able to narrow it down until 30.6Kb where three candidate genes were found. 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.

Keywords: Rice, Open-hull sterile, Mutant, Mapping

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PC-72

Proteolytic processing and chloroplast trafficking inhibition of the chloroplast targeting RING E3 ligase, OsCTR1, involved in ABA-mediated drought tolerance mechanism

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Plant growth under water-deficit conditions adversely affects many key processes. Efforts to understand drought stress-related defense mechanisms have revealed a host of plant genes using molecular approaches in rice. Here, we report the novel finding that OsCTR1 E3 ligase regulates both chloroplast-localized chloroplast protein 12 (OsCP12) and ribosomal protein 1 (OsRP1) in protein levels and subcellular localization. The results of a yeast-two hybrid assay, bimolecular fluorescence complementation assay, ubiquitination assay, subcellular localization, and a protein degradation assay support the hypothesis that OsCTR1 functions in trafficking inhibition and proteolysis of OsCP12 and OsRP1 via the ubiquitin 26S proteasome pathway. Heterogeneous overexpression of OsCTR1 in *Arabidopsis* showed ABA-hypersensitive phenotype in seed germination, seedling growth, and stomatal closure. The transgenic plants also exhibited improvement of water-deficit tolerance with an accumulation of hydrogen peroxide production. These results demonstrate that the OsCTR1 E3 ligase might positively regulate the cellular functions of OsCP12 and RP1 related to photosynthesis under drought stress conditions in rice.

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PC-73

QTL analyses for 8 agronomic characters in two populations of rice derived from wide compatibility line

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Hybrid sterility is a critical barrier of inter-subspecific crosses in rice. However, hybrid sterility can be overcome by wide compatibility variety. The HWC-line of rice had slender grain shape, tall culm length, wide compatibility with both indica and japonica cultivars. For QTL analysis of HWC-line, two F2 populations were derived from the crosses between the HWC-line and each of two Korean variety, Dasan (Korean Tongil-type cultivar) and Hwacheong (temperate japonica cultivar). In the cross between HWC-line/Dasan (HD), 93 STS markers and 13 SSR markers were mapped on 12 chromosomes. In the population from HWC-line/Hwacheong (HH) cross, 28 STS markers, 29 SSR markers and 1 FNP marker were mapped on 11 chromosomes. Eight agronomic characters were evaluated for QTL analysis in two F2 populations and parents. The F2 population from HD cross revealed 21 M-QTLs and 3 E-QTL for culm length, spikelet per panicle, spikelet fertility, grain length, grain width, grain shape and 100 grains weight. 8 QTLs of culm length, grain length, grain width and grain shape were newly detected in this study. In the F2 population from HH cross, 17 M-QTLs were detected for culm length, panicle length, spikelet fertility, grain length, grain width, grain shape and 100 grains weight. 6 QTLs of culm length, grain length, grain width and grain shape were newly found in this study. These QTLs will be able to provide basic information on putative functional genes related with agronomic characters and promote breeding new rice cultivar. HWC-line could be used as bridge for inter-subspecies crosses and in hybrid breeding. 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.

Keywords: rice, QTL analysis, wide compatibility

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PC-74

Qualitative and quantitative analysis of high-molecular-weight subunits in Korean wheat cultivars by two-dimensional electrophoresis

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To evaluate expression level of HMW-GS protein qualitatively and quantitatively, we separated glutenin fractions and conducted two-dimensional electrophoresis (2DE) in 32 cultivars of Korean wheat for the use of as the basis of wheat breeding. The average spot number of HMW-GS in all Korean wheat cultivars was 11.78 which included 1.31, 5.53 and 4.94 to *Glu-A1*, *Glu-B1* and *Glu-D1* loci, respectively. Cultivars harboring 1, 2* subunits had many spots more than ones harboring null allele in *Glu-A1* loci because there is no difference of spots between *Glu-B1* and *Glu-D1* loci. In total spot number of HMW-GS, the highest one was Jokyung as 18 and Dahong the lowest as 7. When the Korean wheat cultivars were compared with the Chinese spring in the average relative expression level, Korean one's were lower as 0.44. Especially, Gobun was the highest as 1.11 and Eunpa was the lowest as 0.24. Also we investigated phylogenetic relationship based on both frequency of HMW-GS spots and quantification value of each spot to all HMW-GS spots. As a result, Korean the varieties of Korean wheat could be classified into six groups.

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PC-75

Qualitative and quantitative analysis of low-molecular-weight subunits in Korean wheat cultivars by two-dimensional electrophoresis

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LMW-GSs represent approximately 1/3 of the total wheat gluten fraction, which have not been widely studied, even though they are important in the context of wheat end-use quality. In this study, we report on the qualitative and quantitative analysis of LMW-GS in korean wheat cultivars by 2DE in 32 cultivars of Korean wheat for the use of the basis of wheat breeding. We firstly identified spots corresponding each of *Glu-3* alleles. The 2DE results for each cultivar will be used as reference map or protein marker discriminating wheat cultivars, wheat and rice, imported and Korean flour. Unexpectedly, five LMW-GS spots were found to be expressed at a common position in hexaploid wheat cultivars, and these spots might play something in glutenin biosynthesis. Total spot numbers were expressed variously between 20 and 10, and average spot number was shown 17.12. The average number of spots in *Glu-A3*, *Glu-B3* and *Glu-D3* were 3.0, 4.56 and 2.96 respectively. When the Korean wheat cultivars were compared with the Chinese spring (1.0) in the average relative expression level, Korean one's were lower as 0.67. Especially, Gobun was the highest as 1.32 and Baekjoong was the lowest as 0.24. Also we investigated phylogenetic relationship based on frequency of HMW-GS spots and quantification value of each spot to all LMW-GS spots. As a result, the varieties of Korean wheat could be classified into five groups.

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PC-76

Requirement of THO2 for miRNA biogenesis and alternative splicing in *Arabidopsis*

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The THO/TREX complex mediates the transport of nascent mRNAs from the nucleus towards the cytoplasm in animals, and it has a role in small RNA-dependent processes in plants. Here we describe five mutant alleles of *Arabidopsis thaliana THO2*, whichencodes a core subunit of the plant THO/TREX complex. *tho2* mutants present strong developmental defects resembling those in plants compromised in microRNA (miRNA) activity. In agreement, not only the levels of siRNAs, but also of mature miRNAs were reduced in *tho2* mutants. As a consequence miRNA target mRNAs accumulated to higher levels than in wild type. Yeast two hybrid experiments showed that THO2 does not seem to interact with any of the known miRNA biogenesis components, implying a more indirect role of THOs in small RNA biogenesis. We also detected alterations in the splicing pattern of genes encoding Serine/Arginine-rich proteins in *tho2* mutants, suggesting a previously unappreciated role of the THO/TREX complex in alternative splicing.

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PC-77

RNA-seq profiling of transcriptomic changes in gibberellic acid-treated seeded grapevine during inflorescence development

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Gibberellic acid (GA) is a well-characterized plant hormone, which plays a critical role in various plant growth and development. including stem elongation, floral indcution and seed development. GA is known to cause enlargement of ripening fruits and, especially in grapevines, GA shows a unique function: the induction of seedlessness in seeded grape varieties. However, despite extensive previous studies about GA, there has been no clear verification of the mechanism that induces seedlessness in grapes. To understand how GA treatment results in artificial parthenocarpy of seeded grapes at molecular levels, we analyzed transcriptional changes in seeded grapes with and without GA application in various inflorescence developmental stages using RNA-seq. At 14 days before flowering (DBF), seeded grapes were treated with 100 ppm GA and clusters were collected at three developmental stages: 7 DBF, full bloom, and 5 days after flowering (DAF). Of a total of 28,974 genes that were mapped to grape genome reference sequences, 7,013 and 9,064 genes were up- and down-regulated, respectively, in the GA-treated grape as compared to the non-GA-treated control at 7 DBF, full bloom, and 5 DAF. Clustering analysis revealed that these genes could be grouped into 9 clusters with different expression patterns. We also carried out functional annotation based on gene ontology categories. There were significant differences in the expression of the GA and auxin-related gene families. These findings expand our understanding of the complex molecular and cellular mechanisms of GA-induced parthenocarpy of grapes and provide a foundation for future studies on seed development in grapevines.

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PC-78

Role of mRNA 3'-end processing in phosphate starvation responsive root architecture changes

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Phosphorus is one of the macronutrients essential for plant growth and development, as well as crop productivity. Many soils around the world are deficient in phosphate (Pi) that plants can utilize. To cope with the stress of Pi starvation, plants have evolved many adaptive strategies, such as changes of root architecture and enhanced Pi acquisition form soil. To understand molecular mechanism underlying Pi starvation stress signaling, we characterized the activation-tagged mutant showing altered responses to Pi deficiency compared to wild type Arabidopsis and named *hsp3* (hypersensitive to Pi starvation3). *hsp3* mutant exhibits enhanced phosphate transporter activity, resulting in higher Pi content than wild type. However, in root architectural change under Pi starvation, *hsp3* shows hyposensitive responses than wild type, such as longer primary root elongation, lower lateral root density. Histochemical analysis using *hsp3* mutant expressing auxin-responsive *DR5::GUS* reporter gene, indicated that auxin allocation from primary to lateral roots under Pi starvation is aborted in *hsp3* mutant. Molecular genetic analysis of *hsp3* mutant revealed that the mutant phenotype is caused by the lesion in ENHANCED SILENCING PHENOTYPE4 (*ESP4*) gene whose function is proposed in mRNA 3' end processing. Here, we propose that mRNA processing plays a crucial role in Pi homeostasis in Arabidopsis.

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PC-79

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-80

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

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Drought tolerance is the ability of a plant to live, grow, and reproduce properly with limited water supply or under periodic conditions of water deficit. However, the climate changes and worldwide water shortages would result in the loss of applied water to irrigated land, increasing soil water deficit. To control the situation, we have carried out the international joint research project for the aim of developing that drought tolerance common wheat and durum wheat in Korea and Tunisia. Total 79 (41 common wheat, 39 durum wheat) Tunisian lines and 33 Korean wheat cultivars were incorporated in this study. Drought stress was applied for 25 days of stopping irrigation from the 3-leaf stage followed by re-watering for restoration in greenhouse. We selected top 13 (5 Korean line, 8 Tunisian line) tolerant lines and 11 (5 Korean, 6 Tunisian) susceptible lines based on growth parameter analysis. Primers (Operon primers and wheat *Dreb1* gene) that have been known to be related drought resistance were applied to explain selected population. The correlation between PCR-based length polymorphism of selected lines and their resistance were evaluated. The obtained primer information will aid selection for drought tolerance durum as well as hexaploid common wheat.
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PC-81

Selection of microsatellite marker set for the analysis of genetic integrity and relationship in rice genetic resources

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Rice genetic resources are composed of various species and ecotypes, and each accession reveals different genetic and phenotypic characters. For the managenment of diverse rice genetic resources, seed integrity is important factor in that the individuals of one accession in self-pollinating crop might be homogeneous. To elevate the management efficiency of rice germplasm contrary to the phenotypic distinction, we focused on applicable microsatellite markers because this markers are widly used for genetic evaluation in diverse genetic resources with a character of high reproducibility and polymorphism. In this regard, we selected microsatellite markers based on genotypes; diversity set including 150 accessions using 249 SSR markers. As SSR loci with high PIC(polymorphism information content) values usually revealed multi bands in one accession, proper genotyping were difficult in these loci. Therefor, we checked the band clarity in addition to PIC values and chose 12 and 6 SSR markers finally. All accessions of rice diversity set were distinguished with the first marker set comprising 12 SSR markers, and only 3 combinations of tested accessions(0.03%, 3/11,175) showed same genotype with second marker set comprising 6 SSR markers. The tested 142 Korean bred varieties revealed 0.19%(19/10,011 combinations) and 0.69%(69/10,011 combinations) genotypic identity using first and second marker set, respectively. These newly selected markers might be useful for the analysis of genetic homogeneity and relationship in rice genetic resources.

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PC-82

Shotgun proteomics approach to identify candidate proteins related with drought stress in *Brassica rapa ssp. pekinensis* (inbred line 'Chiifu')

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As the drought is getting worse, Lot of studies related to drought stress in plant have been conducted. Recently whole genome sequencing of *Brassica rapa ssp* which is important vegetable crop to East Asians has been completed to enable Omic research. It is known that the drought damages occur in the early stage of plant development. Here, we performed shotgun proteomics analysis of *B. rapa* to observe the morphological characters, monitor the expression patterns of the identified proteins during drought stress, and detect the proteins related to drought stress. The three week old B. rapa grown in density of single plant in a single pot were used. Drought stress were treated as that a single plant in soil was removed from the pot and the plant with soil was exposed to air and light without watering. Leaves were immediately harvested before drought treatment, 24hr after drought treatment, and 48hr after drought treatment. The protein expression patterns were monitored by a quantitative shotgun proteomics analysis. Extracted proteins were separated in 1D-SDS-PAGE then the gel sliced into seven pieces. Chopped gels were ingel-digested. Peptides were assigned to mass spectrometry (Q-Exactive). The ms/ms spectra were analyzed through Proteome Discoverer. By combining all of the identified proteins in the seven sliced gel samples, total *B. rapa* proteome reference map was completed. Protein expression patterns were investigated by comparing the quantity of protein. With shotgun proteomic approach, we evaluated the changes in the quantity and finally discovered the candidate proteins related with drought stress.

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PC-83

Sound wave stimulates plant gene response and improve salt stress tolerance of rice seedlings

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We investigated whether sound could alter gene expression in plants. Using a sound-treated subtractive library, a set of sound-responsive genes in plants was demonstrated through mRNA expression analyses. Of them, the *rbcS* and *ald* genes, which are light responsive, up-regulated their expression with sound treatment in both light and in dark conditions. This suggested that sound could be used as a gene regulator instead of light. When we analyzed *ald* gene expression using various single wavelengths, a significant increase in mRNA levels was found at 125 or 250 Hz but decreased at 50 Hz, indicating that the gene responded to sound in a wavelength-specific manner. To determine whether the *ald* promoter respond to sound, we generated transgenic rice plants harboring the chimeric gene consisting of a 1,506-bp promoter fragment of the *ald* gene fused to *Escherichia coli GUS* reporter gene. Analyses of mRNA expressison level of three independent transgenic lines sound-treated with 50 or 250 Hz for 4 h showed that the *Gus* gene expression in all three transgenic lines was up regulated by 250 Hz, but down regulated by 50 Hz. These results correlated with sound responsive mRNA expression pattern observed for the *ald* gene in rice plants, indicating that the 1,506-bp *ald* promoter confers sound-responsiveness on a reporter gene in transgenic rice plants. We also 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, Fv/Fm), 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.

PC-84

SSR 분자마커를 이용한 튀김옥수수 자식계통들에 대한 집단구조 및 association 분석

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본 연구는 강원도 농업기술원 옥수수연구소에서 튀김옥수수 품종개발을 위하여 육성한 79개의 자식계통들에 대하여 SSR 분자마커를 이용하여 집단구조 및 association mapping 분석을 실시하였다. 집단구조 분석결과, 79개의 튀김옥수수 자식계통들은 groups I, II, III, IV, admixed group으로 구분되었다. 4개의 옥수수 자식계통은 group I에 포함되었고, Group II는 총 17개의 자식계통들이 포함되었다. 그리고 6개의 자식계통들은 Group III에 포함되었으며, 22개의 자식계통들은 Group IV에 포함되었다. 그리고 admixed group에는 30개 옥수수 자식계통들로 구성되었다. 더욱이 본 연구에서는 튀김옥수수 자식계통들에서 분석에 이용된 50개 SSR 마커와 13개의 질적, 양적 형질과의 연관성을 분석하기 위해서 association mapping 분석을 실시하였으며, false positive associations을 최소화하기 위해서 population structure(Q), kinship(K) 값을 이용하여 Q GLM과 Q+K MLM 분석을 실시하였다. 0.05의 유의수준에서, Q GLM 분석을 이용하여 총 44개의 SSR 마커가 12개의 형질과 association을 보였고, Q+K MLM을 이용하여 분석하였을 때, 총 25개의 SSR 마커가 12개의 형질과 association을 보였다. 그리고 0.01의 유의수준에서, Q GLM 분석에서는 34개의 SSR 마커와 12개 형질의 association을 확인하였다. 더욱이 Q+K MLM을 이용하여 8개의 SSR 마커는 5개의 형질과 association을 확인하였다. 본 연구에서 79개의 튀김옥수수 자식계통들에 대한 집단구조 및 association mapping 분석의 결과는 앞으로 강원도농업기술원 옥수수연구소에서 튀김옥수수 품종개발을 위한 계통 육성 및 교배조합 구성 등에 유용한 정보를 제공할 것으로 기대한다.

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PC-85

Studies of R2R3-OsMYB4P transcription factor in phosphate starvation signaling

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The molecular processing of upstream regulation of Pi response genes during Pi starvation remains inadequately understood. Several transcription factor have been studied that appear to regulate subsets of the responses to Pi stress either positively or negatively. MYB genes are responsive to one or multiple type of hormone and stress treatments. In this study, cDNA of the MYB have been cloned, and we generated Rice overexpressing plants for characterization of these genes. OsMYB gene function focused on phosphate conditions with rice and Arabidopsis transgenic plants. We selected 30 - T1 transgenic lines from T0 transgenic rices. those are shown high Pi content. The Pi contents of shoots part of transgenic plants were shown 10~20% increased Pi contents than WT, whereas roots have 30% increased Pi contents. As a result, OsMYB genes affect Pi uptake in plants. To investigate interactions between MYB proteins and phosphate signaling related genes. We demonstrate that Myb-binding sites (MBSs) exist in putative promoter of OsPT transporter by analysis of bioinformatics, and its bind specific MYB transcription factor. OsMYB expression is induced by low Pi and Pi deficiency, and its overexpression plants are shown morphological phenotype in Pi stress.

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PC-86

Study on the polymorphism between brown midrib mutants and Hwangkeumchal using SSR markers toward sorghum QTL mapping on excessive water stress

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Excessive water stress can cause severe damage to sorghum and results in significant yield reduction. The aim of this study is to identify quantitative trait loci (QTL) for excessive water stress in sorghum. As a first step, two out of 21 *bmr* mutants were selected for their superior agronomic performance and Chlorophyll a fluorescence OJIP transient, and were crossed with an elite Korean cultivar, Hwangkeumchal, to construct mapping populations. One hundred ten out of 236 SSR primers showed polymorphism between two parens, which cover ten chromosomes of sorghum from different published SSR linkage maps of sorghum. Development of recombinant inbred lines from the crosses '25M2-0698 x Hwangkeumchal' and '25M2-0404 x Hwangkeumchal' are in progress using the single seed descendent method for generation acceleration.

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PC-87

TaGAST genes accelerates spike development by repressing negative growth regulator in wheat

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Over the last decades, increasing natural disasters and climate change are considered as the major environmental problems facing the globe. Numerous studies have been indicated it would cause huge losses on agriculture, especially in the grain productivity. Therefore, several alternatives are suggested for boosting up productivity of wheat as one of the main human food crop. One of important strategy is proper management of inflorescence development and DELLA proteins have been elucidated to play pivotal roles in growth of many plant organs. In this study, putative negative regulator of DELLA protein, *GAST* (Gibberellic acids stimulated transcript) have been isolated to identify their role in the developing spike of wheat. Four genes were isolated from its gene family and designated as *TaGAST1, 2, 3, 4*. Genomic structure was analyzed to demonstrate chromosomal localization of *TaGAST* genes and evolutionary relationships were also verified with GAST genes in other plant species. RT-PCR was conducted to detect transcriptional changes of *TaGAST* genes on external phytohormone. Each of *TaGAST* genes showed considerable changes in transcription level after GA, ABA, PAC treatment, respectively. Through Yeast two-hybrid assay, one protein for *TaGAST1*, and four proteins for *TaGAST2* was isolated as putative interactive proteins in wheat spikes just before and after emergence. Acknowledgement: This work was supported by a grant from the Next-Generation BioGreen 21 Program (Plant Molecular Breeding Center No.{J008031012013}, Rural Development Administration, Republic of Korea.

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PC-88

The effect of chronical irradiation on *Brachypodium distachyon* as a model plant for lignocellulosic bioethanol production

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Brachypodium distachyon is a temperate annual grass that has a short life cycle, a small genome size, self fertility, and a small physical stature. The relationship with major cereal crop including wheat, *Brachypodium* is considered as a monocot model plant. Recently, the cell wall composition of *Brachypodium* is reported closely related with maize and *Miscanthus giganteus*. Therefore, *Brachypodium* is emrging as a powerful model plant for bioethanol production. Here, *Brachypodium* was chronically irradiated with the doses of 50 Gy, 100 Gy, 150 Gy, 200Gy, 250 Gy, and 300 Gy. Plant height and fresh weight were observed dosage-dependent negative effect. However, tiller number and internode diameter were found to be increased their value as compared to control. The cell wall yield showed a decreased tendency with dosage-dependent negative, but cell wall yield of 50 Gy and 200 Gy were detected higher than control. The lignin content of irradiated *Brachypodium* stem was reduced with dosage incease The ratios of lignin content to control were 97.6% (50 Gy), 91.9 (100 Gy), 87.3% (150 Gy), 89.4% (200 Gy), 81.6% (250 Gy), 85.2% (300 Gy). SEM image analysis demonstrated that cell size of 300 Gy plant was decreased by 45% of control. RT-PCR was performed to analyze transcript accumulation of lignin pathway related genes with irradiated *Brachypodium* stem. CCR, PAL, C4H, and 4CL were detected at least 2 times higher expression than control at 150 Gy, 200 Gy, 250 Gy. The preteatment and enzyme hydrolysis will be discussed for bioethanol production.

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PC-89

The rice RING E3 ligase *OsHIR1* participates in positive regulation of arsenic and cadmium uptake

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The metalloid arsenic (As) and the hevy metal cadmium (Cd) are ubiquitously found at low concentrations in the earth, while high concentrations of the both elements in soil and crop are severe dangerous to human health. We have tried to retrieve RING E3 ligase gene, which is believed to regulate substrate proteins in As or Cd uptake via ubiquitin 26S proteasome pathway, related to inhibit metal ion transport system. A total of 48 rice RING E3 ligases were randomly selected and then conducted semi-quantitative RT-PCR for their expression patterns as exposed to As and Cd treatments. We discovered one gene, *Oryza sativa* heavy metal induced RING E3 ligase 1 (OsHIR1) that was significantly up-regulated against both treatments. A total of 31 positive interaction clones with OsHIR1 were screened depending on their strong α-galactosidase activity via yeast-two hybrid screen. Bimolecular fluorescence complementation analysis evidenced that the OsHIR1 protein was clearly interacted with each of six partner protein including aquaporin tonoplast intrinsic protein 4;1 (OsTIP4;1) in the plasma membrane. Protein degradation assay showed that OsHIR1 strongly degraded the protein level of OsTIP4;1 via ubiquitin 26S proteasome system. Heterogeneous overexpression of OsHIR1 in *Arabidopsis* showed As- and Cd-insensitive phenotype. In addition, the transgenic plant showed low levels of As and Cd accumulation than the control plant in leaf and root. Here, we report the novel finding that OsHIR1 E3 ligase positively regulates OsTIP4;1 related to As and Cd uptake.

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PC-90

Towards high-throughput marker-assisted backcrossing system

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The main objectives of IRRI's variety development should meet the needs of customers/farmers from diverse rice sectors in each target region. The dynamic market change asks rapid variety development with highly valued QTLs/genes. Molecular breeding implemented through the efficient crossing, high throughput genotyping and rapid generation advancement will provide packages to breeders to develop new varieties quickly and more economically. The more efficient and cost-effective marker-assisted backcrossing service will provide the more opportunity for the success in molecular breeding platform. To make MABC system more successful, the development of molecular marker system for the high-throughput SNP genotyping is must. Currently Genotyping Service Lab (GSL) of IRRI provides high-throughput SNP genotyping service using BeadXpress and Fluidigm system. Meanwhile, the linked SNP markers for the specific traits are being developed. For abiotic stress tolerances, the markers for submergence, drought, heat, anaerobic germination, salinity, and phosphorus deficiency for Fluidigm system are being developed and tested in variety diversity panel and segregating populations. In MABC, due to the high number of crossings, the labor- and space-saving crossing system is being developed. As a result of an integrated MABC platform will speed up the development of pre-breeding line which are containing single or multiple QTLs/genes.

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PC-91

Transcriptome profiling of Shindongjin and Sugary mutant at grain-filling stages using RNA-Seq

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Rice (Oryza sativa) is an excellent model monocot with a known genome sequence for studying developmental seeds. In the study, the seeds of 10th day after flowering (DAF) were conducted RNA-Seq of the variety Shindongjin and Sugary mutant using RNA-seq technique. Approximately 202 and 214 million high-quality paired-end reads (101-bp in size) were generated in Shindongjin and Sugary mutant, respectively. Comprehensive analysis on the transcript levels of genes which encode starch-synthesis enzymes is fundamental for the assessment of the function of each enzyme and the regulatory mechanism of starch biosynthesis in seeds. Quantitative real-time PCR was also used to validate the expression profiles of 28 rice genes encoding six classes of enzymes, viz., ADPglucose pyrophosphorylase (AGPase), starch synthase, starch branching enzyme, starch debranching enzyme, starch phosphorylase, and disproportionating enzyme at different developmental grain- filling stages (DAF 1-14) between Shindongjin and Sugary mutant. The results showed that the expression of most of starch synthesis genes were up-regulated except the cytosolic AGPase small subunit2b (AGPS2b), which sharply decreased at grain-filling stages in Sugary mutant. These results will expand our understanding of the complex molecular and cellular events in rice grain-filling stages and provide a fundamental understanding of future studies on developmental endosperm in rice and other cereal crops.

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PC-92

Transgenic expression of *MsHSP23* confers enhanced tolerance to multiple abiotic stresses in forage crops

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Abiotic stress is the major limiting factor of forage crops growth and yields. The objective of this work was to study the stress tolerance and regeneration capability of transgenic forage crops carrying a MsHSP23 gene, encoding a alfalfa mitochondrial sHSP protein. The expression of the MsHSP23 gene was confirmed in bacteria, recombinant mHSP23 conferred tolerance to salinity and arsenic stress. Furthermore, mHSP23 was cloned in a plant expressing vector and transformed into forage crops such as alfalfa, tall fescue and bent grass. The transgenic plants exhibited enhanced tolerance to salinity and arsenic stress conditions. In comparison to wild type plants, transgenic plants were exhibited significantly lower electrolyte leakage. Moreover, the transgenic plants had superior germination rates when placed on medium containing arsenic. Taken together, these overexpression results imply that mHSP23 plays an important role in salinity and arsenic stress tolerance in transgenic forage crops. This approach could be useful to develop stress-tolerant plants including forage crops. (This study was supported by a grant from the Next-Generation BioGreen 21 Program (No.PJ0081392013), Rural Development Administration)

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PC-93

Whole transcriptome analysis 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, thin interaction represent a key entry point for reduced nitrogen into the biosphere, and as a consequence this symbiosis in important in both natural and agricultural systems. Symbiotic development of nodule organ in 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 elucidate 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 identify genes and proteins that link Nod factor perception to cellular and physiological responses we are taking a discovery-based strategy on large-scale transcriptome profiling using RNA sequencing 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.

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PD-01

웅성불임 제초제저항성 들잔디 (JG21-MS)의 임성 특성 평가

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현재 작물에서 분자육종학의 기술은 1994년 미국 칼젠사 (Calgene)가 개발한 숙성과정 중 물러지지 않는 토마토, Flavr Savr라는 상품을 개발하여 일반인들에게도 많이 알려지며 관심을 갖는 분야가 되었다. 그 이후 미국 몬산토 (Monsanto)에서 개발한 Round up ready 라는 제초제저항성 콩을 상품으로 발표하면서 외래형질을 도입한 작물에 대한 위해성의 논란이 야기되어, 이를 잠재울 만한 기술 및 방법들이 연구되어 지고 있다.
형질전환 작물, 다시 말하여 유전자변형생물 (GMO, genetically modified organism) 의 위해성의 논란의 하나인 외래유전자가 도입된 형질전환체의 유전자가 야생으로 이동하여 의도치 않은 유전자의 이동에 관한 것이다. 본 연구는 선행 연구에서 제초제저항성을 보이는 잔디, JG21（Jeju Green 21）에 방사선 (감마선)을 처리하여 얻은 여러 형질 중 화분에 이상을 보이는 (웅성불임) 라인을 선발하여 JG21-MS (Male Sterility)라고 명명된 웅성불임 들잔디 화분을 조사하였다. 그 결과 외형적으로 Wild-type, JG21의 정상적인 둥근 공 모양의 형태를 보이는 것에 비해 JG21-MS의 화분은 찌그러진 형태가 관찰되었고, 화분의 활성을 확인할 수 있는 Alexander 염색법을 이용하여 관찰한 결과 JG21-MS의 화분은 대부분 염색되지 않았다. 또한 실제적으로 JG21-MS의 화분이 발아하여 화분관 신장의 가능성을 확인하기 위해 화분관 발아배지를 이용하여 화분관을 유도하였으나 Wild-type, JG21에서 비슷한 수준으로 화분관이 신장된 것에 비해 JG21-MS는 0%의 화분관 신장를 보였다. JG21-MS의 화분은 Wild-type의 화분에 비해 양이 상당히 적고 모양 또한 찌그러진 형태로 유전자 이동의 가능성이 있는 화분관 신장을 보이지 않아 GM 작물의 안정성의 문제를 해소할 수 있을 것이다. 하지만 들잔디의 생육 환경에 따라 화분의 활성에 영향을 미칠 수 있어 이를 명확히 할 필요가 있으며, 한 해의 결과로 속단하기 이르므로 본 연구의 결과를 바탕으로 다음 세대 및 다양한 조건에서의 추가 연구가 필요하다.

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PD-02

유전자변형 벼 안전성평가의 분자생물학적 평가 가이드라인 개발

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국제적으로 유전자변형작물(Genetically Modified, GM)의 개발 및 재배는 지속적으로 증가하고 있으며, 국내에도 GM작물 개발에 대한 많은 연구가 진행되고 있다. 국내에서 GM작물은 상업적 재배 및 이용에 앞서 이들이 인체 및 환경에 미칠 수 있는 잠재적인 위해성을 과학적으로 검토하고 안전성을 입증하도록 법으로 규정하고 있으며, 특히 안전성평가항목에 대해서는 LMO법 통합고시 별표 10-1에 규정되어 있다. GM작물의 안전성평가는 사안별(case-by-case) 평가 원칙에 따라 도입 형질 및 작물별로 평가방법을 달리하여야 하지만 통합고시에서는 모든 유전자변형생물체를 대상으로 기술되어 있어 개발자가 특정 작물의 안전성평가를 수행하여 심사서를 작성하는데 여러 가지 어려움을 제기하고 있는 실정이다. 따라서 본 연구에서는 국내 주요 식량작물이자 가장 많은 유전자변형 연구가 진행되고 있는 벼에 대한 안전성평가 연구 가이드를 제시하여 국내외 개발자 및 안전성평가 연구자를 지원하고자 하였다. 본 발표에서는 안전성평가에 대한 통합고시 별표 10-1의 항목 중 분자생물학적 평가를 대상으로 하였다.

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PD-03

제초제저항성 웅성불임 GM들잔디(JG21-MS)의 분자생물학적 특성 평가

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잔디는 비식용, 비사료용 작물이지만 스포츠공간용, 조경용, 지피용 등으로 전 세계적으로 가장 보편적으로 활용되는 작물이며, 경제성이 매우 높은 작물이다. 본 연구의 목적은 상업적 재배를 위해 개발된 제초제저항성 웅성불임 GM들잔디의 분자생물학적 특성을 평가하는 것이다. JG21-MS 웅성불임계통은 최초 선발된 해로부터 현재까지 6여 년 동안 제초제저항성 뿐만 아니라 웅성불임성을 잘 유지 하고 있다. *BAR* 유전자카세트와 T-DNA 삽입점에서 좌,우 1kb 정도의 주변 염기서열의 동등성 및 *BAR*유전자 발현의 동등성에서 모본과 차이를 보이지 않았다. T-DNA 삽입특성을 조사한 실험에서, T-DNA 오른쪽 경계(RB)의 삽입은 특이한 DNA단편의 첨가 또는 소실 없이 들잔디 DNA와 연결되어 있지만, hygromycin 저항성 유전자(*HPH*)가 위치한 왼쪽 경계(LB)의 삽입은 삽입과정에서 *HPH* 유전자의 4/5 정도가 소실되어 유전자의 기능을 상실하였다. 또한 왼쪽 끝 부분과 연결된 들잔디 DNA 쪽도 620bp가 소실되었다. T-DNA는 Ty1-copia retrotransposon-like 유전자 영역에 삽입 된 것으로 확인되었다. Ty1-copia retrotransposon은 식물 종에 조금 차이가 있지만 전체게놈의 10~50% 정도를 차지하는 것으로 알려져 있다. 또한 retrotransposon-like 유전자는 식물고유기능의 유전자가 아니므로 본 이벤트에서 T-DNA는 비유전자영역에 삽입된 것으로 간주할 수 있을 것으로 사료된다. 결국, JG21과 JG21-MS는 *HPH* 유전자가 소실되어 기능을 상실하였으므로 목표 유전자인 *BAR* 만 single copy로 존재하는 것으로 확인되었다. 차세대바이오그린21 GM작물실용화사업단에서 지원하는 GM작물 이벤트의 분자생물학적 특성의 최소기준은 단일복제수(single copy), 항생제마커 없이 목표유전자 도입(target gene only), 비유전자내 삽입을 장려하고 있고, JG21와 JG21-MS 계통의 제초제저항성 들잔디는 이러한 기본조건을 만족시키고 있는 것으로 평가되었다.

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PD-04

An event of gm peppers tolerant to pepper mottle virus (PepMoV)

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In Korea, CMV (cucumber mosaic virus) is the most frequently occurring virus with a single infection rate of 45%. However, a total occurrence of CMV by co-infection, either couple or multiple, with BBWV (broad bean wilt virus), PepMoV (pepper mottle virus) and PMMoV (pepper mild mottle virus) covers over 90% in the field cultivation of pepper. The PepMoV is transmitted by several aphid species, and it has been considered the most frequently detected potyvirus when it co-infects with CMV or PMMoV. Since F_1 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 T_1 peppers were tested for resistance to the PepMoV, and T_1 peppers tolerant of PepMoV were selected. After consequent self-crossing up to T_4 generation, highly tolerant peppers to PepMoV were selected. So far, BC_3F_1 lines have been selected by back-crossing with 4 elite lines through a breeding program. The horticultural differences of the GM line comparing to inbred lines were investigated and no statistical significance between GM and non-GM lines was found. Based on molecular analysis, One of GM lines, 10-2, contained the transgene in the non-coding region indicating that this line would be a GM event.

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PD-05

Assessment of microbial community in paddy soils cultivated with *Bt* and Nakdong rice

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The cultivation of genetically modified (GM) crops has increased due to their economic and agronomic advantages. Before commercialization of GM crops, however, we must assess the potential risks of GM crops on human health and environment. The aim of this study was to investigate the possible impact of *Bt* rice on the soil microbial community. Microbial communities were isolated from the rhizosphere soil cultivated with *Bt* rice and Nakdong, parental cultivar and were subjected to be analyzed using both culture-dependent and molecular methods. The total counts of bacteria, fungi, and actinomycetes in the rhizosphere of transgenic and conventional rice were not significantly different. Denaturing gradient gel electrophoresis (DGGE) analysis of PCR-amplified 16S rRNA genes revealed that the bacterial community structures during cultural periods were very similar each other. Analysis of dominant isolates in the rhizosphere cultivated with *Bt* and Nakdong rice showed that the dominant isolates from the soil of *Bt* rice and Nakdong belonged to the *Proteobacteria*, *Cloroflexi*, *Actinobacteria*, *Firmicutes*, and *Acidobacteria*.
These results indicate that the *Bt* rice has no significant impact on the soil microbial communities during cultivation period. Further study remains to be investigated whether the residue of *Bt* rice effect on the soil environment.

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PD-06

Characterization of tissue-specific gene promoters in various organs and stage of reproductive development in rice

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Rice is an important model species and one of the most staple crops of the world. The use of rice appropriate promoters suitable for a specific target transgene is important for the control of spatial and temporal transgene expression. To isolate rice tissue-specific promoters, we exploited the potential of whole genome microarrays in 17 stages: callus, germinating seed, leaf, root, the size of the panicles before heading (1, 3, 5, 8, 10, 15, 20, and 22 cm), and the number of days after pollination (1, 3, 5, 11, 21 DAP) using a 300 K Rice Genome Microarray, covering 31,439 genes of the rice. Eight candidate genes for tissue-specific expression were selected in various organs and stage of reproductive development in rice: Histone H4 for constitutive expression, Dehydrin DHN1 for callus-specific expression, germinating seed-specific hypothetical protein, root-specific hypothetical protein, DNA topoisomerase and Retinoblastoma for expression at panicles before heading, heading-specific profiling, and invertase for expression at seed after pollination. Promoter regions of the selected genes were isolated and fused to the β -glucoronidase (GUS) reporter gene, and the constructs were introduced into rice plants. These promoters are highly active in the tissue-specific manner of rice and can be useful for the spatial and temporal enhancement of target gene(s).

PD-07

CMV-CP 바이러스저항성 GM 고추의 농업적 특성

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고추(*Capsicum annuum* L.)는 가지과(Solanaceae)로 분류되는 일년초로서 온대에서 열대까지 널리 재배되고 있다. 또한 세계 50억 인구가 식생활에 활용하고 있고 재배면적이 7위인 세계적인 채소로서 식생 외에도 먹거리의 식품첨가제, 색소, 의약품재료, 화장품 등 산업적으로 많이 사용되고 있으며, 그 산업규모가 계속 증가하고 있다. 고추 관련 산업 매출은 300억불로서 상업적 가치가 매우 높은 채소작물이다. 따라서 고추는 채소류 중 동남아 등 해외로 수출가능성이 가장 높은 작물로써 수출전용 품종 개발이 시급하고, 국내 재배용으로는 바이러스 내병성이 강하고 고품질의 고추 품종 개발이 요구된다. 현대 생물공학은 고추의 병해충에 대한 유전적 개량을 통해 이익을 줄 수 있으며, 첫 번째 유전자 형질전환은 *Agrobacterium tumefaciens*로 neomycin phosphotransferase와 β-glucuronidase 유전자를 삽입한 것으로 (Liu et al., 1990) 그 후로 *C. annuum*에 대한 기술의 발달이 꾸준히 보고되었다. 최근 고추에서 개량하고자 하는 형질에는 CMV, TEV, TMV에 대한 바이러스 저항성(Cai et al., 2003), 담배나방(*Heliothis assulta*)에 대한 해충저항성(Kim et al., 2003), 과실성숙도 조절, 저장기간 연장 등으로 요약되고 있다(OECD 고추표준기술서, 2006).

본 연구에서는 국내에 존재하는 고추 품종과 계통을 모두 이병시키는 새로운 바이러스인 CMVP1에 대한 내성이 있는 GM고추 H15 event의 농업적 특성 포장시험을 실시하였다. 농업환경위해성 평가를 위한 농업적 특성 포장시험을 2012년 5월부터 9월까지 H15 event와 모본 P2377에 대하여 수행하였다. 조사내용은 식물체, 과실 및 꽃의 특성을 조사하였다. 식물체의 특성은 6월부터 9월까지 6항목을 조사하였으며, 8월 최성기는 18항목을 조사하였다. 조사결과는 6월부터 8월까지 식물체 특성은 통계적으로 유의한 차이가 없었으며, 9월에는 P2377 고추의 초폭이 H15 고추에 비해 유의하게 컸지만 초장, 주경장, 경경, 엽장 및 엽폭은 통계적으로 유의한 차이가 없었다. 과실의 특성은 미숙과 20항목과 숙과 19항목을 조사하였으며, 착과상태, 과장, 과경 등 조사대상 항목의 특성은 모두 통계적으로 유의한 차이가 없었다. 꽃의 특성은 화색 등 10가지 항목을 조사하였으며, 화색, 웅예수 등 통계적으로 유의한 차이가 없었다. 종자의 특성은 종자색등 4가지 항목을 조사하였으며, 종자색, 종자크기 등 통계적으로 유의한 차이가 없었다.

이와 같은 연구결과는 포장시험을 통한 농업적 특성의 위해성평가 기초자료로 제시할 수 있을 것이며, GMO 식품안정성평가에 대한 가이드라인으로 제시 할 수 있을 것으로 기대된다.

PD-08

Comparison agronomic characteristic and chemical properties between GM (Genetically modified) drought-tolerant rice and donor rice

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Genetically modified (GM) plant claims to be the solution to global poverty, and potentially solving environmental change and food requirement by increased human population. In this study, we were evaluating agronomic characteristics and chemical properties of two GM drought-tolerant rice (CaMsrB2-8 and CaMsrB2-23) compared with donor cultivars (Ilmi). Statistical analysis agronomic characteristics GM and donor rice showed no significant difference between both of them. Yield and appearance of rice grain, GM rice was a similar to the donor rice. Chemical composition analysis showed that GM drought-tolerant rice has no different with donor rice. This result indicated that GM drought tolerant rice has no big significant difference agronomic character and chemical properties; it can be solve food shortages in spite of drought condition.

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PD-09

Determination of nutrients and anti-nutrients in resveratrol GM rice (*Oryza sativa* L.)

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This study investigated the nutrients and anti-nutrients of produced resveratrol GM rice (Iksan-515, Iksan-526, Dongjin) that were cultivated Iksan and Suwon regions. Among the rice samples, Iksan-515 and Iksan-526 are produced resveratrol GM rice. Reveratrol is health-beneficial compound with strong antioxidant and antitumor activities. Red wine is believed to the main source of resveratrol in the human diet. Recent studies have associated resveratrol with the cardio-protective effect observed among people with moderate resveratrol consumption. Moreover, resveratrol has been possess chemoprotective activity. In present study, we determined the substantial equivalence between GM rice and seedling sort. We investigated the nutrients and anti-nutrients of produced resveratrol GM rice and analyzed nutrients including moisture, crude fat, ash, crude protein, fatty acids, amino acids and minerals. The results of this analysis showed equivalence between GM rice and non-GM rice. We determined phenolic compounds including naringenin, vallin and investigated 4 tocopherols (α-, β-, γ-, δ-tocopherol) and 4 tocotrienols (α-, β-, γ-, δ-tocotrienol). Among the all rice cultivars, they showed substancial equivalence between resveratrol GM rices and non-GM rice.

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PD-10

Differential requirement of *Oryza sativa* RAR1 in immune receptor-mediated resistance of rice to *Magnaporthe oryzae*

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The required for Mla12 resistance (RAR1) protein is essential for the plant immune response. In rice, a model monocot species, the function of *Oryza sativa RAR1 (OsRAR1)* has been little explored. In our current study, we characterized the response of a rice osrar1 T-DNA insertion mutant to infection by *Magnaporthe oryzae*, the causal agent of rice blast disease. *osrar1* mutants displayed reduced resistance compared with wild type rice when inoculated with the normally virulent *M. oryzae* isolate PO6-6, indicating that *OsRAR1* is required for an immune response to this pathogen. We also investigated the function of *OsRAR1* in the resistance mechanism mediated by the immune receptor genes *Pib* and *Pi5* that encode nucleotide binding-leucine rich repeat (NB-LRR) proteins. We inoculated progeny *from Pib/osrar1* and *Pi5/osrar1* heterozygous plants with the avirulent *M. oryzae* isolates, race 007 and PO6-6, respectively. We found that only *Pib*-mediated resistance was compromised by the *osrar1* mutation and that the introduction of the *OsRAR1* cDNA into *Pib/osrar1* rescued *Pib*-mediated resistance. These results indicate that OsRAR1 is required for *Pib*-mediated resistance but not *Pi5*-mediated resistance to *M. oryzae.*

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PD-11

Effects of herbicide tolerance rice cultivation 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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PD-12

Flanking sequence analysis of soybean transgenic plants with three recombinant cry1Ac genes

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Bacillus thuringiensis(Bt) crystal protein (Cry1Ac) 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. Korea soybean variety Kwangan was transformed with Bacillus thuringiensis(Bt) crystal protein genes. We transformed three difference Cry1Ac (Cry1Ac and two modified Cry1Ac) genes into Kwangan using highly efficient soybean transformation system. Transgenic plants with Bt crystal protein genes were confirmed for gene introduction and their expression using PCR, real-time PCR, and RT-PCR. We generated 30 independent lines of transgenic soybean plants. Analysis of the flanking sequences isolated by Inverse PCR revealed complex T-DNA insertion patterns and preferential integration of T-DNA into the intergenic spacer region of the soybean genome. We found 5 different intergenic transgenic soybean lines of soybean genome. Currently, the confirmation of stable gene introduction with Bt genes is also performing by southern blot analysis, physiology test, and agronomic characters are investigating.

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PD-13

Gene flow of GM pepper

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CMVP1 (cucumber mosaic virus pathotype 1) has been frequently occurring virus causing damage in pepper farms, and it is hard to control the outbreak due to lack of the genetic source resistant to this specific pathotype. Therefore, we have developed transgenic peppers tolerant of CMVP1 using a *CP* gene of CMVP0 pathogen. In order to fulfill the requirement of the biosafety assessment criteria, we have studied the horizontal gene flow from GM pepper to non-GM pepper by monitoring the transgene movement. If the pepper farms are located closely each other and the pollen moves from GM pepper to non-GM pepper, it would cause unintended fertilization. Therefore, a buffer zone to separate the cultivation regions is required to avoid the contamination of transgene. Previously, several data regarding the movement distance of pepper pollen were reported by judging the phenotypic change. However, no tool as a trace marker was available. The objective of this study was to assess the frequencies of gene flow from GM peppers to non-GM peppers in neighboring farms using the transgene of *CP* as a trace marker. The GM and non-GM peppers were cultivated in the isolated farm of Nongwoo Bio Co. (NW GM pepper field) and pepper fruits were collected from the NW GM pepper field as well as the neighboring pepper farms. The pepper seeds collected from the farms were planted and the massive PCR analysis was performed to answer the question how far the pollen of GM pepper migrates. The conclusive data based on the consecutive experiments for 6 years is that the gene flow by pollen movement did not occur in peppers that were separated each other over 30 m.

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PD-14

Genome-scale mutagenesis and phenotypic characterization of response regulators in *Xanthomonas oryzae* pv. *oryzae*

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Two-component regulatory system (TCS) is the dominant mechanism that controls almost physiological processes of bacteria, such as nutrition assimilation, cell motility, chemotaxis, biofilm formation, quorum sensing and virulence. The intracellular informing process by a typical TCS accompany transfer of a phosphoryl group from His of a histidine kinase (HK) to Asp of a response regulator (RR). In *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) genome, the TCS genes comprise approximately 3% of the nucleotide sequences with 58 response regulators (RRs), 32 orthodox histidine kinase (HKs) and 13 hybrid histidine kinase (HyHKs). However, there is not much understanding of RRs in *Xoo* except the reported RRs in *Xanthomonas* spp. including RpfC-RpfG, RavS-RavR, HrpG, VgrS-VgrR (also named ColS-ColR), VemR, RaxH-RaxR, and PhoQ-PhoP. Although a genome-scale mutagenesis and phenotypic characterization of TCSs were studied in *Xanthomonas campestris* pv. *campestris* ATCC 33913, there is not any genome-scale research of TCSs in *Xanthomonas oryzae* pv. *oryzae*. We have mutagenized 52 predicted RR genes in *Xoo* PXO99A by marker-exchange mutagenesis method and characterized the phenotype of mutants to identify RR genes involving in pathogenicity of *Xoo* and understand how *Xoo* TCSs work in given conditions. Ours investigation with the RR knock-out mutant strains have identified four novel RR genesthat are likely involved in virulence of *Xoo*. We have studied with these genes in molecular level to elucidate the mechanism for *Xoo* pathogenicity.

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PD-15

Heterologous expression of dehydrin gene from Arctic *Cerastium arcticum* increases abiotic stress tolerance and enhances the fermentation capacity of a genetically modified *Saccharomyces cerevisiae* strain

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We investigated Arctic plants to determine if they have a specific mechanism enabling them to adapt to extreme environments because they are subject to such conditions throughout their life cycles. Among the cell defense systems of the Arctic mouse-ear chickweed *Cerastium arcticum*, we identified a stress-responsive dehydrin gene *CaDHN* that belongs to the SK_5 subclass and contains conserved regions with 1 S-segment at the N-terminus and 5 K-segments from the N-terminus to the C-terminus. To investigate the molecular properties of CaDHN, yeast were transformed with *CaDHN*. *CaDHN*-expressing transgenic yeast (TG) cells recovered more rapidly from challenge with exogenous stimuli, including oxidants (hydrogen peroxide, menadione, and *tert*-butyl hydroperoxide), high salinity, freezing and thawing, and metal (Zn^{2+}), than wild-type (WT) cells. TG cells were sensitive to copper, cobalt, and sodium dodecyl sulfate. In addition, the cell survival of TG cells was higher than that of WT cells when cells at the mid-log and stationary stages were exposed to increased ethanol concentrations. There was a significant difference in cultures that have an ethanol content >16%. During glucose-based batch fermentation at generally used (30℃) and low (18℃) temperatures, TG cells produced a higher alcohol concentration through improved cell survival. Specifically, the final alcohol concentrations were 13.3% and 13.2% in TG cells during fermentation at 30℃ and 18℃, respectively, whereas they were 10.2% and 9.4%, respectively, in WT cells under the same fermentation conditions. An *in vitro* assay revealed that purified CaDHN acted as a reactive oxygen species (ROS)-scavenger by neutralizing H_2O_2 and a chaperone by preventing high temperature-mediated catalase inactivation. Taken together, our results show that *CaDHN* expression in transgenic yeast confers tolerance to various abiotic stresses by improving redox homeostasis and enhances fermentation capacity, especially at low temperatures (18℃).

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PD-16

Improved resistance of soybean mosaic virus with Coat protein and *HC-Pro* genes using RNAi method

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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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PD-17

Introduction of *UGT72E3/2* gene into soybean increases higher content of phenylpropanoids

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UGT72E3/2 gene encodes UDP-glycosyltransferase shown to glucosylate several phenylpropanoids such as syringin and coniferin. Syringin has effect of anti-stress and anti-fatigue. Korean soybean variety Kwangan was transformed with UGT72E3/2 gene. This gene was transformed into Kwangan using highly efficient soybean transformation system. This study used two promoters, beta-conglycinin promoter for seed-specific expression and 35s promoter for total expression. Transgenic plants were confirmed for gene introduction and their expression using PCR and RT-PCR. The analysis of syringin in transgenic plants was performed using HPLC. Currently, the confirmation of stable gene introduction with UGT72E3/2 gene is also performing by Southern blot analysis.

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PD-18

Isolation and functional analysis of glutamine synthetase (*OsGS*) gene in transgenic rice under cadmium stress

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Glutamine synthetase (GS) is an enzyme that plays an essential role in the metabolism of nitrogen by catalyzing the condensation of glutamate and ammonia to form glutamine. Exposure of plants to cadmium (Cd) has been reported to decrease GS activity in maize, pea, bean, and rice. To better understand the function of the *GS* gene under Cd stress in rice, we constructed a recombinant pART vector carrying the *GS* gene under the control of the CaMV 35S promoter and OCS terminator and transformed using *Agrobacterium tumefaciens*. We then investigated GS overexpressing rice lines at the physiological and molecular levels under Cd toxicity. The GS activity along with mRNA expression were found higher in transgenic than in wild type plants. And this is validated by the low malondialdehyde contents observed 10 days after treatment. GS overexpression in rice resulted in the modulation of expression of enzymes responsible for membrane peroxidation, which may result in the sudden death of plants. Our results thus describe the features of a transgenic rice plants with enhanced tolerance to Cd toxicity.

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PD-19

Molecular biological characteristics and biosafety assessment for drought-tolerant transgenic rice (CaMsrB2)

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Genetically modified (GM) crops have been developed worldwide through the recombinant DNA technology and commercialized by various agricultural biotechnological companies. Commercialization of GM crops will be required the assessment of risk associated with the release of GM crops. In this study, we carried out to provide the 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 (CaMsrB2). 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, a selectable marker herbicide resistance unit, and left border in a sequential order. Based on the adaptor-ligation PCR and whole genome sequence database, we confirmed that T-DNA was introduced at the position of 41,737,284 bp of chromosome No. 1. 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. These results will be filed to biosafety assessment document of CaMsrB2 rice.

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2013 한국육종학회-차세대BG21사업단 공동 심포지엄

차세대바이오그린21 사업단 발표

Plant Epigenomics for Breeding

차세대유전체연구사업단 (TAGC)

OD-01

Arabidopsis RNA metabolism by the pre-mRNA processing factor 6 homolog

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Arabidopsis *STABILIZED1* (*STA1*) encodes a protein that is homologous to human U5 snRNP-associated 102-kDa protein (PRPF6), and the yeast pre-mRNA splicing factors, PRP1p (fission yeast) and Prp6p (budding yeast), and is important in pre-mRNA splicing and mRNA stability. The pleiotropic defects of development, chilling sensitivity and hypersensitivity to ABA are observed in *sta1-1*, a weak allele of *sta1*. *sta1-1*, showing enhanced luminescence under cold stress, was originally isolated from a mutant pool generated with the bioluminescent plant harboring the stress-inducible RD29A promoter-driven luciferase gene (RD29A-LUC). Some developmental defects found in *sta1-1* resembled those found in miRNA biogenesis mutants such as *hyponastic leaves1-1* (*hyl1-1*) and *serrate-1* (*se-1*). Similar to these miRNA biogenesis mutants, *sta1-1* accumulated significantly lower levels of mature miRNAs and concurrently higher levels of pri-miRNAs than wild type. The dramatic reductions of mature miRNAs were associated with the accumulation of their target gene transcripts and the corresponding developmental defects. The reduction of miRNA accumulation in *sta1-1* appeared to be because of the *sta1-1* decfects in splicing of intron containing pri-miRNAs. In addition, *sta1-1* decreased transcript levels of *DICER-LIKE1* (*DCL1*) gene. These results suggest that *STA1* is involved in miRNA biogenesis directly by functioning in pri-miRNA splicing and indirectly by modulating the *DCL1* transcript level. Our efforts and recent findings to establish STA1-mediated RNA metabolism will be presented and discussed.

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OD-02

Development of stress-tolerant transgenic plants via RNA metabolism control

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Environmental stresses including drought, extreme temperatures, and high salinity are major factors that severely limit crop productivity worldwide. To overcome yield loss due to these environmental stresses, a large number of researches have been conducted to understand how plants respond to and adapt these environmental stresses. Posttranscriptional regulation as well as transcriptional regulation of gene expression is recognized as a key regulatory process in plant stress responses, and these cellular processes are regulated by diverse RNA-binding proteins (RBPs). Over the last years, we have extensively investigated the functional roles of RBPs that harbor an RNA-recognition motif at the N-terminal half and a glycine-rich region at the C-terminal half (glycine-rich RNA-binding proteins, GRPs), zinc finger-containing GRP, and cold shock domain proteins (CSDPs) in *Arabidopsis thaliana,* rice (*Oryza sativa*), wheat (*Triticum aestivum*), and rapeseed (*Brasicca napus*) under stress conditions. Our comparative analysis demonstrated that certain family members display RNA chaperone function during stress adaptation process in monocotyledonous plants as well as in dicotyledonous plants. These findings point to the importance of the regulation of mRNA metabolism in plant response to environmental stresses and shed new light on the practical application of these RBPs to develop stress-tolerant transgenic crops. [Supported by grants from Next-Generation BioGreen21 and NRF of Korea]

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OD-03

Epigenetic repression of flowering pathway genes by long non-coding RNA in Arabidopsis

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In some plant species, prolonged exposure to low temperature during the winter season is necessary to acquire the competence to flower in the following spring. This process, known as vernalization, is an epigenetic change in which a mitotically stable change of the developmental potential of the meristem (competence to flower) is maintained even in the absence of the inducing signal (prolonged cold exposure). In Arabidopsis, vernalization results in stable epigenetic repression of a potent floral repressor, *FLOWERING LOCUS C* (*FLC*). Increased enrichment of Polycomb Repressive Complex 2 (PRC2) and trimethylated Histone H3 Lys 27 (H3K27me3) at *FLC* chromatin is necessary for the stable maintenance of *FLC* repression by vernalization. A long intronic noncoding RNA (termed as COLDAIR) is required for the vernalization-mediated epigenetic repression of *FLC*. COLDAIR physically associates with a component of PRC2 and targets PRC2 to *FLC*. COLDAIR is required for establishing stable repressive chromatin at *FLC* through its interaction with PRC2. In addition, floral integrator genes are targets of PRC2 complex, resulting in delayed flowering time through repression mechanism of PRC2 complex. Recently another long non-coding RNA was isolated from floral integrator gene and characterized the function of this long non coding RNA.

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OD-04

Role of a histone-modifying enzyme in plant immunity and tomato small RNAome

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In the era of systems biology, plant biologists approach any given phenomena, that they have great interests, from different perspectives. Among them, both epigenomic and epigenetic studies give us new insights into plant immune response as well as development. In plants, recognition of invading pathogenic microorganisms by pattern recognition receptor and race-specific resistance protein activates diverse cellular responses to defend plants against pathogen infection. One of well-known immune responses is the transcriptional reprogramming occurring when pathogen infects plant. Chromatin remodeling caused by change of histone marks and replacement of histone variants affects gene expression that is important for immunity. We are focused on unveiling epigenomic and epigenetic regulatory mechanisms of plant immunity. To address these questions, we have collected knockout mutant plants whose genes might be related to histone modifications, and identified several *enhanced-immune* (*eni*) mutants and *immune-defective* (*imd*) mutants. Here, we will introduce one of mutants showing enhanced disease resistance (EDR) in response to the infection of *Pseudomonas*. Thus we named it *eni2*. Both the growth of virulent bacteria, not avirulent derivatives of *Pseudomonas syringae*, and symptom development were effectively inhibited in the *eni2* mutants, compared with those seen in wild type. Unlike to well-known EDR-type mutants, the levels of salicylic acid in the *eni2* mutant plants were not different from those in wild type. Thus we suggests a few plausible scenarios about role of ENI2 in plant immune response. To examine these possibilities, we are monitoring transcriptional reprogramming occurring in *eni2* mutants through RNA-seq analysis. On the other hand, we have recently initiated the study of tomato small RNAome in order to discover immune-related small RNAs from leaves infected with *Pseudomonas syringae* via next-generation sequencing technology. Here we present the recent progress in this study.

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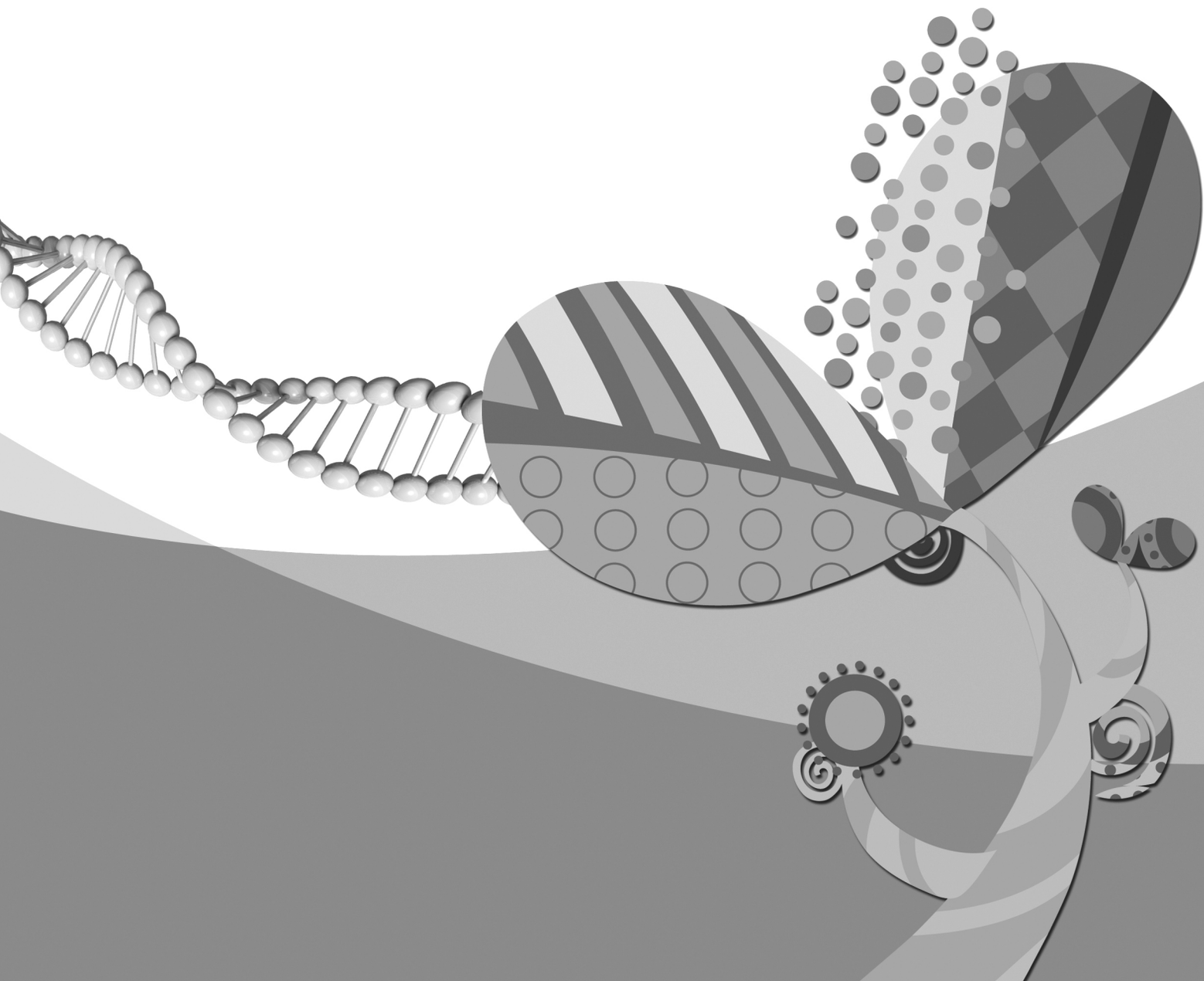
2013 한국육종학회-차세대BG21사업단 공동 심포지엄

차세대바이오그린21 사업단 발표

GM작물실용화사업단 (NCGC/KBIC)



- GM작물실용화사업단 (NCGC/KBIC) -

좌장: 이강섭 (국립농업과학원)

시 간	구 분	내 용
08:30~09:00	주제발표1	글로벌 시장 진출을 위한 GM 작물 개발 전략 ▸김주곤 (서울대학교)
09:00~09:30	주제발표2	쌀 육종기술의 현황과 전망 ▸원용재 (국립식량과학원)
09:30~10:00	주제발표3	중국의 GM 벼 개발과 Hybrid 육종 ▸Piao Zhong Ze (상해시 농업과학원)
10:00~10:30	종합토의	

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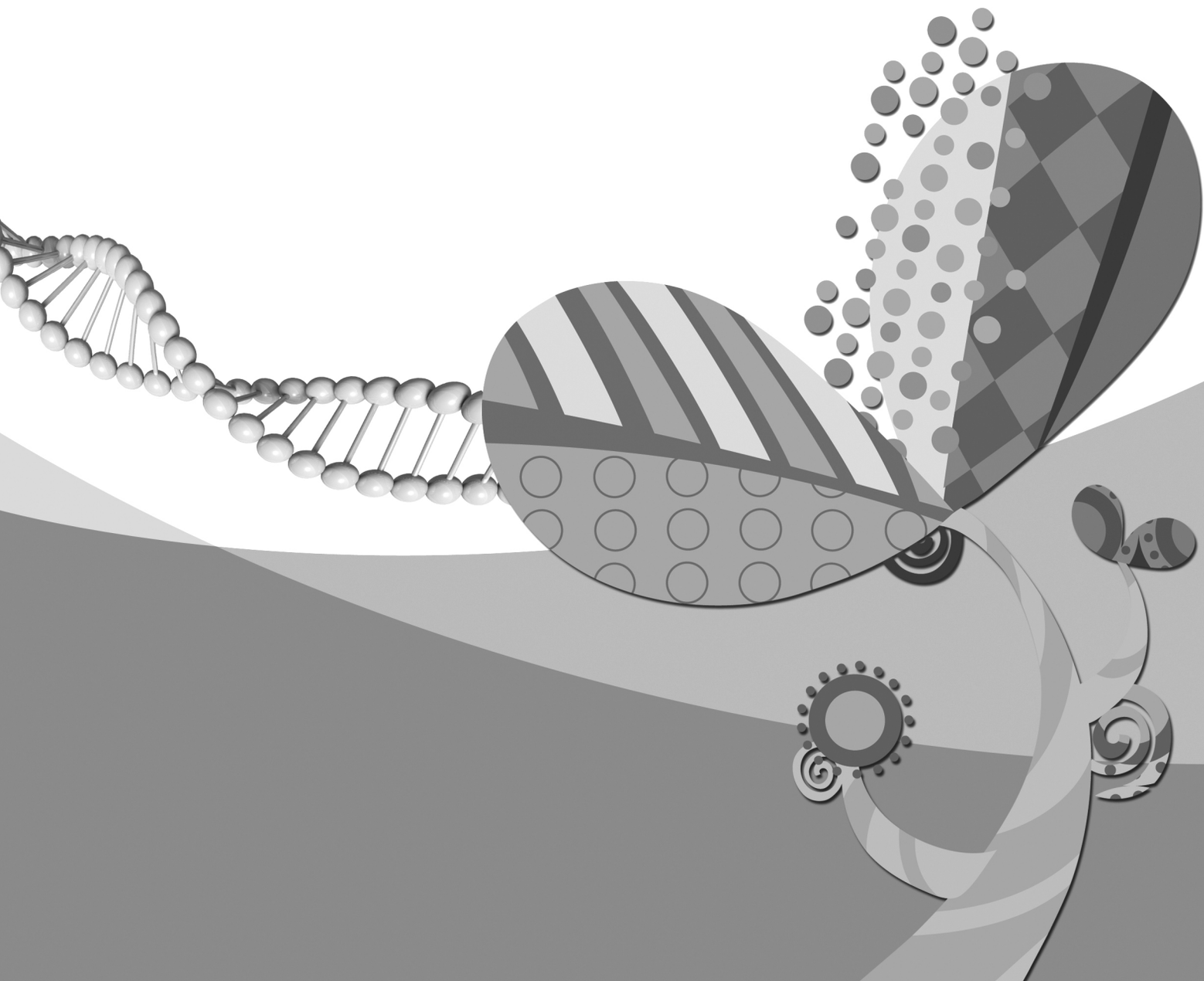
2013년 한국육종학회상



2013년 한국육종학회상 시상 내역

○ 일 시 : 2013년 7월 4일 18:50~
○ 장 소 : 라마다플라자 청주호텔

1. 경산육종학회상

- 유일웅 (삼성종묘주직회사)
- 선정사유 : 청양고추육종 등 민간 육종산업 발전에 기여한 공로

2. 연구상(연구부문)

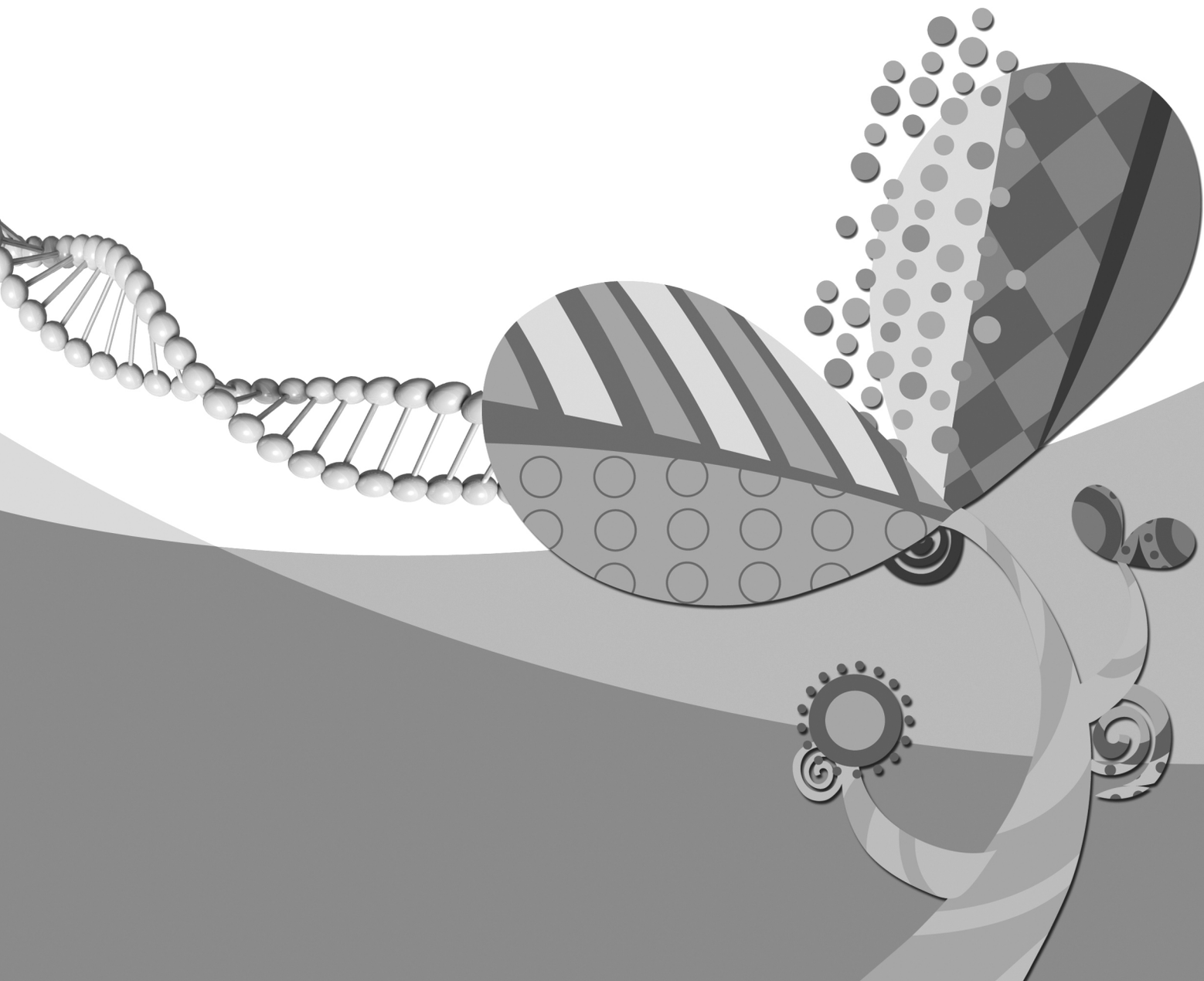
(1) 한국육종학회지 44권, 3호:273-281 (2013년) 발표논문
- 논문제목 : 벼의 밀양23호/기호벼 재조합자식 유전집단을 이용한 PCR 기반 DNA 마커들로 구성된 분자유전자지도 작성
- 논문저자 : 지현소 (국립농업과학원 농업생명자원부 유전자분석개발과)

(2) 한국육종학회지 44권, 4호:476-482 (2013년) 발표논문
- 논문제목 : Genetic Analysis of Carotenoids Content in Red Pepper (*Capsicum annuum* L.) Fruit using Complete Diallel Cross
- 논문저자 : 이우문 (국립원예특작과학원 원예작물부 채소과)

3. 연구상(품종부문)

- 품종명 : 품종보호 제1750호(2007.3.20～2027.3.19)
- 고품질 내도복성 찰옥수수 품종「미백2호」개발
- 논문저자 : 박기진 (강원도농업기술원 옥수수연구소)
- 육성기관 : 강원도농업기술원 옥수수연구소
  (박기진, 류시환, 박종열, 용우식, 고병대, 장진선, 허남기, 민황기, 서정식)

색 인



■ 국 문 ■

한국육종학회
Korean Society of Breeding Science

제 45 권 | 별책 1 호

인 쇄 2012년 7월 1일
발 행 2012년 7월 4일
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