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포스터 세션

GM : Genetics/Molecular Biology

DP : Development/Physiology

ST : Signal Transduction

ETM : Environment/Ecology/Taxonomy/Morphology

PB : Plant Biochemistry

[GM1]

The rice *zebra3* (*z3*) mutation disrupts citrate distribution and produces transverse dark-green/green variegation in mature leaves

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Rice *zebra mutants* are leaf variegation mutants that exhibit transverse sectors of green/yellow or green/white in developing or mature leaves. Here, we examine a new type of leaf variegation mutant in rice, *zebra3* (*z3*), which exhibits transverse dark-green/green sectors in mature leaves and lacks the typical yellow or white sectors. Map-based cloning revealed that the *Z3* locus encodes a putative citrate transporter that belongs to the CitMHS family. To investigate whether Z3 functions as a citrate transporter in rice, we measured citrate levels in the wild-type leaves and in the dark-green and green sectors of the leaves of *z3* mutants. The results showed that citrates accumulated to high levels in the dark-green sectors of *z3* mutant leaves, but not in the green sectors as compared with the wild-type leaves. These results suggest that leaf variegation in the *z3* mutant is caused by an unbalanced accumulation of citrate in a transverse pattern in the leaves. Taking these results together, we propose that Z3 plays an important role in citrate transport and distribution during leaf development and is a possible candidate for a CitMHS family member in plants.

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[GM2]

Overexpression of *MYB50*, a novel MYB-type transcription factor, increases response to drought and salt stress in rice

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MYB-type transcription factors play important roles in response to abiotic stress. Here, we report a rice MYB-type transcription factor, MYB50, and phenotypically characterized the T-DNA insertional *MYB50* overexpressing plant. *MYB50* expression is strongly down-regulated by dehydration, salt, and abscisic acid (ABA) treatments. Growth and development are almost indistinguishable between the wild-type plant and the *MYB50* overexpressing plant under normal growth conditions, but the *MYB50* overexpressing plant is hypersensitive to drought and salt stress in comparison with the wild-typeplant. Moreover, overexpression of *MYB50* decreases sensitivity to ABA at the post-germination stage. These results suggest that *MYB50* increases response to drought and salt stress by decreasing ABA sensitivity. Taken together, we propose that MYB50 functions as a novel MYB-type transcription factor that plays a negative role in dehydration and salt tolerance by regulating sensitivity to ABA.

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[GM3]

The F-box protein inhibits dimerization of COP1 in the control of photoperiodic flowering.

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In Arabidopsis thaliana, CONSTANS (CO) plays an essential role in the regulation of photoperiodic flowering under long-day conditions. CO protein is stable only in the afternoon of long days, when it induces the expression of FLOWERING LOCUS T (FT), which promotes flowering. The blue-light photoreceptor FLAVIN-BINDING, KELCH REPEAT, F-BOX1 (FKF1) interacts with CO and stabilizes it by an unknown mechanism. Here, we provide genetic and biochemical evidence that FKF1 inhibits CONSTITUTIVE PHOTOMORPHOGENIC1 (COP1)-dependent CO degradation. Light-activated FKF1 has no apparent effecton COP1 stability but can interact with and negatively regulate COP1. We show that FKF1 can inhibit COP1 homodimerization. Mutation of the coiled-coil domain in COP1, which prevents dimer formation, impairs COP1 function in coordinating flowering time. Based on these results, we propose a model whereby the light- and day length-dependent interaction between FKF1 and COP1 controls CO stability to regulate flowering time.

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[GM4]

The rice *RADIALIS-LIKE3* (*OsRL3*) connects leaf senescence and salt stress response through ABA signaling pathway

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Abscisic acid (ABA) is associated with multiple developmental processes in higher plants, especially to respond to abiotic stresses. ABA synthesis is triggered by various environmental factors and ABA sensing promotes leaf senescence or stress tolerance. Here, we demonstrate a rice MYB transcription factor *RADIALIS-LIKE3* (*OsRL3*) which promotes dark-induced senescence (DIS) and salt stress response. The gene expression is slightly induced under DIS and some osmotic stress conditions, highly expressed under salt stress. The T-DNA insertion *osrl3* knockout mutant delayed leaf senescence in the dark with a significant retention of chlorophylls and photosynthetic capacity. Furthermore, in high salinity conditions, *osrl3* mutation increased stress response with reduced expression of proline biosynthetic genes *OsP5CS1* and *OsP5CS2* in the leaves. In an exogenous ABA treatment, *OsRL3* expression increased in the WT leaves and *osrl3* mutant exhibit a stay-green phenotype. Under both dark and salt stress treatments, ABA signaling-associated genes were down-regulated in *osrl3*. Yeast one-hybrid assay revealed that *OsRL3* directly targets the promoters of *OsNAP* and *OsRAB16D* that accelerate leaf senescence and abiotic stress response. Taking together, we conclude that *OsRL3* functions as a transcriptional activator for the genes involved in ABA signaling which promotes leaf senescence and abiotic stress response in rice.

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[GM5]

Roles of RNA Methylation in Plant Development and Stress Responses

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Despite the fact that RNA methylation is recently emerging as a potential epigenetic mechanism affecting development and stress responses in animals, our knowledge on the regulation of RNA methylation and its role in plants is limited. Here we show the results of our research focused on RNA methylation and its possible involvement in the regulation of plant development and abiotic stress response. We identified several key enzymes involved in RNA methylation and demethylation, including orthologues of METTL methyltransferases, ALKBH demethylases, and m6A-specific binding protein YTHDF2 in *Arabidopsis thaliana*. Expression levels of these genes were analyzed under various abiotic stress conditions. Confocal analysis of tobacco leaves transiently expressing GFP fusion proteins was used to confirm the localization of these proteins. Analysis of loss-of-function mutants and transgenic *Arabidopsis* plants that overexpress RNA methyltransferase or demethylase revealed that alteration of RNA methylation is important for plant growth and stress responses. Taken together, our results point to the importance of RNA methylation in plant growth, development, and stress responses.

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[GM6]

Overexpression of *ONAC016* promotes leaf senescence and improves drought stress through ABA signaling pathway

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Plant-specific NAC transcription factors are involved in diverse plant processes, including plant developmental programs, cell division, leaf senescence, formation of secondary walls, and biotic/abiotic stress response. While regulatory mechanisms of *Arabidopsis* NAC TFs for leaf senescence have been well-known, in other species, especially in rice, few rice NAC TFs have been associated with leaf senescence. Here, we found that null mutation of *ONAC016* showed delayed leaf senescence in dark-incubated conditions and increased susceptibility to drought stress. However, *onac016-D* dominant mutants, in which transcripts levels of *ONAC016* increased, accelerated leaf senescence and improved the tolerance to drought stress compared with wild-type. The results of RT-qPCR showed that expression of *ONAC016* gradually increased in response to leaf senescence and treatment with abscisic acid (ABA). *onac016* mutants showed reduced sensitivity to ABA-induced senescence by exogenously application of ABA to detached rice leaves. *ONAC016* act as positive regulator of leaf senescence by controlling several chlorophyll degradation, such as *SGR, NYC1* and *RCCR1*. Moreover, deficiency of *ONAC016* left the stomatal status to open under ABA treatment. These results suggest that *ONAC016* plays an important role in leaf senescence and drought stress tolerance via the ABA signaling pathway.

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[GM7]

The rice cryptochrome-Interacting Basic-Helix-Loop-Helix1 (OsCIB1) regulates leaf angle and spikelet shape

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Cryptochrome-Interacting basic-helix-loop-helix (CIB), a critical transcription factor in plant, plays important role associated several development processes, including hypocotyl elongation, flowering, and plastid development. It has been reported that a soybean CIB orthologue gene *Cryptochrome-interacting bHLH1* (*GmCIB1*) promotes leaf senescence by activating transcription of senescence-associated genes such as *WRKY DNA BINDING PROTEIN53b* (*WRKY53b*). However, any functions of *CIB1* have not been studied or reported yet in rice. In this study, we screened two T-DNA mutants to identify the function of *OsCIB1*. Especially, a rice gain of function mutant, *oscib1-D* displayed wide leaf angles and slender grains, similar to plants with increased brassinosteroid (BR) levels or enhanced BR signaling. qRT-PCR analysis showed that genes in brassinosteroid signaling pathway were upregulated in *oscib1-D*, but there was no significant difference of the expression level of BR biosynthesis-related genes between WT and *oscib1-D*. In addition, *oscib1-D* showed more sensitive phenotype than WT to BR. Histological analysis revealed that increased cell length in adaxial surface of lamina joint is responsible for larger angles. Moreover, expression level of genes involved in cell elongation such as expansins and xyloglucan endotransglycosylase/hydrolase(XTH), two major cell wall-loosening enzymes, was significantly increased in *oscib1-D*. Thus, these results strongly suggest that *OsCIB1* is involved in the BR signaling pathway and determines not only leaf inclination but also grain shape by regulating cell-elongation-related genes.

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[GM8]

A rice novel transcription factor *OsWRKY5* promotes leaf senescence by up-regulation of senescence-associated genes.

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Leaf senescence is the final stage of plant development, which is tightly regulated by a variety of external and internal factors such as temperature, light, abiotic and biotic stresses, phytohormones, and transcription factors. WRKY genes are one of most abundant transcription factors which regulate diverse biological processes including leaf senescence. Here we reported *OsWRKY5*, a novel WRKY transcription factor, whose transcriptional level was gradually increased during natural leaf senescence and dark-incubation. A knockdown mutant of *OsWRKY5* (*oswrky5*) exhibited a delayed senescence phenotype during dark-induced senescence; on the contrary, an overexpression mutant of *OsWRKY5* (*OsWRKY5*-D) senesced faster than WT in dark-incubation and natural long-day condition. The transcriptional analysis revealed that several senescence-associated genes, especially chlorophyll degradation genes, were significantly up-regulated in *OsWRKY5*-D mutant and down-regulated in *oswrky5* mutant during dark-induced senescence. These results suggest that *OsWRKY5* participates in regulation of chlorophyll degradation, thereby leading to promotion of senescence.

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[GM9]

Rice *OsDOF24* Delays Leaf Senescence by Downregulating Senescence-Associated and Chlorophyll Degradation Genes

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Leaf senescence is a final stage of leaf development, which largely affectsagronomic traits in cereal production. Although many genetic factors has been reported, it is still necessary to determine the key regulators that delay leaf senescence during grain filling in staple food crops including rice. Here we show that *OsDOF24*, one of DOF (DNA-binding One zinc Finger) transcription factor family, acts as a repressor of leaf senescence in rice. The T-DNA insertion-mediated enhancer-tagged overexpressor of *OsDOF24* (*osdof24-D*) in rice exhibits a stay-green phenotype during both age-dependent natural and dark-incubated senescence. The stay-green phenotype was further confirmed with the detached leaves of transgenic rice overexpressing *OsDOF24* by *35S* CaMV promoter. To elucidate the molecular mechanism of leaf senescence in *osdof24-D* mutants, we performed RT-qPCR analysis, revealing that senescence-associated genes (SAGs), *Osl85* and *Osh36*, and chlorophyll degradation genes (CDGs), *OsNYC1*, *OsNYC3*, and *OsSGR*, are downregulated in *osdof24-D* mutants during dark incubation. In addition, the detached leaves of *osdof24-D*mutants were less sensitive to MeJA (methyl-jasmonate)-induced senescence. Consistent with this stay-green phenotype, expression levels of MeJA-responsive genes, *OsJAmyb* and *OsCOI1a*, decreased in *osdof24-D* mutants. Taken together, our results demonstrate that *OsDOF24* suppresses the induction of leaf senescence during vegetative growth by downregulating MeJA-responsive signaling.

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[GM10]

Quantitative trait locus mapping and candidate gene analysis for agronomic traits in rice

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A lot of agronomic traits are affected by quantitative trait loci (QTLs). Thus, plant breeders have focused on improving plant architecture as an effective means to increase crop yield by using recombinant inbred lines (RILs). Here we identified the main-effect QTLs for plant and grain shape-related traits in rice (Oryza sativa) and found candidate genes by applying genome sequencing of two parental cultivars using genotyping-by-sequencing (GBS). The GBS approach provides reduced time and effort required for QTL mapping. To identify QTLs influencing agromic traits, we analyzed nine traits: plant height, tiller number, panicle diameter, panicle length, flag leaf length, flag leaf width, grain thickness, grain width, and grain length. We performed QTL analysis with 186 F7 RIL lines from a cross of japonica rice line 'Donjin' and indica rice line 'WRDA128'. We identified 12 main-effect QTLs for the nine traits with a threshold LOD value 〉 3.0. These genetic resources will be useful for breeding high-yielding rice cultivars.

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[GM11]

PyMPV17, Pyropia (Rhodophyte) homolog of the human MPV17 enhances abiotic stress tolerance in Chlamydomonas

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Pyropia yezoensis are the most cultured marine red algae (Rhodophyte) in Asia and extremely desiccation tolerant. PyMPV17 from P. yezoensis shares amino acid sequence homology with human MPV17, which are the inner mitochondrial membrane and associated with Mitochondrial DNA depletion syndromes. MPV17 homologs are found in all Eukaryotes, whereby mutants in these cause different phenotypes. The molecular function of the MPV17 protein has remained unclear. Yeast ortholog of MPV17, SYM1 mutant not able to growth on the ethanol containing medium at 37oC. Fluorescence of the PyMPV17-GFP fusion proteins was detected in mitochondria like as MPV17 and SYM1. Expression of PyMPV17 in sym1 knock out mutant cells complements the 37°C ethanol growth defect, suggesting that the PyMPV17 is functional orthologs of SYM1. PyMPV17 showed up-regulation in transcription under desiccation in gametophytes of P. yezoensis. Transcription of the PMPV17 gene was also increased by H2O2 and ABA treatment. The transformed Chlamydomonas overexpressing the PyMPV17 gene grew better than those of the control cells with an empty vector on agar plates containing mannitol. These results suggest that the PyMPV17 contributes to the tolerance mechanism for osmotic stress in Pyropia. This is the first study of the physiological function of MPV17 homolog in plants and will contribute to understanding the function of MPV17 gene.

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[GM12]

Functional Characterization of Chloroplast-targeted RNA Methyltransferases in Plant Growth and Stress Responses

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Nucleotide modifications on RNAs and DNAs contribute to gene expression regulation, which is important for development and many other cellular processes in animals and plants. There are more than 150 different modifications identified in different RNAs, but the functions of many of these modifications are still unclear. One of the most common RNA modifications is methylation, which is catalysed by RNA methyltransferases. This research focuses on RNA methyltransferase that are predicted to be targeted to chloroplasts and are proposed to be involved in rRNA methylation, which is essential for chloroplast rRNA processing and translation. In this study, the effects of abiotic stresses on the methylation patterns of chloroplast RNAs were investigated. In addition, RNA methyltransferase- overexpressing transgenic *Arabidopsis* plants and loss-of-function knockout mutants were generated, and the phenotypes of the plants and the methylation patterns of chloroplast genes under normal and stress conditions were analysed. Our results show novel evidence indicating that regulation of RNA methylation in chloroplasts is crucial for the expression and processing of chloroplast genes, which is important for plant growth and stress responses.

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[GM13]

Rice transcriptional factor *OsMYB44* delays leaf senescence by down-regulating ABA biosynthesis

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MYB-type transcription factors (TFs) play essential roles in plant growth, development and respond to environmental stresses. Role of MYB-related TFs of rice in leaf senescence is not well documented. Here, we report the isolation and characterization of a novel MYB-related TF, *OsMYB44*, of rice. Compared with wild-type (WT) plants, transgenic plants over-expressing *OsMYB44* exhibited much stronger delayed leaf senescence phenotype and repressed by abscisic acid (ABA). *OsMYB44* exhibits persistent green leaves during both dark-induced and natural senescence. Our microarray and qRT-PCR analyses showed that its expression was induced in natural senescence and dark induced senescence at various developmental stages. Further studies demonstrated that overexpression of *OsMYB44* could regulate the expression of some ABA synthesis genes (*ABI5*, *NAP*, *CYP707A6*) under dark-induced conditions. Collectively, these results suggested that *OsMYB44* functions as a novel MYB-related TF which plays a critical role in leaf senescence by down-regulating ABA biosynthesis.

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[GM14]

Proteins putatively interact with viroids during viroidal nuclear import

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Viroid is a plant pathogen consisted of a single-stranded, covalently closed circlular non-coding RNA. Viroids must interact with endogenous plant factors for nuclear import, replication and trafficking because of its non-coding nature. Therefore, the interaction between viroids and endogenous plant proteins should be critical in the pathogenic mechanisms, too. However, the details of the viroid-plant protein interaction are largely unknown. Therefore, we have tried to prepare viroid-interacting proteins to study the interaction modes. Among diverse viroids, we chose *HSVd* (*Hop stunt viroid*) as a model viroid, which is a member of *Pospiviroidae* replicating in plant nuclei. As the model proteins, we chose Virp1 (viroid RNA-binding protein1) and TFIIIa (transcription factor IIIA), which has been reported to bind to another Pospiviroidae member, *PSTVd* (*Potato spindle tuber viroid*). We will scrutinize diverse binding characteristics including the interaction mode and kinetic parameters.
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[GM15]

Functional characterization of TALE transcription factor family from woody perennial, poplar.

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In response to endogenous and/or exogenous stimuli, transcription factor (TF) regulates plant growth and development by modulating the rate of transcription initiation of target genes. Among them, a particular class of TF, the Three-Amino-acid-Loop-Extension (TALE) homeoproteins has been shown to control meristem formation and organ morphogenesis in plants. Poplar, a model woody plant, has a total of 35 TALE transcription factors, which is larger than that of Arabidopsis (22 members). As a first step towards understanding functional role of TALE family in woody perennials, the entire TALE family members of *Populus trichocarpa* werecloned in overexpression (PtrTALE-OX) and suppression (PtrTALE-SRDX) constructs. To characterize the molecular function of the poplar TALE TF family, we performed a phenotype-based screening of transgenic Arabidopsis populations, which were created by transformation of either overexpression or suppression of the TF gene constructs. As expected, many transgenic Arabidopsis plants showed altered plant architecture, leaf shaping and apical dominance. Among them, several PtrTALE genes were found to be orthologous to Arabidopsis homologous genes such as *KNAT1*, *KNAT7*, *STM*, and so on. Especially PtrTALE12, which seems like ortholog of Arabidopsis BLH11, showed significantly unique phenotype, multiple shooting. Some persuadable proof has been appeared showing its interacting partner is *STM*, which plays really significant roles in shoot apical meristem, to control *WUSHEL* gene that is core factor to regulate cell population in SAM. RNA-seq has also provided corresponding result and additional keys to explain the phenotype such as circadian rhythm. We will discuss functional significances of the responsible PtrTALE genes and anticipate that this approach will provide novel insights to understand the functional role of TALE TFs in the tree specific growth habits. This work was funded by the Forest Resources Genome Project (2014071G10-1722-AA04) and by a grant from the Basic Science Research Program through the National Research Foundation of Korea (NRF-2015R1D1A1A01060807).

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[GM16]

Bi-cistronic gene expression system was employed to improve woody biomass in both quantity and quality

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Researches on woody biomass production has been increased for a keen interest on the potential renewable resource of alternate energy. Here, we applied a multi-cistronic gene expression system, known as viral 2A peptide, which allows expressing two or more genes under the same promoter. Thus, this system is very useful to express two or more genes at the exactly same spatio-temporal manner. We produced transgenic poplars designed to express both GA20-oxidase (a key enzyme to produce bioactive gibberellin (GA)) and PtrMYB221, a negative regulator of lignin biosynthesis, in developing xylem (DX) tissue-specific. Our transgenic poplars (designated as DX15::PdGA20ox1-2A-PtrMYB221) resulted in a massively increased biomass during growing season of 3 months in LMO field. For examples, the height and diameter of the DX15::PdGA20ox1-2A-PtrMYB221 poplars were increased 143% and 126%, respectively, compared to those of WT without any undesirable side-effects. Interestingly, we found irregular xylem phenotype of the stem cross section and decreased expression of genes involved in the lignin biosynthesis in the DX15::PdGA20ox1-2A-PtrMYB221 poplars. Accordingly, cell wall analyses showed that the lignin contents were decreased about 16%, while cellulose contents were increased up to 40%. Furthermore, saccharification efficiency was significantly improved in the DX15::PdGA20ox1-2A-PtrMYB221 poplars. Our results demonstrate that the controlledproduction of GAs and secondary wall regulating MYB TF through a DX promoter can be utilized as an efficient biotechnological tool for producing enhanced plant biomass without undesirable side effects. This work was funded by the Forest Resources Genome Project (2014071G10-1722-AA04) and by a grant from the Basic Science Research Program through the National Research Foundation of Korea (NRF-2015R1D1A1A01060807).

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[GM17]

INDETERMINATE DOMAIN (IDD) 11 and 7 function in Arabidopsis thaliana

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The INDETERMINATE DOMAIN (IDD) family are characterized by Cys2His2 zinc-finger domain (C2H2) and involved in diversity progress to control plant growth and development. Many IDDs were discovered the function such as involved in flowering time, hormone signaling, architecture, root/shoot/seed development. To finding the function of two IDD11 and IDD7 transcription factors, we identified single mutations, *idd11* and *idd7*, respectively and *idd11 idd7*double mutation inserted by T-DNA. Analyzed amino acid sequence of two IDD transcription factors shows high identical and their expression level in various tissues and development silique also is similar. In seedling 20 day-old on MS agar without sucrose, while the level expression of *SWEET15* (bidirectional sugar transporter) is the lowest in double mutant, *idd11 idd7* compared with each single mutant, *idd11,* id*d7* and wild-type plants. OX-IDD11 and IDD7 transgenic showed higher expression of *SWEET15* than WT. This result suggest that IDD11 and IDD7 may control expression of SWEET15.

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[GM18]

Identification powdery mildew resistnt genes from MR-1 melon

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Powdery mildew (PM) is a botanical disease of the leaves and stalks of the plant, which is infected with many kinds of plant species. We are conducting to isolate the powdery mildew resistance gene from MR-1 line melon which is resistant to PM. In the MR-1(R-line: resistance line) and Topmark (S-line: susceptible line), PM-resistance candidate genes were cloned and their nucleotides and deduced amino acid sequences were compared to identify the genes that are different. After confirming PM-resistance by overexpression of selected candidate genes in Arabidopsis, PM-resistance gene will be identified and it will be developed a molecular marker for using melon PM-resistance breeding system. Currently, we cloned 4 genes from 7 candidate genes (melo3C002434, melo3C002437, melo3C002439, melo3C002440, melo3C002441, melo3C002443, melo3C002445) for MR-1 resistance. We will present current progress in identification of PM resistant gene from MR-1 melon.

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[GM19]

Three fibrillin 1a, 1b, and 2 are involved in photoprotection under high light stress in Arabidopsis

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Fibrillin (FBN) are lipid-associated proteins of plastids and accumulated under abiotic stress. In previous research, FBN1a and 1b are regulated by abscisic acid (ABA) mediation in high light stress. Triple *FBN1a,1b,2* suppressed transgenic plants by RNA interference (RNAi) showed a lower shoot growth development and reduced anthocyanin accumulation under high light/cold stress. However, these reports did not provide completed function of these three FBNs function. So we are investigating again the major roles of FBN1a,1b and 2 in photoprotection. We identified each T-DNA inserted *fbn1a* and *fbn1b* single mutant and *fbn1a fbn1b* double mutant. In addition *fbn2* mutant and *fbn1a fbn1b fbn2* triple mutant were generated by CRISPR/Cas9 gene editing system. We measured maximum quantum yield of photosystem II photochemistry for mutants. The photosynthesis efficiency of double and triple mutants more decreased than WT under high light/cold stress. This result suggests that FBN1a, 1b and 2 is important to enhance photoprotection. Real-time PCR analysis of *FBN1a*, *1b* and *2* for various tissues showed more expression in leave and flower than non-photosynthetic tissues in Arabidopsis. Furthermore, we conducted yeast two-hybrid screening to find interacting proteins with FBN2. This result showed that the FBN2 interacted with PAPP2C, FMA, PTM, PAP1, EF1B.

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[GM20]

Variations in crop productivity induced by *sp* mutant alleles

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Regulation of shoot growth and termination is a major factor for yield improvement in Tomato. *self pruning* (*sp classic*) mutant inducing shoot termination have been used for breeding field tomatoes for last 90 years. Most recent question addressed that shoot life variation under determinate growth give a new window for manipulating tomato yield in the field. In this study, we isolated new three *sp* mutants from 242 Core Collection (C.C) lines, which show tomato yield variations according to the shoot determinacy. Two deletrious *sp* mutants resulted in knock out *SP* expression and splicing variant eliminating second exon, and represented simlar shoot termination with less yield than *sp classic*. A new single amino acid substitution mutant on external loop domain, *sp-5732,* produced sympodial shoots on main shoot and axilary shoots and improved tomato fruit yield up to 142%. Therefore, we suggest that newly discovered *sp* alleles are new resources for manipulating shoot growth and yield of tomato varieties in the field.

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[GM21]

PtDRG1 from pyropia tenera (Rhodophyta) is red algae specific and confer abiotic stress tolerance

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Water stress is a major environmental factor effect on growth and yield of the plants. *Pyropia tenera*(Kjellman) are marine red algae that grow in the intertidal zone and lose more than 95% of water during hibernal low tides. However, proteins, which share sequence homology with stress response proteins such as LEA or USP well known in green plants, are not found in red algae. These results suggest that *Pyropia* (Rhodophyta) may possess novel red algae specific genes that play a role in abiotic stress tolerance mechanism. We identified desiccation response genes (*DRGs*) based on comparison of the transcriptome of *P. tenera* under control and desiccation stress condition. Among them, *PtDRG1* encodes a polypeptide of 22.6 kDa and located in chloroplast. PtDRG1 homologs are found only in Rhodophyte, but not in green plants and other organisms. Transcription of the *PtDRG1* gene was upregulated by osmotic stress induced by mannitol or H_2O_2 as well as desiccation stress. When *PtDRG1* was over-expressed in *Chlamydomonas*, the transformed cells grew much better than control cells under osmotic stress induced by mannitol and NaCl. In addition, the transformed *Chlamydomonas* and *E. coli* cells also exhibit heat tolerance. In vitro assay results demonstrate that PtDRG1 protect the proteins denaturation and keep enzyme activity under high temperature condition. These results demonstrate that *PtDRG1* is red algae specific stress protein and plays a role in tolerance mechanism for abiotic stress such as temperature and desiccation.

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[GM22]

Molecular cloning and functional characterization of ginseng *PgCYP71D184* and *PgCYP76C9* in *Arabidopsis*

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Cytochrome P450 enzymes are a superfamily of monooxygenases that are found in all living organisms, and which represent extraordinary diversity in their reaction chemistry. These enzymes have been used extensively by plants in their subsequent evolution of complex tissues and organs, signaling compounds, odors and defense compounds. Dammarenediol-II is believed to be the first structural basis for the diversification of triterpenoid ginseng saponin, ginsenoside in ginseng following hydroxylation by P450 enzymes and subsequent glycosylation by glycosyltransferase. In Arabidopsis, only 25% of P450 genes have been characterized by heterologous expression or mutant analyses, but more than 70% remain uncharacterized. Here, we report that *PgCYP*71D184 and *PgCYP*76C9 gene is highly expressed in the root, rhizome, and leaves of ginseng. Cytochrome P450 expression patterns under various abiotic stress conditions were also examined.

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[GM23]

PCA17 modulates glucose responses through cysteine- and AMP-dependent manner in Arabidopsis

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Cysteine (Cys) and AMP are products of sulfate metabolism. Cys is an essential amino acid used for protein and peptide synthesis or reduced sulfur donor for biosynthesis of methionine, coenzyme or cofactor, while AMP (adenosine monophosphate) is a monomerin the production RNA and as a product in many metabolism processes. However, whether theirs function involved in abiotic stress adaptation in *Arabidopsis* remains largely unclear. Here, we identified *pca17* mutant that suppressed the insensitively of the parental line *atrzf1* (*Arabidopsis thaliana ring zinc finger 1*) to glucose (Glc) treatment via reducing Cys and AMP accumulations. Under high Glc condition, the transcript levels of genes involved in primary sulfate pathway were significantly lower in *pca17* lead to reducing 60% and 80% Cys contents compare to WT and *atrzf1*, respectively. Moreover, *PCA17*– overexpressing and complementary lines displayed hyper-insensitive under high Glc concentration treatment manifested by the stress insensitive parameters including cotyledon greening and expansion, root elongation and fresh weigh and also Cys, AMP contents. Noticeably, apply exogenous Cys and AMP lead to rescue the phenotype of *pca17* under high Glc treatment. Taken together, our results indicate that PCA17 plays a role in high Glc response through modulating the sulfate metabolism in which related to Cys and AMP accumulations in *Arabidopsis*.

Keywords: AMP, *atrzf1*, *pca17*, cysteine, glucose, sulfate metabolism.

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[GM24]

Sorghum TCP transcription factor *MULTISEED1* affects grain yield regulating at pedicellate spikelet fertility

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Inflorescence architecture mainly contributes to final grain yield in crops. Sorghum inflorescence is basically composed of one fertile sessile spikelet (SS) and two infertile pedicellate spikelets (PS). To identify regulatory factors involved in the inflorescence architecture, we screened an EMS mutagenesis population from the pedigreed sorghum mutant library. We found inflorescent architecture mutants, named as multi-seed mutants, *msd*, with gained fertile ability in PS and also an increased number of floral branches. In natural sorghum populations, it is not common that are fertile. A detailed dissection of developmental stages of wild type and *msd1* mutant described that the PS in wild type do not have floral organs, including ovary, stigma, filament and anther, while the *msd1* mutants generate intact floral organ in the sessile spikelet. We found *MSD1* encoded a TCP transcription factor using bulk segregant analysis (BSA) of F2 population, and was a strongly enriched expression during inflorescence developmental stages. We proposed that *MSD1* functions to suppress floral organ maintenance at PS during inflorescence development in Sorghum. To explore the regulatory network associated with PS fertility, whole genome expression profiling was performed at 4 different developmental stages in 6 various tissue types between wild type and *msd1*. Taken together, we demonstrated that *MSD1* was involved in the plant hormone and maybe influenced program cell death in PS via the activation of plant hormonal pathway.

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[GM25]

OsWRKY67 Plays a Positive Role in Basal and XA21-Mediated Resistance in Rice

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WRKY proteins play important roles in transcriptional reprogramming in plants in response to various stresses including pathogen attack. In this study, we functionally characterized a rice WRKY gene, *OsWRKY67*, whose expression is upregulated against pathogen challenges. Activation of *OsWRKY67* by T-DNA tagging significantly improved the resistance against two rice pathogens, *Magnaporthe oryzae* and *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). Reactive oxygen species (ROS) rapidly accumulated in *OsWRKY67* activation mutant lines in response to elicitor treatment, compared with the controls. Overexpression of *OsWRKY67* in rice confirmed enhanced disease resistance, but led to a restriction of plant growth in transgenic lines with high levels of OsWRK67 protein. *OsWRKY67* RNAi lines significantly reduced resistance to *M. oryzae* and *Xoo*isolates tested, and abolished XA21-mediated resistance, implying the possibility of broad-spectrum resistance from OsWRKY67. Transcriptional activity and subcellular localization assays indicated that OsWRKY67 is present in the nucleus where it functions as a transcriptional activator. Quantitative PCR revealed that the pathogenesis-related genes, *PR1a*, *PR1b*, *PR4*, *PR10a,* and *PR10b*, are upregulated in *OsWRKY67* overexpression lines. Therefore, these results suggest that OsWRKY67 positively regulates basal and XA21-mediated resistance, and is a promising candidate for genetic improvement of disease resistance in rice.

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[GM26]

Enhancing flower color through simultaneous expression of the *B-Peru* and *mPAP1* transcription factors under control of a flower-specific promoter

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Flower color is a main target for flower breeding. Production of novel flower color in transgenic plants requires a transgene that confers the desired trait with a flower-specific promoter. Here, we expressed the *B-peru* gene encoding a basic helix loop helix (bHLH) transcription factor (TF) together with the *mPAP1* gene encoding an R2R3 MYB TF to enhance flower color in tobacco (*Nicotiana tabacum* L.) plants, using the tobacco *anthocyanidin synthase* (*ANS*) promoter (PANS) to drive flower-specific expression. The transgenic tobacco plants grew normally and produced either dark pink (PANSBP_DP) or dark red (PANSBP_DR) flowers. The expression of four structural genes from the flavonoid biosynthetic pathway increased significantly in both PANSBP_DP and PANSBP_DR lines, compared with the non-transformed (NT) control. Interestingly, the expression of two regulatory genesthat are components of the active MYB-bHLH-WDR (MBW) complex decreased significantly in the PANSBP_DR plants but not the PANSBP_DP plants. Total flavonol and anthocyanin abundance correlated with flower color, with an increase of 1.6 - 43.2 fold in the PANSBP_DP plants and 2.0 - 124.2 fold in the PANSBP_DR plants. Our results indicate that combinatorial expression of *B-peru* and *mPAP1* genes under control of the *ANS* promoter can be a useful strategy for intensifying flower color without growth retardation.

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[GM27]

Genome-wide identification of rice collar preferred genes using meta-expression analysis (RNA-seq) and construction of the regulatory network

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Little and tiny organ, ligule is able to have an effect on whole plant. The ligule is a thin and tongue-like white membrane in some plants including Rice. In rice, the ligule works many things as a column, umbrella and humidifier. However, we actually don't know the ligule specific gene and sequence. To effectively address this limitation, selection of useful candidate genes and identification of major regulatory factors through global approaches are necessary. So This paper used meta-expression analysis data and network analysis data from NCBI Gene Expression Omnibus about collar preferred gene to find out ligule specific gene. And identified 654 rice genes commonly differentially expressed under collar specific conditions. Gene ontology enrichment analysis show the quality and correlation about selected genes for ligule specific genes. Additionally, Regulation, Metabolism, Transcription and biotic stress overview were predicted with MapMan analysis. Using these methods, we can analyze the suitability of candidate genes. uncovering veiled information of the ligule specific genes will contribute to increase major crops production and aid additional experiment.

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[GM28]

CRISPR/Cas9-mediated RabA1 subfamily mutagenesis

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RabA1 members appear to function in divergent processes such as auxin-mediated protein trafficking, cytokinesis. As a sessile organism, the plant has to adjust to the variousenvironmental changes and interact with the variety of environmental microorganisms. However, these molecular mechanisms of RabA1 in the immune responses have not yet been clearly identified in plants. We applied a CRISPR_Cas9 tool to generate specific mutants of the RabA1 group from *RabA1a* to *RabA1i*. These mutants will be compared with previously validated mutants. We will identify gene members that function in a plant immune responsive mechanism to environmental microbes.

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[GM29]

MPSR1 is an early response E3 ligase that immediately eliminates emergent misfolded proteins

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Protein quality control is important cellular process for maintaining proteostasis and ubiquitin E3 ligases are crucial for eliminating misfolded proteins, which form cytotoxic aggregates that inhibit cellular fitness. However, there are few studies about how emerging misfolded proteins in the cytoplasm can be selectively recognized and eliminated by E3 ligases in plants. We found that Misfolded Protein Sensing RING E3 ligase 1 (MPSR1) is an indispensable E3 ligase required for plant survival after protein-damaging stress. Without stress, MPSR1 is prone to rapid degradation by the 26S proteasome, concealing its Protein Quality Control (PQC) E3 ligase activity. Upon proteotoxic stress, MPSR1 directly senses incipient misfolded proteins and tethers ubiquitins for subsequent degradation. Furthermore, MPSR1 sustains the structural integrity of the proteasome complex at the initial stage of proteotoxic stress. Here we suggest that the MPSR1 pathway is a constitutive mechanism for proteostasis under protein-damaging stress, as a novel front-line surveillance system in the cytoplasm.

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[GM30]

ORESARA15, a PLATZ transcription factor, mediates leaf growth and senescence in Arabidopsis

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Plant leaves undergo a series of developmental changes from primordium initiation through growth and maturation to senescence throughout their lifespan. Although the mechanisms underlying leaf senescence have been intensively elucidated, our knowledge of the interrelationship between early development and senescence is still fragmentary because most studies on leaf senescence have mainly focused on the biological processes that occur during the maturation to death stage. Here, we identified the *oresara15-1Dominant* (*ore15-1D*) mutant with an extended leaf longevity under natural and stressed conditions and an enlarged leaf size, from activation-tagged lines of Arabidopsis. ORE15 encodes a PLANT A/T-RICH SEQUENCE- AND ZINC-BINDING PROTEIN family transcription factor. Anatomical and molecular genetic analyses in *ore15-1D* and *ore15-2*, a loss-of-function mutant of ORE15, demonstrated that ORE15 enhanced leaf growth by promoting the rate and duration of cell proliferation in the earlier stage and suppressed leaf senescence in the later stage. Taken together, our study highlighted molecular conjunction through ORE15 between two temporally separated developmental processes during leaf lifespan, growth and senescence, by modulating the *miRNA396*-GROWTH-REGULATING FACTOR (GRF)/GRF-INTERACTING FACTOR regulatory pathway.

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[GM31]

Feedback Loop Mechanisms of LBD18 for RegulatingARF Expression and Transcriptional Activity in Arabidopsis

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The root system of dicotyledonous plants consists of a primary root and lateral roots. Lateral roots are a major determinant of root system architecture that affects the efficiency of water and nutrient acquisition of plants. Plant hormone auxin plays major roles in every step of lateral root development. The auxin signaling pathway in Arabidopsis involves two types of regulators, the AUXIN RESPONSE FACTOR (ARF) transcription factors and the Aux/IAAtranscriptional repressors that are associated with ARFs. In Arabidopsis, a hierarchy of regulatory genes controlling lateral root formation via auxin signaling have been identified, including the *ARF7/ARF19–LATERAL ORGAN BOUNDARIES DOMAIN16 (LBD16)/LBD18* transcriptional network via the *AUX1/LIKE–AUX(LAX)3* auxin influx carriers. ARF7 and ARF19 control lateral root formation in part via the activation of their downstream targets, *LBD16* and *LBD18*. The *LBD* genes encode a class of transcription factors that play important rolesin a plethora of plant growth and development. Here we provide molecular evidence that *LBD18* acts in a positive feedback loop to increase ARF activity. We demonstrated that LBD18 upregulates *ARF19* expression by directly binding the *ARF19* promoter. We further showed that LBD18 enhances ARF7 transcriptional activity by binding to ARF7 and also suppresses Aux/IAA binding to ARFs through the competitive interaction with the PB1 (Phox and Bem1) protein–protein interaction domain (previously referred to as domain III/IV) of ARFs. These results suggest that a dual mode of a positive feedback loop exerted by LBD18 for ARF expression and transcriptional activity may override a negative feedback loop mediated by Aux/IAA proteins. These interwound feedback loops mediated by ARF19 and LBD18 may provide a robust feedback mechanism for sustained lateral root formation in response to auxin. This study was supported by grants from the Next-Generation BioGreen 21 Program (PJ031220), RDA, Republic of Korea and Mid-career Researcher Program (2016R1A2B4015201) and Basic Research Laboratory (2017R1A4A1015620) through the National Research Foundation of Korea, funded by the Ministry of Education, Science, and Technology of Korea to J. Kim.

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[DP1]

Characterization of Three Related Zinc-Finger Protein Genes Expressed in the Outermost Layers of Root Caps in *Arabidopsis*

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To identify genes regulating the root development of *Arabidopsis*, the *UAS* activation tags were introduced into the background of *Q2610* where GAL4-VP16 is highly expressed in the root tip. A dominant mutant developing short and twisted root was isolated and named as *defective root development 2-D* (*drd2-D*). The T-DNA tag was localized in the promoter region of a gene coding for an EAR-motif-containing zinc-finger (ZF) protein. The ectopic expression of the *ZF* gene recapitulated the *drd2-D* phenotype and suppressed the growth of above-ground organs as well. The expression of reporter genes driven by the *ZF* promoter was observed in the border cells of the root cap and this expression pattern was not altered in *sombrero* accumulating additional root cap layers. The *ZF* gene expression was also observed in the tissues undergoing maturation such as cortex, vasculature, and hydathodes. Two related *ZF* genes in Arabidopsis also specifically expressed in the border cell and their misexpression led to severe growth inhibition of the seedlings. These results suggest that these three *ZF*genes might play shared roles in the border cell maturation in the root cap.

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[DP2]

Reduced Expression of a Homeo-Domain Gene Leads to the Defects in the Development of Inflorescence and Abscission of Floral Organs

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Partial loss-of-function mutants could be used to understand the fine functions of a gene of which a null mutation leads to severe defects. *poltergeist* (*pol*) provides a proper genetic background to screen for weak mutants possessing minute defects in shoot meristem. Here, *filamentous gynoecium-1* (*fig-1*) displaying slightly reduced floral meristem together with abscission defects of floral organs has been screened from a mutant pool raised by the activation tagging of *pol-6* background. The tag was localized in the promoter of a homeo-domain gene. *fig-1*single mutant is recessive and exhibits defects in the detachment of floral organs mainly due to the fusion of sepals. *fig-2* and *fig-3*, other T-DNA insertion mutants with reduced expression of the homeo-domain gene exhibited defective inflorescence together with the abscission defects. The expression patterns of the abscission-related reporters such as *HAESApro:GUS* and *KNAT2/6pro:GUS* in the *fig* mutants were not altered compared with those in the wild type suggesting that the homeo-domain gene is involved in the organ boundary determination instead of abscission zone formation itself.

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[DP3]

A Partial Loss-of-Function Allele of PLL1 Reveals the Roles of POL/PLL1 in the Stem Cell Maintenance in Both Shoot and Root Meristems of *Arabidopsis*

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POLTERGEIST (*POL*) and *POL-LIKE1* (*PLL1*) coding for related protein phosphatase 2Cs are required for the establishment of shoot/root meristems during embryogenesis. As strong *pol pll1* mutants are seedling-lethal due to the lack of hypocotyl vasculature, their late developmental phenotypes could be observed only via grafting. To avoid any undesirable effect possibly led by grafting, a weak *pll1* allele (*pll1-4*) has been selected among the T-DNA insertion mutants and a partial loss-of-function double mutant (*pol*-6 *pll1-4*) has been prepared. About 10% of *pol*-6 *pll1-4* seedlings developed the hypocotyl vasculature and were able to grow spontaneously. The above-ground organs of *pol*-6 *pll1-4* phenocopied the *wuschel* mutant by developing adventitious inflorescence and defective flowers lacking any carpel together with reduced *CLV3pro:GUS* expression. *POL/PLL1* is epistatic to *CLV2/3* both in vegetative and reproductive stages. *pol*-6 *pll1-4* also exhibited reduced root meristem with reduced *WOX5pro:GUS* and *SCRpro:GUS* expression. Unexpectedly the weak *pll1-4* was induced by a point mutation in a conserved PP2C motif instead of the T-DNA insertion in the promoter region of *PLL1*.

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[DP4]

The Rice Rolled Fine Striped (RFS) CHD3/Mi-2 chromatin remodeling factor epigenetically regulates genes involved in oxidative stress during development

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In rice (*Oryza sativa*), moderate leaf rolling increases photosynthetic competence and raises grain yield; therefore, this important agronomic trait has attracted much attention from plant biologists and breeders. However, the relevant molecular mechanism remains unclear. Here, we isolated and characterized *Rolled Fine Striped* (*RFS*), a key gene affecting rice leaf rolling, chloroplast development, and reactive oxygen species (ROS) scavenging. The *rfs-1* gamma-ray allele and the *rfs-2* T-DNA insertion allele of *RFS* failed to complement each other and their mutants had similar phenotypes, producing extremely incurved leaves due to defective development of vascular cells on the adaxial side. Map-based cloning showed that the *rfs-1* mutant harbors a 9-bp deletion in a gene encoding a predicted CHD3/Mi-2 chromatin remodeling factor belonging to the SNF2-ATP-dependent chromatin remodeling family. *RFS* was expressed in various tissues and accumulated mainly in the vascular cells throughout leaf development. Furthermore, *RFS* deficiency resulted in a cell death phenotype that was caused by ROS accumulation in developing leaves. We found that expression of five ROS-scavenging genes (encoding catalase C, ascorbate peroxidase 8, a putative copper/zinc superoxide dismutase, a putative superoxide dismutase, and peroxiredoxin IIE2) decreased in *rfs-2* mutants. Western-blot and chromatin immunoprecipitation (ChIP) assays demonstrated that *rfs-2* mutants have reduced H3K4me3 levels of ROS-related genes. Loss-of-function in *RFS* also led to multiple developmental defects, including pollen development, grain filling, and root development. Our results suggest that *RFS* is required for many aspects of plant development and its function is closely associated with epigenetic regulation of genes that modulate ROS homeostasis.

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[DP5]

High Ambient Temperature Represses Anthocyanin Biosynthesis through Degradation of HY5

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Anthocyanins are flavonoid compounds that protect plant tissues from many environmental stresses including high light irradiance, freezing temperatures, and pathogen infection. Regulation of anthocyanin biosynthesis is intimately associated with environmental changes to enhance plant survival under stressful environmental conditions. Various factors, such as UV, visible light, cold, osmotic stress, and pathogen infection, can induce anthocyanin biosynthesis. In contrast, high temperatures are known to reduce anthocyanin accumulation in many plant species, even drastically in the skin of fruits such as grape berries and apples. However, the mechanisms by which high temperatures regulate anthocyanin biosynthesis in Arabidopsis thaliana remain largely unknown. Here, we show that high ambient temperatures repress anthocyanin biosynthesis through the E3 ubiquitin ligase CONSTITUTIVE PHOTOMORPHOGENIC1 (COP1) and the positive regulator of anthocyanin biosynthesis ELONGATED HYPOCOTYL5 (HY5). We show that an increase in ambient temperature decreases expression of genes required in both the early and late steps of the anthocyanin biosynthesis pathway in Arabidopsis seedlings. As a result, seedlings grown at a high temperature (28◦C) accumulate less anthocyanin pigment than those grown at a low temperature (17◦C). We further show that high temperature induces the degradation of the HY5 protein in a COP1 activity–dependent manner. In agreement with this finding, anthocyanin biosynthesis and accumulation do not respond to ambient temperature changes in cop1 and hy5 mutant plants. The degradation of HY5 derepresses the expression of MYBL2, which partially mediates the high temperature repression of anthocyanin biosynthesis. Overall, our study demonstrates that high ambient temperatures repress anthocyanin biosynthesis through a COP1–HY5 signaling module.

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[DP6]

Systemic study of *IDD* gene family in Tomato

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Multiple functions of INDETERMINATE DOMAIN (IDD) family have been evolved as transcriptional regulator controlling plant development such as root, shoot and flowering, which are crucial targets for crop improvement. However, tomato *IDD* gene family are largely uncharacterized and unknown. Here, we studied systemically *IDD* gene family in Tomato. We summarized *IDD* gene family information from publically available database. 18 *IDD* genes were isolated by reciprocal Blast P analysis, gene expression and phylogenetic tree. Interaction partners of *IDD* genes were predicted by prediction of protein binding. *CR-idd*s have been successfully induced by multi-target CRISPR/Cas9 system. On this works, we would characterize an conserved and diversified functions of IDDs from phenotypes of *CR-idds*, functional protein interaction and gene expression on the plant tissue through developmental stages.

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[DP7]

A poplar MYB transcription factor PtrMYB012, identified as orthologous to GAMYB, is incompletely regulated by Arabidopsis miR159 family

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A phenotype-based screening of the T1 transgenic Arabidopsis population transformed by overexpression constructs of the entire poplar MYB TF family found that overexpression of a poplar MYB transcription factor, *PtrMYB012*, in Arabidopsis resulted in upwardly curled rosette leaves, dwarfism, and male sterility. Sequence analysis identified that *PtrMYB012* is homologous to the Arabidopsis GAMYB genes (e.g., *AtMYB65* and *AtMYB33*). Gene expression analysis revealed that *PtrMYB012* is specifically expressed in floral tissues, especially in male catkins, similar to *AtMYB65*. It was well known that Arabidopsis GAMYBs are negatively regulated by microRNA159 (miR159) during vegetative growth; thus, the canonical phenotypes of upwardly curled leaves, dwarfism, and male sterility were only shown in overexpression of GAMYBs with mutations in the miR159 target sequence. To confirm our phenotypic consequences, we independently re-produced transgenic Arabidopsis plants overexpressing *PtrMYB012* without mutations in the miR159 target sequence. The resulting 35S::*PtrMYB012* Arabidopsis plants phenocopied the previous transgenic Arabidopsis plants, suggesting that *PtrMYB012* is probably not a target of Arabidopsis miR159 despite containing the conserved miR159 target sequence. To gain further insight, we produced transgenic poplars overexpressing the intact PtrMYB012. As a result, no conspicuous phenotype was found in *35S::PtrMYB012* poplar plants. These results suggest that *PtrMYB012* transcripts are down-regulated by miR159 in poplar but not in Arabidopsis. Indeed, subsequent 5'-RACE analysis confirmed that *PtrMYB012* transcripts are completely degraded in poplar, probably by miR159, but not in Arabidopsis. These results suggest that species-specific family members of miR159 are important for normal growth and development in plants. This work was funded by the Basic Science Research Program through the National Research Foundation of Korea (NRF) (2011-0008840) and a grant from the Korea Forest Service (S111213L080110).

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[DP8]

Overexpression of RAV1 negatively regulates seed development in *Arabidopsis*

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As plant-specific B3-transcription factor RAV1 also holds AP2 domain for DNA binding domains, its transcriptional regulation covers various aspects of plant development and stress responsiveness. We previously reported that RAV1 is a master negative regulator of growth. In addition to the general growth-retarded phenotypes, in this study, we found that seed development was also defective in RAV1-overexpressing plants. Silique length was reduced and many seeds in the silique were aborted or unfertilized in the RAV1 overexpressing plants. Even normal-looking matured seeds from the RAV1 overexpressing plants were smaller and lighter than those of wild type plants. Around 5 % of seeds exhibited aberrant shape after fully matured and these seeds showed reduced germination efficiency, indicating that seed viability was already lost in developing seeds. To investigate whether the defective seed development is involved with the endosperm and embryo development, we examined expression levels of the genes, *MINI3* and *IKU2* that are known for these processes. Expression of the *MINI3* and *IKU2* were reduced in RAV1-overexpressor comparing with the wild type. Taken together, these results suggest that over expression of RAV1 negatively regulated seed development, leading to the reduced germination.

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[DP9]

stablized1-1 enhancer shows pronounced defects of stabilized1-1 in pre-mRNA splicing, miRNA accumulation, and development

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The *STABLIZED1* (*STA1*) gene encodes an Arabidopsis homolog of *PRP6* pre-mRNA processing factor that is involved in the mRNA splicing and miRNA biogenesis. *STA1*expression is induced by cold and heat stresses, and the *stabilized1-1* (*sta1-1*) mutant accumulates more unspliced transcripts of a set of genes and less mature miRNA compared to wild type. In order to understand the STA1 functions, we EMS-mutagenized *sta1-1* and screened for *sta1-1*modifiers. Here, we report the identification and characterization of a *sta1-1* enhancer, #310-5-3. Splicing defects of *EMB* and *HSFA* were enhanced in #310-5-3 compared to *sta1-1*. Also, pri-miRNA accumulations of #310-5-3 were increased and miRNA accumulations of #310-5-3 were decreased in comparison to *sta1-1*. Moreover, #310-5-3 was smaller than *sta1-1* and defective in apical dominance and phyllotaxy. To identify the gene responsible for the #310-5-3 phenotypes, we performed a map-based cloning combined with the whole genome sequencing and identified a putative mutation in a gene that encodes a zinc finger CCCH domain-containing protein.

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[DP10]

Identification of stl1-1 suppressor that are recovered from the stl1-1 defect.

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Arabidopsis *small and thick leaves1-1* (*stl1-1*) mutant was isolated because of small and thick leaves, hence the name. *stl1-1* also shows pleiotropic defects in developments. Some of these developmental defects include overall small size, uprising leaves, short main inflorescence, sporadic fasciation, and small roots. To identify the genetic interactors of STL1, we chemically mutagenized *stl1-1* and screened for *stl1-1* suppressors that are recovered from small size. We successfully identified *stl1-1* suppressors. Despite the size recovery, these *stl1-1* suppressors showed the various levels of restoration in the other *stl1-1* defects such as uprising leaves, short main inflorescence, sporadic fasciation, and small roots. These results suggest that the *stl1-1* size suppressor genes function at the different development programs.

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[DP11]

Functional analysis of monocotyledonous phytochromes in Arabidopsis thaliana

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Phytochromes are red and far-red photoreceptors that regulate various aspects of plant growth and development. Although their functions have been studied extensively in *Arabidopsis thaliana*, the functional difference between dicotyledonous and monocotyledonous phytochromes has not been studied well. Thus, we generated and analyzed *A. thaliana* transgenic plants overexpressing monocotyledonous phytochromes. In this study, among three phytochrome genes (*BdPHYA*, *BdPHYB*, and *BdPHYC*) in the genome of a monocot model plant *Brachypodium distachyon*, *BdPHYA* and *BdPHYB* genes were introduced into phyA (*phyA-201*), phyB (*phyB-9*), or double (*phyA-201phyB-9*) mutant of *Arabidopsis thaliana* (L*er* ecotype), and functional analysis was performed using homozygous transgenic plants to determine the functional specificity of monocotyledonous phytochromes. The *phyA-201* transgenic plant expressing *BdPHYA* displayed responses to far-red light and the *phyB-9* transgenic plant with *BdPHYB* showed responses to red light, demonstrating that BdphyA mediates far-red photoresponses and BdphyB mediates red photoresponses, similarly in *A. thaliana*. Interestingly, the *phyA-201phyB-9* transgenic plant with *BdPHYA* showed the functional rescues of phyA and phyB deficiency, displaying responses to both far-red and red lights. The transgenic plants with *BdPHYA*recovered phyB-deficient phenotypes such as etiolated hypocotyls under red light, elongated petioles and inflorescence stems, reduced chlorophyll accumulation, and early flowering. In contrast, the *phyA-201phyB-9* transgenic plants with *BdPHYB* showed the functional rescue of phyB only, but not phyA. Therefore, these results suggest that the monocot phyA might play roles in both far-red and red light responses, while the dicot phyA mainly mediates far-red light response only.

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[DP12]

Analysis of phytochrome-mediated light responses in a monocot model plant, Brachypodium distachyon

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Brachypodium distachyon is suggested to be a new and alternative monocot model plant. Phytochromes are photoreceptors that regulate many aspects of plant growth and development in response to red and far-red light signals from the environment. So far, phytochrome-mediated light signaling has been studied extensively in a dicot model plant, *Arabidopsis thaliana*, but it has not been investigated well in monocot plants. Thus, we generated transgenic *B. distachyon* plants overexpressing *Avena sativa* phytochrome A (AsphyA) or *Arabidopsis thaliana* phytochrome B (AtphyB), and investigated phytochrome-mediated light responses using the transgenic plants. Brachypodium plants overexpressing AsphyA were hypersensitive to far-red light and showed early flowering compared with wild-type plants. In contrast, transgenic plants with AtphyB were hypersensitive to red light and showed reduced apical dominance, leading to increases in tiller numbers as well as leaf numbers per plant. Moreover, flowering was delayed in the transgenic plants overexpressing AtphyB, producing more seeds per spikelet and thus total seeds per plant. In the presentation, detailed results of the transgenic Brachypodium plants overexpressing AsphyA and AtphyB will be discussed.

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[DP13]

Patatin domain containing phospholipase A2 gene from ginseng plays a role in cell wall development in *Arabidopsis* and Poplar

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Lipid acyl hydrolase are diverse group of enzymes that hydrolyze the ester or amide bonds of fatty acid in plant lipids. Patatin-related phospholipase A is a major family of lipid acyl hydrolases and plays important roles in diverse cellular processes including phospholipid digestion, metabolism, cell growth, signal transduction, and plant response to environmental stresses. The pPLA gene family can be classified into 3 groups: pPLAI, pPLAII (α, β, γ, δ, ε), and pPLAIII (α, β, γ, δ). pPLAIII proteins are distinguished from the other conventional lipases with a lack of the canonical lipase consensus catalytic motif. Although the function of *pPLAI* and *pPLAII* genes implicated in cell elongation, auxin response, gravitropism, guard cell movement, and defense are reported, enzymatic activity and cellular functions of *pPLAIII* have not yet fully studied. Here we want to discuss about the other unknown functions of a *pPLAIII* gene from one of the well-known medicinal ginseng plant in *Arabidopsis* and Poplar. Cytohistological and its relevant biochemical analysis as well as transcripts changes suggest its role in secondary cell wall development.

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[DP14]

Plant Regeneration of Platycodon grandiflorum Callus by NAA and BA and Tracheary Element Differentiation Rate by Auxin Inhibitors.

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Balloon flower (*Platycodon grandiflorum*) has a saponin component and a high medicinal value for asthma. In this study, calli from 3 kinds of ballon flowers were induced on MS medium supplemented with 0.1 ppm 2,4-D and 1.0 ppm BA. And regeneration frequency of shoots and roots formation from calli was the highest on 2.0 ppm NAA and 1.0 ppm BA with 25.71% (in *P. grandiflorum* for. *albiflorum* leaf originated callus) and 47.37% (in *P. grandiflorum*stem originated callus), respectively. Also we investigated the effect of three auxin inhibitors NPA, mepiquat, and paclobutrazol on the differentiation of tracheary element (TE), an key requirement for plant regeneration. The inhibitors were treated at 10, 20 and 50 ¥Íì¥Ìand the length(or area) of TE formed was measured. The higher the concentrations of paclobutrazol, the higher was the TE differentiation rate. But in the case of mepiquat and NPA the TE differentiation rate was inversely proportional to concentrations. However, the length or area of TE was not related to the concentrations of the auxin inhibitors.

Key word : Platycodon grandiflorum, Plant Regeneration, Auxin Inhibitors

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[DP15]

Overexpression of Antarctic moss genes in *Arabidopsis* improves stress tolerance

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Antarctic plants survive the extreme conditions of very low temperatures, high lights, and high salt conditions. These stress tolerance traits in polar plants could be introduced to other plants by heterologous expression. To test this, two genes from *Polytrichastrum alpinum*, an Antarctic moss, were isolated and individually overexpressed in Arabidopsis. Homozygous T4 generation lines of the polar gene overexpressing Arabidopsis were analyzed for growth/development characteristics and stress tolerance. Overexpression of each of two *P. alpinum* genes resulted in increased growth in transgenic lines compared to wild type (WT) under normal conditions. One polar moss gene overexpressing line also showed enhanced photosynthesis compared to wild type (WT) under salt stress. In germination, all overexpressors germinated better than WT in salt or osmotic stress, but not in ABA treatment. One overexpressor of the two polar gene overexpressing plants was hyposensitive to ABA treatment in chlorophyll retaining. At post-germination stage, not all overexpressors displayed higher root elongation in these conditions; only in salt conditions the overexpressing plants grew longer roots than WT. In summary, our results suggest that two *P. alpinum* genes function differently at germination and post-germination stages in terms of stress tolerance.

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[DP16]

Global analysis of differentially expressed genes between japonica and indica rice roots reveals the molecular basis for enhanced cold tolerance in japonica rice

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Plant roots provide important support for plant growth, acquiring water and nutrients, and anchoring the plants. Rice varieties have been cultivated and improved through crossbreeding of *japonica* (Dongjin) rice and *indica*(IR64) rice varieties, which have various contrasting characteristics in important traits including root development. Using Agilent 44K array analysis, we isolated 564 genes from Dongjin that were significantly upregulated relative to expression in IR64 and 251 genes upregulated in IR64 compared with Dongjin. Through MapMan analysis, we determined that four ascorbate peroxidase (APX) and glutathione peroxidase (GPX)-related genes closely associated with response to oxidative stress from Gene ontology (GO) enrichment analysis were more important in the roots of Dongjin than in IR64. We further confirmed that the APX and GPX enzyme activities under cold stress were higher in Dongjin than in IR64. These results explain why the *japonica* cultivar is more resistant to cold stress than the *indica*cultivar. Our results can be used as an important basis for future studies on useful traits related to root development and abiotic stress tolerance in rice.

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[DP17]

Characterization and cloning of the wow (WONDER WOMAN) mutant related with the shoot meristem development

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All of tissues and organs of aerial parts of mature plants are originated from the stem cells in the shoot apical meristem (SAM). Thus, mutants involved in the SAM development signaling pathway usually present the abnormal structure of the SAM and unbalanced organ growth and development. Here we report a new recessive mutant originally isolated from an activation-tagging mutant pool. Because of the increased number of carpel in its flowers, we designated it as *wonder woman* (*wow*). This mutant showed increased stem cell population leading to enlarged SAM and increased flower organ number like *clv3*. Moreover, since the enlarged shoot meristem of *wow*is less sensitive to constitutive treatment of synthetic CLV3 peptide (CLV3p), it indicates that WOW is probably involved in CLV signaling pathway related the shoot meristem development. In addition, through the epistatic analysis among *wow*, *clv3* and *wus* mutants, we confirmed that *WOW* acts in the *CLV-WUS* genetic pathway. Thus, our results suggest that WOW plays a role inthe shoot meristem development and may be a factor affecting plant growth and development. Map-based cloning revealed that the mutation site is located on chromosome 3 and narrowed into 244 kb region (8,068,104 - 8,312,407 bp) containing 62 genes. We selected 10 candidate genes located at near center position between narrowed SNP markers. Seven of them are related with signaling cascades. Currently, we have been investigating the mutation site by comparing gene sequences of *wow* with those of WT. Moreover, we also try to confirm that the knock-out phenotype of candidate genes is consistent with *wow* phenotype shown in *wow*.

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[DP18]

Genome-wide identification of genes involved in the cold stress response and circadian rhythm and analysis of its crosstalk in rice by using meta-expression analyses.

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To understand the crosstalk between low temperature stress and circadian regulation in rice, a model crop plant, we used two different meta-expression databases. The first database contains Affymetrix array data for abiotic stresses, whereas the other contains Agilent 44K array data from 202 leaf samples collected from 9 developmental stages and can be used for circadian expression analysis. We identified 885 genes that were upregulated at least 2-fold under low temperature conditions and 572 genes that were downregulated. Of the upregulated genes, 119 showed circadian expression patterns; of the downregulated genes, 346 showed circadian expressionpatterns. Gene Ontology (GO) enrichment analysis revealed that polysaccharide catabolic processes and protein amino acid dephosphorylation were overrepresented in the genes upregulated under cold stress with circadian rhythm, whereas cytokinin metabolic processes and photosynthesis were overrepresented in the genes downregulated under cold stress with circadian rhythm. MapMan regulation overview analysis suggested that the candidate genes were likely to be involved in photoinhibition and hormonal regulation, indicating that cold stress and hormone responses might be linked. These results expand our knowledge about the circadian rhythm-mediated cold stress response.

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[DP19]

The Role of *LBD14* in Lateral Root Development during ABA Response in Arabidopsis

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The *LATERAL ORGAN BOUNDARIES* (*LOB*) *DOMAIN/ASYMMETRIC LEAVES2-LIKE* (*LBD/ASL*) gene family encodes plant-specific transcription factors, which harbour a conserved LOB domain in the N-terminus, and this gene family plays an important role in regulating diverse aspects of plant development. There are 42 *LBD* genes in Arabidopsis, 35 *LBD* genes in rice, and 43 *LBD* genes in maize, and *LBD* homologues have been further identified in various other plant species. The plant root system consists of a primary root derived during embryogenesis and lateral roots (LRs) and secondary roots that form post-embryonically. LRs are a major determinant of the root system architecture, which is important for root anchoring, nutrient and water uptake, and storage, and it is vital for the growth and survival of plants. Auxin critically regulates every step of the process of Arabidopsis LR development. Accumulating evidence has suggested that ABA plays an important role in LR formation. In this study, we showed that LBD14 is a transcriptional activator promoting LR formation and is involved in the ABA response to suppress the LR formation in Arabidopsis. Our RNA interference (RNAi) and gain-of-function studies suggested that *LBD14* promotes LR formation by enhancing developmental kinetics of both LR primordium and LR emergence. Analysis of β-glucuronidase (GUS) expression showed that *LBD14* is expressed in the root stele and in primordium during LR development and that exogenous treatment of ABA downregulates *LBD14* expression in those root tissues. ABA further suppresses the LR formation in dexamethasone(DEX)-inducible *LBD14-RNAi* transgenic Arabidopsis lines upon DEX treatment, relative to that observed with mock treatment, indicating that *LBD14* is involved in the ABA response to suppress LR formation. Taken together, these results suggest that *LBD14* promoting LR formation is one of the critical factors regulated by ABA to inhibit LR growth, contributing to the regulation of the Arabidopsis root system architecture in response to ABA. This work was supported by grants from the Next-Generation BioGreen 21 Program (PJ0013220), Rural Development Administration, Republic of Korea, and Mid-career Researcher Program (2016R1A2B4015201) and Basic Research Laboratory (2017R1A4A1015620) through the National Research Foundation of Korea, funded by the Ministry of Education, Science, and Technology of Korea, to J. Kim.

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[DP20]

OsVIL2 encoding a chromatin remodeling factor controls spikelet development in rice.

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Flower organ patterning is accomplished by spatial and temporal functioning of various regulatory genes. We previously reported that *OsVIL2* induces flowering by mediating the trimethylation of Histone H3 on *LFL1* chromatin. In this study, we report that *OsVIL2* also plays crucial roles during spikelet development. Two lines of T-DNA insertional mutants in the gene displayed abnormal spikelet development and altered organ numbers. Whereas the number of rudimentary glumes was increased in *osvil2* mutant spikelets, that of empty glumes was decreased. The mutants also had more lemma, palea, and lodicules, but the extra organs were often abnormal. Although stamen numbers either increased or decreased, two carpels were produced instead of one, and they were often fused in the mutant florets. Transcriptome analysis of developing spikelets revealed that several regulatory genes involved in that process and the formation of floral organs were down-regulated in *osvil2*. These results suggest that *OsVIL2* is required for proper expression of the regulatory genes that control floral organ number and morphology.

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[DP21]

The advantages of toxoflavin in plant pathogenic Burkholderia spp. for plant interactions.

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Burkholderia glumae and *gladioli* are causal agents of bacterial panicle and grain blight in rice in many countries. Many strains produce the yellow pigment toxoflavin, which is highly toxic to plants, fungi, animals, and microorganisms. Although there have been several studies on the toxoflavin biosynthesis system of *B. glumae*, it is still unclear how *B. gladioli* activates toxoflavin biosynthesis. Using a *B. gladioli* strain without production of toxoflavin in nature, we demonstrated that the toxoflavin biosynthetic system enhanced the virulence of *B. gladioli* and can expand the host ranges. In addition, a seed-borne plant pathogenic bacterium, *Burkholderia glumae* and an air-borne plant pathogenic fungus, *Fusarium graminearum*, interact to promote bacterial survival, bacterial and fungal dispersal, and disease progression on rice plants. This key component in this interaction is toxoflavin.

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[DP22]

Natural allelic variation of GVS1 confers diversity in the regulation of leaf senescence in Arabidopsis

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Leaf senescence affects plant fitness. Plants that evolve in different environments are expected to acquire distinct regulations of leaf senescence. In this study, we investigated leaf senescence in 259 natural accessions of *Arabidopsis* by quantitatively assaying dark-induced senescence responses using a high-throughput chlorophyll fluorescence imaging system. A meta-analysis of our data with phenotypic and climatic information demonstrated biological and environmental links with leaf senescence. Through genome-wide association mapping, we uncovered a single nucleotide polymorphism (SNP) in the new locus Genetic Variants in Leaf Senescence (*GVS1*) that underlies the natural diversity in leaf senescence among a wide range of *Arabidopsis* accessions. *GVS1* encodes a protein with a high similarity to reductases. Loss-of-function mutations of *GVS1* in Columbia-0 delayed leaf senescence and increased sensitivity to oxidative stress, suggesting that this *GVS1* variant promotes optimal responses to developmental and environmental signals. Intriguingly, *gvs1* loss-of-function mutants in accessions with *GVS1* variants and transgenic lines complemented with its SNP variants display accession- and SNP-dependent phenotypes, revealing the functional diversity of *GVS1* alleles not only in leaf senescence but also oxidative stress. Our discovery of *GVS1* as the genetic basis of natural variation in senescence programs reinforces its adaptive potential in modulating life histories across diverse environments.

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[ST1]

Degradation of the BR-Responsive Transcription Factor BZR1 in *Arabidopsis* Root

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Plants are sessile organisms that encounter diverse environmental changes in temperature, light, water availability, nutrient, and pathogen. In response to both endogenous and exogenous stimuli, plants precisely control their physiological processes through appropriate intracellular responses. Brassinosteroid (BR) is an essential steroid hormone that regulates a wide range of plant growth and development through the activation of BR-responsive transcription factors, BZR1 (BRASSINAZOLE RESISTANT 1) and BES1 *(bri1* EMS-SUPPRESSOR). Recent studies showed that three E3 ligases (MAX2, COP1 and SINATs) are involved in BZR1/BES1 degradation under different hormonal and environmental conditions, respectively. In addition, BZR1/BES1 can be degraded by autophagy-mediated pathway (TOR, DSK2).
In this study, we identified another ubiquitin E3 ligase that degrades BZR1 with a distinct way. Biochemical analysis demonstrated that U-box type E3 ligase (TGS7) interacts with BZR1 in vitro and in vivo. TGS7 strongly bound to phosphorylated BZR1 rather than unphosphorylated BZR1, suggesting that BIN2 phosphorylation of BZR1 promotes BZR1 binding to TGS7. Interestingly, TGS7 regulated BZR1 stability in a root-specific manner. We found that TGS7 is cell-layer specifically expressed in the root tip, results in selective BZR1 accumulation in the epidermal layer. BZR1 was highly accumulated in most of cell-layers of the *tgs7* loss-of-function mutant. In contrast, the *bzr1-1D* gain-of-function mutation reduced the interaction with TGS7, which suppressed TGS7-mediated BZR1 degradation. Consistent with root-specific function of TGS7, the *tgs7*triple mutant displayed significantly increased BR sensitivity in root but not hypocotyl. In addition, it revealed that BIN2 interacts with and phosphorylates TGS7, leading to the elevation of interaction with BZR1 as well as TGS7 stability. Our study suggests that BZR1 stability in the roots is specifically controlled by BIN2-regulated TGS7.

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[ST2]

Arabidopsis basic Helix-Loop-Helix 34 (bHLH34) regulates glucose signaling through binding to a novel cis-element and its overexpression enhances abiotic stress tolerance

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The modulation of glucose (Glc) homeostasis and signaling is crucial for plant growth and development. Nevertheless, the molecular signaling mechanism by which a plant senses a cellular Glc level and coordinates the expression of Glc-responsive genes is still incompletely understood. Previous studies have shown that *Arabidopsis thaliana*plasma membrane Glc-responsive regulator (AtPGR) is a component of the Glc-responsive pathway. Here, we demonstrated that a transcription factor bHLH34 binds to 5′-GAGA-3′element of the promoter region of *AtPGR in vitro*, and activates beta-glucuronidase (GUS) activity upon Glc treatment in *AtPGR* promoter-GUS transgenic plants.Gain- and loss-of-function analyses suggested that the bHLH34 involved in the responses to not only Glc, but also abscisic acid (ABA) and salinity. These results suggest that bHLH34 functions as a transcription factor in the Glc-mediated stress responsive pathway as well as an activator of *AtPGR* transcription. Furthermore, genetic experiments revealed that in Glc response, the functions of bHLH34 are different from that of a bHLH104, a homologue of bHLH34. Collectively, our findings indicate that bHLH34 isa positive regulator of Glc, and may affect ABA or salinity response, whereas bHLH104 is a negative regulator and epistatic to bHLH34 in the Glc response.

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[ST3]

Identification of Plant Raptor-Binding Motif in TOR Signaling Components

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A putative raptor-binding fragment was identified from Arabidopsis S6 kinase (AtS6K1) N-terminal domain in our previous study. Here, we report a further characterization of this fragment, which identified a 12-aa core element absolutely required for the interaction. Although the amino acid sequence of the element *per se* had no significant homology with the canonical consensus of the TOS (TOR-signaling) motif found in the mammalian TOR (target of rapamycin) kinase substrates, its overall sequence composition is similar to that of the TOS motif in that the acidic and non-polar amino acids residues are arranged in alternating fashion and having one or two of the bulky hydrophobic amino acid (F) buried in the interior. Substitution of this bulky residue completely abolished the binding of the fragment to AtRaptor, as in the case of the mammalian TOS motif. Taken together with its position relative to the catalytic domain of the kinase, which also show a resemblance with the TOS motif, these results appear to suggest that this core binding element in the N-terminus of AtS6K1 represents a plant version of the TOS motif.

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[ST4]

Functional study of GIGANTEA in transcriptional regulatory system of ABA biosynthesis under drought stress

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Drought is one of the critical environmental stresses that limit on the plant growth and crop productivity. Even though numerous transcription factors involved in drought stress responses have been characterized, how plants cope with various signals and integrate them into biological and physiological adaptation is not clear. GIGANTEA (GI), a key regulator in photoperiod-dependent flowering and circadian rhythmicity is involved in various abiotic stress signaling. ENHANCED EM LEVEL (EEL)/bZIP12 was isolated as a GI interactor by yeast two-hybrid system. The *eel*, *gi-1* and *eelgi-1* mutants are hypersensitive to drought because ABA induced stomata closure was impaired. The expression of *NCED3*, a rate-limiting enzyme in ABA biosynthesis, was down-regulated in *eel*, *gi-1* and *eelgi-1* mutants. ChIP and EMSA assays showed that GI and EEL directly bound the ABRE motif on the promoter regions of *NCED3*. In addition, during drought stress *eel*, *gi-1* and *eelgi-1* mutants reduced endogenous ABA levels than WT plants. Our results suggested that the EEL-GI complex modulated drought tolerance through ABA biosynthesis. Moreover, EEL could be applicable for the enhancement of plant stress tolerance through transcriptional regulatory systems of stress-responsive genes.

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[ETM1]

Mutation of ONAC096 delays leaf senescence and enhances grain production in rice

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Leaf senescence is a complex process in which regulatory cascades of several transcription factors are involved. *NAC* genes are one of the major transcription factor families that control the gene mechanism of senescence. Here, we report that *ONAC096* is directly associated with promotion of leaf senescence, and investigated its preliminary function during the process of leaf senescence. The qRT-PCR showed that expression of *ONAC096* gradually increases in response to leaf aging and abscisic acid (ABA) treatment. Knockout mutant of *ONAC096* delayed leaf senescence, whereas overexpression of *ONAC096* accelerated leaf senescence, by controlling several chlorophyll degradation genes (CDGs) and senescence-associated genes (SAGs). These results indicate that *ONAC096* acts as a positive regulator of leaf senescence. In addition, detached leaves of *onac096* mutants showed the reduced sensitivity to ABA-induced senescence, which might be caused by decreased expression of the ABA-signaling genes, *OsABI5* and *OsEEL*. More importantly, loss-of-function in *ONAC096* increases number of panicles per plant, resulting in about 9% increase in grain yield per plant. These results suggest that ONAC096 has a regulatory role in accelerating the process of leaf senescence, probably via ABA signaling pathway.

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[ETM2]

Development of Growth-promoting and Stress-tolerant Plants via the Regulation of Chloroplast Gene Expression

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Chloroplasts are essential organelle for the growth and development of plants under both normal and stress conditions. Expression of chloroplast genes is mainly regulated at posttranscriptional levels, and the posttranscriptional RNA metabolism in chloroplasts is affected by developmental and environmental cues. To obtain insight into the significance of chloroplast RNA metabolism during stress responses, we analyzed the splicing patterns of chloroplast introns in cabbage, rice, and Arabidopsis under different environmental conditions, such as drought, salt, cold, UV, ABA, or heat stress. To determine the importance of splicing of chloroplast introns in stress responses, the cabbage and Arabidopsis chloroplast genes whose intron splicing was affected by environmental stresses were introduced into Arabidopsis, and their functional roles during stress response were determined using thetransgenic Arabidopsis plants. The results showed increased thermo-tolerance and growth as well as much better seedling growth under normal growth conditions. Taken together, our results suggest that plants with higher adaptability to stresses can be generated by modulating the splicing of chloroplast introns.

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[ETM3]

Characterization of Chloroplast-targeted tRNA Methyltransferases in Plant Growth and Abiotic Stress Responses

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Abiotic stresses, including salt, drought, cold, and heat, are environmental factors that reduce plant growth and crop productivity worldwide. Photosynthesis in chloroplasts is considered as a stress sensor, and chloroplasts play an important role in stress response. Methylation of tRNAs, rRNA, and mRNAs in chloroplasts is emerging as an important way to regulate chloroplast gene expression, which is crucial for plant growth and stress responses. In this study, we aimed to determine the roles of chloroplast-targeted tRNA methyltransferases (Trms) in plant growth and response to abiotic stresses. Genome-wide analysis revealed a total of 104 potential *Trms* in *Arabidopsis thaliana*, among which 35 *Trms* contained putative chloroplast transit peptides. Expression patterns of these chloroplast-targeted *Trms* were analyzed under various abiotic stresses, and chloroplast localization of selected *Trms* was confirmed by confocal analysis. Functions of several Trms were analyzed by investigating *Trm*-overexpressing transgenic plants and loss-of-function mutants. We found that the *trm* mutants and overexpression plants respond differently to diverse abiotic stresses. These results suggest that regulation of tRNA methylation in chloroplasts is important for plant growth and adaptation to abiotic stresses.

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[ETM4]

CCOAOMT1, a potential cargo secreted via VAMP721/722 vesicles in Arabidopsis

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Flagellin, a bacterial PAMP that induces plant innate immunity, has been previously reported to increase the expression of *VAMP721/722*genes. This indicates that immune molecules may be secreted via the VAMP721/722-associated exocytosis in response to flagellin. Hence, we tried to isolate and identify proteins that are differently accumulated between WT and the VAMP721/722-depleted plants (*VAMP721+/-722-/-* and *VAMP721-/-722+/-*)treated with flagellin, in order to obtain an information on immune molecules secreted via the VAMP721/722 exocytosis. We assume that an immune protein secreted through this exocytosis would accumulate more in VAMP721/722-depleted plantsthan WT plants. Therefore, we isolated and identified proteins accumulated more in in VAMP721/722-depleted plants by mass spectrometry. Interestingly, we found that one of the more accumulated proteins in VAMP721/722-depleted plants is caffeoyl-CoA O-methyltransferase 1 (CCOAOMT1) which is involved in the synthesis of lignin, the main component of the plant secondary cell wall. It was reported that plants form the secondary cell wall in response to pathogen attack likely to physically inhibit the pathogen infection. Thus, our results suggest that plants may form the secondary cell walls by secreting CCOAOMT1 via the VAMP721/722-related exocytosis during immune responses.

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[ETM5]

Synaptotagmin 4 and 5 are involved in Arabidopsis immunity to bacteria by facilitating the formation of SYP132-SNAP33-VAMP721/722 SNARE complex

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Synaptotagmin (SYT) is a well-known regulator of vesicle fusion in animals. We found that the Arabidopsis SYT4 and SYT5 are most similar to the mouse SYT1 which is involved in the secretion of neurotransmitters by stimulating vesicle fusion. To understand how the same VAMP721/722 can be engaged in diverse biological processes in plants, we isolated corresponding *syt4* and *syt5* mutant plants and generated the *syt4 syt5* double mutant. Although SYT5 is partially co-localized with VAMP722, the respective single and double mutant plants show compromised resistance to *Pseudomonas syringae* DC3000 bacterium but not to *Erysiphe pisi* fungus. It was previously reported that SYP132 is involved in resistance to bacteria, whereas PEN1 in immunity to fungi. Indeed, we found that SYT5 promotes the interactions between SYP132, SNAP33 and VAMP722. The elevated growth of *P. syringae* DC3000 in VAMP721/722-deficient plants suggest that VAMP721/722 is engaged in plant immunity to bacterial pathogens by secreting unknown antibacterial(s) via the SYP132-SNAP33-VAMP721/722 SNARE complex, which is facilitated by SYT4/5.

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[ETM6]

Functional deficiency of phytochrome B improves salt tolerance in rice

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Soil degradation affects agriculture worldwide. Soils with high salt can result from local geological conditions or accumulation of salt from irrigation. Salt limits water uptake and reduces crop yields; therefore, salt tolerance is an important trait for crops grown in highsalt soils. Here, we show that the rice (*Oryza sativa*) *phytochrome B* (*osphyB*) mutant has greater tolerance to salt stress than its parent *japonica* rice (cv. Dongjin). We found that the osphyB mutant showed a higher survival rate, fresh weight, and levels of total chlorophylls and carotenoids, as well as enhanced membrane integrity under salt stress compared to the wild type. *OsPHYB* transcripts increased in tissues of the wild type after salt treatment; *OsPHYB* expression was much higher in the leaf blade than in the stem and root. The *osphyB* mutant accumulated less Na+ in the shoot and considerably more K+ in both the shoot and root, maintaining a significantly lower Na+ to K+ ratio, possibly due to a lower rate of Na+ uptake and a higher rate of K+ uptake. To elucidate the possible mechanism of salt tolerance in the *osphyB* mutant, we performed quantitative reverse transcription PCR analysis, which indicated that salt stress-associated genes, including transcription factors and highaffinity K+ transporters, are upregulated in the *osphyB* mutant under high-salinity conditions. Taken together, our findings show that the null mutation of *OsPHYB* contributes to a decrease in the Na+/K+ ratio and enhances cell membrane integrity through upregulation of salt stressassociated genes, resulting in improved tolerance to salt stress.

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[PB1]

Sodium and Potassium ions selectivity by Two closely related HKT1 Homologs, EpHKT1;1 and EpHKT1;2 in *extr* emophile, *Eutrema parvula*

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A balance between sodium and potassium ions under salinity stress is crucial for plants. HKT1-type transporters play key role in regulating high salinity stress by reducing Na^+ toxicity through K^+ uptake. Previously we have shown that a homolog of HKT1, EsHKT1;2 in *Eutrema salsuginea* (formerly *Thellungiella salsuginea*), contribute to salinity tolerance and halophytic characteristic of this specie. *Eutrema parvula*, another halophyte contains two copies of *HKT1*, that code for EpHKT1;1 and EpHKT1;2. In response to high salinity *EpHKT1;2* induces dramatically compare to *EpHKT1;1*. Moreover EpHKT1;2 tolerate high salinity whereas EpHKT1;1 showed the same response to salt stress as shown by AtHKT1 when expressed in heterologous system. Amino acid sequence alignment showed that AtHKT1 and EpHKT1;1 (*E. parvula*), contain two asparagine residues, one in the 2nd pore loop domain and another one in the next transmembrance domain. In contrast, EpHKT1;2 contains conserved aspartic acid residues at the same position similar to EsHKT1;2. *Arabidopsis* plants (Col-*gl*), overexpressing *AtHKT1*or *EpHKT1;1* were sensitive to salt stress both in early germination as well as in adult stage. However, overexpression of *EpHKT1;2* made the plants more tolerant to salt stress compare to all tested lines. From these results we hypothesized that presence of Asn and Asp can determined the mode of cation selectivity of the HKT1-type transporters, which is at least true for a few dicot like *Arabidopsis*, *E. salsuginea* and *E. parvula*.

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[PB2]

DEWAX transcription factor plays a role in resistance to the necrotrophic fungal pathogens *Botrytis cinerea* in *Arabidopsis thaliana* and *Camelina sativa*

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Plant cuticle is the first physical barrier to protect their aerial parts from biotic and abiotic stresses. DEWAX, an AP2/ERF-type transcription factor, negatively regulates cuticular wax biosynthesis. In this study, we investigated the resistance to the necrotrophic fugal pathogens *Botrytis cinerea* in *Arabidopsis thaliana* and *Camelina sativa* overexpressing *DEWAX* and in *Arabidopsis dewax* mutant. Compared to wild type (WT) leaves, *Arabidopsis DEWAX* OX and *dewax* leaves were more and less permeable to toluidine blue dye, respectively. The ROS levels increased in *DEWAX* OX leaves, but decreased in *dewax* relative to WT leaves. Compared to WT, *DEWAX* OX was more resistant, while *dewax* was more sensitive to *B. cinerea* however, defense responses to *Pseudomonas syringae* pv. tomato DC3000:GFP were inversely modulated. Microarray and RT-PCR analyses indicated that the expression of defense-related genes was upregulated in *DEWAX* OX, but downregulated in *dewax* relative to WT. Transactivation assay showed that DEWAX upregulated the expression of defense-related genes *PDF1.2a*, *IGMT1*, and *PRX37*. Chromatin immunoprecipitation assay revealed that DEWAX directly interacts with the GCC-box motifs of PDF1.2a promoter. In addition, ectopic expression of *DEWAX* increased the tolerance to *B. cinerea* in *C. sativa*. Taken together, we suggest that increased ROS accumulation and *DEWAX*-mediated upregulation of defense-related genes are closely associated with enhanced resistance to *B. cinerea* in *Arabidopsis* and *C. sativa*.

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[PB3]

Malonyl CoA-ACP malonyltransferase, which is targeted to both the chloroplast and the mitochondria is essential for growth and development of Arabidopsis and its overexpression increases seed storage oil content

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Fatty acids are essential precursors for the synthesis of cell membranes, storage oils, and lipid-signaling molecules. Malonyl CoA-acyl carrier protein (ACP) malonyltransferase (MCAMT) catalyzes the conversion of the malonyl-CoA and ACP to CoA and malonyl-ACP, which is the key building block for fatty acid biosynthesis in both the plastids and the mitochondria. In this study, we report molecular and functional characterizations of Arabidopsis MCAMT. Quantitative RT-PCR and MCAMT promoter:GUS analyses showed that *MCAMT* is predominantly expressed in shoot and root apical meristems, hydathodes, and developing embryos. The fluorescent signals of MCAMT:eYFP were observed in the chloroplasts and the mitochondria of tobacco leaf protoplasts. In particular, the N-terminal region (1 to 30 amino acid residues) of MCAMT is required for mitochondrial targeting. Arabidopsis *mcamt-1 and -2* mutants exhibited embryo lethal phenotype due to an arrest of embryo development at the globular stage. T*ransgenic* Arabidopsis *lines* expressing antisense *MCAMT* RNA showed growth retardation by defects in cell division, rather than expansion. Overexpression of *MCAMT* increased growth, yield, and seed oil content. Taken together, MCAMT, which are dual-targeted to mitochondria and plastids, is essential for growth and development of Arabidopsis and could be useful for increasing seed oil content.

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[PB4]

Functional study of Hot pepper NADPH-Cytochrome P450 reductase 2 (CaCPR2) gene

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There are various P450s exist in plant and they need electron to do function. Plant NADPH-cytochrome P450 (CPR) is membrane protein that transfer the electron to various plant P450s. Two kinds of CPR genes (*CaCPR1, CaCPR2*) were isolated from hot pepper (*Capsicum annuum* L. *cv. Bukang*). Quantitative PCR analysis was used for determining CaCPRs mRNA expression levels in various hot pepper tissues. During the fruit ripening, the mRNA expression level was gradually increased. But in case of CaCPR2, mRNA level was expressed constitutively and lower than *CaCPR1*. To identify the enzymatic properties of CaCPR2, this protein was heterogously expressed in *Escherichia coli*. The enzymatic properties of *CaCPR2* were confirmed by characteristic absorption spectrum and catalytic activities measurement, which were assessed using protein and chemical substrates including P450, cytochrome c, cytochrome b_5, MTT, and CTC. As a results of these studies, *CaCPR2* can plays important role under many stress conditions although it is no major CPR in almost tissues in hot pepper.

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[PB5]

Functional analysis of Cytochrome P450 736A72 gene isolated from Tomato

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Cytochrome P450 proteins is very abundant in plant with catalysis for a large-scale of reactions, typically in production of primary and secondary metabolites.Functions of P450s normally concern the biochemical synthesis pathways comprise terpenoids, fatty acids, lipids, alkaloids,…as well biosynthesis of plant hormones, especially, chemical defense mechanism. Tomato is well-known as one of plants containing numerous CYP genes in its genome, however, the majority of them is unknown function. In order to reveal their function, one of P450 in CYP736A subfamily, CYP736A72, which express in most of whole tomato tissues, was isolated by using RT-PCR. With regard to studying enzyme character of CYP736A72, this gene was expressed in *E. coli*by cloning into pCW vector and the protein obtained after induction was used for enzymatic assays. The initial results show that this enzyme has 7-ethoxycoumarin *O*-deethylation activity. For identifying its function in plant, the transgenic lines of tobacco (*Nicotiana tabacum* cv.Xanthi-NC) and tomato (*Solanum lycopersicum*cv.Micro-Tom) which over-expressed CYP736A72 gene were produced.

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[PB6]

Enhancement to Heat Shock Tolerance of Arabidopsis is caused by the Redox-dependent Holdase Chaperone of Thioredoxin Reductase Type C (NTRC)

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NTRC has been identified as heat shock induction of transcripts by Genevestiator analysis. We find the NTRC overexpression (NTRC OE) enhanced tolerance to heat shock stress but the NTRC knockout mutant (*ntrc KO*) is sensitive to it. To understand the mechanism of this phenotype, we analyzed its biochemical qualities and structural changes. NTRC can alter its structure forms and functions as a disulfide reductase, a foldase chaperone, and as a holdase chaperone. High molecular weight (HMW) showed stronger activity as a holdase chaperone and low molecular weight (LMW) showed weaker holdase chaperone activity but stronger disulfide reductase and foldase chaperone acitivities. LMW proteins altered into the HMW complexes by the heat stress. Mutations of active site Cys residues of NTRC into Ser (C217/454S NTRC) guided inactivation of disulfide reductase and foldase, chaperoene functions, but holdase chaperone function decreased slightly. When NTRC-OE plants is treated under heat stress, it showed stronger phenotype than C217/454SNTRC plants. Our results suggest that the heat shock- mediated holdase chaperon function in NTRC is responsible for the increased heat tolerance in *Arabidopsis*.

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[PB7]

PtrERF109, a member of ERF transcription factor family from Populus involved in the adventitious root formation in plants.

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Improved root architecture is crucial for crop productivity and a very important contributor to drought resistance. The rooting system of plants is fundamentally important not only for water and nutrient uptake but also for anchoring a plant to its substrate. Adventitious roots (AR) have the same function as lateral roots but derived from aerial tissues (e.g., stem, hypocotyl, and leaf) by dedifferentiation. The induction of AR formation is an essential step in the vegetative propagation of economically important agricultural, horticultural and woody species. However, the molecular mechanisms underlying the AR formation are still poorly understood. Here we report a gene encoding a member of AP2/ERF transcription factor family from Populus (named PtrERF109). Gain-of-function mutation of PtrERF109 in Arabidopsis (35S::PtrERF109) shows a dramatic increase of adventitious roots (ARs) formation with a reduction of primary root growth. Gene expression and phenotypic analysis after various hormone treatments showed that both ethylene and auxin affect AR formation and upregulation of PtrERF109 could induce auxin biosynthetic genes. In addition, treatment of methyl jasmonateincreased PtrERF109 expression in poplar and enhances AR formation in 35S::PtrERF109 plants. Taken together, these results suggest that the PtrERF109 may be involved in AR formation by facilitating auxin biosynthesis in response to ethylene and/or methyl jasmonate. To gain further insights, we produced transgenic poplars overexpressing PtrERF109. Resulting phenotypic consequences will be presented. This work was funded by the Forest Resources Genome Project (2014071G10-1722-AA04) and by a grant from the Basic Science Research Program through the National Research Foundation of Korea (NRF-2015R1D1A1A01060807).

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[PB8]

Identification of a novel function of SAMLL RUBBER PARTICLE PROTEIN HOMOLOG, AtSRP1, in relation to pollen growth and development in Arabidopsis

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Despite the Small Rubber Particle Protein (SRP) – one of the major protein components in rubber tree – plays an important role in rubber biosynthesis, only a few functions of SRP Proteins in non-rubber-producing *Arabidopsis* (AtSRPs) containing high sequence homology with SRP have been identified in relation to stress-resistance. To identify physiological functions of AtSRP1, we isolated T-DNA-inserted knock-out mutant *Arabidopsis* (*FLAG_543A05*) and analyzed its phenotypes. *AtSRP1* was predominantly expressed in reproductive organs and localized to lipid droplets (LDs), ER and Golgi complexes. Furthermore, *atsrp1* mutants contained smallsilique sizes with reduced seed numbers and heterogeneous seed shapes in compared with wild type plants. By using Alexander- and DAPI-staining to analyze the anther- and pollen-grain structures in *atsrp1* mutants, their sizes were highly irregular and the grain numbers of *atsrp1* were lower than WT containing homogeneous shapes and higher grain numbers. In this paper, we identify a novel function of AtSRP1 in relation to pollen growth and development in non-rubber-producing plants.

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[PB9]

Suppression of plant shade avoidance responses using bathochromic mutants of Avena sativa phytochrome A

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The search for sunlight is critical for plants to optimize growth and development, which makes plants to evolve complex photoreceptor systems including red/far-red light (R/FR) sensing phytochromes. Particularly, phytochrome A (phyA) is a unique photoreceptor to perceive FR as a de-etiolation signal in seedlings and acts antagonistically to phytochrome B (phyB) upon exposure to low R: FR ratio. Phytochromes enables to transfer the light signal through photocycling between two photoisomers, R-absorbing Pr (¥ë$_{max}$ = 660 nm) and FR-absorbing Pfr (λ_{max} = 730 nm) forms. The absorption spectra of phytochrome are determined by interactions between a chromophore and specific amino acid residues in a GAF (cGMP phosphodiesterase/adenylyl cyclase/FhlI) domain. To suppress shade avoidance responses in plants using spectral properties of phytochromes, we mutated *Avena sativa* phyA (AsphyA) and developed bathochromic mutants whose Pr-absorption maximum was shifted to a longer wavelength when compared to wild-type phytochrome. Transgenic Arabidopsis plants bearing bathochromic AsphyA with 8 nm shift exhibited approximately 100 fold-increases in FR-sensitivity, long-lived signal from intermittent FR pulse in seedlings, and i.e., shade-tolerant phenotypes including shortened petioles, suppressed early-flowering and sustained chlorophyll contents against shade avoidance responses. Furthermore, the bathochromic AsphyA reduced the transcript levels of shade-avoidance responsive elements, such as PIF4 and PIF5, whereas those of positive regulators in photomorphogenesis, such as HY5 and HYH, were kept high under shade. These results demonstrate that light responses in plants are affected by the spectral properties of phytochrome and the photoequilibrium shift toward the increase of Pfr counteracts the shade avoidance reactions more effectively.

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[PB10]

Functional analysis of constitutively active phytochrome mutants using chimeric constructs

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Phytochromes, plant red and far-red photoreceptors, consist of globular N-terminal chromophore-binding photosensory domain and structurally extended C-terminal domain. Previously, a domain swap experiment demonstrated that the N-domains of phytochrome A (phyA) and phyB determine the photosensory specificity of phytochromes. On the other hand, the C-domain has been suggested to play roles in dimerization and nuclear localization. The nuclear import of phyA is known to be regulated by far-red elongated hypocotyl 1 (FHY1) and FHY1-like (FHL), whereas phyB has been proposed to have an intrinsic nuclear localization signal (NLS) in the C-domain. Recently, we obtained constitutively active mutants of phytochromes, which include *Arabidopsis thaliana* Y269V mutant ofphyA (AtYVA) and Y303V mutant of phyB (AtYVB). Although both transgenic plants exhibited a constitutive photomorphogenic (*cop*) phenotype, the AtYVA transgenic plant showed a weak *cop* phenotype (i.e., shortened hypocotyls in the dark, but longer than light-grown seedlings) due to impaired nuclear localization of AtYVA, whereas the AtYVB transgenic plant showed a strong *cop* phenotype. In this study, assuming that the C-domain of phyB has an intrinsic NLS, we generated chimeric phytochrome constructs by domain swapping using the constitutively active mutants, which include N-domain of AtYVA and C-domain of AtphyB (i.e., YVAN/BC), and N-domain of AtYVB and C-domain of AtphyA (i.e., YVBN/AC). Interestingly, the results showed that the YVAN/BC transgenic plant exhibited a weak *cop*phenotype, similar to the AtYVA plant, suggesting that the fusion with C-domain of phyB is not sufficient for the nuclear localization. In addition, the YVBN/AC transgenic plant exhibited a strong *cop* phenotype, suggesting that the N-domain of AtYVB is sufficient to be constitutively active. Therefore, our results reinforce that the N-terminal photosensory domain is critical for the function of phytochromes, including nuclear localization.

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[PB11]

Arabidopsis PDAT1 and PDAT2 genes editing to increase the hydroxy fatty acid production in transgenic Arabidopsis seed

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Triacylglycerol

Triacylglycerol (TAG) is accumulated in plant seeds that is composed of a glycerol with three fatty acids. Fattyacids of most plants are composed of common fatty acids, like saturated and unsaturated fatty acids, but some plants accumulate unusual fatty acid, like hydroxy fatty acid (HFA) in seeds. The HFAs are used as a chemical feedstock, including soaps, lubricants, plastics. Castor plant has a large amount of HFA in seeds, but it also have a toxin ricin and allergenic 2S albumin in seeds. Because of this drawback as a crop plants, we are interested to produce HFA in oil crop, like camelina. In first step, we are trying to produce HFA in Arabidopsis model plant by transformation of HFA synthase (*RcFAH12*) and HFA accumulating gene (*RcPDAT1-2*) identified from castor plant. We generated an Arabidopsis transgenic plant producing 27% of HFA in seed by transformation with castor *RcFAH12* and *RcPDAT1-2*genes. Current our result is not enough to use in industrial purpose compared with castor that accumulate HFA up to 80~90%. So we are going to knock-out *AtPDAT1* and *AtPDAT*2 genes using CRISPR-Cas9 to remove of competitive endogenous TAG biosynthesis genes for boosting transformed castor RcPDAT1-2 to accumulate more HFA in TAG. In this conference, we will present our strategy to produce HFA in transgenic plants.

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[PB12]

Isolation and characterization of two allelic variants of flavonol synthases from *Allium cepa*

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The major class of flavonoids in onion (*Allium cepa* L.) bulb is flavonol, which is synthesized from dihydroflavonol by the action of flavonol synthase (FLS). In this study, the cDNAs encoding FLSs were isolated from the red onion "H6" (AcFLS-H6) and the yellow onion "Hwangryongball" (AcFLS-HRB). The two cDNA sequences were found to have differences in the three amino acids at positions 45, 65, and 213. Kinetic analysis with recombinant proteins revealed that both proteins preferred dihydroquercetin (DHQ) to dihydrokaempferol (DHK), but AcFLS-HRB-GST exhibited approximately 2-fold higher catalytic efficiencies than AcFLS-H6-GST for the dihydroflavonol substrates. The flavonoid biosynthesis genes were mainly expressed in the sheaths of H6 and HRB onions, which corresponded to the accumulation pattern of flavonoid aglycones in both onions. The gene expression levels of most of the genes in H6 were higher than those in HRB, whereas *FLS* expression levels were similar in both onions. This relatively enhanced FLS expression, along with the higher activity of AcFLS-HRB, seems to bring about the increase in quercetin production in the HRB sheath. The quercetin content was approximately 12-fold higher than the cyanidin content in the H6 sheath, suggesting that FLS is dominant over dihydroflavonol 4-reductase (DFR) in competition for their substrate DHQ.

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