

Identification of novel genes involved in FT function or transport

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polar auxin transport through the control of subcelluar localization of PIN1 proteins in cotyledon development. *MAB4* has four paralogues, named *MAB4/ENP LIKE (MEL) 1, MEL2, MEL3 and MEL4. mel1 mel2 mel3 mel4* quadruple mutants exhibit abnormal gravitropism like *pin2* mutants, although each single mutant does not exhibit any phenotypes in root gravitropism. In root tips of quadruple mutants, PIN2 abundance was severely reduced and PIN2 polarization was weakened. To investigate the mechanism by which the *MAB4* subfamily genes regulate PIN2 localization, we used pharmacological approaches in PIN2-GFP expressing mutants. When treated with BFA or wortmannin, PIN2 protein accumulated in induced intracellular compartments of *mel1 mel2 mel3 mel4* roots, as well as wild-type roots. Furthermore, when BFA was washed out, the BFA compartments were disappeared and PIN2-GFP was normally reverted to the plasma membrane in the mutants. These results suggest that the *MAB4* subfamily genes are not involved in intracellular trafficking of PIN2 proteins. Meanwhile, the MAB4 subfamily proteins are localized at the cell periphery with polarity in plant cells. The MAB4 polarity is almost identical to PIN polarity. However, peripheral MAB4 localization did not change by treatment with BFA, indicating that the MAB4 subfamily proteins do not exist in intracellular compartment and that their functional domain is limited to cell periphery. Taken together, it is suggested that the MAB4 subfamily proteins would retain PIN proteins with polarity in the plasma membrane.

08096

AMINO ACID SEQUENCES THAT ARE REQUIRED FOR LOCALIZATION OF ASYMMETRIC LEAVES2 (AS2) TO THE SUB-NUCLEOLAR BODY ADJACENT TO THE NUCLEOLUS

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ASYMMETRIC LEAVES2 (AS2) gene is one of key regulators of morphogenesis of leaves in Arabidopsis thaliana. It encodes a plantspecific nuclear protein with a AS2/LOB domain that consists of the C motif containing four cysteine residues, the single conserved glycine residue and the leucine-zipper-like sequence in its amino-terminal half. The AS2/LOB domain includes a short stretch of basic residues (RRK) in the C-motif. The AS2 protein localizes to a sub-nuclear body that is adjacent to nucleoli and we designated this body as the AS2 body. In order to identify the signal in AS2 that is required for the localization of AS2 to the AS2 body, we have made DNA constructs that encoded mutant AS2 proteins with various deletions and amino acid substitutions in the AS2/LOB domain such as the cysteine residues in the C motif, the basic strech RRK and the deletion of the leucine zipper like sequence. We have investigated sub-nuclear localization of these mutant proteins. We also have examined whether the localization to the AS2 body might be required for the function of AS2 in morphogenesis of leaves. We will present latest results of these experiments.

08097

IDENTIFICATION OF NOVEL GENES INVOLVED IN FT FUNCTION OR TRANSPORT

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Flowering of *Arabidopsis* is influenced by seasonal changes in day length, so that plants flower early in long days of summer and late under short days of winter. In *Arabidopsis*, *FLOWERING LOCUS T (FT)* is a component of the photoperiodic pathway and its transcription is activated under long days. FT protein is expressed in the leaf vascular tissue and then moves through the phloem to the shoot apex, where it causes changes in gene expression that reprogram the shoot apical meristem to form flowers instead of leaves. Recent studies demonstrated that the *FT* homolog *TSF* also participates in the photoperiodic flowering pathway redundantly with FT. To deepen our knowledge of the function and transport of FT, we performed different genetic and genomic approaches. First, we have generated a mutant collection from the *ft tsf* double mutant, which is insensitive to day length and very late flowering under long days, and from *GAS1: FT ft tsf* plants which are early flowering. We have already identified many early and late flowering mutants in both genetic backgrounds. The genes affected in the most promising mutants will be identified using Illumina next generation sequencing. Second, we investigated the global effects of FT on gene expression in leaves by studying which genes are specifically affected by FT and/or TSF by comparing Col-0 with *ft tsf* and *GAS1:FT tsf* ft genotypes. Our Tiling Array experiment showed that several differentially expressed genes affected by FT in leaves encode proteins which potentially can modify cellular membranes. Further studies are being performed in order to test the contribution of these candidate genes to FT function or transport.

08098

EARLY IN SHORT DAYS 6 (ESD6), A FLORAL REPRESSOR IN ARABIDOPSIS, ENCODES A RING MOTIF-CONTAINING E3 UBIQUITIN LIGASE

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Genetic analyses performed by combining *esd6* and mutants affected in flowering inductive pathways suggest that flowering inhibition mediated by ESD6 occurs through both *FLC*-dependent and independent pathways. *ESD6* has been cloned by a map-based approach and encodes HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENE 1 (HOS1), an E3 ubiquitin ligase previously demonstrated to negatively regulate the low-temperature responses. Progress in understanding the role of *ESD6 / HOS1* in the repression of floral initiation will be presented.

08099

MAPK CASCADE REGULATES THE HOMEOSTASIS OF STEM CELL POPULATION IN *ARABIDOPSIS* SHOOT APICAL MERISTEM *Horim Lee (Harvard Medical School/MGH, USA), Ok-Kyong Cha (Harvard Medical School/MGH, USA), Jen Sheen (Harvard Medical School/MGH, USA)

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Arabidopsis shoot stem cells generate all aerial parts of plants throughout the whole lifespan. The constant population size of the shoot

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Flowering time control must be tightly regulated as it is essential for reproductive success in plants. Both promotive and repressive factors are involved in the control of the floral transition. We have isolated a recessive mutation, named *early in short days 6 (esd6)*, causing an acceleration of flowering. Besides their flowering phenotype, *esd6* mutant plants also displayed complex pleiotropic alterations of both vegetative and reproductive development. Mutant plants are smaller than wild type and *esd6* leaves showed slightly reduced size in comparison to wild type leaves. Moreover, *esd6* primary root showed a significant decrease on elongation with lower production of adventitious roots. *esd6* flowers and siliques also displayed some developmental abnormalities including a reduction in size in comparison to wild type plants.