virus (SMV) was examined by reverse trnscription-polymerase chain reaction (RT-PCR) and restriction fragment length polymorphism (RFLP) analysis. The P1 protein is the least conserved region of the entire polyprotein of SMV, particulary in the N-terminal half having hypervariation in length and in sequence, which is the best target for strain discrimination. Among 14 symptomatic collected soybean plants, 12 yielded an array of amplification products of expected size 924 bp fragments following RT-PCR with specific primers. Successful amplification produced the entire P1 gene except cleavage site between P1 and HC-Pro. The amplified products were digested with *Afl*II, *Bcl*I, *Hha*I, *Mbo*I, and *Xho*I, the restriction enzyme chosen to discriminate between the collected isolates and known strains. The distinctive restriction patterns generated by the listed enzymes classified in certain types and subtypes and showed as a marker to discriminate between PCR products generated from field isolates including 4 reference strains.

F205 Characterization and cloning of SUF1 (suppressor of FRI 1) that regulates flowering time in Arabidopsis

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Flowering of Arabidopsis is promoted by several interacting genetic pathways; photoperiod, vernalization and autonomous pathways. In the autonomous pathway, *FLOWERING LOCUS C (FLC)* is known as a central molecule, which acts as a floral repressor. *FLC* is positively regulated by *FRI*, while it is negatively regulated by *LD, FVE, FCA* and vernalization treatment. By fast neutron mutagenesis of *FRI-Col*, a very late flowering line, we isolated mutants that flower as early as Columbia ecotype. By genetic complementation of these mutants, five mutants (FN6, 24, 108, 202 and 225) were shown to be allelic and the mutants were named as *suf1-1* to *suf1-5* (suppressor of *FRI*). Our physiological data showed that the *suf1-1* allele is sensitive to photoperiods (short day vs long day) and vernalization (4?, 8 weeks). The RT-PCR analysis showed that the expression of FLC in *suf1-1* was not change in comparision to *FRI-Col*, but *ALG20* and *FT* were expressed as Col. Thus SUF1 acts located between FLC and AGL20 on the autonomous pathway. The mapping of *suf1* showed that *suf1* is tightly linked to a molecular marker *AtGABab* on chromosome III. Currently, the cloning of SUF1 gene is in progress.

F206 AGAMOUS-LIKE 20 gene integrates gibberellin signals for flowering in *Arabidopsis thaliana*

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Flowering in Arabidopsis is triggered by endogenous and environmental signals. Genes that regulate this transition have been assigned to separate genetic pathways that control the response to stimuli. A MADS-box gene, *AGAMOUS-LIKE 20* (*AGL20*) promotes flowering by responding to the signals from autonomous, vernalization and photoperiod pathways. In this study, we show that the *AGL20* gene expression also responds to gibberellins which are absolutely required for flowering in short day conditions. Grown under non-inductive conditions, *ga1* mutants never produce flowers and also showed low levels of *AGL20*. When the mutants were treated with gibberellin, they produced flowers and this phenotype was also accompanied with an increase in *AGL20* expression. Transgenic plants constitutively overexpressing *AGL20* gene (*35S::AGL20*) were insensitive to gibberellins and paclobutrazol, an inhibitor of gibberellin biosynthesis. Our results indicate that

gibberellin signals are integrated to *AGL20*. We suggest that AGL20 protein integrates signals from different pathways of floral induction including the gibberellin pathway which is crucial in short day conditions and is a central component for the induction of flowering in Arabidopsis.

F207 Arabidopsis Cytochrome P450 Mutants Involved in Maintaining Apical Dominance and Fruit Elongation

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Cytochrome P450s are involved in the metabolism of most phytohormones as well as many secondary metabolites in plant cells. Sequencing of the Arabidopsis genome revealed that it contains six different CYP78A genes, CYP78A5 to 78A10. In an effort to elucidate the functional roles of CYP78A genes in A. thaliana, we isolated knock-out mutants for these genes by reverse genetics method. Only cyp78A5 mutant showed a visible phenotype having slightly reduced apical dominance. To further elucidate function and to circumvent gene redundancy, we generated double mutant lines based on gene expression patterns (cyp78A5/78A7) and sequence identity (cyp78A6/78A9). A double mutant, cyp78A5/78A7, showed pleiotropic phenotypes; dwarfism, sterility, multiple inflorescences, short hypocotyls, and delayed senescence. The double mutant also displayed very abnormal inflorescence growth pattern where flower inflorescence progressively arose out of disorganized clusters of cauline leaves. Trasngenic lines overexpressing CYP78A7 showed strong apical dominance and defects in floral development. The other double mutant, cyp78A6/78A9, shows short silique phenotype. The silique length of cyp78A6/78A9 double mutant reduced by 40% compared to wild-type, and single mutants, cyp78A6 and cyp78A9, but the seed number and the seed size were not changed. We will discuss the putative functional roles of the CYP78A genes in growth and development of Arabidopsis.

F301 PCR Cloning of mmoZ Gene Encoding a Hydroxylase of Soluble Methane Monooxygenase from Methylocystis sp. strain 2

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Several methanotrophs synthesize a soluble cytoplasmic methane monooxygenase (sMMO) when they are grown in copper-depleted conditions. A 348 bp fragment of the *mmoZ* gene encoding the binding protein of soluble methane monooxygenase was cloned by polymerase chain reaction (PCR) and sequenced from *Methylocystis* sp. strain 2. The cloned gene had approximately 91.6% homology with other *mmoZ* genes in nucleotide sequence level. The deduced amino acid sequence showed about 46% homology with those from other methanotrophic and methylotrophic bacteria and several key amino acids were also found. These results suggest that this strain has the same methane-oxidizing system as in other methanotrophic bacteria.

F302 Purification and Characterization of Methanol Dehydrogenase (MDH) from a Marine Methylotroph Methylophaga sp. strain YC

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