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Genetic analysis of *FT* and other late-flowering mutations

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In higher plants, the proper timing of flowering is of crucial importance for reproductive success. Flowering is a complicated phenomenon which is regulated by both environmental conditions and endogenous factors. Recently, it was suggested that at least 80 genes are involved in the regulation of flowering[1].

To understand the regulation of flowering, we have been focusing on the flowering-time gene *FT*, and have shown that *FT* acts in part downstream of *CO* and mediates signals for flowering in an antagonistic manner with its homologous gene, *TFL1*[2].

Genetic interaction between *FT* and other flowering-time genes will be discussed.

1. Levy and Dean (1998) *Plant Cell* 10, 1973-1989.
2. Kobayashi *et al.* (1999) *Science* 286, 1960-1962.

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MOLECULAR GENETIC ANALYSIS OF *corymbosa2*, AN ARABIDOPSIS MUTANT WITH CORYMB-LIKE INFLORESCENCE.

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Arabidopsis thaliana is a typical rosette plant with distinct vegetative and reproductive growth phases. The reproductive growth is characterized by the elongation of stem internodes in parallel with the production of flower buds.

corymbosa2 has been identified as a mutant with corymb-like inflorescence morphology. The corymb-like phenotype of the tip of the inflorescence in *crm2* mutants was caused by the increase in the number of flower buds at the tip.

Genetic analysis indicated that the *CRM2* locus was mapped between the CAPS markers, g13838 and *GA5*, on chromosome 4. Fine mapping experiments revealed that the *CRM2* gene was mapped to a 80kbp region which was covered with 2 BAC clones. Isolation of the gene is currently in progress and will be presented.

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Analysis of petal and sepal-specific floral mutant, *sep1* in Arabidopsis

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The *sep1* (*serrated petals and sepals1*) mutant has serrated petals and sepals but the other floral and vegetative organs appear to be normal. The petals and sepals were not different in length between *sep1* and wild type, but those of the *sep1* mutant were broader. In the distal region of *sep1* petal, there were fewer number of larger epidermal cells. Also, highly-expanded cells with larger nuclei were sometimes found, indicating that endoreduplication had occurred. The *SEP1* gene may regulate late stage of petal and sepal development by maintaining the mitotic state or inhibiting transition to the endoreduplication cycle.

Double mutants with *ap3-1* and *ag* showed additive phenotypes. Ectopic petals and sepals of *sep1 ag* flowers were serrated. On the other hand, the *sep1* phenotype appears to be weak in the *sep1 ap2-1* background. These results indicate that *SEP1* function is subordinate to organ identity but not to organ position, and that *SEP1* gene is positively regulated by class A function.

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Analysis of *rabbit ears* mutant that affects petal development in *Arabidopsis*

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Arabidopsis wild-type flowers have four symmetrically-positioned petals. In *rabbit ears* mutant (*rab*), most of the adaxial petals change to filamentous, small, or abnormally-shaped organs. Since the other floral organs are as normal as those are in wild type, we consider *RAB* gene is involved especially in the development of the adaxial petals.

To investigate the genetic interactions between *RAB* and other genes in floral development, we are examining double mutants between *rab* and mutants of ABC genes, *clv1* and *pan1*. We are also trying to isolate *RAB* gene by positional cloning procedure.

Phenotypic analysis of *rab* mutant and progress of *RAB* gene cloning will be presented.