Plant Gene Register

Isolation and Analysis of SaMADS C, the APETALA 1 cDNA Homolog from Mustard

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Genetic studies on floral development in Antirrhinum majus and Arabidopsis thaliana have led to the identification of floral homeotic genes that determine floral organ identity. Supplemented with molecular analyses of the cloned homeotic genes, the simple ABC model of floral organogenesis was confirmed (Weigel and Meyerowitz, 1994). All but one of the cloned genes of the model encode an amino-terminal DNA-binding domain (Okamura et al., 1993), which shows homologies to the DNA-binding domain of the transcription factors MCM1 from yeast and SRF from mammals. This domain was named the MADS-box.

We are interested in the transition from vegetative to reproductive development and are working for this purpose with the LDP Sinapis alba (Melzer et al., 1990). Working with a plant in which flowering is inducible by a simple, experimentally manageable condition has the advantage that molecular and biochemical studies can be applied to very small samples of tissue, such as the apical meristem, by using large plant populations that are synchronized in their development.

To analyze whether there are MADS-box genes involved in the transition from a vegetative meristem to a reproductive meristem, we first cloned the AGAMOUS MADS-box-encoding region from mustard via PCR by using two primers that were derived from the Arabidopsis AGAMOUS sequence (Yanojofsky et al., 1990). The 168-bp PCR fragment was subsequently used to screen cDNA libraries of transition stages from apical meristems (Table I).

Of 40 positive signals, three different transcript classes named SaMADS A, B, and C were determined. The temporal expression of the genes was analyzed by northern blots. Whereas SaMADS A and B are activated early after induction of flowering, SaMADS C is first detectable 3 d after floral induction. The nucleotide sequence of SaMADS C was determined by dideoxy sequencing of both strands.

SaMADS C contains 1023 bp and encodes a protein with 254 amino acid residues and a predicted molecular mass of 29,900. A data bank search showed that SaMADS C is highly homologous to the APETALA1 (API) gene of A. thaliana (Mandel et al., 1992) and to SQUAMOSA (SQUA) of A. majus (Huijser et al., 1992). The amino acid identity within the amino-terminal MADS-box region is 100% to API and 87.7% to SQUA, and in the remaining part of the protein, it is 94.9 and 61.7%, respectively. On in situ hybridizations with longitudinal sections through apical meristems the expression of SaMADS C is first detectable in flower primordia, emerging on the flanks of the inflorescence meristem. This is in accordance with the expression pattern of the Arabidopsis API gene. Thus, we have cloned the S. alba API cDNA and are now able to analyze possible interactions with other MADS-box genes we have isolated from mustard and that are activated earlier during the transition to flowering.

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LITERATURE CITED

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