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Isolation of MADS-box Genes and Patterns of Their Expression in *Panax ginseng*

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Objectives

To study in vitro early flowering of *Panax ginseng*, we isolated MADS-box genes and analyzed their expression pattern by RT-PCR.

Materials& Methods

1. Materials

Dehusked ginseng(*Panax ginseng*) seeds, four years old ginseng(*Panax ginseng*).

2. Methods

1) Isolation of MADS-box genes

Total RNA and mRNA were extracted from flower of *Panax ginseng* and cDNA synthesized mRNA. Using RACE(Rapid Amplification cDNA Ends) PCR, we obtain the sequence of MADS-box. The nucleotide and deduced amino acid sequence were used for BLAST searches. Phylogenetic relationships of the sequences were performed using the Neighbor-Joining Method.

2) Induction of in vitro early flowering

Zygotic embryos were threw out for 1 week in 1/3MS. To induce in vitro flowering, we treated 1/2MS medium with 2 ㎎/ℓ BA and 5 ㎎/ℓ GA_3.

3) RT-PCR analysis

The RT-PCR performed with synthesized cDNA from four years old ginseng in different tissues and hormone treated node of embryo in different time.

Results & Discussion

We isolated 9 genes encoding MADS-domain transcription factor from *Panax ginseng*,. Phylogenetic tree analysis revealed that 9 genes were belong to AG-like genes(C-function), DEF-like gene(B-function), SQUA-like genes(A-function) as ABC model. RT-PCR revealed that the transcript level of PGAG group are specific in flower and the transcript level of PGSQ group are expressed in vegetative organ as well as in flower. PGSQ1 revealed expression specifically in MS medium with BA and GA_3. These results suggest that PGSQ1 regulates the transcription of genes required for early flowering.

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