

(05-1-26)

Redundant gene expression of duplicate *AGAMOUS* orthologues during floral development in *Phalaenopsis*

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Objectives

The aim of our study is attempted to isolate and characterize *AGAMOUS* (*AG*)-like genes from *Phalaenopsis* and compared them with previously isolated genes affecting the floral development.

Materials and Methods

Material:

Plant - *Phalaenopsis* sp. 'Hatsuyuki'

Methods:

AG-like genes were isolated by using the RACE method from *Phalaenopsis*. A *Phylogenetic* tree was constructed by the neighbor joining (NJ) method and drawn by Njplot. To investigate the expression pattern of *PhalAG1* and *PhalAG2* during floral development was performed RT-PCR and *in situ* hybridization.

Results and Discussion

Two *Phalaenopsis* *AG*-like genes, *PhalAG1* and *PhalAG2*, were isolated in this study. Our alignment data showed that *PhalAG1* and *PhalAG2* had MADS-domain and K-domain. In addition, these genes had the diagnostic amino acid motifs typical of the C-terminal, the *AG* motif I and the *AG* motif II. Moreover, the MD-motif was located at the C-terminal of *PhalAG2*. Phylogenetic analysis indicated that *PhalAG1* and *PhalAG2* fall into different phylogenetic positions in the *AG* gene family since they belonged to the C- and D-lineages, respectively.

RT-PCR analyses showed that *PhalAG1* and *PhalAG2* transcripts were detected in flower buds but not in vegetative organs. Moreover, *in situ* hybridization experiments revealed that hybridization signals of *PhalAG1* and *PhalAG2* were observed in the lip, column and ovule. These results suggested that two *AG*-like genes in *Phalaenopsis* maintained functional redundancy with each other.