



# A putative miR172-targeted *CeAPETALA2-like* gene is involved in floral patterning regulation of the orchid *Cymbidium ensifolium*

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**ABSTRACT.** APETALA2 plays critical roles in establishing meristem and organ identity during plant floral development. In this study, we obtained a *CeAP2-like* gene by using the mRNA differential display technique to analyze the wild type and a *multitepal* mutant of the orchid *Cymbidium ensifolium*. The full-length cDNA encoding the *CeAP2-like* transcription factor shows significant similarity to the cDNA of *AP2* from *Erycina pusilla* and contains nucleotides complementary to miR172. Using a transient gene expression system of *Arabidopsis* protoplasts, we found that the accumulation of *CeAP2-like* protein and transcripts was negatively regulated by miR172, indicating this gene as a putative target of miR172. Northern blotting revealed that *CeAP2-like* is dominantly

expressed in the sepals and petals of the wild-type flower, and shows low expression in the gynostemium. In contrast, the accumulation of *CeAP2-like* transcripts decreased significantly, especially in the central part of the mutant flower, corresponding to its abnormal petals and the absence of the gynostemium. Furthermore, we found an antagonistic expression pattern between *CeAP2-like* and *AGAMOUS* in the wild type, representing A- and C-class genes that specify floral organ fate. However, this antagonistic distribution was modified in the *multitepal* mutant, and both genes showed lower expression than that in the wild type. This result suggested that the balance between *CeAP2-like* and *AGAMOUS* activity was important for the regulation of floral patterning in *C. ensifolium*. This study represents the first report on a class A gene and its regulatory role for floral development in the orchid *C. ensifolium*.

**Key words:** Orchid; *Cymbidium ensifolium*; Floral patterning; *APETALA2-like*; miR172; *AGAMOUS*