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# SEP-class genes in *Prunus mume* and their likely role in floral organ development

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## Abstract

**Background:** Flower phylogenetics and genetically controlled development have been revolutionised during the last two decades. However, some of these evolutionary aspects are still debatable. MADS-box genes are known to play essential role in specifying the floral organogenesis and differentiation in numerous model plants like *Petunia hybrida*, *Arabidopsis thaliana* and *Antirrhinum majus*. SEPALLATA (SEP) genes, belonging to the MADS-box gene family, are members of the ABCDE and quartet models of floral organ development and play a vital role in flower development. However, few studies of the genes in *Prunus mume* have yet been conducted.

**Results:** In this study, we cloned four *PmSEPs* and investigated their phylogenetic relationship with other species. Expression pattern analyses and yeast two-hybrid assays of these four genes indicated their involvement in the floral organogenesis with *PmSEP4* specifically related to specification of the proliferated flowers in *P. mume*. It was observed that the flower meristem was specified by *PmSEP1* and *PmSEP4*, the sepal by *PmSEP1* and *PmSEP4*, petals by *PmSEP2* and *PmSEP3*, stamens by *PmSEP2* and *PmSEP3* and pistils by *PmSEP2* and *PmSEP3*.

**Conclusion:** With the above in mind, flower development in *P. mume* might be due to an expression of SEP genes. Our findings can provide a foundation for further investigations of the transcriptional factors governing flower development, their molecular mechanisms and genetic basis.

**Keywords:** SEP genes, *Prunus mume*, Floral organ development, Expression analysis, Yeast two-hybrid assay

## Background

Flower emergence is a vast step in the evolutionary history of plants [1], and its diversification overtime has largely altered the interaction patterns of the plant kingdom [2]. Furthermore, floral structures are controlled by a number of environmental and genetic factors. In recent years, consistent strides have been made to uncover the molecular basis behind flowering [3].

*Prunus mume* Sieb. et Zucc. (Rosaceae, Prunoideae), a traditional ornamental plant, has been cultivated in China for more than 3,000 years. During this long period of domestication and cultivation, the phenotypic characteristics of its flowers (such as single petal, double petal, multi-sepals, multi-pistils and proliferated flowers) have revolutionised. These variations have added more ornamental

value to *P. mume* and are also useful when studying floral organ development. A series of flower development models are proposed for specimen plans [4, 5]. Genetic control of flower identity has been largely affected by the ABC model [6]. According to this model, three different gene classes signal floral organogenesis. The outermost sepals are specified by the A class (*API* and *AP2*), petals are controlled by the combination of A and B (*AP3* and *PI*) and C class genes (*AG*) and the carpels are specified by C class genes [7, 8]. MADS-box genes are of vital importance for ascertaining the genetic basis of plant development [9]. Among these, E class genes play a significant role in flower development. Scientists have already carried out investigations of the MADS-box gene family and the cloning of C class genes in *P. mume* [10]; however, the molecular mechanisms behind flower organ development and morphology remain unclear. Therefore, an expression and functional analysis of SEP genes is required to uncover these processes. Transcriptional regulators encoded by MADS-box genes have critical role in flower organ development [11]. A series of genes controlling flower

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