



Genome-Wide Identification, Characterization and Expression Analysis of the *TCP* Gene Family in *Prunus mume*

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TCP proteins, belonging to a plant-specific transcription factors family, are known to have great functions in plant development, especially flower and leaf development. However, there is little information about this gene family in *Prunus mume*, which is widely cultivated in China as an ornamental and fruit tree. Here a genome-wide analysis of *TCP* genes was performed to explore their evolution in *P. mume*. Nineteen *PmTCP*s were identified and three of them contained putative miR319 target sites. Phylogenetic and comprehensive bioinformatics analyses of these genes revealed that different types of *TCP* genes had undergone different evolutionary processes and the genes in the same clade had similar chromosomal location, gene structure, and conserved domains. Expression analysis of these *PmTCP*s indicated that there were diverse expression patterns among different clades. Most *TCP* genes were predominantly expressed in flower, leaf, and stem, and showed high expression levels in the different stages of flower bud differentiation, especially in petal formation stage and gametophyte development. Genes in *TCP-P* subfamily had main roles in both flower development and gametophyte development. The *CIN* genes in double petal cultivars might have key roles in the formation of petal, while they were correlated with gametophyte development in the single petal cultivar. The *CYC/TB1* type genes were highly detected in the formation of petal and pistil. The less-complex flower types of *P. mume* might result from the fact that there were only two *CYC* type genes present in *P. mume* and a lack of *CYC2* genes to control the identity of flower types. These results lay the foundation for further study on the functions of *TCP* genes during flower development.

Keywords: Genome-wide, *TCP* genes, expression analysis, *Prunus mume*, flower development

INTRODUCTION

Prunus mume Sieb. et Zucc. (Rosaceae, Prunoideae) has been cultivated in China for over 3,000 years for its prominent ornamental and economic value. This species has acquired favorable ornamental characteristics with various types of flowers, colorful corollas, pleasing fragrance, and early blooming in the *Prunus* genus (Zhang et al., 2012; Xu Z. et al., 2014). The flower development plays a vital role in ornamental value. In *P. mume*, the studies of the *MADS*-box gene family and *SBP*-box gene family have been performed to gain insights into flower development