



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

Yuzhen Zhou<sup>1†</sup>, Zongda Xu<sup>1,2†</sup>, Kai Zhao<sup>1</sup>, Weiru Yang<sup>1</sup>, Tangren Cheng<sup>1</sup>, Jia Wang<sup>1</sup> and Qixiang Zhang<sup>1\*</sup>

<sup>1</sup> Beijing Key Laboratory of Ornamental Plants Germplasm Innovation and Molecular Breeding, National Engineering Research Center for Floriculture, Beijing Laboratory of Urban and Rural Ecological Environment, Key Laboratory of Genetics and Breeding in Forest Trees and Ornamental Plants of Ministry of Education, School of Landscape Architecture, Beijing Forestry University, Beijing, China, <sup>2</sup> College of Forestry, Shandong Agricultural University, Tai'an, China

## OPEN ACCESS

### Edited by:

Xiaowu Wang,  
Chinese Academy of Agricultural  
Sciences, China

### Reviewed by:

Sachiko Narita Isobe,  
Kazusa DNA Research Institute,  
Japan  
Jianfei Zhao,  
University of Pennsylvania, USA

### \*Correspondence:

Qixiang Zhang  
zqxjfu@126.com

<sup>†</sup> These authors have contributed  
equally to this work.

### Specialty section:

This article was submitted to  
Plant Genetics and Genomics,  
a section of the journal  
Frontiers in Plant Science

**Received:** 04 June 2016

**Accepted:** 15 August 2016

**Published:** 31 August 2016

### Citation:

Zhou Y, Xu Z, Zhao K, Yang W,  
Cheng T, Wang J and Zhang Q  
(2016) Genome-Wide Identification,  
Characterization and Expression  
Analysis of the *TCP* Gene Family  
in *Prunus mume*.  
*Front. Plant Sci.* 7:1301.  
doi: 10.3389/fpls.2016.01301

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