

Isolation and functional characterization of a R2R3-MYB regulator of *Prunus mume* anthocyanin biosynthetic pathway

Qin Zhang^{1,2} · Ruijie Hao¹ · Zongda Xu¹ · Weiru Yang¹ · Jia Wang¹ · Tangren Cheng¹ · Huitang Pan¹ · Qixiang Zhang¹ 

Received: 28 January 2017 / Accepted: 10 August 2017
© Springer Science+Business Media B.V. 2017

Abstract Flower color is an important economic trait of *Prunus mume*, a famous ornamental plant widely cultivated in East Asia. Anthocyanins, acting as major pigments of flower coloration, are biosynthesized via transcriptional regulation of transcription factors (TFs). Many R2R3-MYB TFs have been identified to regulate anthocyanin biosynthetic pathways. However, very little is known about the role of R2R3-MYB TFs regulating anthocyanin biosynthesis in *P. mume*. In our study, the first R2R3-MYB TF (*PmMYBa1*) from *P. mume* has been isolated and characterized. Sequence analysis revealed that *PmMYBa1* contains conserved R2R3 MYB domain and belongs to anthocyanin-related subgroup 6 of R2R3-MYB family. Overexpression of *PmMYBa1* in tobacco contributed to anthocyanin accumulation by activating endogenous anthocyanin-relating genes in the flowers and fruits of transgenic lines. Gene expression analysis showed that almost all of the endogenous structural genes

of anthocyanin biosynthesis were obviously up-regulated, as well as bHLH TFs An1a and An1b in the flowers and fruits of *PmMYBa1*-overexpressing tobacco. In contrast, only three structural genes *NtCHS*, *NtF3H*, and *NtANS* were up-regulated in the leaves. In addition, the expression level of *PmMYBa1* was higher in the anthocyanin-rich red flowers than in white ones and strongly correlated with anthocyanin content in the developing petals of *P. mume*. These findings strongly suggest that *PmMYBa1* is involved in regulating anthocyanin biosynthesis in *P. mume*. Moreover, *PmDFR* and *PmANS* might be potential target genes regulated by *PmMYBa1* in *P. mume* according to the correlation analysis. Isolation and functional characterization of *PmMYBa1* laid a foundation for further exploring the mechanisms of anthocyanin synthesis and provide a potential candidate gene for breeding to manipulate flower colors in *P. mume*.

Keywords Anthocyanin · MYB transcription factor · Transcriptional regulation · *Prunus mume*

Communicated by T. Winkelmann.

Electronic supplementary material The online version of this article (doi:10.1007/s11240-017-1294-4) contains supplementary material, which is available to authorized users.

✉ Qixiang Zhang
zqxbjfu@126.com

¹ Beijing Key Laboratory of Ornamental Plants Germplasm Innovation & 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 100083, China

² College of Landscape and Travel, Hebei Agricultural University, Baoding 071000, China

Abbreviations

CHS	Chalcone synthase
CHI	Chalcone isomerase
CaMV	Cauliflower mosaic virus
F3H	Flavanone 3-hydroxylase
DFR	Dihydroflavonol 4-reductase
ANS	Anthocyanidin synthase
UFGT UDP-glucose	Flavonoid glucosyltransferase
F3'H	Flavanone 3'-hydroxylase
F3'5'H	Flavanone 3'5'-hydroxylase
TAC	Total anthocyanin content