ORIGINAL ARTICLE



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

Qin Zhang $^{1,2} \cdot$ Ruijie Hao $^1 \cdot$ Zongda Xu $^1 \cdot$ Weiru Yang $^1 \cdot$ Jia Wang $^1 \cdot$ Tangren Cheng $^1 \cdot$ Huitang Pan $^1 \cdot$ Qixiang Zhang $^1 \oplus$

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

Communicated by T. Winkelmann.

Published online: 18 August 2017

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

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 upregulated 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*

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

