

# Genome-wide analysis of MYB transcription factors and screening of *MYBs* involved in flower color formation in *Rhododendron delavayi*

Fenfang Long, Hairong Wu, Huie Li\*, Weiwei Zuo, Qian Ao

College of Agriculture, Guizhou University, Guiyang 550025, People's Republic of China

**Abstract:** Flower color is a vital trait of ornamental plants. *Rhododendron delavayi* Franch. is a famous ornamental plant species distributed in the mountain areas of southwest China with red inflorescences and young branches, but the molecular basis of its color formation is unclear. Based on the released genome of *R. delavayi*, in this study, 184 *MYB* genes were identified in its genome, including 78 1R-MYB, 101 R2R3-MYB, four 3R-MYB and one 4R-MYB; these MYBs were divided into 32 subgroups by phylogenetic analysis together with those of *Arabidopsis*. The members of the same subgroup had similar conserved domains and motifs, gene structures, and promoter cis-regulatory elements, indicating their relative conserved function. In addition, transcriptome analysis of spotted petals, unspotted petals, spotted throat, unspotted throat, and branchlet cortex showed significant differences in the expression levels of R2R3-MYB genes. Furthermore, weighted co-expression network analysis showed that MYBs were the most common transcription factors involved in color formation, of which seven were R2-R3MYB and three were 1R-MYB. Besides, bHLH and WD40 transcription factors, and gene glucose-flavonoid 3-O-glucosyl-transferase were also involved in the regulation of color formation in *R. delavayi*. The genes screened in this study provide references for the study of transcriptional regulation of flower color formation of *Rhododendron delavayi*.

**Keywords:** *Rhododendron delavayi*; color formation; transcriptome analysis; MYB transcription factors; WGCNA