

Some genes have a more significant impact on the shade of leaf color. Comparative studies on different varieties of red maples revealed that in some red maples, there is a situation of UFGT gene duplication. When both UFGT genes maintain high expression simultaneously, the anthocyanin content in the leaves will significantly increase, indicating that this gene plays an important role in the formation of red leaves (Zhang et al., 2023). DFR is also one of the important genes affecting leaf color. When this gene undergoes mutation or its expression level decreases, the anthocyanin content will also decrease (Recinos and Puck, 2023). In maples, the expression changes of DFR and ANS usually correspond with the changes in anthocyanin content in red leaves (Chen et al., 2019; Chen et al., 2022; Gong et al., 2025; Li et al., 2025). Therefore, the quantity and expression level of these genes affect the accumulation of anthocyanins, and thereby influence the final color of the leaves.

#### 4.2 Regulatory role of transcription factors

Apart from structural genes, transcription factors can also regulate the formation of pigments at a higher level. The production of anthocyanins is usually controlled by the MBW complex. This complex consists of three types of proteins: MYB, bHLH, and WD40, and it is activated during plant growth stages or when influenced by external environmental signals (Figure 3) (Gao et al., 2020; Yan et al., 2021; Chen et al., 2022; Fan et al., 2024; Liu et al., 2024). Studies have found that in many plants, the influence of transcription factors on pigment differences is often more significant than that of structural genes, and MYB-type transcription factors play a particularly crucial role (Recinos and Pucker, 2023). Generally speaking, MYB mainly regulates the process, while bHLH and WD40 play more auxiliary and stabilizing roles in maintaining the complex.

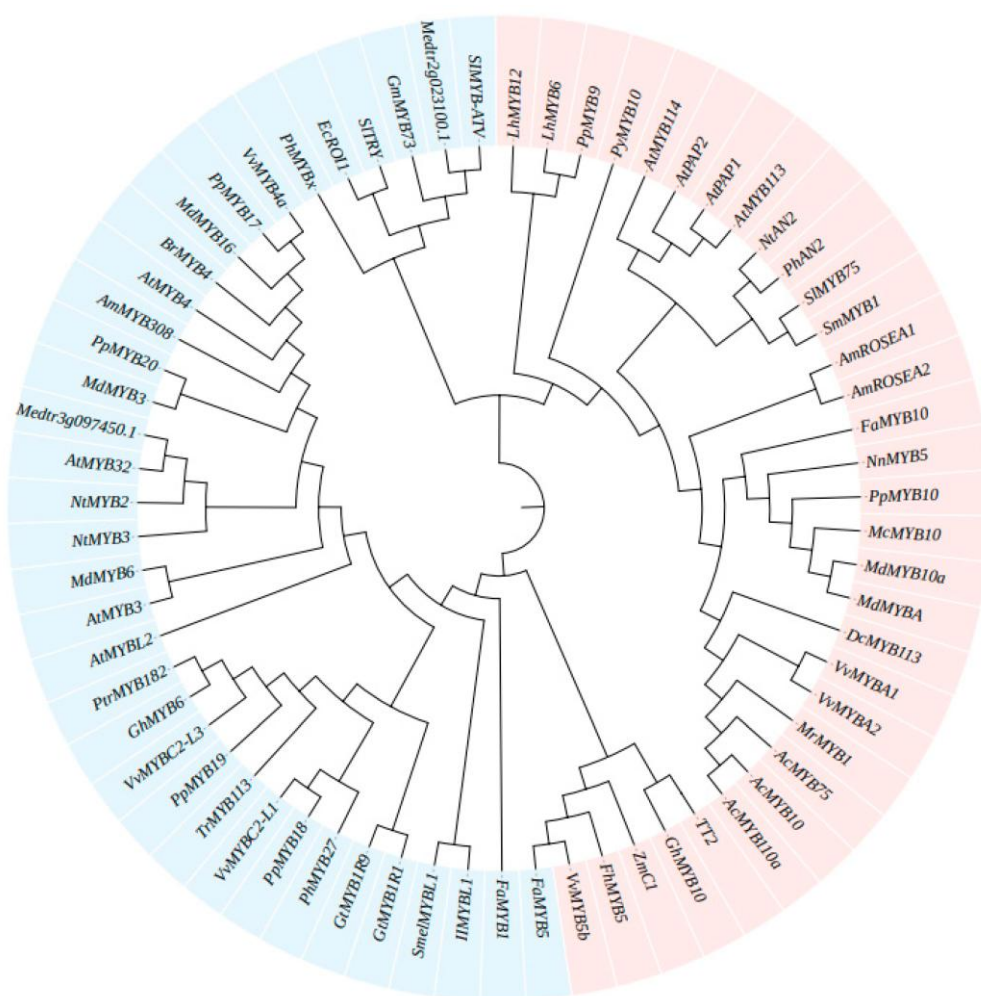


Figure 3 Phylogenetic tree of the regulation of anthocyanin biosynthesis by MYB genes (Adopted from Yan et al., 2021)

Image caption: The tree was constructed based on the entire protein sequences using MEGA 6 software. Blue represents the antagonistic effects of MYB factors in the anthocyanin biosynthetic pathway, and red represents the MYBs as activators to promote the biosynthesis of anthocyanin (Adopted from Yan et al., 2021)