Complexity and robustness of the flavonoid transcriptional regulatory network revealed by comprehensive analyses of MYB-bHLH-WDR complexes and their targets in Arabidopsis seed.

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Résumé en anglais	In Arabidopsis thaliana, proanthocyanidins (PAs) accumulate in the innermost cell layer of the seed coat (i.e. endothelium, chalaza and micropyle). The expression of the biosynthetic genes involved relies on the transcriptional activity of R2R3-MYB and basic helix-loop-helix (bHLH) proteins which form ternary complexes ('MBW') with TRANSPARENT TESTA GLABRA1 (TTG1) (WD repeat protein). The identification of the direct targets and the determination of the nature and spatio-temporal activity of these MBW complexes are essential steps towards a comprehensive understanding of the transcriptional mechanisms that control flavonoid biosynthesis. In this study, various molecular, genetic and biochemical approaches were used. Here, we have demonstrated that, of the 12 studied genes of the pathway, only dihydroflavonol-4-reductase (DFR), leucoanthocyanidin dioxygenase (LDOX), BANYULS (BAN), TRANSPARENT TESTA 19 (TT19), TT12 and H(+) -ATPase isoform 10 (AHA10) are direct targets of the MBW complexes. Interestingly, although the TT2-TT8-TTG1 complex plays the major role in developing seeds, three additional MBW complexes (i.e. MYB5-TT8-TTG1, TT2-EGL3-TTG1 and TT2-GL3-TTG1) were also shown to be involved, in a tissue-specific manner. Finally, a minimal promoter was identified for each of the target genes of the MBW complexes. Altogether, by answering fundamental questions and by demonstrating or invalidating previously made hypotheses, this study provides a new and comprehensive view of the transcriptional regulatory mechanisms controlling PA and anthocyanin biosynthesis in Arabidopsis.
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