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CsMYB5a and CsMYB5e from *Camellia sinensis* differentially regulate anthocyanin and proanthocyanidin biosynthesis

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Highlights

- A total of 140 R2R3-MYBs were screened from different tea transcriptome databases.
- CsMYB5a reduced the accumulation of anthocyanin but promoted the accumulation of PAs.
- DMACA-stained PAs increased significantly in CsMYB5e-overexpressing tobacco flowers.
- Genes related to PA and anthocyanin biosynthesis pathways were markedly up regulated.
- 3 UGTs and 4 GSTs involved in anthocyanin glycosylation and transportation.

Abstract

Tea is one of the most widely consumed nonalcoholic beverages worldwide. Polyphenols are nutritional compounds present in the leaves of tea plants. Although numerous genes are functionally characterized to encode enzymes that catalyze the formation of diverse polyphenolic metabolites,