Functional genomic study on flavonoid-glycosyltransferases in *Arabidopsis thaliana*

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Abstract

Over 110 putative family1 UDP-glycosyltransferases (UGTs) have been postulated to exist in Arabidopsis genome. Currently, there are only a few reports on functional characterization of flavonoid glycosyltransferases in Arabidopsis. Based on the sequence homology of known flavonoid glycosyltransferases of other plant species, such as P. hybrida and Scutellaria baicalensis, we have been focusing on seven flavonoid glycosyltransferase genes in Arabidopsis. To understand where the putative flavonoid glycosyltransferase genes are expressed in Arabidopsis, we performed real-time RT-PCR with flowers, rosette leaves, stems, and roots. In our results, one putative glycosyltransferase gene, UGT73B1, is mainly expressed in flowers and rosette leaves. To further characterize the functions of the flavonoid glycosyltransferase and the relationships between the functions and flavonoid biosynthesis pathway in Arabidopsis, we isolated T-DNA insertion mutations for each GT. Comparative study of metabolic profiling on wild type, T-DNA mutant lines and over-expression lines is in progress.

References

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