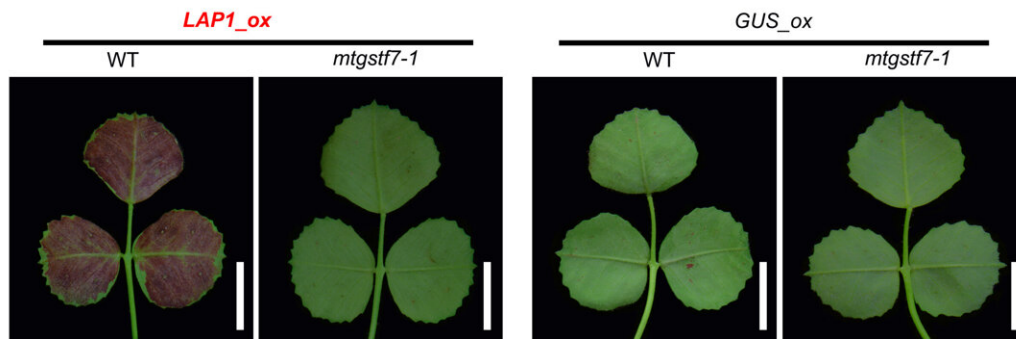


New target gene found for engineering anthocyanins in plants

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MtGSTF7 specifically participates in anthocyanin accumulation in *Medicago truncatula*. Credit: ANG Ruoruo

Anthocyanins and proanthocyanins are two classes of flavonoids with benefits for human health. The biosynthesis of anthocyanins and proanthocyanins shares a common up-stream biosynthetic pathway. The genes regulating their biosynthesis, namely the ternary MYB-bHLH-WD40 protein complexes, are conserved in higher plants. In *Arabidopsis thaliana*, AtTT19 is necessary for both anthocyanin and proanthocyanin accumulation. However, it remains unclear whether TT19-like glutathione S-transferase (GST) is recruited to participate in proanthocyanin accumulation in other plants.

In a study published in the *Journal of Experimental Botany*, researchers

from the Xishuangbanna Tropical Botanical Garden (XTBG) of the Chinese Academy of Sciences demonstrated that MtGSTF7, a TT19-like GST gene, was activated by the [anthocyanin](#) regulator LAP1 to determine the accumulation of anthocyanins, but not proanthocyanins, in *Medicago truncatula*, a model legume plant.

The researchers carried out analysis of previous transcriptomic data, expression pattern detection, phenotypic analysis of knockout mutants, and genetic complementation assays.

They found that MtGSTF7 plays a critical role for anthocyanin accumulation in *M. truncatula*. The transcript levels of anthocyanin [biosynthetic pathway genes](#) in MtGSTF7 had no significant differences compared with those in wild type.

In addition, the ectopic expression of MtGSTF7 could rescue the anthocyanin deficiency of *tt19* mutants, demonstrating that MtGSTF7 plays an analogous function with AtTT19 in terms of facilitating anthocyanin transport from estrogen receptor to vacuole.

After analyzing the yeast-one-hybridization and dual-luciferase reporter assays, they found that LAP1 could bind to the MtGSTF7 promoter to activate its expression. Ectopic expression of MtGSTF7 in *tt19* mutants could rescue their anthocyanin deficiency, but not their proanthocyanin defect.

Moreover, they found that the proanthocyanin accumulation was not affected in the MtGSTF7 mutants.

"Our results show that the mechanism of anthocyanin and proanthocyanin accumulation in *M. truncatula* is different from that in *A. thaliana*. This study provides a new target gene, MtGSTF7, for engineering anthocyanins in plants," said Chen Jianghua of XTBG.

More information: Ruoruo Wang et al, MtGSTF7, activated by the MYB transcription factor LAP1, specifically participates in anthocyanin accumulation in *Medicago truncatula*, *Journal of Experimental Botany* (2022). [DOI: 10.1093/jxb/erac112](https://doi.org/10.1093/jxb/erac112)

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