Elucidation of the Biosynthesis Pathway of Acylated Flavonoid Glycosides in Pseudognaphalium affine and Exploration of Its Key Enzymes

Liu, Dongtian (School: Shanghai Foreign Language School Affiliated to SISU)

The acylated flavonoid glycosides (AFGs) in Pseudognaphalium affine (D. Don) Anderberg, a plant resource that has the concomitant function of both medicine and foodstuff in China, exhibited strong anti-complementary activity, which have potential applicable prospect in drug development. However, AFGs are limited by the low contents from the herb and the few source plants. Therefore, exploring more methods to improve the productive rate of the AFGs is necessary. Recently, with the development of plant secondary metabolism engineering and synthetic biology, the target compound can be obtained by regulating the expression of the key gene or constructing the synthetic pathways in vitro to achieve the high yield, which based on elucidation of the biosynthesis pathways. According to the known biosynthetic pathway of AFGs, the flavonoid glycoside is catalytically generated by the corresponding flavonoid via uridine diphosphate glycosyltransferase (UGT), which is then used as a substrate to combine with the corresponding acyl-donor via BAHD-acyltransferases (BAHD) acyltransferase to form AFGs. Nonetheless, how the AFGs are synthesized by UTG and BAHD in Pseudognaphalium affine is still unclear. In this project, eight potential UGT genes and three potential BAHD genes were screened through annotation of the full-length transcriptome of Pseudognaphalium affine, and we found the two key enzymes in the biosynthesis of AFGs in Pseudognaphalium affine. This study provided a basis for further illustration of biosynthetic pathway of AFGs in Pseudognaphalium affine and would prompt the large-scale production of these bioactive AFGs through synthetic biology, and also lies the foundation for sustainable utilization of resources using AFGs as the natural anti-complementary ingredients.

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