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2、代表性论文



Article

Metabolome and Transcriptome Analyses Reveal Flower Color Differentiation Mechanisms in Various *Sophora japonica* L. Petal Types

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Simple Summary: Flower color is one of the most important ornamental characteristics of *Sophora japonica*. The most common *S. japonica* flower color is generally yellow and white, with no exceptional characteristics. The monotonous flower color seriously affects the ornamental value of this species. Therefore, the elucidation of the underlying biosynthetic mechanisms and the role of anthocyanins in the development and cultivation of new flower color varieties in *S. japonica* is of significant importance but has remained unclear to date. In this study, the *S. japonica* ‘AM’ mutant was investigated due to its flower color mutation. The key structural genes involved in the synthesis and accumulation of anthocyanins in *S. japonica* ‘AM’ were screened out using metabolomics and transcriptomics approaches. Bioinformatics analysis demonstrated that the primary key metabolites that affect the color variation in ‘AM’ petals are cyanidin-type anthocyanins. The *lcy* gene and the *MYB1* transcription factor are the key genes affecting the anthocyanin synthesis and responsible for color variation in *S. japonica* ‘AM’ petals. This study analyzed the variation patterns and the synthesis pathways of anthocyanin components in *S. japonica* petals. The major relevant regulatory genes were also explored to provide a theoretical basis for the innovative utilization of *S. japonica* flower color germplasm resources.

Abstract: *Sophora japonica* L. is an important landscaping and ornamental tree species throughout southern and northern parts of China. The most common color of *S. japonica* petals is yellow and white. In this study, *S. japonica* flower color mutants with yellow and white flag petals and light purple-red wing and keel petals were used for transcriptomics and metabolomics analyses. To investigate the underlying mechanisms of flower color variation in *S. japonica* ‘AM’ mutant, 36 anthocyanin metabolites were screened in the anthocyanin-targeting metabolome. The results demonstrated that cyanidins such as cyanidin-3-O-glucoside and cyanidin-3-O-rutinoside in the ‘AM’ mutant were the key metabolites responsible for the red color of the wing and keel petals. Transcriptome sequencing and differentially expressed gene (DEG) analysis identified the key structural genes and transcription factors related to anthocyanin biosynthesis. Among these, *F3’5’H*, *ANS*, *UFGT75B1*, *MYB1*, and *WRKY* expression was significantly correlated with the cyanidin-type anthocyanins (key regulatory factors affecting anthocyanin biosynthesis) in the flag, wing, and keel petals in *S. japonica* at various flower development stages.

Keywords: *Sophora japonica*; anthocyanin; metabolome; transcriptome

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3、代表性成果

