

Integrated Analysis of Metabolome and Transcriptome Provides Insights into the Mechanisms of Anthocyanin Biosynthesis in Chinese Cherry (*Cerasus pseudocerasus* Lindl.) Fruit

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Abstract

Chinese cherry [*Cerasus pseudocerasus* (Lindl.) G.Don], native to China, has excellent nutritional, economic, and ornamental values with different fruit color. The red coloration of fruit is determined by anthocyanin pigmentation, which is an attractive trait for consumers. To date, the mechanisms underlying fruit color formation in Chinese cherry fruit have not been reported yet. In this study, the pigmentation patterns in (dark)-red and yellow fruit of Chinese cherry were illustrated by integrated widely-targeted metabolome and transcriptome analyses. Anthocyanin content and color ratio (a^*/b^*) in (dark)-red fruit was significantly higher compared with yellow fruit at mature stage. Metabolomic profiling revealed that cyanidin-3-*O*-rutinoside was the predominant anthocyanin compound in both fruit, while it was 6.23-fold higher in dark-red than in yellow fruit. Pelargonidin-3-*O*-rutinoside, pelargonidin-3-*O*-glucoside, peonidin-3-*O*-glucoside, and pelargonidin-3-*O*-glucoside-5-*O*-arabinoside were present only in dark-red fruit, also being responsible for the dark-red peel color. In addition, more accumulated procyanidins, flavanols, and isoflavones might result in less anthocyanins in flavonoid pathway for yellow fruit. Through comparative transcriptomics and weighted gene co-expression network analysis, ten genes were identified to be involved in anthocyanin biosynthesis and transport pathway, including seven biosynthesis genes (*CpCHS*, *CpCHI*, *CpF3H*, *CpF3'H*, *CpDFR*, *CpANS*, *CpUFGT*), one transport gene (*CpGST*), and two transcription factors (MYB10, IBH1). Transcriptome data and real-time PCR showed that the transcript levels of these genes were significantly higher in dark-red fruit than in yellow fruit at later stage, especially *CpANS*, *CpUFGT*, and *CpGST*, suggesting they may play important roles in red-colored fruit formation. *CpLAR* was higher in yellow fruit than dark-red fruit, especially at the early stage, which promoted the accumulation of flavanols, isoflavones, and procyanidins in yellow fruit. These results provide novel insights into color patterns formation mechanisms of Chinese cherry fruit, and the candidate key genes identified in anthocyanin biosynthesis may provide a valuable resource for Chinese cherry breeding program in the future.

Keywords: Chinese cherry, *Cerasus pseudocerasus* (Lindl.) G.Don, metabolome, transcriptome, anthocyanin, key candidate gene

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