



Identification of differentially expressed genes associated with flower color in peach using genome-wide transcriptional analysis

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Genet. Mol. Res. 14 (2): 4724-4739 (2015)

Received June 11, 2014

Accepted October 27, 2014

Published May 11, 2015

DOI <http://dx.doi.org/10.4238/2015.May.11.5>

ABSTRACT. Flower color is an important trait of the ornamental peach (*Prunus persica* L.). However, the mechanism responsible for the different colors that appear in the same genotype remains unclear. In this study, red samples showed higher anthocyanins content (0.122 ± 0.009 mg/g), which was significantly different from that in white samples (0.066 ± 0.010 mg/g). Similarly to carotenoids content, red extract (0.058 ± 0.004 mg/L) was significantly higher in white extract (0.015 ± 0.004 mg/L). We estimated gene expression using Illumina sequencing technology in libraries from white and red flower buds. A total of 3,599,960 and 3,464,141 tags were sequenced from the 2 libraries, respectively. Moreover, we identified 106 significantly differentially expressed genes between the 2 libraries. Among these, 78 and 28 represented transcripts with a higher or lower abundance of more than 2-fold than in the white flower library, respectively. GO annotation indicated that highly ranked genes were involved in the pigment biosynthetic process. Expression patterns of 11 genes were verified using quantitative reverse transcription-polymerase chain reaction assays. The results suggest that hydroxycinnamoyl-coenzyme A shikimate/quinic

hydroxycinnamoyltransferase, 2-oxoglutarate-dependent dioxygenase, isoflavone reductase, riboflavin kinase, zeta-carotene desaturase, and ATP binding cassette transporter may be associated with the flower color formation. Our results may be useful for scientists focusing on *Prunus persica* floral development and biotechnology.

Key words: Differentially expressed genes; Flower color; *Prunus persica*; Illumina sequencing