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Transcriptome sequencing of *Paeonia suffruticosa* 'Shima Nishiki' to identify differentially expressed genes mediating double-color formation

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1 **Transcriptome sequencing of *Paeonia suffruticosa* ‘Shima Nishiki’ to identify**  
2 **differentially expressed genes mediating double-color formation**

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15 **Abstract**

16 *Paeonia suffruticosa* ‘Shima Nishiki’ is one of extremely rare double-color cultivars in the world. It  
17 usually shows the two beautiful colors of red and white in the same flower, and this trait undoubtedly  
18 makes the flowers more charming for the ornamental market. However, few studies have been done to  
19 unravel the molecular mechanisms of double-color formation in *P. suffruticosa* ‘Shima Nishiki’. In this  
20 study, we measured the anthocyanin composition and concentration, and sequenced the transcriptomes  
21 of the red and white petals. We found that the total content of Pg-based glycosides was at a  
22 significantly higher level in the red petals. Furthermore, we assembled and annotated 92,671 unigenes.  
23 Comparative analyses of the two transcriptomes showed 227 differentially expressed genes (DEGs),  
24 among which 57 were up-regulated, and 170 were down-regulated in the red petals. Subsequently, we  
25 identified 3 DEGs and the other 6 structural genes in the anthocyanin biosynthetic pathway including  
26 *PsCHS*, *PsCHI*, *PsF3H*, *PsF3’H*, *PsDFR*, *PsANS*, *PsAOMT*, *PsMYB*, and *PsWD40*. Among them,  
27 *PsDFR* and *PsMYB* expressed at a significantly higher level and showed positive correlations between  
28 their expression and anthocyanin concentration in the red petals. However, *PsWD40* expressed at a  
29 significantly lower level and exhibited an inverse relationship in the red petals. Furthermore, we further

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