

## **Identification and characterization of genes involved in the fruit color development of european plum**

### **ABSTRACT**

European plum fruit (*Prunus domestica*) are normally blue-black to dark purple. However, some genotypes remain green/yellow after ripening. We hypothesized that in such genotypes anthocyanin biosynthesis is genetically disturbed. To examine this hypothesis, six european plum genotypes with diverse fruit colors were investigated for the expression pattern of several anthocyanin biosynthetic genes (ABGs)—e.g., phenylalanine ammonia-lyase, chalcone synthase (CHS), dihydroflavonol 4-reductase (DFR), anthocyanin synthase (ANS), and UDP-glucose:flavonoid 3-O-glucosyltransferase 1 and 2 (UFGT 1 and 2). Expression profiles indicated that ABGs, especially Pd-CHS and UFGT 2, were significantly downregulated in the green/yellow fruit compared with the dark-purple fruit. Furthermore, the quantification of total polyphenols and individual flavonoid compounds showed substantial differences between the off-colored and the purple genotype. To further examine the contribution of each of the ABGs in color development, the open reading frame (ORF) of Pd-CHS, Pd-DFR, Pd-ANS, and Pd-UFGT 2 was ectopically expressed in tobacco (*Nicotiana tabacum*). The characterization of transgenic plants showed that the petals of plants expressing Pd-CHS were darker in color and had higher anthocyanin content than control or even other transgenic types, suggesting the significant contribution of CHS in determining anthocyanin production levels and hence fruit coloration. The results of this study provides better understanding of color development in european plum, which can be rewarding in developing european plum cultivars with desired colors through classical or modern breeding tools.

**Keyword:** *Prunus domestica*; Anthocyanin biosynthetic genes; Polyphenols; Chalcone synthase