

## bHLH Transcription Factors involved on the regulation of anthocyanin genes during fruit development in wild strawberry (*Fragaria vesca*) and red raspberry (*Rubus idaeus*)

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Red coloration on berry fruits is caused due the presence of anthocyanin pigments mainly produced during the late stages of the fruit maturation process. In the past years the interest on anthocyanins and other phenylpropanoids compounds has increased due the proof antioxidant effect both *in vitro* and *in vivo* systems, making consider plant breeders around the world consider this plant metabolites as an important trait to follow up.

Anthocyanin and proanthocyanidin synthesis is regulated through the interaction of the MYB-bHLH-WD40 complex, which has been characterized in several crops from diverse families, including some Rosaceae species such as strawberry and apple. To date it is not clear which bHLH proteins are involved in this pathway in strawberries and raspberry species, including their correct identification and expression levels during the physiological changes that occur during fruit development and ripening. Here we show the activity of some “key” genes of the anthocyanin pathway like CHS, DFR, UFGT.

Using genome wide phylogenetic analysis and the public genome available, we identified three possible bHLH candidates from *F vesca* and two from *R. idaeus* based on sequence homology with previously reported bHLH proteins from *Malus*, *Arabidopsis* and *Fragaria*. In order to quantify the activity of the candidate genes involved in this study, we analyze the RNA expression levels trough quantitative Real Time PCR (qRT-PCR) of 6 different fruit stages for *Fragaria* and 3 for *Rubus*, young leaves were used as a control tissue.

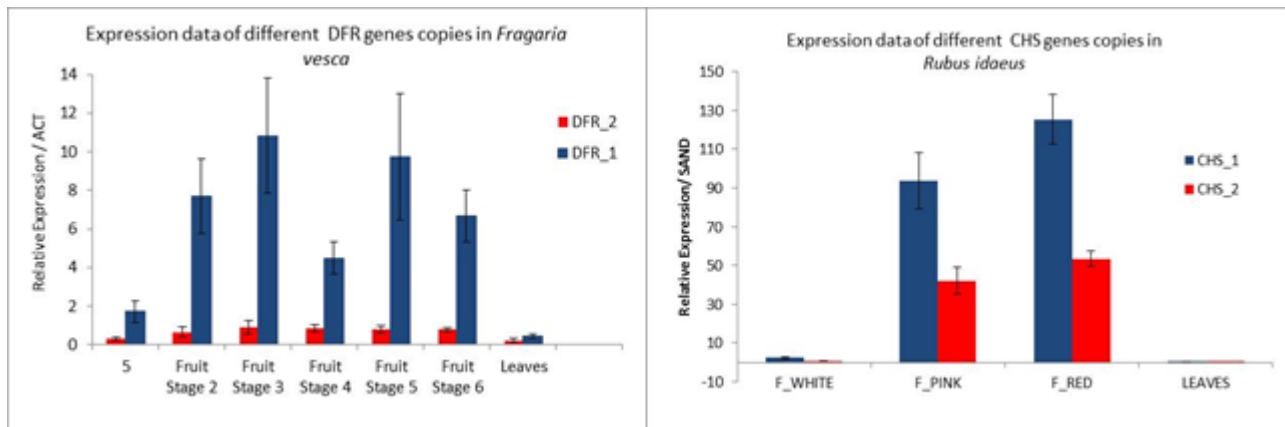


Figure 1: Example of expression data analysis of two DFR or two CHS genes in *F. vesca* or *R. idaeus*, respectively, to determine which gene copy is involved in anthocyanin biosynthesis.