P11-Analysis of Anthocyanin-related Transcription Factors during Fruit Development in *Rubus idaeus* and *Fragaria vesca*

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Anthocyanin synthesis is regulated through the interaction of the MYB-bHLH-WD40 complex, which has been characterized in several crops from diverse families (1), including some Rosaceae species such as strawberry and apple (2, 3). 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.

Using the available published genome data and genomes under construction, we identified three possible bHLH candidates from *F vesca* and two from *R. idaeus*. These candidates were evaluated for sequence homology with previous bHLH characterized proteins. We also performed sequence analysis of all the bHLH proteins of each species to determine the phylogenetic relationships amongst them and identify subgroups of interest. Preliminary results suggest which bHLH proteins are anthocyanin related, by examining expression during the fruit development, with experiments to define which proteins are involved in the regulation of "late-step" enzymes as LDOX and the UFGT family.

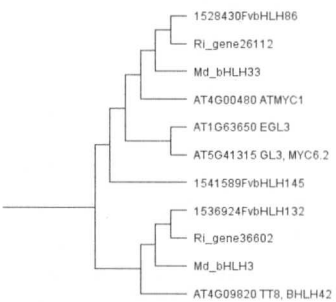

Figure 1: Phylogenetic analysis of the bHLH subgroup III f (4) involved in anthocyanin biosynthesis.

References:

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