

RGC 7

7th International
Rosaceae
Genomics
Conference



June 24-26, 2014
Seattle, Washington, USA

Program and Abstracts



Activation of anthocyanin-related biosynthetic genes by bHLH transcription factors in *Rubus idaeus* and *Fragaria vesca*

Andrea Lorena Herrera Valderrama¹, Antje Feller¹, Stefan Martens¹, Andrew Allan²

¹Fondazione Edmund Mach, Trento, TN, Italy; ²The New Zealand Institute for Plant & Food Research, Auckland, Auckland, New Zealand

Abstract:

Anthocyanin biosynthesis is regulated through the interaction of the MYB-bHLH-WD40 complex, which has already been characterized in several crops from diverse plant families, including some Rosaceae species. Using genome wide phylogenetic analysis, we identified three possible bHLH candidates from *F. vesca* and two from *R. idaeus* based on sequence homology with reported bHLH proteins from *Malus*, *Arabidopsis* and *Fragaria*. To date it is not clear which of these bHLH proteins are regulators of anthocyanin biosynthesis, and how this regulation is occurring in strawberries and raspberries. Here we show the results of gene expression studies of these bHLH genes as well as of putative anthocyanin biosynthetic genes at several fruit developmental stages. In addition, we show the results of promoter activation studies of “key” genes of the anthocyanin pathway like CHS, DFR, UFGT. Gene activation was determined by co-transformation of the promoter regions of biosynthetic genes fused to the luciferase gene and bHLH genes under 35S promoter expression in *Nicotiana benthamiana*, followed by luciferase transient assay; we determined that some of the bHLH candidate proteins are essential components for activation of key genes involved in the anthocyanin pathway.

Keywords: *Fragaria vesca*, *Rubus idaeus*, anthocyanins, bHLH transcription factors

Poster number: 2