

## W1011: Strawberry Genomics

### Natural Variation in Fruit Color Among *Fragaria* Species Explained by Independent Mutations in a Single Transcriptional Factor: *MYB10*

Cristina Castillejo<sup>1</sup>, Julie Caruana<sup>2</sup>, Veronica Waurich<sup>3,4</sup>, Henning Wagner<sup>3,4</sup>, Rubén Ramos<sup>1</sup>, José Vallarino<sup>5</sup>, Nicolás Oiza<sup>1</sup>, Pilar Muñoz-del Río<sup>1</sup>, Juan C. Triviño<sup>6</sup>, Sonia Osorio<sup>5</sup>, Zhongchi Liu<sup>2</sup>, David Posé<sup>5</sup>, Tuomas Toivainen<sup>7</sup>, Timo Hytönen<sup>7</sup>, José F. Sánchez-Sevilla<sup>1</sup>, Klaus Olbrich<sup>3</sup> and **Iraida Amaya**<sup>1</sup>, (1)IFAPA Centro de Málaga, Málaga, Spain, (2)Dept. of Cell Biology and Molecular Genetics, University of Maryland, College Park, MD, (3)Hansabred GmbH & Co, Dresden, Germany, (4)Institut für Botanik, Dresden, Germany, (5)IHSM - University of Málaga - CSIC, Málaga, Spain, (6)Sistemas Genómicos, Valencia, Spain, (7)University of Helsinki, Helsinki, Finland

Anthocyanins are the pigments responsible for the red color of strawberries. Their biosynthesis is controlled at the transcriptional level by a ternary complex consisting of R2R3-MYB and bHLH transcription factors associated with a WD40-repeat protein.

In order to map the genetic factors involved in fruit coloring we generated a mapping population crossing a *F. vesca* accession bearing white fruits (ESP138.596) with the red-fruited 'Reine des Vallées'. DNA from white- or red-fruited F2 individuals was pooled to perform a bulk segregant analysis (BSA) linked with high-throughput genome sequencing. This analysis revealed the presence of a *gypsy*-like retrotransposon inserted in the third exon of *FvMYB10*. The presence of this retroelement in homozygosis co-segregated with white fruits in the complete F2 population. We further extended this analysis to other white-fruited *F. vesca* accessions but none of them harbored this retroelement in *FvMYB10*. Instead we identified two additional polymorphisms affecting *FvMYB10*, (1) a single nucleotide insertion, which generates a truncated protein, and (2) a large deletion of ~100 Kb spanning a genomic region that contains 7 genes, one of them being *FvMYB10*. The three newly identified polymorphisms on *FvMYB10* differ from the previously described single nucleotide mutation, responsible for the lack of anthocyanins in other *F. vesca* white/yellow fruited accessions<sup>1</sup>.

We next analyzed QTL for fruit color in a segregating population derived from the red-fruited *F. x ananassa* 'Senga Sengana' and a *F. chiloensis* accession with white flesh. A major QTL controlling 45.7 - 54.7% of variance in internal flesh color was detected on LG I-3. The confidence interval spans the orthologous region where *FvMYB10* is located. Furthermore, transient overexpression on *FvMYB10* on different *F. chiloensis* accessions resulted in red sectors both in the epidermis and fruit flesh.

Altogether, these results show that a single R2R3-MYB, *FvMYB10*, regulates fruit color in different *Fragaria* species, indicating convergent evolution for anthocyanin biosynthesis in strawberry fruit.

<sup>1</sup>Hawkins, C., et al. (2016). Genome-scale DNA variant analysis and functional validation of a SNP underlying yellow fruit color in wild strawberry. *Sci. Rep.* 6, 29017.