

Study of Transcriptional Regulatory Network controlling Strawberry Fruit Ripening and Quality

Carmen Martín Pizarro¹, Eva Lucas Reina¹, Almudena Traperero Mozos¹, Victoriano Meco¹, Carlos Sánchez Gómez¹, José Vallarino¹, Maria A. De Luis Balaguer², José L. Rambla³, Tuomas Toivainen⁴, Sonia Osorio¹, Rosangela Sozzani², Antonio Granell³, Miguel A. Botella¹, Timo Hytönen⁴, Victoriano Valpuesta¹ and **David Posé**¹, (1)IHSM - University of Málaga - CSIC, Málaga, Spain, (2)North Carolina State University, Raleigh, NC, (3)IBMCP, Valencia, Spain, (4)University of Helsinki, Helsinki, Finland

Abstract Text:

Ripening is a critical step for the development of flavor quality in fruits. This character has significantly declined in many fleshy fruits over recent decades. This is particularly significant in strawberry (*Fragaria × ananassa*), where current cultivars are derived from a narrow germplasm collection. Improving fruit quality requires two important breakthroughs: 1) a precise understanding of the fruit ripening process that will allow the targeting of relevant genes, and 2) the identification of novel alleles responsible for fruit quality traits.

In our project (TRANSFR-Q, Starting Grant-ERC), we aim at the identification and characterization of key transcription factors involved in fruit ripening regulation and their target genes, in order to infer the Gene Regulatory Network controlling this process. On the other hand, we are carrying out a Genome-Wide Association Study using a germplasm collection of the woodland strawberry (*Fragaria vesca*) in order to identify loci involved in important traits such as aroma, fruit size, and resistance to pathogens. Finally, we have implemented the use of the genome-editing tool CRISPR/Cas9 in the cultivated strawberry, which we expect to open opportunities for engineering this species to improve traits of economic importance.