

## Spk12.

### **Strawberry GRN forever: insights into the transcriptional regulatory network controlling strawberry fruit ripening and quality**

Carmen Martín-Pizarro<sup>1</sup>, Carlos Sánchez Gómez<sup>1</sup>, Victoriano Meco<sup>1</sup>, María Urrutia<sup>1</sup>, Jeremy Pillet<sup>1</sup>, Eva Lucas Reina<sup>1</sup>, Almudena Trapero Mozos<sup>1</sup>, José Vallarino<sup>1</sup>, Maria A. De Luis Balaguer<sup>2</sup>, Jessica Pérez-Sancho<sup>3</sup>, Emmanuelle M. Bayer<sup>3</sup>, José M. Franco-Zorrilla<sup>4</sup>, Sonia Osorio<sup>1</sup>, Rosangela Sozzani<sup>2</sup>, Miguel A. Botella<sup>1</sup>, Victoriano Valpuesta<sup>1</sup>, David Posé<sup>1</sup>

<sup>1</sup>Laboratorio de Bioquímica y Biotecnología Vegetal, Instituto de Hortofruticultura Subtropical y Mediterránea (IHSM)-UMA-CSIC, Málaga, Spain. <sup>2</sup>North Carolina State University, Raleigh, NC. <sup>3</sup>Laboratory of Membrane Biogenesis, Université de Bordeaux-CNRS, 33140 Villenave d'Ornon, France. <sup>4</sup>Genomics Unit, Department of Plant Molecular Genetics, Centro Nacional de Biotecnología, CSIC, C/Darwin 3, 28049 Madrid, Spain.

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, we aim at the identification and characterization of key transcription factors (TF) involved in fruit ripening regulation and their target genes, in order to infer the Gene Regulatory Network controlling this process. Among them, we have identified two TFs belonging to the NAC (FaRIF) and the BLH9 (FaRPL) family. Functional analyses establishing stable silencing and overexpression lines support that both TFs play a critical role in the regulation of fruit ripening and development. Furthermore, using a stage- and tissue-specific transcriptome analysis, we have identified TFs specifically expressed in the external layer of ripe receptacles of *F. vesca* fruits, which are involved in the regulation of wax and cuticle formation.

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.

*This work was supported by the ERC Starting Grant ERC-2014-StG 638134 and the Plan Estatal de Investigación Científica y Técnica y de Innovación RTI2018-097309-A-I00.*