

XIV REUNIÓN DE BIOLOGÍA MOLECULAR DE PLANTAS

SALAMANCA, 4-6 de Julio 2018

Name & Surname of the presenting author: Eva Lucas-Reina

E-mail: elucas@uma.es

Session: Desarrollo

Communication (Oral or Poster): Poster

Deciphering Strawberry Ripening by Tissue Specific Gene Regulatory Networks

Eva Lucas-Reina¹, Almudena Trapero-Mozos¹, María Angels de Luis Balaguer², Carmen Martín-Pizarro¹, Martín Ramos-Alvelo, Rosangela Sozzani², Miguel Ángel Botella, Victoriano Valpuesta¹ and David Posé¹

¹*Departamento de Biología Molecular y Bioquímica, IHSM-UMA-CSIC, Málaga, Spain.*

²*Plant and Microbial Biology Department, North Carolina State University, Raleigh, NC, USA.*

Corresponding author: David Posé Padilla (dpose@uma)

During ripening, fruits undergo a number of metabolic and physiological changes leading to softening and improvement of characters such as flavor and palatability. Insights into transcriptome changes during strawberry fruit ripening have been reported, but always using either complete fruits in the analysis or separating achenes and the fleshy part (receptacle). However, the receptacle is composed of heterogeneous cell types, each of them with different characteristics and functions. Hence, transcriptomic studies performed so far may have lost important regulatory elements which expression is low but important in a specific cell-type.

In our study, we use Laser Capture Microdissection (LCM) technique for the isolation of cells from specific tissue types such as the epidermis, vascular bundles, cortex, and pith. Transcriptome profiling of these tissue types was performed by RNAseq. A gene co-expression analysis was performed by Weighted Correlation Network Analysis (WGCNA). Ontology analysis of each module showed wax biosynthesis as the main biological pathway enriched at the red epidermis specific module. In order to elucidate the putative regulatory elements that control the synthesis of waxes in this tissue, a Gene Regulatory Network (GRN) was inferred using GENIST (de Luis Balaguer, 2017). As a result, we have identified a set of transcription factors that might regulate the expression of *Eceriferum* genes and a fatty acid elongase necessary for wax biosynthesis in ripe epidermis.

Ultimately, our results open the possibility of implementing novel targeted breeding approaches. Moreover, this work shows that LCM followed by RNAseq is a powerful tool that can be used to clarify the regulatory scenario of tissue-specific biological processes during strawberry fruit ripening.

References

1. *de Luis Balaguer et al (2017). PNAS. 5;114 (36)*

Acknowledgements & Funding. This work was supported by the Grant ERC-2014-StG 638134 (European Research Council) and the Ramón y Cajal program RYC 2013-1269 (MINECO-Universidad de Málaga, Spain). The authors also acknowledge the support by the Plan Propio from University of Malaga, Campus de Excelencia Internacional de Andalucía.