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Deciphering Strawberry Ripening by Tissue Specific Gene Regulatory Networks

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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)*

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