

Fruit ripening behaviour: Ethylene and the Regulation of Sugar Metabolism

Macarena Farcuh*, HoYoun Kim, Bosheng Li and Eduardo Blumwald

Department of Plant Sciences, University of California, Davis, CA 95616. *mfarcuh@ucdavis.edu

Introduction

Japanese plums represent the most abundant and variable group among tree species and include most of the fresh-market plums commercialized worldwide. We recently reported the existence of two Japanese plum cultivars, 'Santa Rosa' (SR) and its bud-sport mutant 'Sweet Miriam' (SM), that share the same genetic background but display contrasting ripening behaviors (SR, climacteric and SM, non-climacteric) (Kim et al., 2015). Besides, both cultivars differ in their sugar composition conferring the SM fruits with unusual quality properties. The main objective of this research is to characterize the role(s) of ethylene in the regulation of sugar metabolic pathways and its influence in climacteric (SR) and non-climacteric (SM) fruit ripening behaviors. In order to achieve this, fruits from each cultivar were harvested at early (S2: pit hardening) and late (S4: fully-ripe) stages of fruit development and assessed using transcriptomics, proteomics and metabolomics methodologies, together with targeted gene expression, metabolite and enzymatic activity assays.

Results and discussion

Fruit quality-related traits

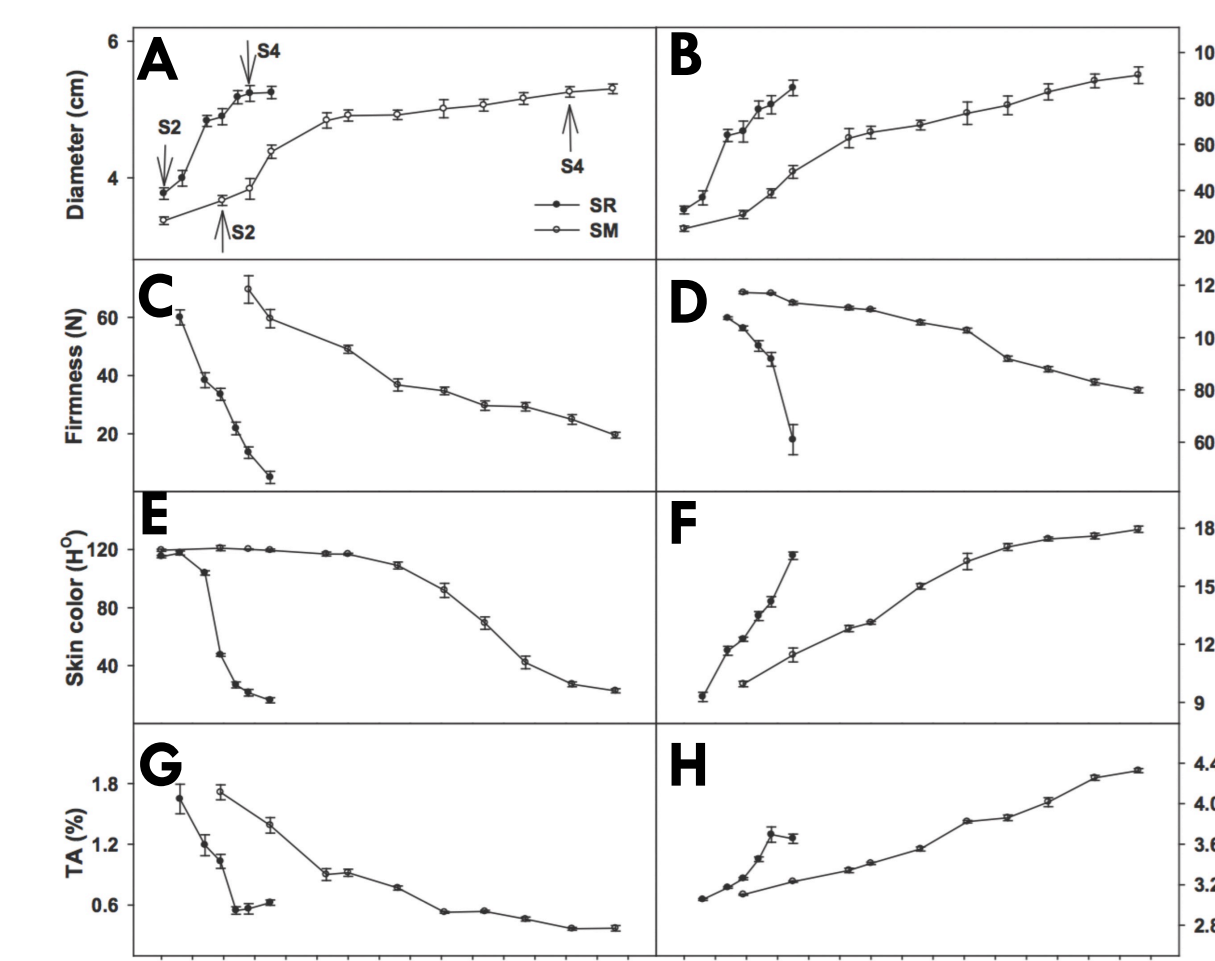


Fig. 1. Fruit quality traits. (A) Fruit diameter, (B) fruit weight, (C) fruit firmness, (D) fruit flesh color, (E) fruit skin color, (F) fruit soluble solid contents, (G) fruit titratable acidity and (H) fruit pH. SR, Santa Rosa (closed circles); SM, Sweet Miriam (open circles). Values are mean \pm SE (n=6). Arrows indicate stages S2 and S4 in each cultivar.

CO₂ and Ethylene production rates

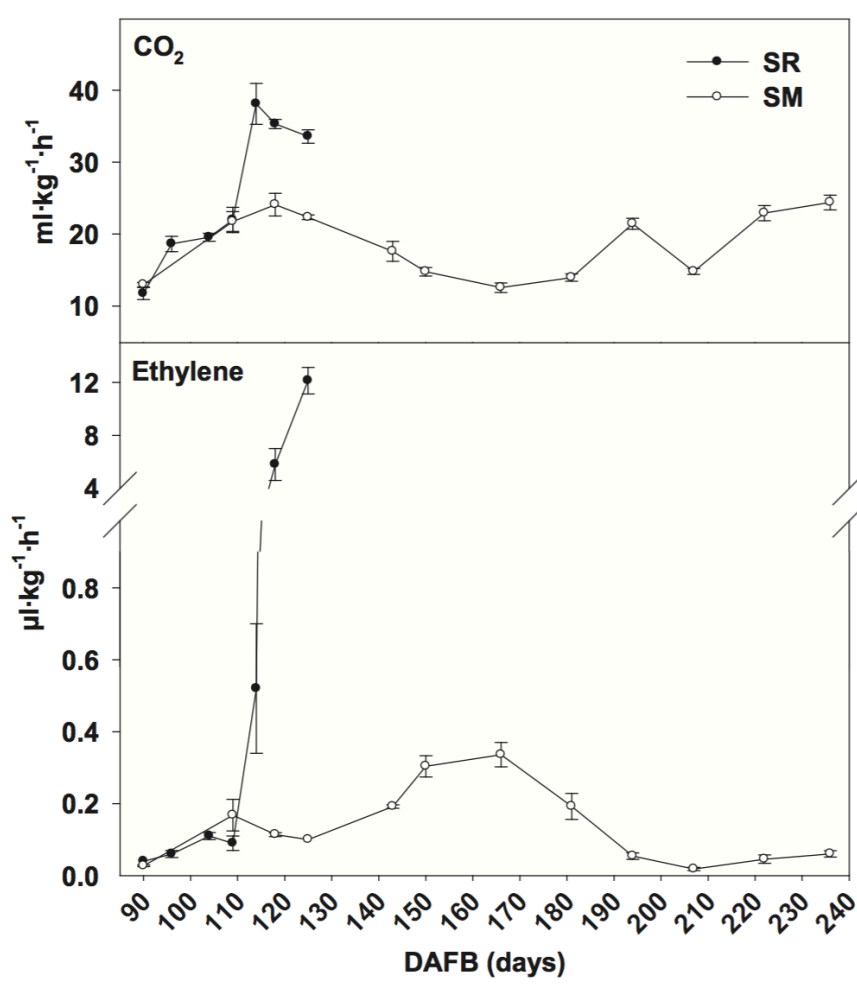


Fig. 2. Ethylene and CO₂ production rates during maturation and ripening on the tree. SR, Santa Rosa (closed circles); SM, Sweet Miriam (open circles). Values are mean \pm SE (n=6).

Transcriptomics, Proteomics and Metabolomics

TRANSCRIPTOMICS DATA SUMMARY	
Number of samples	12 from two developmental stages (S2 and S4) of plum cultivars SR (climacteric) and SM (non-climacteric)
Number of run/lanes	Two HiSeq lanes to produce approximately 25 million 100 × 100 nt paired-end reads per sample
Reads before trimming	526 million raw reads (263 million pairs)
Reads after trimming	511 million reads
Unique Reads	42 million reads
PROTEOMICS DATA SUMMARY	
Number of samples	12 from two developmental stages (S2 and S4) of plum cultivars SR (climacteric) and SM (non-climacteric)
Soluble proteins detected	624 proteins detected
Membrane proteins detected	892 proteins detected
METABOLOMICS DATA SUMMARY	
Number of samples	12 from two developmental stages (S2 and S4) of plum cultivars SR (climacteric) and SM (non-climacteric)
Total number of compounds detected	248 compounds
Number of identified compounds	90 compounds
Number of unknown compounds	158 compounds

Table 1. Data summary for transcriptomics, proteomics and metabolomics methodologies used in this study for both plum cultivars.

Results and discussion

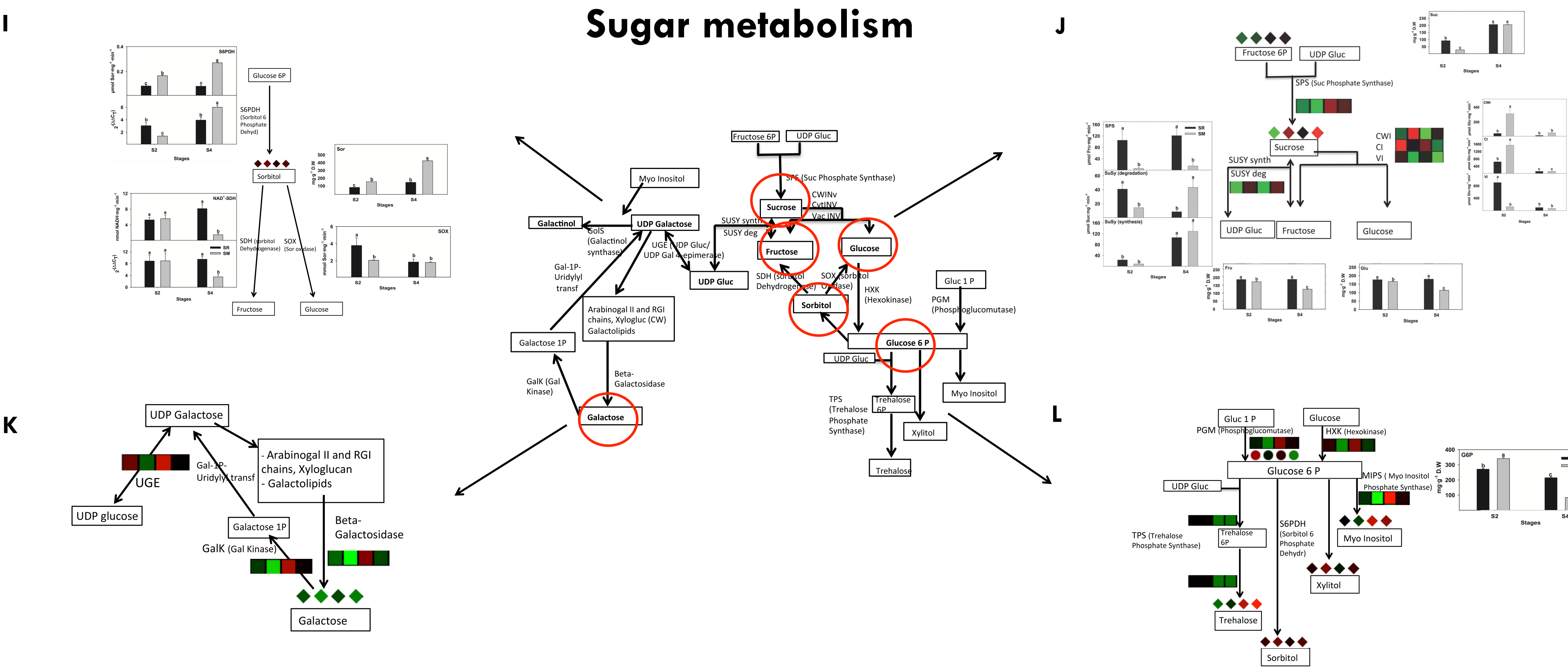


Figure 3. Sugar metabolism-related pathways for SR and SM cultivars during an early (S2: pit hardening) and late (S4: fully-ripe fruit) developmental stage, characterized using transcriptomics, proteomics and metabolomics methodologies together with targeted gene expression, metabolite and enzymatic activity assays. (I) Sorbitol-related pathways; (J) Sucrose, Glucose and Fructose-related pathways; (K) Galactose-related pathways; (L) Glucose 6P-related pathways.

Ethylene biosynthesis, perception and signaling

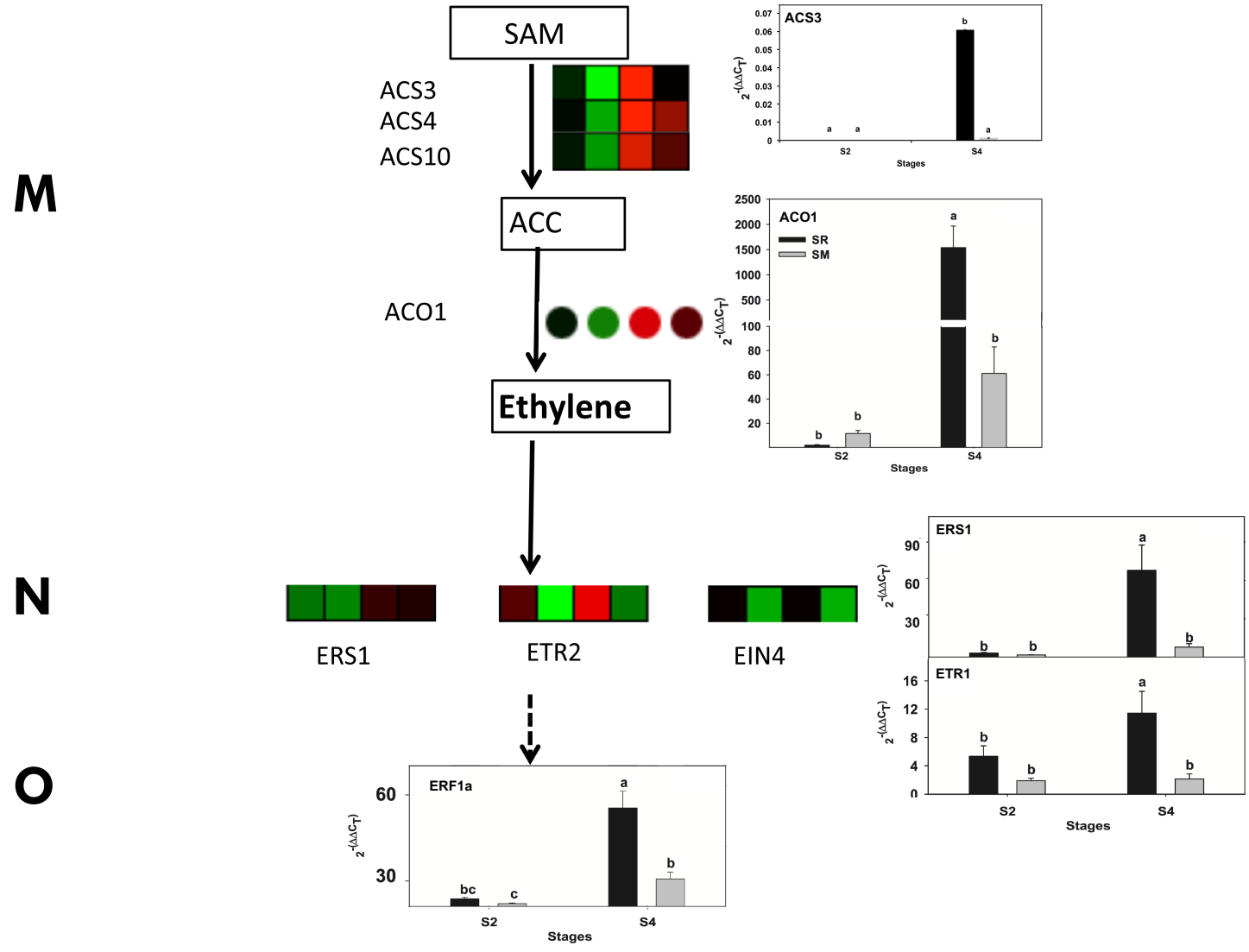
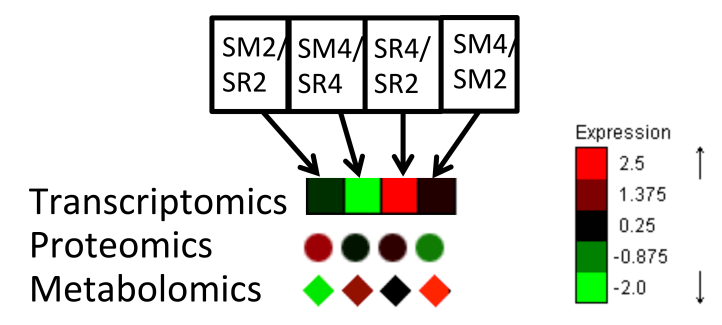


Figure 4. Ethylene biosynthesis, perception and signaling-related pathways for SR and SM cultivars during an early (S2: pit hardening) and late (S4: fully-ripe fruit) developmental stage, characterized using transcriptomics, proteomics and metabolomics methodologies together with targeted gene expression, metabolite and enzymatic activity assays. (M) Biosynthesis-related pathways; (N) Perception-related pathways; (O) Signaling-related pathways.



Conclusions

Our results indicate that there are significant differences in ethylene biosynthesis, perception and signaling as well as in sugar metabolism-related pathways between both cultivars. The non-climacteric cultivar, SM, presents lower glucose, fructose and galactose but higher sorbitol concentrations with respect to SR at both developmental stages analyzed. These differences can affect fruit quality characteristics (sweetness), nutritional value and even ROS scavenging capacity of both cultivars. Ongoing work is focused on further understanding ethylene and its regulation of sugar metabolism.

References

Kim et al. 2015, Plant Science 231:30-39.

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