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8TH International Rosaceae Genomics Conference, Angers (France), 2016/06/21-24. Oral presentation

From gene to phenotype: genetic control and modeling of sugar metabolism during peach fruit development

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Fruit quality is a multi-criteria character with frequent antagonistic relationships. Among the three so-called major sugars in fruit, fructose is the sweetest and its concentration is the factor that most affects the fruit sweetness. The objective of the present study is to analyze the sugar metabolism in peach fruit from metabolic, enzymatic and genetic aspects and integrate into a mathematical model all information obtained. This work focuses on the identification of the effect of a low fructose concentration on the whole sugar metabolism and the understanding of the mechanisms responsible for this phenotype called 'low-fructose-to-glucose-ratio'. A nearly exhaustive biochemical characterization of sugar metabolism was conducted during peach fruit development. For this, 6 metabolites and 12 enzyme capacities were assayed in 106 genotypes of a population derived from an interspecific cross. This study revealed a high stability of the enzyme capacities despite large variations of metabolites. A QTL analysis performed on this dataset highlighted the instability of the effect of certain loci during fruit development. Co-locations of QTLs for metabolites and enzyme capacities and candidate genes were observed. In addition, the genomic region responsible for the 'low-fructose-to-glucose-ratio' phenotype was confirmed, and functional candidate genes were identified. An analysis of this gene has started to validate its function and its involvement in this particular phenotype. Based on data from 10 genotypes, a kinetic metabolic model that simulates the sugar accumulation in fruit was developed and validated. This model simulates contrasting phenotypes and helps in understanding the underlying mechanisms of the 'low-fructose-to-glucose-ratio' phenotype. In the future, the integration of the genetic control into the metabolic model will allow simulating virtual genotypes with different combinations of alleles and predict their sugar content.

Topic: Flower and fruit development and quality (primary and secondary metabolism,...)

Type of presentation: oral

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