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High or low fructose? Consequences for sugar metabolism in peach fruit

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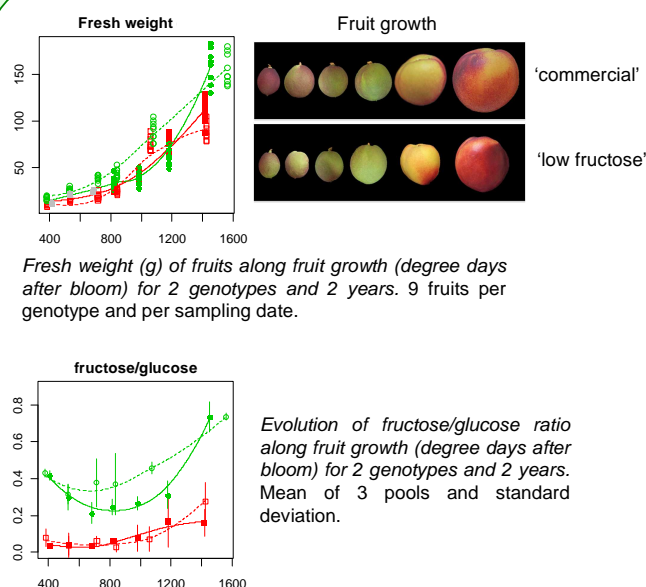
Introduction

Fruit taste is largely affected by the content of sugars and acids. Fructose is the sweetest tasting sugar. In commercial peach fruit, sucrose is the main sugar, followed by fructose and glucose which have similar levels. Interestingly low fructose accessions have been described in wild peaches^{1,2}. Through an extensive profiling of metabolites and enzymatic activities, this study aims at i) describing sugar metabolism in peach fruit at different developmental stages and ii) comparing two genotypes with contrasted fructose/glucose ratios.

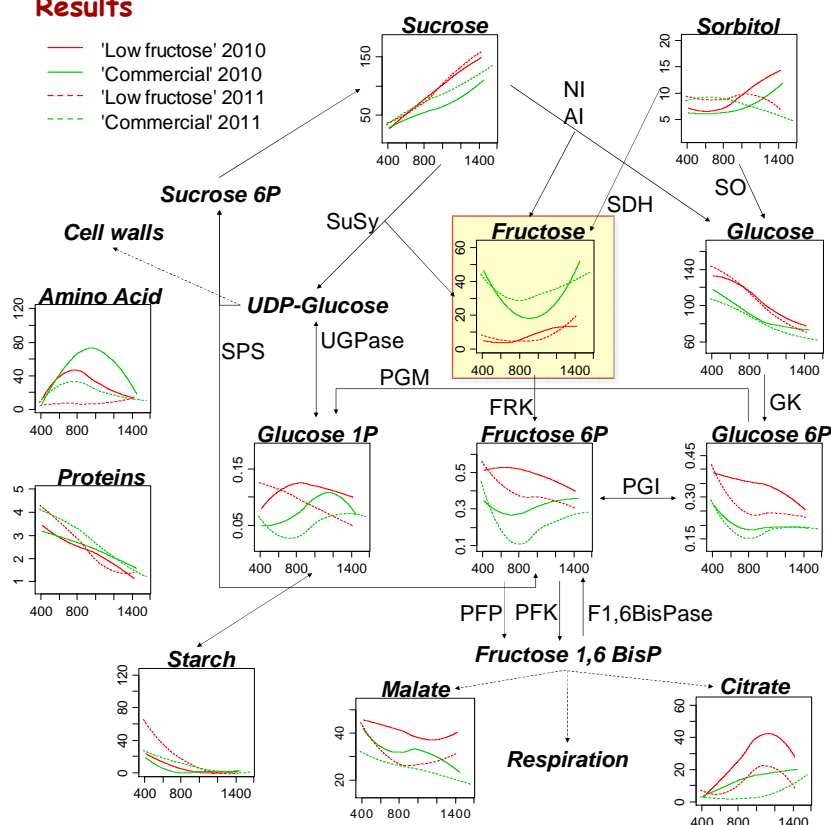
Materials and methods

Fruit samples were collected at 6 or 7 developmental stages respectively in 2010 and 2011. Three pools of 3 fruits were collected for each stage. Fruit mesocarp was cut in little pieces, immediately frozen in liquid nitrogen, ground to a fine powder and stored at -80°C. Twelve metabolites and 12 enzyme activities were measured by enzymatic methods³.

Hypotheses to explain 'low fructose' genotype : reduced synthesis and/or increased degradation



Results



Sugar metabolism in peach and time courses smoothed from concentration data of the different metabolites (mg/gFW), proteins and amino acids (mol/FW) along fruit growth (degree days after bloom) for 2 genotypes and 2 years.

Main results

- Genotypic effect was observed for all metabolites
- Year effect was observed for sorbitol and citrate
- The enzyme activities were stable between genotypes and years

No difference was detected in the activities of the enzymes responsible for synthesis or degradation of fructose

SO	SDH	SuSy	SPS	F1,6bisP	NI	PFK	FRK	PGM	GK	AI	UGPase
0 - 0.1	0.2 - 0.7	1 - 3	1 - 5	10 - 60	20 - 80	10 - 150	50 - 150	60 - 150	60 - 200	50 - 800	450 - 600
→	→	→	→	→	→	→	→	→	→	→	→

Min and max activities (nmol/gFW/min) and mean tendency of evolution along fruit growth of 12 enzymes for 2 genotypes and 2 years

UGPase : UDP-glucose pyrophosphorylase; PGI : phosphoglucosomerase; PGM : phosphoglucosomutase; PFP : phosphotransférase; PFK : phosphofructokinase; F1,6BisPase : fructose 1,6-bisphosphatase; SPS : sucrose phosphate synthase; FRK : fructokinase; GK : glucokinase; SuSy : sucrose synthase; NI : neutral invertase; AI : acid invertase; SDH : sorbitol dehydrogenase; SO : sorbitol oxidase

Sugar metabolism is a highly regulated system in which a major perturbation in a central compound has only slight repercussions on other metabolites and on enzyme activities

Other explanations for the low fructose phenotype

- **Differential affinities for substrate between iso-enzymes.** In peach fructokinase has two isoforms with different affinities for fructose².
- **Limited fructose storage resulting in higher degradation.** Fructose and glucose are stored in the vacuole. If fructose cannot be stored or if it 'destocked' to cytosol, it is more degraded than glucose.
- **Differential consumption of the two hexoses for respiration, cell wall or synthesis of other carbon compounds.** First results suggest that the 'low fructose' genotype has more carbon than the 'commercial' genotype though there is no difference between the two genotypes for dry mass.