Metabolomic analyses in sweet cherry

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Introduction

In sweet cherry (*Prunus avium* L.) organoleptic quality is part of the main fruit traits for breeders and consumers. Fruit acidity and the composition in sugars and acids have an important impact on fruit taste. In this work, we present the quantitative trait locus (QTLs) detection for pH, titratable acidity (TA) and content of the main sugars and acids. The two first traits were evaluated during three years whereas the sugar and acids contents were evaluated for one year.

Material & Methods

Fig. 1: R×L hybrids

Plant material

Two intraspecific F_1 mapping progenies Regina×Lapins (R×L) and Fercer×INRA-X (F×X) composed of 124 and 67 hybrids respectively, were evaluated for fruit quality traits. Trees were planted on their own roots in orchard (Fig. 1).

Linkage maps

The two progenies were genotyped using the 6k cherry chip SNP developed in the RosBREED project. Linkage map was constructed for each parent. For the R×L progeny, Regina and Lapins maps include respectively 142 SNPs (619 cM) and 126 SNPs (610 cM); for the F×X progeny, Fercer and INRA-X maps include respectively 107 SNPs (covering 715 cM) and 87 SNPs (644 cM).

Phenotypic evaluation of titratable acidity, pH and metabolite concentrations

AT and pH were evaluated during 3 years on R×L and were estimated with titroLine®Easy.

Metabolite concentrations in fruits (glucose, fructose, sorbitol and malic acid) were evaluated in 2012 on both progenies by high-throughput enzymatic analyses.

QTL detection

QTL analyses were performed separately for each year and combined for all years using MultiQTL software.

Results

- QTLs for both pH and TA were detected on three linkage groups (LG) in RxL (Fig.2). A high stability between years of evaluation was observed on LG6 in Regina for pH and TA. Multi-years QTL of pH and TA explain respectively 24.6% and 28.3 % of the EV (Fig.3).
- QTLs for fructose with major effects were detected in LG1 and LG4 in FxX. They explain 14.4%, 20.4 % et 36.4 % of the EV in Fercer in LG1, and in INRA-X in LG1 and LG3, respectively (Fig.2).
- Only one QTL for sucrose was detected, located on L3.
- For glucose, one QTL on F1 with high effect (20.3% EV) and a second one on L4 with lower effect (8.3 % EV) were detected.
- QTLs for sorbitol were detected in LG1, LG2, LG3, LG4 and LG8, the one with the highest effect (17.3%) located on LG4 (FxX).
- A QTL for malate with major effect was observed on LG6 for Regina and INRA-X. It explains 30,8% of EV in R6 and 31% in X6 (Fig.2 and Fig.3). The QTL for malate co-localize with the QTLs with high effect for pH and TA observed also in R6.

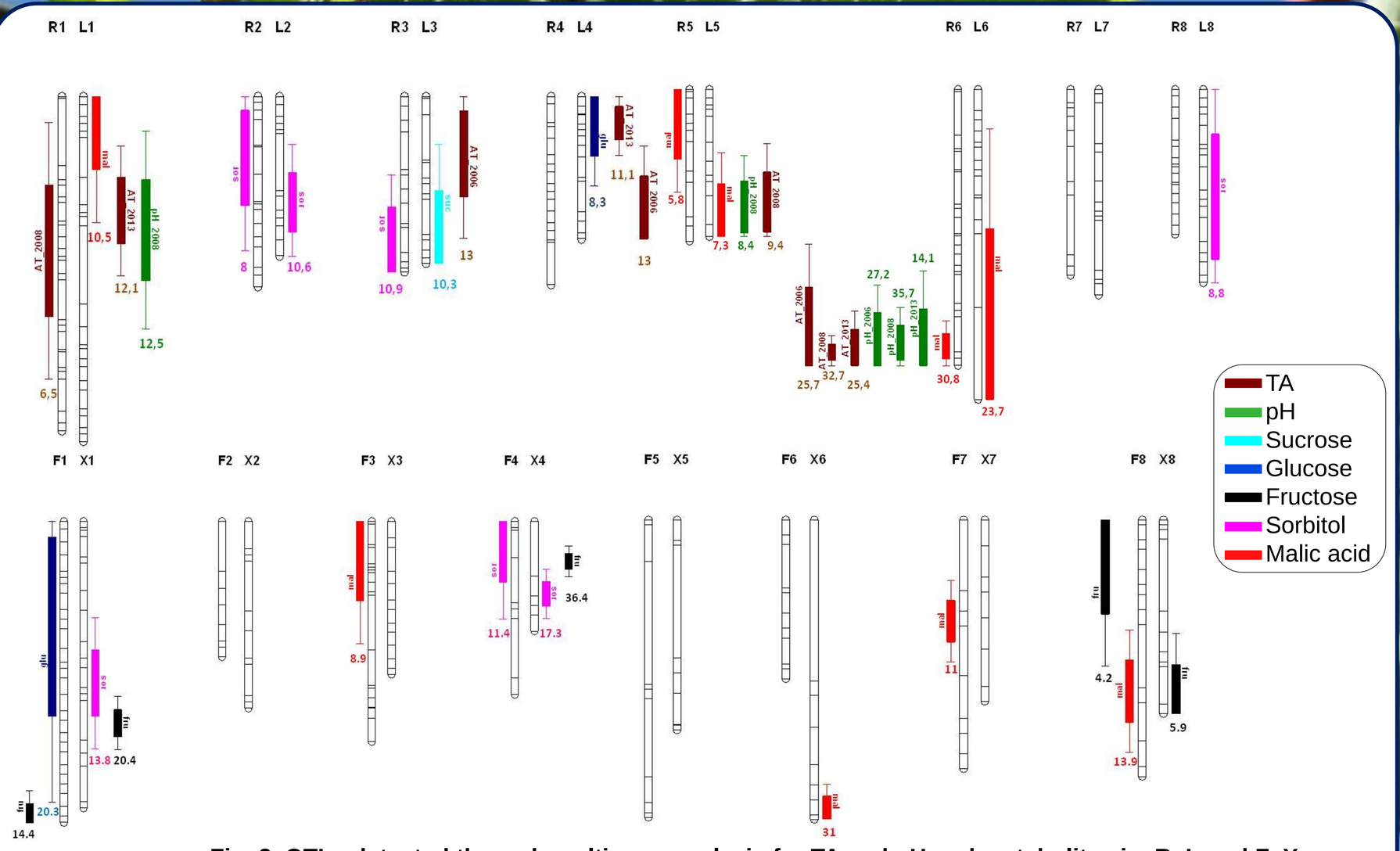

Fig. 2: **QTLs detected through multi-year analysis for TA and pH and metabolites in R×L and FxX.**
For each QTL the percentage of explained variation (PEV(%)) value is indicated in bold near the QTL.

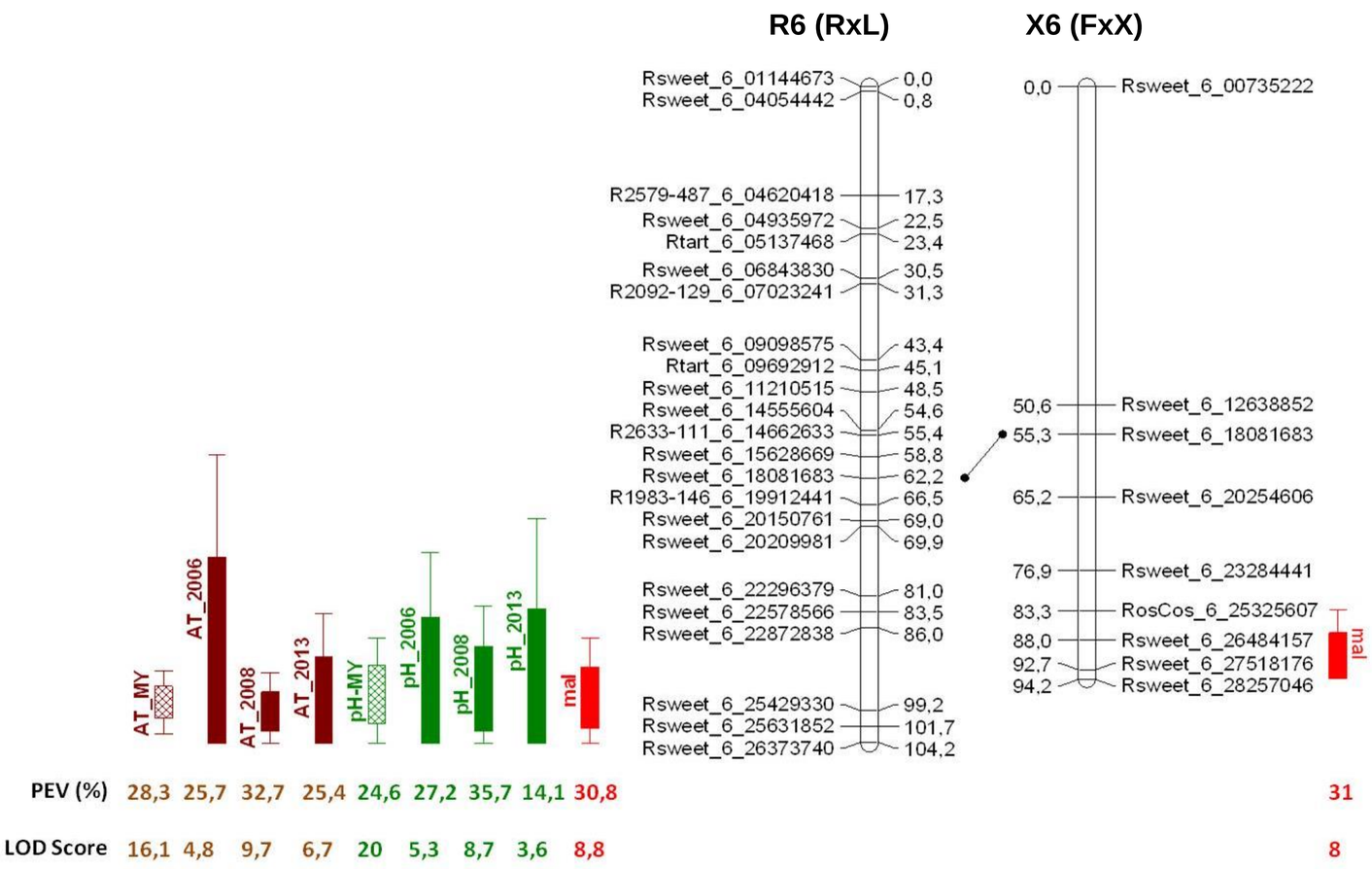

Fig. 3: QTLs detected for TA, pH and malic acid on LG6 of the parents 'Regina' and 'INRA-X'.
QTLs from multiyear's evaluation are represented by brown and green hatched boxes respectively for AT and pH. QTLs from year evaluation are represented by full boxes. QTLs for malic acid are represented on LG6 of both parents by red boxes. Anchored markers are indicated by connecting lines. Marker names include the LG and physical position corresponding to the peach genome v1.0.

Acknowledgements

We thank the Fruit Experimental Unit of INRA – Bordeaux for growing the trees.

RGC7 7th International Rosaceae Genomics Conference

Seattle June 24-26 2014 -Breeding and Genetics