QTL MAPPING AND CANDIDATE GENE RESEARCH FOR THE PHENOLIC CONTENT OF FRUITS AND JUICES PREPARED FROM A CIDER APPLE PROGENY

VERDU C.F.[1,2], Guyot S.[3], Childebrand N.[1], Lasserre-Zuber P.[1], Gaillard S.[1], Celton J.-M.[1], Troggio M.[4], Guilet D.[2] and Laurens F.[1]

[1]INRA, UMR1345 Institut de Recherche en Horticulture et Semences, SFR 4207 QUASAV, PRES L'UNAM, F-49045 Angers, France, [2]Université d'Angers, EA 921 laboratoire Substance d'Origine Naturelle et Analogues Structuraux, SFR 4207 QUASAV, 49045 Angers, France, [3]INRA, UR117 Recherches Cidricoles et Biotransformation des Fruits et Légumes, 35653 Le Rheu, France, [4]IASMA Research and Innovation Centre, S. Michele all'Adige, TN, Italy.
Corresponding author: cindyverdu@gmail.com

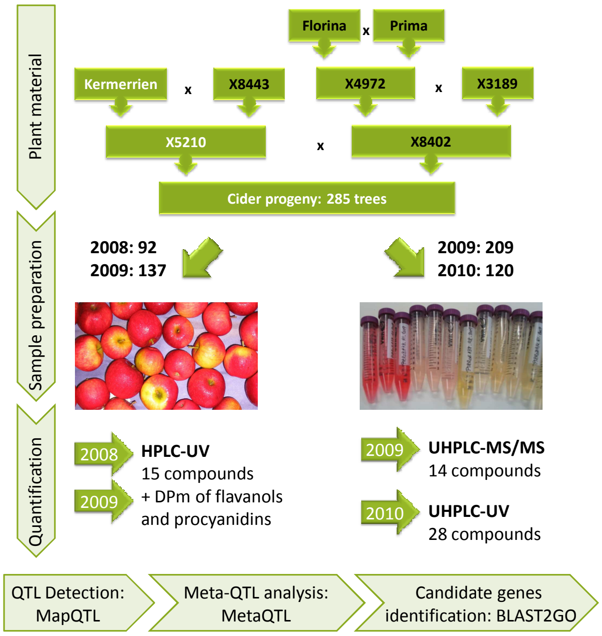
Introduction

Cider quality is dependant on polyphenol content : they affect astringency, bitterness, color and aroma. Five main groups of phenolic compounds are present in the apple fruit: flavanols, hydroxycinnamic acids, dihydrochalcones, flavonols and anthocyanins. Their regulation by transcription factors is well known as well as their biosynthesis. Furthermore, the apple genome has been sequenced and annotated, which facilitate candidate gene identification.

Variability of phenolic compounds has been widely studied in apple germplasm. But until now, only two QTL studies have been performed, both on dessert apple progenies.

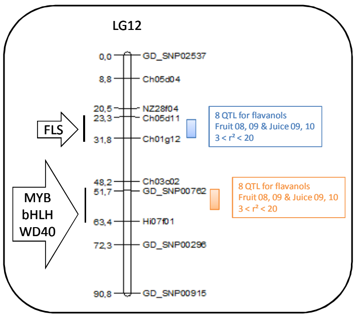
> The aim of this work is to perform a QTL analysis and a candidate gene research on the phenolic compounds present in fruit extracts and juices prepared from a cider apple progeny.

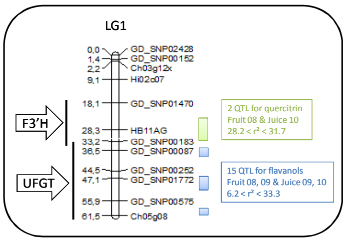
Material and Methods

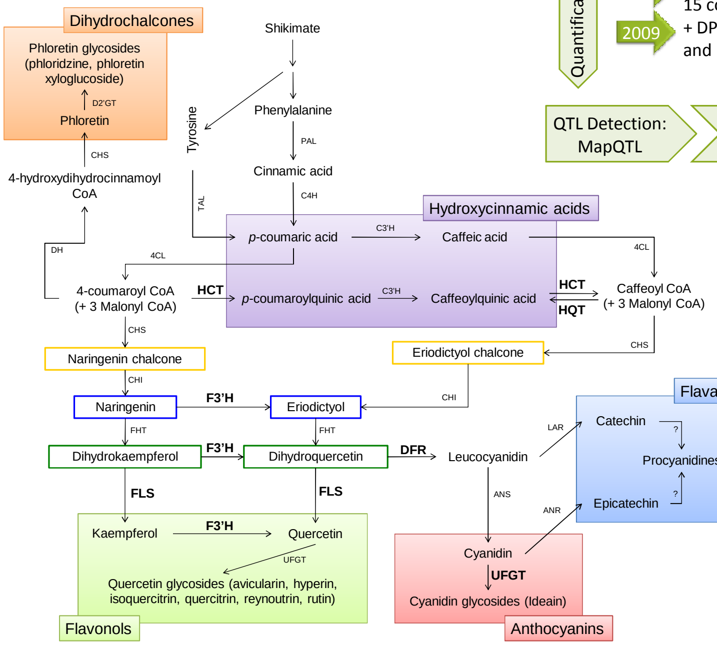


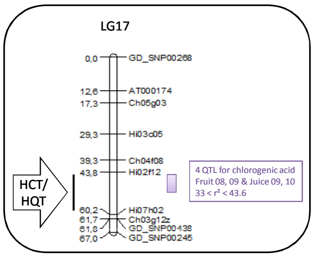
Results

- o 48 QTL identified at genome wide (GW) threshold on nine linkage groups (LG) of the integrated map for flavanols, flavonols, dihydrochalcones and hydroxycinnamic acids.
- o 11 main clusters located on six LG including QTL obtained at GW and LG threshold.
- o Confidence interval for clusters on LG 1, 3, 12, 15 and 17 significantly reduced with Meta-QTL analysis.
- o Several enzymes and transcription factors implicated in the phenolic pathway identified by *in silico* candidate gene research.









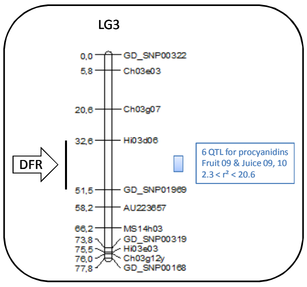


Figure. QTL meta-analysis for phenolic compounds quantified in fruit and juice prepared for two harvest years and candidate gene related to the biosynthethic pathway. *Meta-QTLs are represented as full bars on the right side of the LG. Details on QTL included in meta-QTL analysis are described close to the meta-QTL. Candidate genes found close to the meta-QTL are indicated in the arrow on the left side of the LG.*

Conclusion

- o Many QTL obtained for phenolic compounds quantified in fruit extracts and apple juices prepared in two harvest years. Several clusters identified for four phenolic groups.
- o The meta-QTL analysis was a powerful tool to reduce confidence interval of these clusters.
- o BLAST2GO software allowed a rapid analysis of putative gene functions present underneath QTL confidence interval.

Acknowledgment

This work was supported by a PhD grant funding from the SFR 149 QUASAV (Structure Fédérative de Recherche: Qualité et Santé du Végétal), Angers, France and the inter-regional (Bretagne-Pays de la Loire) project INNOVACIDRE. Participation to RGC6 was funded by a grant awarded by the "Académie d'Agriculture de France".

Sixth Rosaceous Genomics Conference
30th september-4th october 2012