

# QTLs mapping for primary metabolites responsible of the organoleptic and nutritional characteristics of strawberry (*Fragaria x ananassa*)

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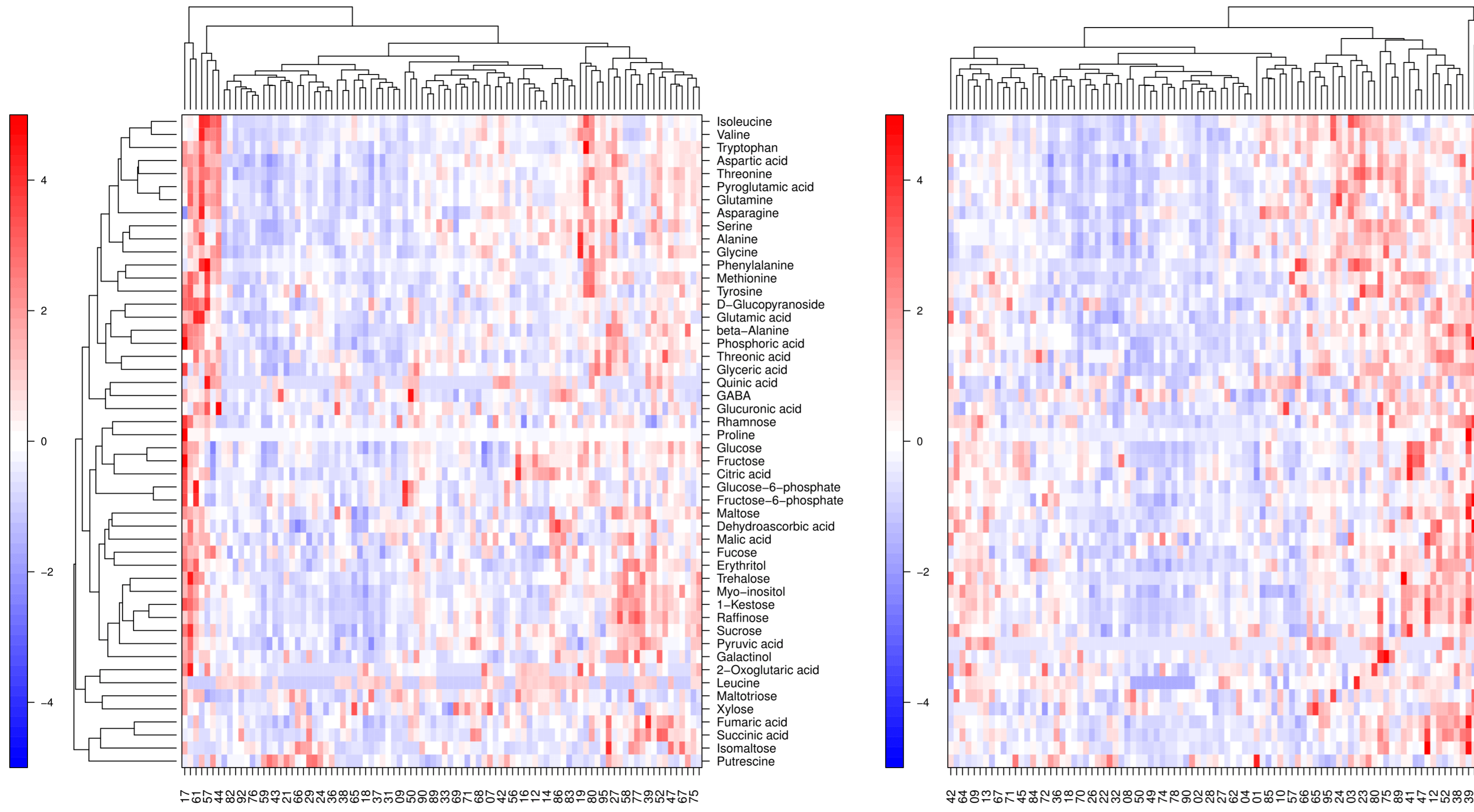
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## INTRODUCTION

The cultivated strawberry (*Fragaria x ananassa*) is a highly consumed fruit known for its delicate flavour and nutritional characteristics. However, as fruit quality attributes have been lost after years of traditional breeding, new technological tools, such as genomics and high throughput metabolomics are necessary for the identification of factors responsible of these traits. Here we present the quantitative trait loci (QTLs) mapping for the content of primary metabolites of a 95 F<sub>1</sub> individuals strawberry population derived from genotype "1392", selected for its superior flavour, and "232" (Zorrilla-Fontanesi et al., 2011; Zorrilla-Fontanesi et al., 2012).

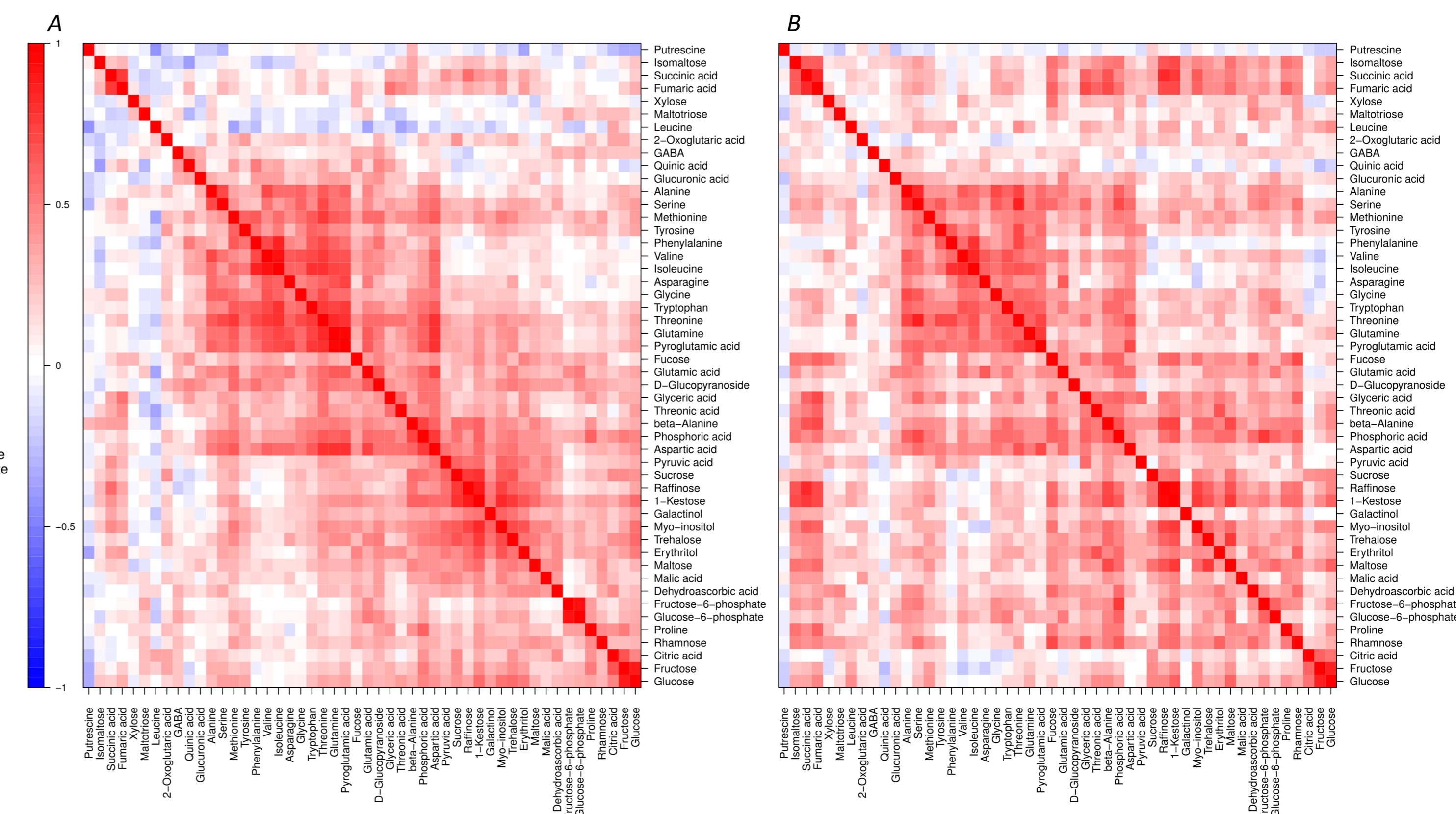
Metabolite profiling was performed on red stage fruits of the strawberry population using gas chromatography hyphenated to time-of-flight mass spectrometry. QTLs mapping was performed on the "232x1392" population separately over two successive years, based on integrated linkage maps using mapQTL5 software.

## RESULTS

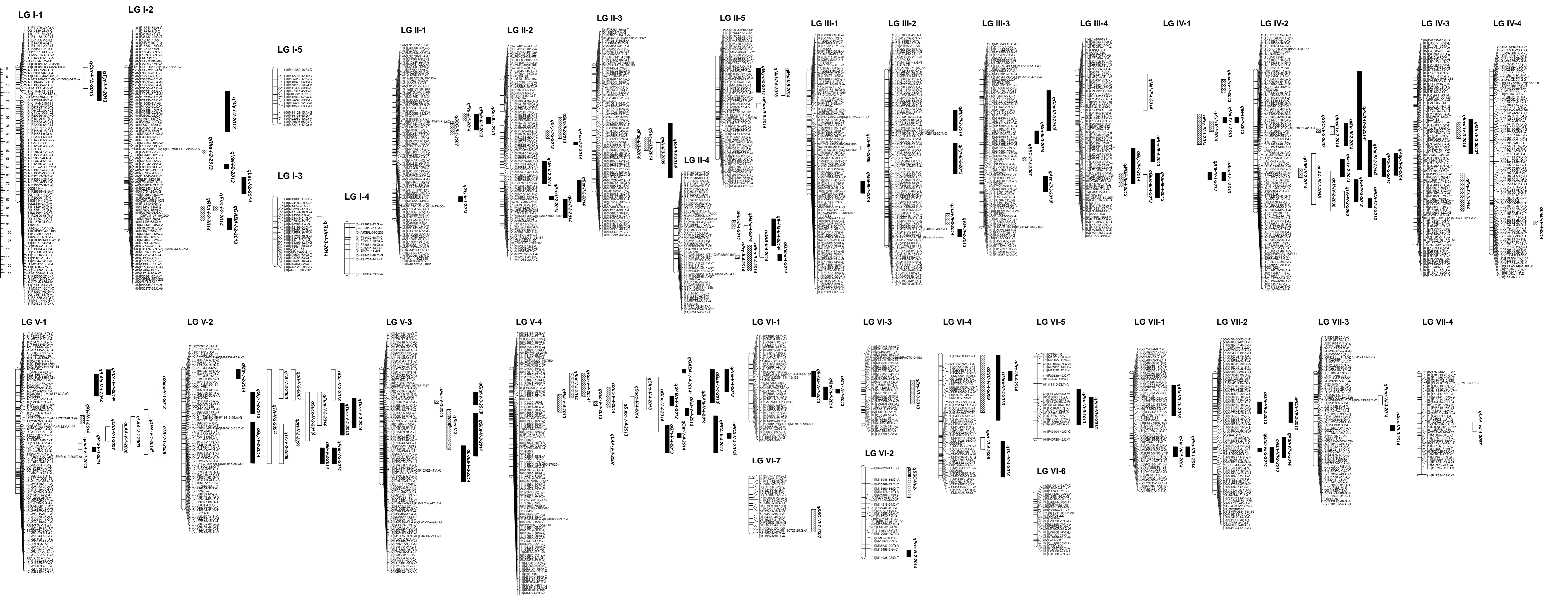


**Figure 1.** Heat map representing the levels of metabolites in the '1392 x 232' strawberry population in the harvest 2013. Metabolites and population's lines are grouped by clusters, using Pearson's coefficient. Lowest levels of metabolites are represented in blue, highest levels in red.

**Figure 2.** Heat map representing the levels of metabolites in the '1392 x 232' strawberry population in the harvest 2014. Population's lines are grouped by clusters, using Pearson's coefficient. Metabolites are ordered after cluster analysis of the 2013 harvest. Lowest levels of metabolites are represented in blue, highest levels in red.



**Figure 3.** Heat map of metabolite-metabolite correlations in the '1392 x 232' strawberry population. Correlation coefficients were calculated with Pearson algorithm. Dark blue squares indicate negative correlation and dark red squares a positive correlation. A Metabolite-metabolite correlations in the 2013 harvest. B Metabolite-metabolite correlations in the 2014 harvest.



**Figure 4.** Location of QTLs controlling primary metabolites analyzed in two consecutive years (2013–2014) using rMQM. Bars on the right of the linkage groups represent 2-LOD support intervals and are white, dashed or black for acids, sugars and amino acids, respectively. Segregation distortion is indicated by \*P ≤ 0.05; \*\*P ≤ 0.01; \*\*\*P ≤ 0.001. §, QTLs detected below the threshold but significant in other years or detected by Kruskal Wallis.

## CONCLUSIONS

A total of 132 QTLs were detected in all the linkage groups over the two years for 42 metabolites out of 50. Among them, 4 (9.8%) QTLs for sugars, 9 (25%) for acids and 7 (12.7%) for amino acids were stable and detected in the two successive years. We are now studying the QTLs regions in order to find candidate genes to explain differences of metabolites content in the different individuals of the population, and we expect to identify interactions between genes and metabolites which will help us to understand their role in quality traits of strawberry fruit.

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References  
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Zorrilla-Fontanesi, et al (2012) *Plant Physiol*, 159: 851-870.