



Metabolomics profiling of a strawberry (*Fragaria x ananassa*) F1 population to characterize flavour and nutritional traits

Delphine Pott^{1*}, Juan Jesús Medina³, Alisdair R. Fernie², Irida Amaya⁴, José G. Vallarino², Sonia Osorio^{1¶}

¹Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", University of Malaga-Consejo Superior de Investigaciones Científicas, Department of Molecular Biology and Biochemistry, Campus de Teatinos, 29071 Malaga, Spain. ²Max-Planck-Institute für Molekulare Pflanzenphysiologie, Am Mühlenberg 1, 14476 Golm, Germany. ³Instituto Andaluz de Investigación y Formación Agraria y Pesquera (IFAPA), Centro de Huelva. Julio Caro Baroja s/n, Huelva, Spain. ⁴IFAPA, Centro de Churriana, Cortijo de la Cruz S/N, Churriana, 29140 Malaga, Spain.

* dpott@uma.es; ¶ sosorio@uma.es

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 high throughput metabolomics, are necessary for the identification of factors responsible of these traits. Here we present the metabolomics profiling for the content of primary and secondary metabolites of a 95 F₁ 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 mature fruits of the strawberry population using gas chromatography hyphenated to time-of-flight mass spectrometry for primary metabolites and ultra performance liquid chromatography Exactive Orbitrap tandem mass spectrometry for secondary metabolites.

RESULTS

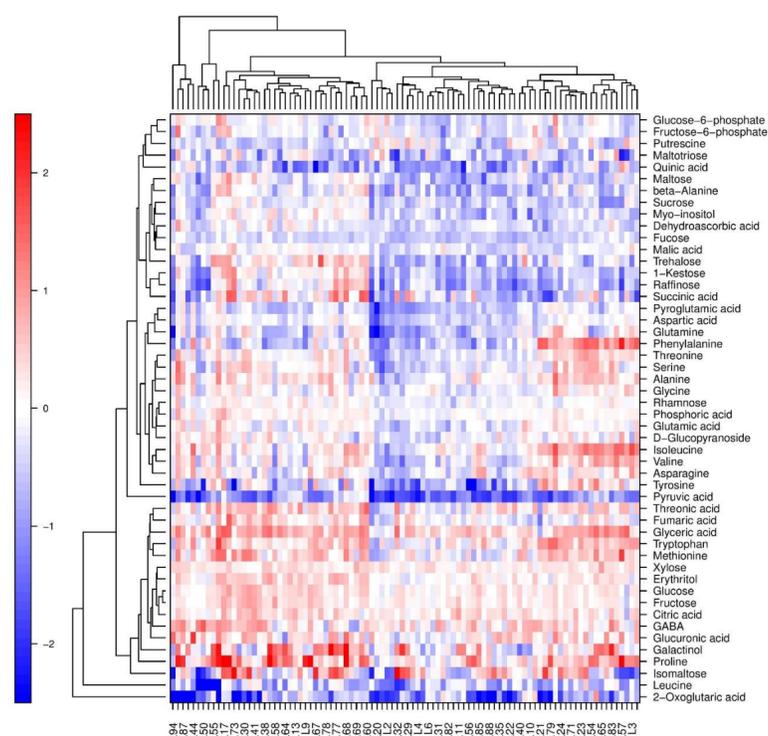


Figure 1. Heat map representing the mean value of the levels of primary metabolites in the '232 x 1392' strawberry population in the harvests 2013 and 2014. Metabolites and population's lines are grouped by clusters, using Pearson's coefficient. Values are represented as the fold change relativized to the '1392' parental. Lowest levels of metabolites are represented in blue, highest levels in red.

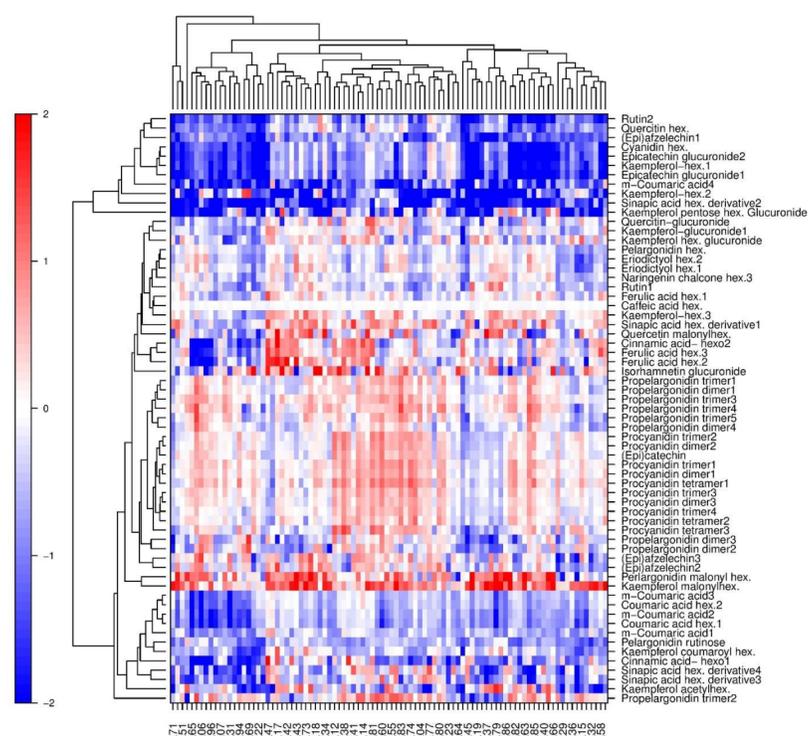


Figure 2. Heat map representing the mean value of the levels of the main class of secondary metabolites (flavonoids) in the '232 x 1392' strawberry population in the harvests 2013 and 2014. Metabolites and population's lines are grouped by clusters, using Pearson's coefficient. Values are represented as the fold change relativized to the '1392' parental. Lowest levels of metabolites are represented in blue, highest levels in red.

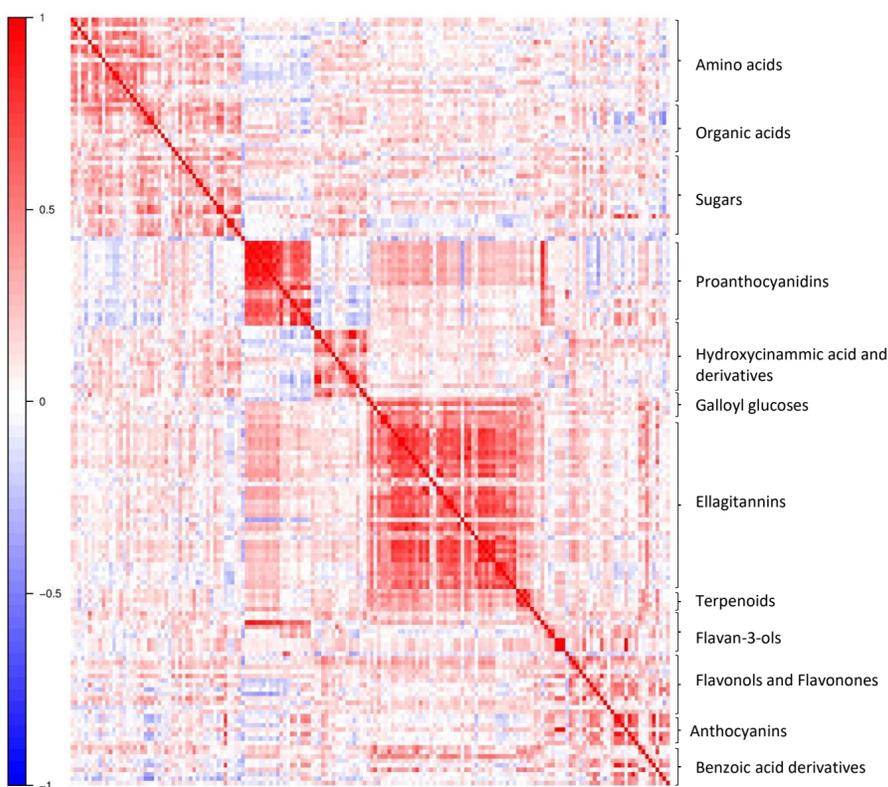


Figure 3. Heat map of metabolites-metabolites correlation in the '232 x 1392' strawberry population. Correlation coefficients were calculated with Pearson algorithm. Dark blue squares indicate a negative correlation and dark red squares a positive correlation.

CONCLUSION

- Primary metabolites include **sugars** and **acids**, which are directly responsible of the **taste** perceived by the human sensory system. In addition, they are precursors for secondary metabolites, including **volatiles**, which confer to strawberry its delicate **aroma**.
- **Phenolic compounds**, which are synthesized via phenylalanine and the phenylpropanoid pathway, are the main class of secondary metabolites in strawberry fruits. They are essential constituents of human diet because of their **antioxidant** function.
- A **quantitative trait loci mapping** has been performed with the results of the metabolomic profiling of the '232 x 1392' population, in order to find **candidate genes** which influence the levels of metabolites involved in strawberry quality traits.

The work was supported by the MINECO (grant AGL2012-40066-C02-02, Spain). SO acknowledges the support by Spanish Ministry of Science and Innovation (Ramón and Cajal contract, RYC2011-09170). DP has received a predoctoral grant from MINECO (grant BES-2013-062856). JJM and IA has been supported by the grant AGL2012-40066-C02-01. The authors also acknowledge the support by the University of Malaga, Campus de Excelencia Internacional de Andalucía.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement Number 679303.

References
Zorrilla-Fontanesi, et al. (2011) *Theor Appl Genet*, 123: 755-778.
Zorrilla-Fontanesi, et al (2012) *Plant Physiol*, 159: 851-870.

