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A MULTIDISCIPLINARY APPROACH TO IDENTIFY THE GENETIC DETERMINANTS OF FLAVONOID CONTENT IN GRAPES

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Anthocyanins and flavonols are among the most abundant flavonoids in grapes and they are synthesized starting from the aminoacid phenylalanine via the well characterized flavonoid biosynthetic pathway. They are important for the quality of grapes and wines since they contribute to their colour, taste and health properties. Although the genetic and biochemical bases of the biosynthesis of these compounds and to lesser extent of its regulation have been recently characterized also in grapevine, the molecular reasons of the varietal variability in terms of quality and quantity are still unclear.

To shed light on this issue we have characterized a mapping population derived from the cross Syrah x Pinot Noir by integrating metabolic, genetic and transcriptional sources of information.

Berries of 170 F1 individuals of the cross were harvested at technological maturity in three different seasons and analyzed for anthocyanins and flavonols content. QTL analysis for these traits identified several QTLs on the available dense genetic map of the cross with different effects and stability among seasons.

The analysis of flavonols allowed also the selection of two groups of individuals having either very low or very high content of these compounds in the berry skin. Gene expression profiling of these two groups by means of microarrays, identified a large set of transcripts differentially modulated between the groups.

Co-localization of some of these transcripts with the QTL regions highlighted in the QTL analysis is helping in the selection of the best candidate genes for further characterization.