Proceedings of the 57th Italian Society of Agricultural Genetics Annual Congress
Foggia, Italy – 16/19 September, 2013
ISBN **978-88-904570-3-6**

Oral Communication Abstract – 4.05

THE FINE GENETIC REGULATION OF ANTHOCYANIN AND FLAVONOL CONTENT IN GRAPES

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grapevine, flavonoids, quantitative trait loci, microarray analysis, metabolome

Anthocyanins and flavonols are natural compounds that accumulate preferentially in grapevine fruits and flowers. They are among the most abundant flavonoids and play a very important role in grape and wine quality. In particular, they confer and stabilize colour and contribute to other organoleptic characteristics of the final product. Their complex profile in terms of concentration and relative abundance varies among cultivars and contributes to wine typicity. Although the general flavonoid pathway has been genetically and biochemically elucidated and the main determinants of colour have been identified, the molecular reasons of the fine variation among grape cultivars are still not completely understood. To shed light on this issue, a segregating population derived from the cross 'Syrah' x 'Pinot Noir' was characterized by integrating metabolic, genetic and transcriptional sources of information. Berries of 170 F1 individuals were harvested at technological maturity in four different seasons and analyzed for ca. 60 traits, including specific forms of the two classes of compounds, their sums and ratios. QTL analysis detected several new QTLs, most with small phenotypic effect. Within the confidence intervals genes were identified which may contribute to fine tune the global regulation of the biosynthetic pathway (i.e. transcription factors, hydroxylases, glycosyltransferases, methyltransferases and acyltransferases). The same analysis allowed the selection of two groups of individuals having either very low or very high anthocyanin and flavonol content. Gene expression profiling of these two groups by means of microarrays identified a large set of differentially modulated transcripts. Co-localization of some transcripts with the QTLs helped in the selection of the best candidate genes for further characterization. A metabolomic characterization of both the Syrah x Pinot Noir progeny and a germplasm collection was also undertaken in order to test the effect of the candidate genomic regions on plant metabolome.