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BERRY AND PHENOLOGY RELATED TRAITS IN GRAPEVINE (*VITIS VINIFERA* L.): FROM QTLS TO UNDERLYING GENES

COSTANTINI L.*, BATTILANA J.*, EMANUELLI F.*, FANIZZA G.**, GRANDO M.S.*

*) IASMA Research Center, Genetics and Molecular Biology Department, Via E. Mach 1, 38010 San Michele all'Adige (Italy) - laura.costantini@iasma.it
**) DIBCA, University of Bari, Via Amendola 165/A, 70100 Bari (Italy)

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The timing of grape ripening initiation, length of maturation period, berry size and seed content are major concerns to viticulturalists and wine makers. Understanding the genetic control of grapevine phenology is desirable for staggering harvest along growing season, expanding the production towards periods when the fruit gets a higher value in the market and finally ensuring an optimal adaptation to climatic and geographic conditions. Fruit size determines grape productivity and has a role in wine quality. Seedlessness is especially demanded in the table grape market and is negatively correlated to berry size. All these traits result from complex developmental processes modified by genetic, physiological and environmental factors. In order to elucidate their genetic determinism we carried out a quantitative analysis in a F_1 segregating progeny obtained by crossing two table grape cultivars. Molecular linkage maps covering most of the genome were generated for each parent and integrated into a consensus map. Segregating traits were evaluated in three growing seasons by recording flowering, veraison and ripening dates and by measuring berry size, seed number and weight. QTL (Quantitative Trait Loci) analysis was carried out based on single marker and interval mapping methods. QTLs could be identified for all the investigated traits, a number of which were stable over more than one year. In order to characterize the most significant QTLs at the gene level, the underlying SSR markers were used as anchors to identify the corresponding Pinot noir genomic sequence, which was analysed by means of bioinformatic tools. Gene prediction and protein similarity search suggested the involvement in the studied phenotypes of some interesting proteins, whose role in flower and fruit development is reported also in literature. These results will be validated by analysing the gene expression profile in contrasting phenotypes at different phenological stages and by testing allelic variation at the gene trait-associations in a grapevine germplasm collection.