

QTLs AND CANDIDATE GENES FOR BERRY QUALITY AND RIPENING TRAITS IN GRAPE

L. COSTANTINI*, J. BATTILANA*, F. EMANUELLI*, C. SEGALA*, S. MOSER*,
G. FANIZZA**, G. VERSINI*, M.S. GRANDO*

*) IASMA Research Centre, Istituto Agrario San Michele all'Adige, Via E. Mach 1,
38010 San Michele all'Adige (Trento), Italy - laura.costantini@iasma.it

***) DIBCA, University of Bari, Via Amendola 165/A, 70100 Bari, Italy

QTLs, candidate genes, berry quality, ripening, grapevine

The identification of genes underlying agriculturally important traits is a major goal of plant functional genomics, which has been significantly aided by the explosive growth of large-scale expressed sequence tag (EST) sequencing projects. Co-localization of candidate genes and QTLs represents a valuable strategy to find associations between genes involved in relevant pathways and trait variation. Here we report on mapping of QTLs and candidate genes for berry quality and ripening traits in the 163 F₁ individuals derived from the cross between the *Vitis vinifera* cultivars Italia and Big Perlon. A number of genes, mainly related to aromatic compound metabolism, were selected according to predicted functions and gene ontologies. About 40 EST-based markers were developed by revealing molecular polymorphisms through SSCP analysis and minisequencing and placed on a linkage map based on approximately 350 markers, mainly AFLPs and SSRs. Segregating characteristics were scored as quantitative traits in three growing seasons by recording flowering, veraison and ripening dates, by measuring number and weight of seeds, berry size, and finally by quantifying through HRGC-MS the free monoterpenes responsible for Muscat aroma. QTL analysis, based on single marker and interval mapping methods, revealed the existence of QTLs for all the investigated traits, a number of which were repeatedly obtained in the same genetic regions by independently analysing field data from the different years. Interestingly map co-localization of some CG markers and QTLs was observed, which provides clues regarding the possible role of these genes in the regulation of the investigated traits. The existence of linkage disequilibrium between these sequence polymorphisms and quantitative traits, as well as the predictive value of some SSR markers in MAS processes, is now under evaluation by testing allelic variation in a germplasm collection representing most of the phenotypic variance.