

CHARACTERIZATION OF MAJOR QUANTITATIVE TRAIT LOCI CONTROLLING BERRY AND PHENOLOGY-RELATED TRAITS

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Background and Aims: Most traits of interest for viticulturalists and winemakers have a complex nature, being attributable to the interactions of multiple genes and their environment. Statistical genetics using QTL (Quantitative Trait Locus) mapping is a powerful tool to determine the genetic architecture of phenotypic traits and provides a basis for the identification of candidate genes underlying trait variation. The aim of our work was to investigate the genetic determinism of relevant traits related to berry composition and development.

Methods and Results: Target features were evaluated in two segregating progenies in three growing seasons. To this purpose we recorded flowering, veraison and ripening dates, we measured berry size, seed number and weight, and we quantified the main monoterpenes responsible for Muscat flavour through high-resolution gas chromatography-mass spectrometry (HRGC-MS). A number of QTLs were found with reproducible effects over years, which in some cases clustered in genomic regions controlling different characters. Interesting findings came out from the molecular characterization of the main QTLs for phenology and monoterpene content based on the whole grapevine genomic sequence. Candidate genes playing a potential regulatory role in trait variation were suggested according to their predicted function and their observed co-localization with QTLs. The functional significance of these associations is currently being evaluated through expression and association analysis. Focusing on the most promising candidate gene for Muscat flavour, we investigated the quantitative and temporal relationship existing between transcript level (RT-PCR) and monoterpene accumulation (HRGC-MS) in a small set of aromatic and non-aromatic grapevine varieties collected from pre-veraison to over-ripening. Moreover, we exploited the natural variation of a grape germplasm collection including aromatic and non-aromatic varieties (150 accessions) in order to test the existence of correlations between specific polymorphisms and aroma degree.

Conclusions: In this work we located the genomic determinants of berry and phenology-related traits. We observed interesting associations between candidate genes and QTLs, which provided the basis for functional studies testing their significance.

Significance of the study: This research revealed new insights into the genetic control of relevant grapevine features. Testing the role of specific genes in trait variation will contribute not only to the understanding of plant biology but also to crop improvement by breeding.