P71 – The genetic architecture of berry size in seedless grapevine: From QTLs discovery to the validation of a candidate panel of markers for assisted selection

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Abstract

Although the table grape breeding industry is achieving a maturity and programs are close to regime and release tens of new varieties every year, it is still a low performance innovation sector. The development of molecular techniques, combined with classic and newly genetic-genomic resources, allowed the discovery and description of genomic regions involved in qualitative, semi-quantitative and quantitative traits in more than 50 studies in the last 20 years, very few tools for assisted selection or the prediction of the phenotype for breeding purposes are being used.

In this work we have characterized the genetic architecture of the berry size in a framework of genetic improvement of seedless table grapes. To reduce the outcome of underpowered or biased results we used a large biparental cross (n~530), between a table seedless vine (Crimson Seedless) and a multipurpose vine (Muscat of Alexandria). The progeny was genotyped using a GrapeReSeq Illumina 20K SNP chip and phenotyped for five seasons to perform a fine QTL mapping experiment. To reduce the effects of environmental variance, Best Linear Unbiased Predictors were used to discover QTLs and individual seasonal data was used to evaluate the reproducibility across seasons. Up to 15 QTLs for berry weight describe a complex nature of this trait. For the five most stable QTLs we defined several candidate genes and developed SSR markers that were individually tested for its association in a larger panel of the biparental population (n~770). Considering an additive model built on the favorable alleles of the most associated five genes (SSR), up to 42% of the phenotypic variation of berry weight was explained. Finally, in a panel consisting in n~663 genotypes, including 100 common varieties and 563 seedlings derived from 13 crosses held by CREA-Turi and INIA breeding programs, in which 60% are seedless, we validated the associations and development of SSR markers for assisted selection for Berry Weight in a context of seedlessness. With five markers we are able to apply negative selection to close to 90% of breeding material, encouraging for an efficient breeding.