

Genome Wide Association Study using table grape breeding families provide new QTLs for berry, seed and cluster traits

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Abstract

Breeding programs use several sources of genetic diversity for the improvement of their objective traits, such as seedlessness, berry size, shape, firmness and good quality and condition after cold storage, generating several families derived from a good x good crossing strategy. In contrast, many QTL have been obtained using bi-parental mapping, which gains resolution power by using parents with contrasting phenotypes in one single large family. As result, these QTL must to be validated before their use in the complex genetic background of a breeding program.

In this work, we take advantage of low-coverage genotyping and phenotypic data produced for breeding materials at INIA's table grape breeding program during three consecutive seasons. We use a large set of 536 table grape progenies generated from from 7 related F₁ families, as well as a diverse germplasm panel of 68 seedless and seeded vines. Using genotyping-by-sequencing we produced a set of 20,013 reliable markers distributed across the 12X.2 grapevine reference genome. To perform genome wide association analysis, we used BLINK and a robust Bonferroni adjunted p-values to determine 78 statistically significant associations between these genetic variants and measurements of eight berry and seeds traits at harvest, as well as cluster weight both at harvest and after cold storage. About half of these markers co-localize with previously described QTL, but many others are novel and overlap, or are located nearby, genes of biological significance in grapevines' seed and berry development. Due to the suggestive functional impact of these genes on final trait outcomes of interest, these variants may represent potential useful loci for table grape breeding.

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