

Comprehensive family-based SNV association analysis shows new alleles associated to mealy traits in *Prunus persica*

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Identification of DNA markers associated with mealiness trait is an important tool to agricultural industry. Many peach breeding initiatives have as aim to improve early selection of varieties with better postharvest performance. We present a family-based approach to identify and develop an association panel to evaluate potential varieties susceptible to mealiness induced by chilling. We used whole-genome sequencing and SNV genotyping of parents and ten contrasting siblings (Juicy and mealy) obtained from segregating population of self-cross 'Venus'.

Results show that there are differences regarding SNVs and structural variants (SVs) that could be associated with mealy to be contrasted with individuals without such damage phenotype. Preliminary results showed a total of 30.564 SNVs and 2.297 SVs having a non-synonymous change in genes.

Comparison of SNVs between segregants and parental revealed 1.963 SNVs associated genes presents in juicy segregants and 6.162 SNVs associated genes in segregants mealiness. We found 230 and 244 SVs with functional impact in genomes mealy and juicy. As proof of concept, all SNVs obtained were correlated with the information published in peach related to chilling injury (QTL genomic region, dbSNP, SDR chillpeach, upeach and RNA-seq available). Guided by preliminary analysis, we selected pools of alleles that display a frequency difference between mealy and juicy fruit and a selective sweep is observed around those alleles. Some of the SNVs have been previously correlated with chilling injury through transcriptome analysis. Additionally, we identify new genome regions associated with mealy susceptibility.

Most of these genes were related to negative regulation of programmed cell death, cell surface receptors signaling pathways and cell wall remodeling. On the other hand, the genes affected by SV in the juicy segregating are classified according to the biological process in metabolism of sugars and fatty acid biosynthetic process.

These results provide insights into genetics determinants related with susceptibility to mealiness. Analysis of the sequences revealed the existence of a high polymorphism rate in nectarines, and statistical analysis showed that the segments could be used as genetic barcodes that should be informative enough to allow reliable identification of cultivars. This study proposes a predictive panel of biomarkers to identify varieties at susceptible for mealiness and identifies new candidates genes linked to mealiness in peach.

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