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Identification and characterization of QTLs for peach fruit quality by pedigree-based analyses (PBA) in the FruitBreedomics project

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Abstract:

The European project FruitBreedomics was conceived with the aim of improving the efficiency of peach and apple breeding. One of the strategies consists of enhancing the use of molecular markers in progeny selection (Marker Assisted Selection, MAS). In peach, many QTLs linked to more than one hundred agronomic traits have been identified and published so far, in all instances detected after analyzing single mapping populations. Despite the great amount of information, the number of molecular markers available to be used in MAS is still reduced. One of the reasons is the too large QTL intervals, which are due to low marker density and/or limited progeny size. With the final goal of reducing the confidence intervals of some relevant agronomic QTLs, in FruitBreedomics we have genotyped with the 9K peach SNP chip about 1,500 progeny from 18 peach and other *Prunus* crosses with phenotypic data from several years. Hereby, we present first results on fruit quality QTL mapping using pedigree-based analysis (PBA) methodology. PBA has its power in the joint analysis of progenies from different crosses at a time, enlarging the population size and consequently narrowing the candidate genomic regions. Moreover, as multiple parents with different genetic backgrounds are included in the analysis, this method may detect multiple favorable alleles. Additionally, the subsequent analyses of identity by descent (IBD) give insight into the peach founders that brought some of the favorable QTL alleles into these breeding populations.

Keywords: Peach quality traits, QTL mapping, Pedigree-based Analysis (PBA), FruitBreedomics