

## **IDENTIFICATION OF QTLs CONTROLLING FRUIT QUALITY, PHENOLOGICAL AND TREE ARCHITECTURE TRAITS BY A GENOME WIDE SCAN APPROACH**

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A genome-wide genotyping approach with the IPSC 9K SNP array was performed on a BC<sub>1</sub> progeny coming from the cross between IF7310828, a peach selection used as female recurrent parent, and the oriental accession Ferganensis (formerly *P. ferganensis*). After filtering for quality (GenTrain >0.4 and missing data <10%), out of a total of 8144 markers screened, 3326 (40.8%) resulted polymorphic: 1669 segregating 1:1 were informative for the F<sub>1</sub> parent, 1016 segregating 1:1 were informative for the recurrent parent and 641 segregating 1:2:1 were informative for both parents.

SNPs informative for the F<sub>1</sub> parent were considered for linkage map construction, using JoinMap 4.1 and the Maximum Likelihood mapping algorithm. The raw map, obtained at >10 LOD score, grouped 1660 SNP markers plus additional 15 SSR loci, chosen from a set previously mapped in the same population. After filtering for identical SNP markers, the final map was composed of 242 loci distributed along the expected 8 peach chromosomes and covering a genetic distance of 607 Haldane cM. This map was used to scan the genome for QTLs detection using Interval mapping and MQM mapping tools implemented in MapQTL6, both with the mixture Model Algorithm. Phenotypic data of traits related to plant structure (internode length, plant height, trunk perimeter), plant physiology (blooming and maturity date), fruit quality (fruit weight, fruit juice pH, titratable acidity, soluble solid content, fruit red overcolor) were collected for at least two years and were analysed. Several QTLs were identified, the major ones for blooming and maturity date, soluble solid content, fruit red overcolor. Analysis of QTLs eventually segregating in the recurrent parent is also in progress.