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FONDAZIONE EDMUND MACH



ISTITUTO AGRARIO
DI SAN MICHELE ALL'ADIGE



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Autonomous Province of Trento

Furthermore, comparative analyses show that peach has not undergone recent whole genome duplication (WGD) and even though the ancestral triplicated blocks in peach are fragmentary compared to those in grape, all seven paleosets of paralogues from the putative paleoancestor are detectable.

A second generation peach linkage map using the IPSC 9K SNP chip for advanced QTL identification

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Peach [*Prunus persica* (L.) Batsch] is one of the most important fruit crops in temperate area. Peach breeding is costly and time consuming due to the size of the plants and the relatively long (3-4 years) intergeneration period. Marker assisted breeding can help in reducing the cost and time in obtaining improved cultivars. The availability of the complete peach genome sequence (International Peach Genome Initiative) allowed the development of a powerful genetic tool, a 9K SNP chip delivered by the International Peach SNP Consortium. The chip is being employed within the EU funded project FruitBreedomics to dissect QTL and identify SNPs linked to important agricultural traits. Here we report a peach linkage map obtained with 1279 SNPs of the IPSC 9K chip using 232 individuals of a BC1 progeny. The map is distributed in 8 linkage groups and covers 610.8 cM with an average distance between adjacent markers of 0.5 cM (1.2cM excluding co-mapping markers). The map aligns completely with the eight peach V1.0 pseudomolecules, a few incongruences highlight putative misassembly occurred in Peach v1.0 release. A QTL analysis was performed for the flowering time recorded in spring 2012 (2 years old plants) using MapQTL6. A single major QTL was identified in Group 4 (SNP_IGA_420819 at 13939118 bp in Peach v1.0). The variance explained was 39.7% with an additive effect of -4.035 days.

QTL mapping for content of phenolic compounds extracted from fruit and juice in a cider apple progeny

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Genetic variability description in a wide germplasm of domesticated peach through high throughput genotyping

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Peach (*Prunus persica* (L.) Batsch) is one of the most economically important fruit crops in temperate areas. Classical fruit tree breeding is generally slow and inefficient. Molecular markers could improve its efficiency but, although nowadays many Mendelian traits are mapped in peach and SSR markers have been found to be linked to some of the key major genes, its use in breeding programs is still limited. Main reasons for that are insufficient linkage between the markers and the genes and the lack of markers suitable for medium-high degree of multiplexing. To address this limitation, about 1,300 peach cultivars were genotyped with the 9K peach SNP chip (Verde et al. 2012) in the frame of FruitBreedomics project. This germplasm was chosen to be representative of the genetic diversity present in five germplasm collection in Europe and in China. Out of the 8144 SNPs present in the chip, about 4300 were positively genotyped and used for the further analysis. The average number of heterozygous loci in the genotyped accessions was 1186 (spanning from 13 to 2775). The preliminary results of the population structure reveal three main subpopulations and the presence of high number of admixed individuals. LD seems to decay at distance longer than ca. 1 Mb. These results will be instrumental for implementing LD-based mapping of QTLs and genes in peach.