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 compl etely with the eight peach V1.0 pseudomolecules, a few incongurences 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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Polyphenols have favorable antioxidant potential on human health suggesting that their high content in apple is responsible for the beneficial effects of apple consumption. They are also related to the quality of ciders as they predominantly account for astringency, bitterness, color and aroma. Five groups of phenolic compounds are described in the apple fruit: flavanols, hydroxycinnamic acids, dihydrochalcones, flavonols and anthocyanins. So far, only two studies have been published on the genetic basis of the phenolic content of dessert apples. As cider apples are commonly described to be much more concentrated in phenolic compounds than dessert varieties, the present study focuses on a cider apple progeny. 32 compounds belonging to the five groups were identified and quantified by HPLC-UV and UHPLC-UV-MS/MS in fruit extracts and juices. 53 QTL controlling phenolic compounds concentration were detected on nine linkage groups (LG) on the integrated linkage map, for all p henolic groups except anthocyanins. QTL clusters located on LG1, 12, 14, 15 and 17 were stable across the year or the studied material. QTL detected on LG1, 14 and 17 for quercitrin, p-coumaroylquinic acid, rutin and chlorogenic acid confirmed results of previous studies. However, no significant QTL was obtained on the LG16 where a major locus for flavanols was previously located. With the two previous studies, this study shows the diversity of genomic regions controlling traits of interest in apple.

Genetic diversity of wild European and Mediterranean pear species

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Many pear species are native to Europe, the Middle East, and Northern Africa. These seemingly distinct species readily hybridize resulting in nomenclatures that do not reflect their phylogenetic history. We have used microsatellite and chloroplast sequence markers as well as phenotypic traits to differentiate between European and Mediterranean wild pear species in the world pear collection at the USDA-ARS National Clonal Germplasm Repository in Corvallis, Oregon. Species include *Pyrus communis*, *P. eleagrifolia*, *P. gharbiana*, *P. mamorensis*, *P. regelii*, *P. sachokiana*, *P. salicifolia*, *P. spinosa*, and *P. syriaca*. We took a population genetic approach when evaluating the diversity within and among these described species by using a model based clustering method to distinguish genetic lineages. These estimated lineages often contained individual genotypes that were from different species. These groups were then assessed geographically and genetically to better understand specie s distribution and differentiation. Our data revealed hybridization among species as well as diagnostic