

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 8144SNPs 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.