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P0492 Application of High Throughput Genotyping Techniques in Peach Germplasm and Breeding Lines within the FruitBreedomics Project

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Peach (*Prunus persica* (L.) Batsch) is one of the most economically important fruit crops in temperate areas. Every year new varieties are released from breeding programmes trying to meet the requirements imposed by the market. 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 programmes 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. FruitBreedomics is a European project conceived with the strategic goal to improve the efficiency of fruit breeding by bridging the gap between scientific knowledge and application in breeding. In the frame of this project, and with the goal of obtaining SNP closely linked to agronomic interesting traits, the 9K peach SNP chip (Illumina Inc.) developed by the International Peach SNP Consortium (IPSC) has been used in both segregating populations and in germplasm collections. This chip, containing 8144 SNPs scattered on the 8 peach chromosomes, has been used in about 1,500 individuals belonging to seventeen *Prunus* crosses (12 peach x peach and 5 interspecific) and in 1,300 peach cultivars from different origins, including some of the founders of the current breeding programs.

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