P0620: Definition of a Core Collection and Construction of a Reference Set for Genome-Wide Association Studies from a Large *Prunus persica* Germplasm Collection

Genome-wide association studies take advantage of the natural variation present in germplasm repositories for identifying genes underlying agronomic traits, through plant molecular and phenotypic characterization. For tree crops, *in vivo* maintenance and phenotyping are particularly onerous and the reduction of redundancy and duplicates could help lowering management costs. In the frame of the European project FruitBreedomics, a collection of 1580 *Prunus* accessions from different institutions in Europe and China has been genotyped with the IPSC 9K SNP Array and phenotyped for different agronomic traits and a GWAS analysis with 4271 SNPs on 7 monogenic traits has been carried out (Micheletti et al. 2015). In the present work, the same set of 4271 SNP markers was used to identify a peach core collection by applying the maximization strategy implemented in the software PowerCore v 1.0 (Kim et al. 2007). Out of a total of 1540 a core of 72 (C72) accessions was identified, representing 4.7% sampling size. C72 contains the accessions with higher diversity representing the total allelic coverage with an efficiency index of 0.83 with respect to random sampling. In the view of setting up a genomic tool for GWAS analyses a reference subset of 150 accessions was also developed taking into account allelic and phenotypic traits representativeness through the maximization strategy, population stratification and controlled redundancy required to have enough statistical power. Preliminary PCA analysis shows population structure to explain less than 30% of variability due to the local varieties. Validation of the reference set will also be presented.

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