Abstract

Genetic characterization of Apple genotypes of the German National Fruit Genebank with an optimized SNP marker array

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The Julius Kühn-Institute, Institute for Breeding Research on Fruit Crops in Dresden-Pillnitz, coordinates the nationwide conservation, genetic characterization and evaluation of the national fruit genetic resources and is supported by the advisory council and the Federal Office for Agriculture and Food (BLE). The aim of the project was the characterization of 954 apple genotypes from the Deutsche Genbank Obst (DGO) and 80 international apple varieties using an optimized SNP marker array for apple. Basis was the development of the optimized and cost-effective SNP marker array for apple with around 50,000 markers on the Thermo Fisher Axiom platform.

For the new array, 48,138 markers were selected according to the following criteria:

- good and even coverage of the current apple genome (HFTH1)
- comparability to the 20K Infinium and 480K Axiom SNP arrays
- integration of trait-specific and maternally inherited SNP markers
- integration of some specific markers for wild *Malus*-species

Using an optimized protocol, DNA of the genotypes was successfully extracted from leaf samples supplied by the DGO. Since the capacity of the Axiom Array Analysis with three 384 arrays was more than the originally planned number of 1034 samples, a cost-neutral adjustment to 1152 samples was agreed with the DGO in order to use the full capacity. Finally, 1128 di- and triploid apple genotypes, 12 biological duplicates and 12 internal controls were successfully analyzed. 950 genotypes were identified as diploid and 178 genotypes as triploid. The quality of the analysis of the diploid genotypes was very high. Over 87% of the markers could be recommended for the genetic characterization of the apple genotypes. Such a classification of the markers was not possible for the triploid samples, since the analysis was carried out with an R-script, which does not provide the relevant quality parameters. Here, the quality of the markers needed to be assessed on an individual case-by-case using bar graphs. The genotypes were also analyzed for duplicates. For the diploid genotypes, the genetic fingerprints of the varieties were compared across all markers using a newly developed script which allows the assignment of a unique ID to each different fingerprint. Duplicate analysis of the triploid samples was conventionally performed using NTSYS relatedness analysis. A total of 717 different haplotypes were identified for the diploid genotypes and 126 for the triploid genotypes.

The new SNP array provides a high quality tool for the reproducible characterization of apple genotypes in the future. By integrating markers from existing arrays, namely the 20K Infinium and the 480K Axiom array, existing data sets that were generated with these arrays can be integrated into future analyses. The public availability of the new array offers the opportunity for diverse cooperations in research and development projects worldwide and a standardized exploitation of the results as well as progress in the targeted coordination of gene banks regarding maintenance, characterization and evaluation of genetic resources.