



Development of the Axiom[®] Apple480K SNP genotyping array and its application for genome wide association study in apple S2P6

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During the last decade, high-throughput genotyping has facilitated the dissection of complex traits in species with large/complex genomes and high level of genetic diversity. Array-based marker systems have been increasingly adopted for high-throughput genotyping, not only in model organisms, but also in many non-model plant species for which genomic resources are now available. A new high-density Affymetrix Axiom[®] SNP array has been built for the domesticated apple (*Malus x domestica*). It gathers more than 487K SNPs that are evenly distributed over the 17 chromosomes. The array has been built from the high-depth resequencing (~10-20x) of 63 different varieties covering most of the genetic diversity in cultivated apple. SNPs have been chosen by applying a focal points approach to enrich genic regions, but also to reach a uniform coverage of non-genic regions as to support SNP haplotype approaches. A total of 1324 apple accessions, including the 92 progenies of two mapping populations, have been genotyped with the Axiom[®]Apple480K to assess the effectiveness of the array. The majority of SNPs (359,994; 74%) fell in the most interesting class of Poly High Resolution polymorphisms. A novel filtering procedure was also devised to identify a subset of 275K robust markers that can be safely used for germplasm surveys in apple. A first application to genome wide association (GWA) study of two phenology traits (flowering time and maturity date) in six European germplasm collections is also presented. The Axiom[®]Apple480K has been publicly released and will likely be a reference tool for GWA studies in apple.