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W173: Towards GWAS and Genomic Prediction in Coffee: Development and Validation of a 26K SNP Chip for *Coffea canephora*

ABSTRACT

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Pacific Salon 3

Genome-wide SNP genotyping platforms aiming at high-throughput and high-precision genotyping constitute an essential tool to advance breeding by genomic prediction and gene discovery by GWAS. Recent advances in coffee genomics with the sequencing of the *Coffea canephora* reference genome, has provided the coffee scientific community the necessary resource to develop a SNPs toolbox for genome-wide genotyping. *C. canephora*, an allogamous diploid species, and one of the parents of the allotetraploid *C. arabica*, has been an important source of genetic variability for breeding programs of both cultivated species. Highly heterozygous genomes such as *C. canephora* require a much higher sequence depth to reach acceptable marker call rates and genotype accuracy, when using sequence-based genotyping methods such that their cost effectiveness may not be realized. Here we describe the development and validation of a 26K Axiom SNP array (Affymetrix) whose genome-wide distributed SNP content was discovered from pooled whole-genome resequencing of *C. canephora* accessions covering most of its known genetic diversity. Besides facilitating low cost, high marker density, polymorphism and speed of data generation, the platform displays high genotype call accuracy and reproducibility. Genotyping validation resulted in 24,073 SNPs (94.6%) successfully converted out of the 25,456 SNPs on the array. 20,982 markers (87.1%) were scored as providing high-resolution genotypic data in a set of 800 individuals of a breeding population in which 19,586 (81.4%) were polymorphic and 1,396 (5.8%) were monomorphic. The remaining set of 3,091 (12.8%) successfully converted markers were of lower accuracy in the studied sample and may require additional cluster analysis to proper biological interpretation, *i.e.* targeting CNVs. This large validated SNP collection provides a powerful tool for molecular breeding and population genetics investigation within coffee species. Some preliminary results of a GWAS using this genotyping platform will be presented.

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