VIII SIMPÓSIO INTERNACIONAL DE GENÉTICA E MELHORAMENTO
ÔMICAS: do gene ao fenótipo

Development and Validation of a 26K Axiom® SNP array for *Coffea canephora*

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World coffee production is higly affected by climate changes due to the occurrence of severe droughts and high temperatures resulting in low flower viability, fruit development and yield. Faster breeding methods are required to obtain adapted coffee plants to a changed climate cenario, as conventional breeding in perennial crops such as coffee, requires a long time. With the recent advances in coffee genomics, such as the availability of a *C. canephora* reference genome, the objective of this work was to develop and validate a 26K Axiom SNP array for *C. canephora* aiming at a reliable high throughput genotyping platform to be used in the breeding programmes of the species. The *chip* design was based on a whole-genome resequencing panel comprised by DNA pools of *C. canephora* Conilon and pools formed by individuals representing the different genetic diversity groups of *C. canephora*. This panel was chosen to provide a representative sample of the genetic diversity in the species studied. After mapping the resequencing reads against the *C. canephora* reference genome a selection of 25,456 SNP variants was choosen to compose the array. About 170 *C. canephora* individuals were genotyped using the chip to evaluate the array performance and some of the DNA samples were included as a technical replicates. For each sample, 200 ng of genomic DNA was extracted, fragmented and hybridized to arrays using the Affymetrix GeneTitan platform following Affymetrix's guidelines. Samples with a Dish Quality Control (DQC) value <0.82 and sample call rate <0.97 were excluded from further genotyping analysis The positioning of the probes along the chromosomes showed to be uniform, covering the entire genome. The vast majority of SNPs fell in the more thoroughly defined class of Poly High Resolution (PHR) polymorphisms, approximately 82% (20,920 SNPs). The reproducibility of the technique was satisfactory, since the same samples included were identified between 99.5 and 100% similarity. The development of the chip, the large number of SNPs identified and, above all, of high quality, represents a novelty and a powerful tool to be used in different studies, such as GWAS and in the development of predictive models, which may represent a time reduction in coffee breeding programs.

Financial Support: Consórcio Pesquisa Café, INCT-Café (CNPq/Fapemig),CAPES –
Concentration area: Genomics

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