

55. Analysis of genetic diversity in a population of *Coffea canephora* conilon through nextRAD genotyping

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Of all the different activities related to agricultural industry worldwide, coffee agribusiness is among the most important, both economically and socially, being the main livelihood for more than 125 million people in more than 60 countries. Commercial coffee production is mostly based on two species, *Coffea arabica* and *C. canephora*. The high genetic variability of *C. canephora*, due to its level of allogamy, is of great importance for breeding programs of coffee as a source of new genes. A very important tool in the study of genetic diversity is the discovery of SNPs (Single Nucleotide Polymorphism) molecular markers. In the case of *C. canephora* diversity studies may benefit breeding programs in selecting progenitors for hybridization or genotypes for clonal varieties composition. The present study aimed to evaluate and characterize through nextRAD genotyping technique the genetic diversity of 480 individuals from *C. canephora*. It also aims to validate the genotyping technique here in used in genomic scale. A list of 5,412 SNPs was obtained for 421 individuals, however 4,769 SNPs were analyzed. The chromosome 2 obtained higher density of probes mapped. More than 60% of the identified SNPs occurred in genic (coding) regions. The indices of genetic diversity, calculated by Cervus software, suggest that to 1,413 locus the H_o was greater than H_e and 48% of SNPs marks had PIC above 0,3 which means that they are informative. The results of this work indicate that the nextRAD method is efficient for simultaneous SNP discovery and genotyping. Nevertheless, the variable call rates observed across the sampled SNPs is a concern when considering its routine application in molecular breeding applications that require fast and genome-wide SNP genotyping for thousands of individuals. Regarding the *C. canephora* population we studied, the genome-wide data revealed considerable genetic variability among individuals, confirming the previously reported genetic proximity of the set of parents to the Niaouli diversity group SG1 of *C. canephora*. The genotyping data generated for the population will be useful in upcoming studies to investigate full parentage and genetic relatedness of the individuals as well as the extent of linkage disequilibrium to better inform the development of genomic prediction models.

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