Analysis Of Nucleotide Diversity In Coffea spp.

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Marker-assisted selection becomes a reality for many crops; in perennial crops, the utilization of molecular markers in breeding programs can speed up genotype selection. However, the most important commercial coffee species - allotetraploid C. arabica - has a restrict number of available polymorphic markers, which is a consequence of the narrow genetic basis and low molecular variability among cultivars. In order to study the nucleotide diversity in C. arabica, as well in other diploid Coffea relatives, we sequenced PCR amplified fragments of nine genes in 20 Coffea genotypes: twelve C. arabica, including eight wild genotypes and four commercial cultivars; and eight C. canephora genotypes. Genotypes of C. eugenioides, C. racemosa and Psylanthus bengalensis were also included in this analysis. From a total of 9 Kb analyzed, we found 573 polymorphisms: 500 SNPs; 39 INDELs and 34 SSRs. In C. canephora genotypes, we detected 188 polymorphisms (frequency of 2.09/100bp). For C. arabica we obtained similar results: 144 polymorphism (frequency of 2.13/100bp). Most of the polymorphism found in C. arabica only reflected the differences between ancestral homeologs, and they were monomorphic among different genotypes. However, 19% of these polymorphisms (27 SNPs) were interespecific for C. arabica, and 13 of them were fixed among genotypes. The strategy of this work reflects the importance in using a more diverse panel of genotypes in order to identify SNPs in C. arabica, pointing out that the exploitation of wild germplasm will be an important source of genetic variability.