

Development of a molecular method for the identification of clone varieties of *Coffea canephora* via PCR

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Conilon coffee belongs to the *Coffea canephora* species, which is a diploid ($2n = 2 \times = 22$), perennial, allogamous plant with a high genetic variability. Consequently, a plantation established from seeds will likely have plants with highly diversified characteristics. Accordingly, the production of cuttings is of great value for the success of crop implementation. Using clones produced from superior genotypes instead of seeds has some advantages such as lower implementation costs, higher productivity, higher uniformity of maturation, better grain quality, differentiated cycle of maturation and staggered harvest scheduling. Brazil is an important coffee producer, and the development of new varieties is important to maintain or even increase its production. Trading new seeds and cuttings, which involves the concepts of registration and protection of cultivars, depends on Brazilian legislation. Law No. 10.711 of August 5, 2003 and Law No. 9,456 of April 25, 1997 and their regulations on the National System of Seeds and Cuttings and regulates the right of protection of cultivars, respectively. Registering a cultivar in the National Register of Cultivars allows the production, processing and marketing of seeds and cuttings. Conversely, the protection of a cultivar in the National Service of Protection of Cultivars gives right to the intellectual property to its owner. The registration and protection are based only on morphological characteristics, which are described and assured by the breeder, which can not be prior diagnosis of the clones, since morphological characteristics only can be analyzed after the development of the plant. Therefore, the objective of this work is to develop a molecular method for the identification of the different clones of *C. canephora*, registered and/or protected in Brazil. The clones that compose those varieties were genotyped, using the Axiom chip (Affymetrix) developed by Embrapa, containing around 25,000 SNPs (Single Nucleotide Polymorphism). As a result of this genotyping we had 25,456 SNPs, while 22,889 markers (89.88%) were classified with high resolution, of which 20,424 (80.23%) were polymorphic for this set of clones. The SNPs were analyzed and 18 of them were selected as potential candidates for the allelic distinction during the identification of Conilon clones that compose all varieties that are registered and/or protected in Ministry of Agriculture, Livestock and Food Supply.

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