

AFLP Analysis of Genetic Diversity within and among *Coffea arabica* Varieties

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SUMMARY

Genetic diversity of *Coffea arabica* varieties was estimated using amplified fragment length polymorphism (AFLP) markers. The natural variation within arabica varieties is the source of variants of genes that control agronomic traits. The degree of this natural variation has direct impact on coffee variety improvement program. Fifty-seven arabica accessions representing five major arabica variety groups, including Typica, Bourbon, Catimor, Catuai, and Mokka hybrid, and two related *Coffea* species were analyzed with six *EcoR* I – *Mse* I primer combinations. A total of 274 informative AFLP markers was generated and scored as binary data. These data were analyzed using cluster methods in the software package NTSYSpc. The differences among varieties at the DNA level were small with an average genetic similarity of 0.933. Most accessions within a variety clustered together, although deviant samples occurred in all five varieties examined due to residue heterozygosity from the ancestral materials each variety was derived from. Among the five varieties fingerprinted, the highest level of genetic diversity was found within the variety Catimor, with an average genetic similarity of 0.880. The lowest level was found within Typica accessions with an average genetic similarity of 0.966. The genetic similarities of Bourbon, Catuai, and Mokka hybrid were 0.933, 0.942, and 0.944, respectively. We also compared the diversity between arabica and two other *Coffea* species, *C. canephora* and *C. liberica* with average genetic similarities of 0.540 and 0.413, respectively, indicating that *C. canephora* is more closely related to *C. arabica*. Although arabica varieties appear to have a very narrow genetic base, our results show that sufficient polymorphism can be found among some arabica varieties with genetic similarity as low as 0.767. AFLP appears to be applicable to genetic and QTL mapping in coffee, as it rapidly generates a large number of informative markers. This information is necessary as a first step in using marker-assisted selection for coffee breeding.