

Application of DNA Marker Technologies in Characterizing Genome Diversity of Selected Coffee Varieties and Accessions from India

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SUMMARY

Assessment of genome diversity in a genepool of any particular species offers great promise for better exploitation and management of genetic resources. The development of molecular markers in coffee trees (*Coffea* L.) has opened new perspectives for analysing genetic relationships and in marker assisted breeding. In this study, we report the successful use of two efficient PCR based DNA marker technologies, Amplified Fragment Length Polymorphism (AFLPs) and Simple Sequence Repeats (SSRs) for generating DNA profiles of the selected *C. arabica* accessions under cultivation and genebank collections of *C. canephora* available in India. Eighteen arabica genotypes covering the commercial accessions S.288, S.795 and S.1934 were subjected to AFLP analysis using 36 different primer combinations. Analysis of the DNA fingerprints revealed 18 to 45 amplified products depending on the genotype and primer set. In all, a total of 115 polymorphic bands were scored. The high polymorphism is mainly attributed to the introgression of *C. liberica* genetic material as these commercial lines were derived from S.26, a putative natural interspecific hybrid (*C. arabica* x *C. liberica*) and thus the molecular data established the natural hybrid lineage. Further, 39 accessions of *C. canephora* representing indigenous as well as exotic genebank collections were analyzed for genetic diversity in comparison with 16 IRD collections from different geographical regions of the world, using 15 AFLP primer combinations and 12 SSR primer sets. A total of 205 polymorphic bands were scored from the AFLP marker data while 72 alleles were identified with 12 SSR primers. Analysis of data for genetic relationships revealed the structure of Indian germplasm and the outcome is almost similar with both marker approaches. The potential use of AFLPs and SSRs for evaluating genetic diversity and in other molecular genetic applications are discussed.