

DNA Polymorphisms in *Coffea arabica* L.

R. RAJKUMAR, B. DE NARDI, E. ASQUINI, P. TORNINCASA, C. MARTELLOSI,
A. PALLAVICINI, G. GRAZIOSI

Department of Biology, University of Trieste, P.le Valmaura 9, Trieste-34143, Italy

SUMMARY

Due to the tremendous developments in the field of molecular genetics, variety of techniques to analyze and utilize genetic variation has emerged during the last few decades. Genetic improvement of coffee (*Coffea arabica* L.) is particularly constrained by low genetic diversity, lack of genetic markers, lack of information on the genetic makeup and prolonged generation time. In this context, the use of DNA markers to detect and exploit the variation in the available genetic pool of *C. arabica* becomes highly imperative. Here, we describe three high genetic-resolution marker systems, viz., simple sequence repeats (SSR), sequence-specific amplification polymorphism (SSAP) and single nucleotide polymorphisms (SNPs) to possibly detect and exploit the genetic variation in the in *C. arabica* gene pool maintained in Italy. Analysis of 161 SSR markers, 20 retro-transposons based markers in various arabica genotypes though, have revealed low genetic variation in the arabica pool, it has led to the better understanding of the allo-tetraploid origin of arabcia genome. Analysis of 69 expressed sequence tag sequences (ESTs) have resulted to the detection of 4 new SNPs in arabica varieties and 30 polymorphic restriction pattern in other wild species, which intern could be used as potential markers for genotyping and genetic dissection of complex traits and disease. Furthermore, the data also suggests that arabica genome maintains a high level of heterozygosity particularly through paralogous genes.