

Coffee Genomics : Disclosing the Possibilities

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Coffee, being the beverage of tremendous economic importance, continuous efforts to develop better genotypes for sustainability is the need of the day. Genetic improvement of coffee is constrained predominantly due to narrow genetic base, limited molecular information, autogamous nature and long generation period. In the view of the above, our research is focussed particularly, to identify and exploit the largest possible number of polymorphic loci in cultivated species using molecular markers and to develop an inventory of the expressed genes through microarray based functional analysis of Expressed Sequence Tags (ESTs).

We have successfully developed a total of 159 *C. arabica* specific microsatellite markers and validated across different varieties. These makers were screened for parental polymorphism in 5 different crosses and a total of 17 polymorphic loci were identified, despite of limited genetic variation among *arabica* varieties. The selected polymorphic markers are being analysed in the segregating population for constructing map. Sequence-specific amplification polymorphisms (S-SAP) is a technique that exploits the widespread transposable elements to screen large number of sites for polymorphisms. We have isolated sequences encompassing the start of the 3' large terminal repeat (LTR) from *Ty1*-copia-like elements to generate required primers for further S-SAP analysis. Preliminary experiments detected polymorphisms among more distantly related samples. The ESTs are single-pass sequences of cDNA clones randomly chosen from a library, can be used for characterization as well as expression studies. We have recovered a total of 2069 ESTs from two cDNA libraries and some of them have been used in varietal characterization. The amplification of some of the ESTs on *arabica* varieties resulted in identification of 3 single nucleotide polymorphic (SNPs), and several heterozygous loci. These markers are being analysed against different arabica varieties to develop diagnostic markers. The DNA microarray technology is a most promising and dynamically evolving approach fulfilling all the requirements of functional genomics. The identified ESTs have been assembled into 1520 contigs (900 from roots and 620 from leaves). A set of 48 gene fragments with an NBS-LRR domain have been sequenced from two genomic library enriched for gene linked to the resistance to several pathogen. Attempts are under way to construct microarray using these transcripts to further understand the tissue specific expression pattern. A query based user-friendly web-interface was developed, conceptually an effort for graphical display of large amount of information pertaining to coffee genomics generated from our lab. The database would also serve as a web portal for sequence analysis using in-house/web resources. The details of the above investigations will be discussed.