

Genetic relatedness of coconut genetic resources in Sri Lanka as revealed by simple sequence repeat markers

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Seventeen pairs of coconut specific simple sequence repeat (SSR) primers were used to analyse the genetic relatedness of coconut palm populations in Sri Lanka. Forty three accessions were screened in this study among approximately 100 *ex-situ* conserved accessions at the gene banks of the Coconut Research Institute (CRI). The 17 primers detected a total of 82 alleles, with an average of 4.8 alleles per locus within the range 2 to 10 per locus. All loci exhibited polymorphism in the 43 genotypes screened. Eight accession specific-alleles were found characterizing six accessions. A distance matrix was constructed using Nei and Li pair-wise genetic distances. The distances among accessions ranged from 0.13 to 1.0 averaging 0.63 is quite high compared to previous observations with RAPDs. The clustering of 43 accessions based on genetic distances grouped them into two major groups. The first group comprised all the dwarf, semi tall, semi dwarf and king coconut forms and bodiri and two Philippine coconuts; clovis and Nipuni. The second cluster comprised all Sri Lanka Tall coconut accessions irrespective of morphological and geographic differences. Further clustering of first group showed separation of more heterozygous types such as semi tall, clovis, Nipuni and bodiri from more homozygous pure dwarf types. The pattern of the genetic structure of 43 coconut accessions unveiled by simple sequence repeat polymorphism exemplifies the genetic relationships of coconut in Sri Lanka with respect to true evolutionary links than what was explained before by morphological classifications.

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