SUMMARY

This project was undertaken to study the levels and distribution of genetic diversity in coconuts with special reference to Sri Lankan coconut germplasm. Such information will allow plant breeders and conservationists to select better breeding materials and formulate appropriate conservation strategies. PCR-based DNA profiling of coconut palms indigenous to Sri Lanka was conducted using both Amplified Fragment Length Polymorphism (AFLPs) and Microsatellites (SSRs). In the AFLP study 322 amplification products were generated from the 42 genotypes with eight pairs of primers (*Eco*RI and *Mse*I). Thirty-nine microsatellite primers specific to coconut were developed by small insert genomic library construction. Eighteen of those primers were used to analyse Sri Lankan coconut materials. Overall, the results generated by both AFLPs and SSRs were in agreement. Most diversity was found in the tall variety (Typica) (0.92 and 0.62 for AFLPs and SSRs respectively) rather than the intermediate (Aurantiaca) and dwarf (Nana) varieties (0.82 and 0.25 for AFLPs and SSRs respectively). A hierarchical analysis of molecular variance (AMOVA) based on AFLP data was used to quantify and partition levels of variability into between and within forms components. This revealed that for the inbreeding dwarf and intermediate forms most variation was observed between rather than within forms. In contrast, the out-breeding tall forms exhibited as much variation within as between forms.

Under the coconut bio-diversity conservation programme, several collections of form typica coconuts were planted *ex-situ*. Thirty-three populations were subjected to SSR assay with eight microsatellite primers. A high level of genetic diversity (0.68) and high level of within population variation (98%) were detected. There was very little population differentiation. It was concluded that a single large collection would adequately represent the genetic diversity in the targeted area. These results generated useful information for the coconut bio-diversity conservation programme in Sri Lanka.

Twelve pairs of SSR primers were used to screen worldwide collections of coconut germplasm. Eightyfour alleles were detected in talls compared with only 42 in dwarfs and average diversity value in talls was significantly higher (0.703) than in dwarfs (0.374). It was concluded that dwarfs are a subset of the tall coconuts and are directly evolved from tall and moreover from 'Niu vai' types of tall coconuts. These results provided evidence in support of previous hypotheses concerning the dissemination of coconut, as well as important new information for conservation and breeding purposes.

Levels of cytoplasmic diversity in coconut were assessed by using both restriction digestions of PCR products using universal primers in the chloroplast genome and mitochondrial genome and chloroplast SSRs . No variation was found suggesting coconut has gone through a severe cytoplasmic bottleneck and only one cytoplasmic type may have participated in the colonisation process.

The information emerging from this study enhances the knowledge of amount and distribution of genetic diversity, origin, evolution and dissemination of coconut. The use of the results generated for formulating conservation strategies and selection of parents for the breeding programme is discussed.