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Genetic relatedness of coconut germplasm in Sri Lanka as revealed by Random Amplified Polymorphic DNA (RAPD)

Seventeen germplasm accessions and three improved cultivars of coconut (talls; typical, gonthebili, St Ann's, Moorock, Palugaswewa, Goyambokka, Ambakelle special, Kasagala, Debarayaya, Margaret and San Ramoon (SR), intermediate king coconut, dwarfs; yellow, green, brown, Cameroon red and Brazilian green and improved cultivars; Tall x San Roman, Dwarf Green + x Tall and Dwarf Yellow+ x Tall) were assessed by the RAPD technique. The DNA of each accession /cultivate was amplified by 20 previously selected random primers (Operon) and Nei and Li pairwise distances were calculated on band sharing and a dendrogram was constructed to reveal the genetic relationships.

A total of 129 fragments were amplified (6-7 per primer) with 65% exhibiting polymorphism. A close genetic relatedness(0.15 0.04) was observed among all with tall and dwarf groups averaging 0.12 and 0.08 distances respectively. Brazilian Green Dwarf was the most deviant of all type swhile San Ramon deviated from at all coconuts. In the dendrogram tall and dwarf types separated while San Romon, the Philippine coconut maintained its evolutionary links by grouping dwarfs. King Coconut too indicated a South East Asian origin similar to dwarfs. As expected hybrids with tall types as all these cultivars have a tall as one parent.

The coconut germplasm conserved ex-situ in the Coconut Research Institute has a narrow genetic base indicating fewer chances for substantial genetic improvement. The two accessions somewhat distant being exotic types,Brazilian Green Dwarf and San Ramon suggest the possibility of gene pool enrichment by introduction of exotic coconuts. +Female parent