

D-33: A molecular approach to improve the efficiency of breeding of *Cocos nucifera* by marker assisted selection

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Currently used improved cultivars of coconut are inter- and intra-varietal hybrids of coconut types, tall, dwarf and San Ramon, all of proven hybrid vigor on average nut yield and copra. A major drawback of these materials is that they lack uniformity in plantings due to their inherent heterozygosity. Construction of a genetic map saturated with molecular markers facilitates effective and efficient selection of characters and is therefore a major research priority in coconut. Despite lack of appropriate populations for linkage analysis and while measures are being taken to establish segregating populations, a molecular marker assay was initiated to detect DNA polymorphisms (RAPD, RFLP and SSR/VNTR) among parental coconut forms.

DNA was isolated from immature leaf tissue from 3 individuals, each from tall, dwarf and San Ramon coconut types, using the procedure described by Doyle and Doyle (1990) and quantified by 'Genequant' (Pharmacia). Sixty arbitrary decanucleotide primers from kits OPA, OPB, and OPC from Operon Tech. (USA) were used for the RAPD-PCR (standard protocol). The amplified fragments of DNA were visualized under UV in 2% agarose/ethidium bromide.

The primers detected 24, 18 and 6 bands specific to tall, dwarf and San Ramon respectively. Further tall and dwarf (3), tall and San Ramon (26) and dwarf and San Ramon (36) shared another 65 polymorphic bands.

Detection of 113 type (bulk) specific RAPDs among tall, dwarf and San Ramon genotypes by just 60 primers within a very short period of time is remarkable in terms of generating a high density linkage map. Screening of more primers in similar manner is appreciable in parallel with the establishment of time consuming detection procedures required for RFLP and SSR/VNTR screening.

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