

Genetic Variation of Selected Progeny Lines of Coconut (*Cocos nucifera* L.) Based on Simple Sequence Repeat Markers

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Genetic variation of selected coconut progeny lines was estimated using simple sequence repeat (SSR) markers. A total of 15 progenies derived from selfing and reciprocal crossing of Laccadive Tall (LCT) and Gangobondam Dwarf (GBD) were used. Cluster and principal coordinate analysis were performed using the software NTSYS pc. Ten coconut specific primer pairs detected a total of 42 alleles. Jaccard's similarity coefficient varied from 0.136 to 1.000 with a mean of 0.590. The dendrogram based on UPGMA resulted in two clusters. Cluster I comprised of individuals of LCT and LCT x GBD and cluster II comprised of individuals of GBD and GBD x LCT. The principal coordinate plot exhibited close grouping of individuals of GBD and GBD x LCT than LCT and LCT x GBD. It showed that there were more genetic variation present among LCT and LCT x GBD progenies than among GBD and GBD x LCT.

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