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MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF SRI LANKAN *MANILKARA HEXANDRA* (PALU) GERMPLASM

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Manilkara hexandra (Palu) is a dominant canopy tree species in dry forests of Sri Lanka. It appears that *M. hexandra* shows a phenotypic variability among the different populations and there must be underlying genetic variability explaining the phenotypic variance. The genetic variations present in different provenances should be considered in selecting species for restoration programmes. The present study was conducted to study the morphological and genetic variation of Sri Lankan *M. hexandra* germplasm. Samples were collected to represent all the areas of Sri Lanka where *M. hexandra* grows. Tree morphological parameters, total height, dbh, height to first branch and crown diameter were measured for 91 trees in five Agro Ecological Zones (AEZ) in the dry zone of Sri Lanka. Young leaves were collected from each tree and were stored at -80 ^{o}C. DNA was isolated from each leaf sample by using QIAGEN DNeasy Plant Mini Kit. Ten RAPD markers and 12 microsatellite markers designed for *Manilkara huberi* were tested for *M. hexandra* DNA samples. The data were statistically analyzed. The trees sampled from five different AEZ exhibited varying morphometric parameters. Dbh was significantly higher in trees found in DL1 than those found in other AEZs. The trees in DL1, DL2 and DL3 AEZs were significantly taller than those in DL4 and DL5. The trees found in DL5 tend to branch at significantly a lower height than those found in other AEZs. The average crown width was significantly lower in trees at DL4 and DL5 than the trees in DL1, DL2 and DL3 ($P < 0.05$). The dendrogram showed that overall trees in DL2, DL4 and DL5 are morphologically more similar (>70%) and the trees from DL1 and DL3 exhibited 60% similarity. Basically two broad clusters could be observed (DL1 and DL3 together and DL2, DL4 and DL5 together) and therefore it is logical to consider as two subpopulations present in five AEZ. However, none of the RAPD markers yielded reproducible bands. The microsatellite markers Mh07, Mh19, Mh24 and Mh22 didn't amplify any band but Mh03, Mh04, Mh06, Mh08, Mh12, Mh20, and Mh22 produced polymorphic bands. A total of 11 alleles/bands were detected by these seven markers indicating the power of comparative mapping with genera. The dendrogram resulted from these polymorphic DNA banding data yielded five clusters which indicated a very high level of diversity. However, each cluster has trees from all the AEZs indicating that the recorded marker data has no apparent relationship with the morphological diversity. More robust species specific molecular markers must be developed to have greater insight into the molecular diversity of this species.

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