

Teak (*Tectona grandis* Linn. f.) is a tropical forest tree species naturally occurring in India, Lao, Myanmar and Thailand, while dahat (*Tectona hamiltoniana* Wall.) is an endemic tree species confined to Myanmar. Genetic variation of four *T. grandis* populations and three *T. hamiltoniana* populations in Myanmar was investigated using Amplified Fragment Length Polymorphisms (AFLPs) and chloroplast Simple Sequence Repeats (cpSSR). 85 samples from *T. grandis* populations and 72 samples from *T. hamiltoniana* were used for AFLP analysis while 86 samples from *T. grandis* and 71 samples from *T. hamiltoniana* were used for cpSSR analysis. 69 AFLP markers were employed for the analysis while two conserved chloroplast microsatellite primers (ccmp4 and ccmp6 primers) were applied for cpSSR analysis. AFLP analysis showed that genetic diversity varied between species, showing a slightly higher variation in *T. grandis* (PPL=94.23%,  $H_e=0.31829$ ) than in *T. hamiltoniana* (PPL=90.37%,  $H_e=0.30520$ ). Genetic diversity also varied among populations. Analysis of Molecular Variance (AMOVA) from AFLP revealed that the two species were significantly differentiated (38.42%,  $p < 0.05$ ). AMOVA also showed higher genetic variation within populations ((*T. grandis* (94.39%) and *T. hamiltoniana* (97.69%)) and lower but significant genetic differentiation among populations (*T. grandis* (5.61%;  $p < 0.001$ ) and *T. hamiltoniana* (2.31%;  $p < 0.05$ ). Similarly, pairwise  $F_{st}$  generated from AMOVA revealed that all except three population pairs were significantly differentiated ( $p < 0.05$ ) with  $F_{st}$  values ranging from 0.04155 to 0.47348. An Unweighted Pair Group Method with Arithmetic Mean (UPGMA) cluster based on Nei's genetic distance illustrated a clear genetic differentiation between species and among populations. AFLP diagnostic markers were also detected to differentiate between species and among populations. The cpSSR analysis confirmed a clear genetic differentiation between species, showing only a single haplotype (h1) in *T. grandis* populations while detecting two haplotypes (h2 and h3) in *T. hamiltoniana*. All *T. grandis* populations were fixed for a single haplotype. Both species were unambiguously distinguished at cpDNA markers and at AFLPs, indicating strong phylogenetic divergence.