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Conservation and Genetic Variation of Teak (*Tectona grandis* Linn. f.) in Natural Populations in Myanmar

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Abstract

Teak (*Tectona grandis*) is a valuable tropical forest tree species which naturally occurs in India, Laos, Myanmar and Thailand. Ten polymorphic nuclear microsatellite markers (SSRs) and seventy-one AFLP markers (Amplified Fragment Length Polymorphisms) were used to investigate genetic variation of teak in natural populations in Myanmar for conservation and sustainable utilisation of genetic resources. Adult trees and young regeneration were sampled in selectively logged and unlogged populations in four regions, each in the northern and southern parts of Myanmar, and two plantations in Benin. A total of 1667 samples and 1573 samples were used for SSRs and AFLPs, respectively. In general, genetic diversity within teak populations was relatively high but not significantly different between management types and between regeneration and adults. Myanmar populations were less diverse than Benin populations with SSR markers and the allelic richness was significantly higher in southern than in northern populations of Myanmar. Additionally, inbreeding was significantly higher in the regeneration in unlogged than in selectively logged populations. AFLP markers showed contrasting patterns as the Myanmar populations were more diverse than those of Benin, and genetic diversity in northern populations was significantly higher than in the South of Myanmar. Furthermore, genetic diversity of adult trees was significantly higher than in the teak regeneration in unlogged populations. For both markers, cluster and structure analyses revealed two major clusters: one with northern populations and another one with southern populations of Myanmar and those of Benin. A Mantel test showed significant positive correlation between genetic and geographical distances among populations. Analyses of molecular variance (AMOVA) detected the highest genetic variation within populations. The F_{st} values were significantly different among all teak populations and higher between than within the regions in Myanmar. This study suggests applying different conservation strategies for northern and southern Myanmar.

Keywords: AFLPs, genetic variation, SSRs, teak