Genetic Differentiation among Natural Populations of *Shorea contorta* and *Parashorea malaanonan* (Dipterocarpaceae) in the Philippines

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Abstract

The rapid decline of the Philippine forests during the past century has resulted in highly fragmented tree populations. To conserve the remaining forest genetic diversity and to better support an effective forest restoration activities in the country, genetic differentiation among the remaining natural populations of the ecologically important and critically endangered timber species, *Shorea contorta* and *Parashorea malaanonan* (Dipterocarpaceae), was investigated using microsatellite markers developed for *Shorea* species.

Results revealed a higher mean values for populations in the northern than in the central region, in both dipterocarps, concerning on their allelic richness, effective number of alleles, and observed and expected heterozygosities. Further, population differentiation was higher in the northern (F_{ST}=0.187) than in the central region (F_{ST}=0.134) for *P. malaanonan*. An opposite trend of F_{ST} value, on the other hand, was obtained for *S. contorta* populations (northern: 0.017; central: 0.038). Analysis for inbreeding coefficient (F_{IS}) among populations within region generally showed an excess of heterozygotes for the studied dipterocarps. The groupwise differentiation of these different genetic parameters between populations from two regions in both dipterocarps, however, was not significant based from the two-sided test.

Analysis of molecular variance (AMOVA) showed significant difference between populations from northern and central region for both dipterocarps (*P. malaanonan*: 12.48 % variation, P= <0.05; *S. contorta*: 6.31 % variation, P= <0.01). This was supported by principal coordinate analysis and clustering of the populations based from the UPGMA dendrogram. Mantel test also revealed highly significant ($p < 0.0001$), in both species, after regressing Nei genetic distance against the geographic distance (P. malaanonan: r = 0.599; *S. contorta*: r = 0.511). Further, a high significant ($p < 0.001$) genetic structure among populations within region was also revealed in the studied dipterocarps (*P. malaanonan*: 3.37 % variation; *S. contorta*: 2.26 % variation). This result was supported by an analysis of a model-based Bayesian inference clustering, which was estimated from an optimal K population.

Keywords: Dipterocarpaceae, genetic differentiation, microsatellites

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