

Spatial Structure and Impact of Logging on Genetic Diversity of Selected Tropical Tree Species

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Analyses of the spatial distribution pattern, spatial genetic structure and of genetic diversity were carried out in two tropical tree species with contrasting breeding systems and different ploidy levels using a 50-ha demographic plot in a lowland dipterocarp forest in Peninsular Malaysia. *Shorea leprosula* is a diploid and predominantly outcrossed species, whereas *S. ovalis* ssp. *sericea* is an autotetraploid species with apomictic mode of reproduction. In comparisons with *S. leprosula* and other tropical tree species, *S. ovalis* ssp. *sericea* also displayed relatively high levels of genetic diversity. This might be explained by the lower pressure of genetic drift due to tetrasomic inheritance, and for autotetraploids each locus can accommodate up to four different alleles and this allows maintenance of more alleles at individual loci. The observed high levels of genetic diversity in *S. ovalis* ssp. *sericea* can also be due to a random retention of more heterogeneous individuals in the past, and the apomictic mode of reproduction might be an evolutionary strategy, which allows the species to maintain high levels of genetic diversity. The spatial distribution pattern analyses of both species showed significant levels of aggregation at small and medium but random distribution at the large-diameter class. The decrease in magnitude of spatial aggregation from small- to large-diameter classes might be due to compensatory mortality during recruitment and survival under competitive thinning process. Spatial genetic structure analyses for both species revealed significant spatial genetic structure for short distances in all the three diameter classes. The magnitude of spatial genetic structure in both species was observed to be decreasing from smaller- to larger-diameter classes. The high spatial genetic structuring observed in *S. ovalis* ssp. *sericea* at the small-diameter class is due primarily to limited seed dispersal and apomictic mode of reproduction. The similar observation in *S. leprosula*, however, can be explained by limited seed and pollen dispersal, which supports further the fact that the species is pollinated by weak fliers, mainly of thrips and megalurothrips in the lowland dipterocarp forest.

Analyses of the spatial distribution pattern, spatial genetic structure and genetic diversity were also carried out using a 33-ha plot in a hill dipterocarp forest for *S. curtisii* (habitat specific: dominates the ridges), *S. leprosula* (habitat specific: dominates the valleys), and *S. macroptera* (habitat generalist: common in ridges as well in the valleys). The levels of genetic diversity estimated based on five microsatellite loci were high in all the three species. The spatial distribution pattern analyses showed significant aggregation at small-diameter trees of all the three species and this was explained by limited seed dispersal. Intense aggregation of *S. curtisii* and *S.*

leprosula but random distribution of *S. macroptera* at the large-diameter trees might further prove that *S. curtisii* and *S. leprosula* are habitat specific, whereas *S. macroptera* is habitat generalist. The spatial genetic structure analyses revealed significant spatial genetic structure only at large-diameter trees of all the three species. Given the high degree of environmental heterogeneity in hill dipterocarp forest, for habitat specific species (*S. curtisii* and *S. leprosula*), the spatial genetic structure at the large-diameter trees can be explained by intense selection in favour of certain genotypes at the small-diameter trees; seedlings with suitable genotypes for a specific habitat will be selected to exist continuously and subsequently to become adults. The lack of spatial genetic structure but significant aggregation at the small-diameter trees of all the three species might indicate extensive pollen flow. Hence, if seed dispersal is restricted but pollen flow is extensive, no spatial genetic structure but significant spatial aggregation will be observed at the small-diameter trees, regardless of whether the species is habitat specific or habitat generalist. The inferred extensive pollen flow also allows us to postulate that energetic and generalist pollinators might be involved in the pollination of dipterocarps in the hill dipterocarp forests.

The impact of selective logging on the genetic diversity of *S. leprosula* and *S. ovalis* ssp. *sericea* was examined using direct comparison and simulation methods. Direct comparison of adjacent natural and logged-over stands showed substantial loss of genetic diversity on *S. leprosula*, but not on *S. ovalis* ssp. *sericea*. This indicates that outcrossing species are more susceptible to negative impacts of logging than apomictic species. Simulation studies were conducted using three approaches: (1) simulated-removal of individuals based on diameter size classes; (2) simulated-removal of individuals at random; and (3) simulated-removal of individuals in clump. The simulation study based on the first approach showed that the loss of genetic diversity was higher for the Malayan Uniform System (MUS) compared with the Selective Management System (SMS) in lowland and hill dipterocarp forests. This might suggest that the SMS is more orientated towards the conservation of genetic diversity. This simulation study also showed that to conserve 95% of the total number of alleles, the tolerable cutting limits of *S. leprosula* in a 50-ha plot of Pasoh Forest Reserve (FR) and a 33-ha plot of Sungai Lalang FR were > 70 cm diameter at breast height (dbh) and > 80 cm dbh, respectively. Comparison of simulation studies based on the second and third approaches showed that the loss of genetic diversity was more rigorous if logging activities were anticipated to extract trees in clumps rather than at random.