

Understanding local patterns of genetic diversity in dipterocarps using a multi-site, multi-species approach: Implications for forest management and restoration

Abstract

The lowland tropical forests of Southeast Asia are dominated by a single family of canopy and emergent trees, the Dipterocarpaceae. The seeds of dipterocarps are gravity or gyration dispersed. Short distance and limited seed dispersal via these mechanisms result in the aggregation of related individuals and strong fine-scale spatial genetic structure (FSGS). In logged and fragmented forests, where gene flow may be disrupted, tree species with strong FSGS are predicted to exhibit increased inbreeding, which consequently can erode genetic diversity, fitness and might limit the potential for natural regeneration of dipterocarps. Developing a set of indirect operational indicators for FSGS provides a solid basis for informing conservation and management of forest genetic resources in logged forests. Our main objective was to use an information theoretic approach to identify these indicators of FSGS in dipterocarps. We quantify FSGS in 19 dipterocarp species across four forest sites in Malaysian Borneo, India and the Seychelles. We detected FSGS in 15 (79%) of our study species, most of which displayed significant inbreeding. Our results suggest that wood density and flower size offer useful indicators of FSGS. We propose some simple guidelines to allow forest managers to account for FSGS when planning approaches to maintain genetically diverse stands in logged dipterocarp forests. The integration of improved understanding of genetic processes is essential for conserving forest tree genetic resources and ensuring the resilience of logged forests.