



Sustaining tropical timber trees in production forests of Asia - ensuring their genetic viability

Sustainable timber production in approximately 400 million hectares of production forests in the tropics would be enhanced by incorporating genetic conservation measures in their management. This would also enhance the conservation value of these forests while contributing to maintaining carbon sequestration and provision of other ecosystem services in a changing environment. Natural forests in the humid and subhumid tropics are commonly managed under selection logging regimes, applying minimum diameter cutting limits. The larger trees which exceed these minimum diameter limits and can, therefore, be harvested, generally produce more pollen and seed than smaller trees because their crowns are larger. They can also attract more pollinators than smaller trees which reduces the risk of self-pollination.



When there are fewer remaining reproductive trees per species per hectare, inbreeding can increase. Smaller populations are also at a higher risk of loss of genetic diversity.

Inbreeding and loss of genetic diversity can have severe negative effects on timber tree populations, for instance, reducing growth, reproductive output, ability to resist pests and diseases and the capacity to adapt to climate change. Over time these can reduce quantity and quality of timber yields.

Since trees have a life span of a century or more, it is evident that today's seedlings will grow to mature trees under very different environmental conditions than those they experienced during seedling establishment, which underlines the importance of maintaining adaptive capacity.



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Why are tropical Asian timber trees vulnerable?

Most of the logging activities in natural forests of Southeast Asia occur in mixed dipterocarp forests, which are among the most diverse and, in terms of timber production, most valuable tropical forests. These forests commonly harbour 150–250 tree species per hectare, with correspondingly low densities of individual species. The canopy is dominated by hardwood species of the family *Dipterocarpaceae*, which are long-lived and can grow to exceptional sizes. Important commercial timbers include chengal (*Neobalanocarpus* spp.), giam (*Hopea* spp.), kapur (*Dryobalanops* spp.), keruing (*Dipterocarpus* spp.), meranti (*Shorea* spp.), mersawa (*Anisoptera* spp.), resak (*Cotylelobium* spp.) and white seraya (*Parashorea* spp.).

Biological characteristics and ecological requirements vary among dipterocarp species. However, they have many characteristics which suggest that they are particularly vulnerable to logging and habitat fragmentation. Typically, they:

- Are slow in reaching reproductive maturity
- Flower and produce seeds at irregular intervals during synchronized general flowering events occurring every few years (also known as mast fruiting)
- Are pollinated by insects, many of which are small, which limits the distance of pollen flow
- Have relatively high outcrossing rates and, in case of inbreeding, exhibit strong negative impacts e.g. on seed production and germination and seedling growth
- Disperse seed mainly via gravity over short distances, typically 20–50 m

- Lack a soil seedbank of dormant seed
- Require an increase in light for satisfactory establishment and growth of seedlings
- Trees tend to be closely related to their neighbors, which increases the risk of inbreeding.

How do logging and fragmentation affect the genetic diversity of tropical Asian trees?

Biodiversity International and the Forest Research Institute of Malaysia (FRIM) reviewed genetic research on the impacts of logging and fragmentation on tropical Asian timber species and found that when the density of trees per species was reduced by logging or was naturally low compared to adjacent stands, trees produced more inbred seed and seedlings. Inbreeding in these studies was associated with reduced fruit set, smaller seed and slower growth of seedlings. Some studies also reported that overall genetic diversity (typically measured as allelic richness i.e. the number of genetic variants per locus in the population) was lost, although this was less common than increased inbreeding.

When a tree population is exposed to disturbance, changes are often first seen in mating patterns, for instance, as increased self-pollination. Effects on genetic diversity may be delayed because many of the alleles that were present before harvest are also present in residual trees, although in reduced numbers. In small populations, alleles can then be lost by chance when the trees harbouring those alleles fail to produce surviving offspring, for example as a result of inbreeding.

Our review showed that loss of genetic diversity was more common in fragmented than selectively logged populations. This was probably because in most cases the effect of habitat fragmentation had lasted at least 100 years, whereas logging

had started less than 50 years ago and most of the forests had been logged only once. This suggests that negative genetic impacts of logging can become more severe during subsequent cutting cycles.

At the same time, in several of the studies in logged forests the loss of genetic diversity was still evident decades after a single logging event. This suggests that in species in which pollen or seed dispersal or both are limited, genetic diversity may not be easily restored through gene flow from surrounding forests, contrary to what is commonly assumed. Fragmentation reduced pollen flow distances and it may increase the negative genetic impacts of logging. These results underline the importance of integrating genetic conservation measures in logging guidelines.

International criteria and indicators for sustainable forest management, such as those developed by the International Tropical Timber Organization (ITTO), the Forest Stewardship Council (FSC) and the Programme for the Endorsement of Forest Certification (PEFC) already require that forest managers take measures to conserve genetic diversity in production forests. However, there has been lack of guidance for policy makers and forest managers on what kind of measures are required.

What can policymakers do to reduce the risk of genetic erosion of timber tree species in production forests?

- Support the development and use of harvesting guidelines that are specific to species or species groups
- Initiate requirements for average minimum population densities as a precondition for harvesting, to avoid inbreeding
- Consider introducing maximum diameter cutting limits, to avoid systematic removal of large trees which are often

particularly important seed sources and may contain genetic variants that are rare or absent in younger tree cohorts

- Support training of forest botanists and their inclusion in field inventory teams to improve species identification
- Require systematic documentation of the origin of forest reproductive material (FRM) and commission the development of guidelines for seed zones and transfer of FRM as well as for increasing diversity of FRM to support adaptation to climate change.
- Improve land use planning to increase connectivity among forest patches, to avoid habitat fragmentation which could augment the risks of genetic erosion in logged forests.

What can forest managers do to maintain productivity and resilience of timber tree populations?

- Avoid systematic removal of all trees that exceed the diameter cutting limits
- For species with clumped distributions, remove trees randomly rather than in clumps to reduce the risk of inbreeding
- Monitor numbers of seedlings and saplings, by species where possible, and postpone logging if they are few
- Include forest botanists in field inventory teams
- If planting, use genetically diverse forest reproductive material (FRM) from conditions that are ecologically similar to the planting site and document the origin of FRM.

*This factsheet is based on the following scientific article: Jalonen R, Hong LT, Lee SL, Loo J, Snook L. 2014. Integrating genetic factors into management of tropical Asian production forests: a review of current knowledge. **Forest Ecology and Management**, 315: 191-201.*

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