

Forest Genetic Resources

Basic Knowledge



This module is intended for managers of forests and conservation areas as well as for silviculturists, restoration ecologists and others involved in conserving and managing tree-based resources or who work with forest planting materials. The module provides information on the conservation and management of forest genetic resources and gives links to other useful materials.

What are forest genetic resources?

Forest genetic resources are the heritable materials within and among tree species and other woody plants (FAO, 2014a). Forest genetic resources underpin the adaptive potential that has enabled trees to be, in evolutionary terms, among the planet's most successful types of organism. The practice of genetic conservation is not intended to conserve every genetic variant (or "genotype") – indeed, this would be impossible because individuals of sexually reproducing species are genetically unique. Rather, the aim is to conserve the evolutionary potential of species, which means ensuring the continuation and functioning of the processes that shape and maintain genetic diversity. Conservation efforts may also focus on conserving particular traits (characteristics) of trees and other woody plants, such as resistance to pests, diseases or drought.

Although genetic resources are often neglected in planning and implementing forest management, their conservation is essential for sustainability. It is critical, therefore, that forest managers understand the point at which ignoring genetic aspects can prevent the achievement of forest management goals.

Why are genetic resources important?

Trees vary – both within and among species – in their growth rates; stem form; seed production; tolerance to pests, drought, heat, salinity and heavy metal toxicity; and many other characteristics. The ability of trees to adapt to environmental changes depends on the level of genetic variability in their "adaptive traits" – characteristics that confer tolerance of, or resistance to, new environmental challenges.

Most tree species have high levels of genetic diversity, presenting great (and largely untapped) potential for improving tree products such as food, fibre, solid wood and forage and increasing the delivery of environmental services (such as water supply regulation and carbon sequestration). Tree selection and breeding programmes attempt to take advantage of genetic variability to improve valuable traits; such programmes have the potential to achieve the same dramatic improvements in forest production that have been made in food crops. The time required to achieve such improvements is longer for trees than for most agricultural crops, however, because of the late initiation of sexual reproduction in trees and their longevity. Evaluating, conserving, testing and using genetic diversity is vital for ensuring the future

production of goods and environmental services from trees.

Genetic diversity of forest trees

Genetic diversity in any species originates as mutations in the genetic code, DNA. Although most mutations are deleterious and are removed rapidly through natural selection, beneficial mutations can confer selective advantages on individuals carrying the variant genes. Thus, the carriers of beneficial genes have higher "fitness" (that is, they are capable of producing more surviving offspring) and are better adapted to their environmental conditions compared with individuals not carrying those genes.

Genetic diversity is maintained by gene flow via pollen and seed movement within and among populations. In general, large populations maintain more genetic diversity than smaller ones; conversely, genetic diversity is restricted by small population size and isolation. Isolation may be the result of distance from other populations of the same species or due to physical barriers preventing the movement of pollinators or the dispersal of seeds across landscapes.

Adaptation to conditions as they vary along environmental gradients maintains genetic diversity among distinct and overlapping tree populations. Understanding patterns of variation in adaptive traits is important in selecting suitable seed sources for planting.

Most tree species are out-crossing, which means that:

- flowers on one tree are usually pollinated by another tree;
- they respond poorly to inbreeding (i.e. mating between close relatives); and
- they have high genetic diversity relative to many other species.

In their natural state, therefore, most tree species have considerable potential for both adaptation to environmental change and genetic improvement in productive traits, thereby increasing their usefulness to people.

Forest genetic resources contributes to SDGs:





Related modules

- [Agroforestry](#)
- [Forest reproductive material](#)
- [Forest restoration](#)
- [Management of non-wood forest products](#)
- [Wood harvesting](#)

In more depth

How is genetic diversity measured?

Genetic variation in the traits of trees can be measured in field trials designed to allow the separation of genetic from environmental effects using appropriate statistical analyses. Provenance and progeny trials have been conducted for many species used in commercial plantations. In provenance trials, seed collected from many individual trees in a population is planted to increase understanding of the large-scale variation among different locations in the broad geographic range of a species and to identify the most suitable seed sources for planting at specific sites. Progeny trials are used to determine the heritable variation in useful traits and to identify the best-performing individuals.

Although the term “genetic diversity” is generally taken to mean genetic variation in traits, it also refers to DNA-level variability that may or may not be associated with measurable trait differences. Most commonly, genetic diversity is measured using molecular markers assumed to be neutral with respect to selection. Rapid advances have been made in recent years in the power of molecular genetic tools while reducing their cost. To date, however, the potential associations between molecular markers and traits of interest to tree-breeders are unknown. Field trials are still needed, therefore, to estimate genetic variation in the traits of interest for adaptation to changing environmental conditions and for improving tree products.

Conservation of forest genetic resources

Forest genetic resources may be conserved in place (“*in situ*”), or outside the natural habitat of a species in gene banks (“*ex situ*”). Of the two approaches, *in situ* conservation is usually the preferred option because it allows natural evolutionary processes to continue through adaptation to changing conditions. *Ex situ* conservation is necessary, however, if species or populations are threatened in the wild. Many countries and some international organizations maintain seed banks for forest trees, but accessions are generally limited to species with “orthodox” seed. Many tree species in the humid tropics in particular, such as dipterocarps in Southeast Asia, are “recalcitrant” (the opposite to orthodox, in this sense), meaning that their seed cannot be stored under conventional conditions in seed banks without the rapid loss of viability. Live gene banks (plots of planted trees designed to conserve genetic diversity) have been established for some species, but these require considerable space and must be tended over long periods.

The *in situ* conservation of forest genetic resources is compatible with sustainable use – as long as genetic considerations are accounted for explicitly in forest management. Protected areas that have been established for other purposes may not effectively conserve the genetic resources of priority tree species. Indeed, forest genetic resources can sometimes be conserved more effectively in managed forests than in protected areas. Genetic reserves established specifically for conserving forest genetic resources, such as those in European countries monitored by the [EUFORGEN programme](#), are ideal; few countries have such reserves, however.

Key considerations in the conservation of forest genetic diversity include:

- maintaining sufficient population sizes to promote out-crossing between unrelated individuals and to maintain genetic variation within populations; and
- ensuring that genetic processes that affect diversity, such as gene flow and natural selection, are functioning, and that genetic drift by which alleles (alternative forms of genes) are lost through sampling error from one generation to the next is minimized.

Effective population size is an important concept in managing and conserving genetic diversity because it is a much more accurate indicator of potential genetic problems than the census population size (the actual number of individuals), and it is almost always smaller. The effective population size equals the census size if:

- the population has equal numbers of males and females, all of which are reproducing at a rate that varies no more than by random chance;
- mating is equally likely between any two individuals and occurs at random; and
- the number of reproducing individuals is constant from generation to generation, and only one generation is of reproductive age at any time.

The effective size of a population of tree species is always likely to be considerably smaller than the census population because, even if the other conditions are met, the long life-cycles of trees result in overlapping generations. The probability of inbreeding and the random loss of alleles increases as effective population size decreases. Inbreeding, particularly self-pollination (its most extreme form), is harmful to most tree species, which generally carry high genetic loads of deleterious recessive alleles. The first expression of inbreeding is often reduced fertility; inbred seedlings and saplings are also likely to exhibit lower growth rates and less resistance to biotic and abiotic attacks.

Effective population size is reduced relative to the census size as the level of relatedness in a population increases. Therefore, the lower the effective population size compared with the census size, the larger the area required for conservation.

Analysing threats to genetic resources and prioritizing species and populations are important steps in developing conservation strategies for forest genetic resources. Some of the most serious threats globally are overexploitation, livestock grazing, agricultural expansion, and climate change.

Most forest genetic resource conservation to date has been *in situ* (in contrast, the conservation of agricultural crop genetic resources is usually *ex situ*). With a few exceptions, tree species are still wild; capturing the variability of a set of provenances of a tree species therefore requires a much larger sample than would be needed to capture the diversity of a similar number of crop varieties. Ideally, forest genetic resource conservation strategies would combine genetic reserves (designed specifically to conserve the genetic resources of targeted tree species) with well-designed forest management practices to ensure that the evolutionary potential of valuable and at-risk tree species is maintained. Implementing such a strategy would imply a change in conservation paradigms and require the strengthening of capacity among a variety of actors.

Key genetic considerations in managing forest resources in natural forests

It is feasible to conserve genetic resources while harvesting wood products and non-wood forest products, but care must be taken in forest management to avoid detrimental impacts. Most sustainable management practices and guidelines do not explicitly consider the role of genetic resources in long-term sustainability.

The type of product harvested, and the way in which it is harvested, matters. The harvesting of wood products kills trees, but it is usually carried out after trees have reached reproductive maturity and have shed seed. The harvesting of fruit, bark and leaves affect trees in different ways, with the degree of impact on genetic resources related largely to the intensity of harvest. It is unusual for the harvest of fruit to kill trees, unless branches or entire trees are cut in a one-time harvest. If, however, the entire fruit production is harvested year after year, there will be little or no regeneration. The harvesting of bark, if too intensive, can be just as destructive as cutting trees.

Even when reduced impact harvesting practices are employed, logging can result in a serious reduction in genetic diversity, with associated impacts on a species' adaptability and long-term persistence. Selective logging reduces population density and hence the distance between large trees – which are likely contributing more than smaller trees to reproduction in the population. Depending on the species, pollinators may be less likely to travel between widely separated trees, which may result in higher levels of self-pollination. For many tree species, knowledge is incomplete about reproduction, pollinators and genetics, so prescribing a harvesting regime that does not reduce the ability of a tree population to reproduce can be difficult.

Another consideration is the successional status of harvested species. Even when diameter limits are set to ensure that logged trees are well past the age of initial reproduction, regeneration is not assured because it depends on the light requirements of seedlings and saplings and the corresponding conditions in the stand. Light-demanding species do not regenerate under shade. The soil seedbank is effective only for seed that remains viable for extended periods, which is not the case for many tree species: even if the canopy is opened during logging to permit sufficient light, therefore, there may be no seed available to establish regeneration. Such considerations demonstrate that effective forest genetic resource conservation requires an understanding of the reproductive biology and ecology of species. Species may differ in their requirements for adequate regeneration, and these differences should be taken into account to ensure the long-term adaptability and persistence of affected species and effective forest genetic resource conservation.

Dysgenic selection – in which harvesting leads to an (unintentional) undesirable directional change in genetic quality over one or more generations – has long been a preoccupation of forest managers. This is the idea that removing the best-quality trees (for example in terms of their form or growth rates) and leaving the rest leads to genetic shifts in important traits by increasing the relative reproductive contributions of poor-quality trees. This is more likely to occur in trees that are shade-intolerant because they tend to leave behind less regeneration at the time of harvest; the extent to which this is a problem is open to debate, however, and further knowledge is required.

Genetic considerations in establishing planted forests

Tree-planting is carried out for many reasons, ranging from small-scale and industrial wood production to landscape restoration, conservation and agroforestry. Regardless of the purpose, a sufficient supply of seed (or some other form of propagule) with high physiological and genetic quality is necessary. Most industrial planting employs genetically improved material and the seed supply chain is well established; for many other plantings, however, the planting material is obtained from the wild.

There are three primary considerations related to genetic quality in sourcing seeds from the wild, with their importance varying depending on the purpose of planting:

1. The seed source must be well adapted to the planting site – this does not necessarily mean using seed that is geographically closest to a target site because other factors may reduce the suitability of such material.
2. The seed must be obtained from a sufficient number of trees to ensure that it is genetically diverse.
3. The seed-source trees must not be closely related, to avoid collecting inbred seed.

Ambitious forest restoration initiatives are in the early stages of implementation in various regions of the world; in many cases, however, the planning of seed supply is lagging behind. Although restoration has many possible objectives and methods, the restored forest should be self-sustaining, meaning that ecosystem functions should be restored sufficiently to ensure the ongoing reproduction and regeneration of desired tree species. This requires attention to the genetic characteristics of seed sources to ensure that planting material is well adapted to site conditions and sufficiently diverse to allow adaptation to changing conditions through natural selection.

The best way to ensure that seed sources are well adapted to planting sites is to conduct provenance trials at test sites covering the range of environmental conditions encountered in the targeted restoration areas. If provenance trial data are unavailable and time does not allow field tests to be established, the next best option is to source seed from localities where environmental conditions are similar to those of the target restoration areas (see also [Forest Reproductive Material](#)).

Problems associated with collecting seed from small populations

If a population of trees is isolated and has consisted of a small number of reproductive trees over several generations, the effective population size is likely to be much smaller than the census population. It therefore may have been subject to genetic drift, and trees may have become increasingly closely related in each generation, leading to inbreeding.

Any individual produced through sexual reproduction obtains half its DNA from each of its two parents. The degree to which the alleles received from each parent are the same is a measure of the “homozygosity” of an individual – the more closely related the parents, the higher the homozygosity of the offspring. Thus, an outcome of inbreeding is higher-than-expected homozygosity, which can be detrimental because of an accumulation of deleterious alleles that have not been removed through natural selection. High heterozygosity (i.e. the extent to which the alleles of a given gene received from two parents differ), on the other hand, has been found to be associated positively with survival, growth and reproductive capacity in some tree species. If possible, therefore, seed for planting purposes should not be collected from populations with fewer than 500 reproductively mature individuals.

If seed is collected from a small number of trees at a location, even if the population is large, the seed will represent a small sample of the available genetic diversity and the resulting planted forest will have lower genetic diversity than the source population if no additional seed sources are used. This would constitute a genetic bottleneck and may lead to inbreeding and the loss of adaptive potential in subsequent generations. The bottleneck effect would be exacerbated by variability among source trees in their seed production, which would further reduce the effective size of the source population. The problem would be further compounded if the planted trees later became the source of germplasm for future plantings.

Assuming that seed is collected in such a way as to ensure diverse planting sources, the system for properly distributing genetic diversity to planting sites (which may be small and scattered across a landscape) must be well designed and executed. Ensuring that planting material is diverse and well adapted to planting sites is not a trivial issue: measures range from the molecular monitoring of populations, nursery material and established trees to ensure that the system is functioning well at each stage, to more easily and cheaply applied surveys of seed production variability, germination rates, and the survival and vigour of trees after planting.

Key genetic considerations in managing trees outside forests

As the area of intact forest declines and the area of agricultural land expands, the need to manage the genetic diversity of trees in agricultural landscapes increases. *In situ* genetic conservation in protected areas and managed forests does not include populations confined to primarily agricultural landscapes – trees that have been planted by farmers or retained in agroforestry systems and natural patches. Likewise, *ex situ* conservation in the tropics excludes many valuable tree species because of the difficulty and cost involved in storing tropical tree seeds. The conservation of forest genetic resources through their use on farms, where trees may grow outside their natural habitats but within their natural ranges, has a potentially important complementary role. The long-term survival of some species (such as savannah agroforestry species in sub-Saharan Africa) may depend on the appropriate management of their genetic resources in agricultural landscapes.

An important issue in forest genetic resource conservation in agricultural landscapes is the fragmentation of tree populations and the effects of this on gene flow and population viability. If regeneration is hindered by inadequate gene flow within and among tree populations, those populations may disappear as mature trees die. On the other hand, some tree species are adapted to low population densities, and in some cases gene flow may even be boosted by an increase in open space between trees. The key to forest genetic resource conservation in

agricultural landscapes, therefore, is to understand the reproductive biology and ecology of the species, including their mating systems and modes of pollination, what constitutes barriers to gene flow, and the potential consequences of changes in the landscape matrix.

Generalizations are open to debate: an extreme view is that isolated trees in agricultural landscapes are the “standing dead”, with no apparent prospects for reproduction. Long-distance pollination and seed dispersal events have been observed, however, in many tree species; in some cases, too, regeneration occurs naturally in pulses when conditions are suitable (rather than continuously). Thus, relatively isolated individual trees may be important as genetic repositories and as stepping stones for maintaining gene flow, at least for some species.

Where landscape fragmentation disrupts gene flow it can lead to inbreeding, which in turn can reduce seed yields and the vigour of seedlings. Dioecious fruit tree species (that is, trees that produce either male or female flowers but not both) may fare badly in agroforestry systems because non-producers (i.e. those that do not produce fruits because they lack the female reproductive organs) may largely be removed, reducing the effective population size and leading to increased inbreeding in subsequent generations. On the other hand, when it is known that cross-pollination is needed for fruit production, farmers are more likely to see the value in maintaining connectivity, thereby increasing the prospects for effective genetic conservation. In general, the importance of conserving genetic diversity may be more obvious in agricultural landscapes than in intact forests simply because farmers recognize the usefulness of the trees.

Although productive trees may be maintained in agroforestry landscapes, regeneration may be limited by crop production or grazing among mature trees. This means that, to conserve the viability of populations of valuable tree species in agricultural landscapes, managers should devise strategies to enable priority species to reproduce and regenerate to ensure their perpetuation.

E-learning

[Planning seed and seedling supply for forest and landscape restoration](#)



This course explores how to plan seed and seedling supply for forest and landscape restoration (FLR). This includes the importance of considering seed and seedling origin and genetic quality, the reproductive and supply chain bottlenecks that reduce genetic diversity or adaptive capacity, and ...

Further Learning

Boffa, J. 2000. West African agroforestry parklands: keys to conservation and sustainable management. *Unasylva*, 51: 11–17.

Boshier, D.H., Gordon, J.E. & Barrance, A.J. 2004. Prospects for *in situ* tree conservation in Mesoamerican dry forest agro-ecosystems. In: G.W. Frankie, A. Mata & S.B. Vinson, eds. *Biodiversity conservation in Costa Rica: learning the lessons in the seasonal dry forest*, pp. 210–226. Berkeley, USA, University of California Press.

Boshier, D.H. 2004. Agroforestry systems: important components in conserving the genetic viability of native tropical tree species? In: G. Schroth, G. Fonseca, C.A. Harvey, C. Gascon, H.L. Vasconcelos & A.M.N. Izac, eds. *Agroforestry and biodiversity conservation in tropical landscapes*, pp. 290–314. USA, Island Press.

Bozzano, M., Jalonen, R., Thomas, E., Boshier, D., Gallo, L., Cavers, S., Bordács, S., Smith, P. & Loo, J. 2014. [Genetic considerations in ecosystem restoration using native tree species](#). Thematic Study 10. Food and Agriculture Organization of the United Nations (FAO) and Bioversity International.

Dawson, I.K., Lengkeek, A., Weber, J.C. & Jamnadass, R. 2009. Managing genetic variation in tropical trees: linking knowledge with action in agroforestry ecosystems for improved conservation and enhanced livelihoods. *Biodiversity and Conservation*, 18: 969–986.

Dawson, I.K., Vinceti, B., Weber, J.C., Neufeldt, H., Russell, J.R., Lengkeek, A.G. et al. 2011. Climate change and tree genetic resource management: maintaining and enhancing the productivity and value of smallholder tropical agroforestry landscapes. *Agroforestry Systems*, 81: 67–78.

Dawson, I.K., Guariguata, M.R., Loo, J., Weber, J.C., Lengkeek, A., Bush, D., Cornelius, J., Guarino, L., Kindt, R., Orwa, C., Russell, J. & Jamnadass, R. 2013. What is the relevance of smallholders' agroforestry systems for conserving tropical tree species and genetic diversity in *in situ*, *in situ* and *ex situ* settings? A review. *Biodiversity and Conservation*, 22: 301–324.

FAO, DFSC & IPGRI. 2001. *Forest genetic resources conservation and management. Vol. 2: In managed natural forests and protected areas (in situ)*. Rome, Food and Agriculture Organization of the United Nations (FAO), DANIDA Forest Seed Center (DFSC) and International Plant Genetic Resources Institute (IPGRI).

FAO, FLD & IPGRI. 2004. *Forest genetic resources conservation and management. Vol. 1: Overview, concepts and some systematic approaches*. Rome, Food and Agriculture Organization of the United Nations (FAO), Forest and Landscape Denmark (FLD) and International Plant Genetic Resources Institute (IPGRI).

FAO, FLD & IPGRI. 2004. *Forest genetic resources conservation and management. Vol. 3: In plantations and genebanks (ex situ)*. Rome, Food and Agriculture Organization of the United Nations (FAO), Forest and Landscape Denmark (FLD) and International Plant Genetic Resources Institute (IPGRI).

FAO. 2014a. [State of the World's Forest Genetic Resources](#). Rome.

FAO. 2014b. [Global Plan of Action for Conservation, Management and Development of Forest Genetic Resources](#). Rome.

Finkeldey, R. 2005. *An introduction to tropical forest genetics*. Göttingen, Germany, Georg-August-University Institute of Forest Genetics and Forest Tree Breeding.

Geburek, T. & Turok, J., eds. 2005. *Conservation and management of forest genetic resources in Europe*. Zvolen, Slovakia, Arbora Publishers.

Hubert, J. & Cottrell, J. 2007. [The role of forest genetic resources in helping British forests respond to climate change](#). Forestry Commission Information Note FCIN086.

IUCN Species Survival Commission. 2008. *Strategic planning for species conservation: an overview*. Version 1.0. Gland, Switzerland, International Union for Conservation of Nature (IUCN).

Jalonen, R., Hong, L.T., Lee, S.L., 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.

Jennings, S.B., Brown, N.D., Boshier, D.H., Whitmore, T.C. & Lopes, J.d.C.A. 2001. Ecology provides a pragmatic solution to the maintenance of genetic diversity in sustainably managed tropical rain forests. *Forest Ecology and Management*, 154: 1–10.

Koskela, J., Lefèvre, F., Schueler, S., Kraigher, H., Olrik, D.C., Hubert, J. et al. 2013. Translating conservation genetics into management: pan-European minimum requirements for dynamic conservation units of forest tree genetic diversity. *Biological Conservation*, 157: 39–49.

Koskela, J. & Lefèvre, F. 2013. Genetic diversity of forest trees. *In*: D. Kraus & F. Krumm, eds. [*Integrative approaches as an opportunity for the conservation of forest biodiversity*](#), pp. 232–241. Freiburg, Germany, European Forest Institute.

Ledig, F.T. 1992. Human impacts on genetic diversity in forest ecosystems. *Oikos*, 63: 87–108.

Loo, J., Souvannavong, O. & Dawson, I., eds. 2014. [Global forest genetic resources: taking stock](#). Special issue. *Forest Ecology and Management*, 333: 1–98.

McNeely, J.A. & Schroth, G. 2006. Agroforestry and biodiversity conservation: traditional practices, present dynamics, and lessons for the future. *Biodiversity and Conservation*, 15: 549–554.

Credits

This module was developed with the kind collaboration of the following people and/or institutions:

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