

# Regional guidelines for identifying genetic conservation units and seed sources for Asian tree species



Bioversity International & Asia-Pacific Forest Genetic Resources Programme



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Seed source of the critically endangered Siamese rosewood (*Dalbergia cochinchinensis*) in Lao PDR. Credit: R. Jalonen / Bioversity

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## List of Acronyms

APFORGEN	Asia-Pacific Forest Genetic Resources Programme
EUFORGEN	European Forest Genetic Resources Network
GBIF	Global Biodiversity Information Facility
FAO	Food and Agriculture Organization of the United Nations
IUCN	International Union for Conservation of Nature

## Introduction

Across Asia, thousands of socio-economically important tree species are threatened [1,2]. These species and their genetic resources offer vital sources of income, food and environmental services for hundreds of millions of people. Genetic diversity underlies the species' productivity and allows them to adapt to climate change and other potential threats. Today's large-scale commitments to forest and landscape restoration mean a growing demand for seeds and seedlings of native tree species, the genetic diversity and origin of which determines the survival and growth of the newly established forests into the future. For many species the dwindling natural populations are currently the only available source of seed and seedlings for meeting the restoration targets [3,4].

Conserving the genetic diversity and adaptive capacity is the cornerstone of effective conservation of tree species and maintaining quality natural seed sources. This was recognised in the Kunming- Montreal Global Biodiversity Framework which set, for the first time, global targets for maintaining and restoring the genetic diversity of wild species, by 2030 [2]. Genetic conservation requires a network of viable, large enough tree populations across each species' range and the diversity of environments in which they are found and adapted to. Minimum viable population size that minimises the risk of genetic erosion depends on the species and site characteristics such as typical population densities, growth rates, pollen and seed dispersal patterns and mating system [5,6]. The minimum number and location of the conserved populations, in turn, depends on the diversity of the environments where the species is found and the geneflow patterns that determine how distinct the populations have developed over time.

For many tropical Asian tree species, this information to aid conservation and restoration planning is widely lacking – not only on the genetic diversity patterns and reproductive traits, but even on the distributions of the species [7]. According to the State of the World's Trees (2021) report, the conservation status of one in three tree species from the Indo-Malaya region remains unknown, highest among world's major floristic regions [2]. Conservation approaches also vary between countries depending on priority species, socio-economic contexts, resources and capacities, and currently there are no commonly agreed, specific definitions of *in situ* species conservation units that would ensure the conservation of genetic diversity and species' evolutionary potential. This gap makes it difficult to assess the conservation status of the species across their distribution ranges and country borders, and to identify spatial conservation priorities to safeguard unique local adaptations.

## Objectives

The objectives of this guideline are to:

- enable a regional assessment of the conservation status of native Asian tree species and their genetic resources using readily available information
- enable the identification and recognition of sites that already serve, or have the potential to serve, as genetic conservation units and seed sources for native tree species, so that relevant measures can be taken to safeguard them

- support the identification of priorities and collaboration opportunities for ecological and genetic research on native Asian tree species across country borders
- raise forest managers' and conservation practitioners' awareness about the importance of conserving genetic diversity, by highlighting related gaps and priorities that may differ from gaps and priorities identified solely at species or ecosystem level.

The process contributes directly to the strategic objectives of the Asia Pacific Forest Genetic Resources Programme (APFORGEN) for 2023-2030 [8]:

- 1) Mobilize political and financial support for integrated management of forest genetic resources in land use, biodiversity and climate policies, strategies and programmes
- 2) Make information about the region's forest and tree genetic resources available and accessible to support their sustainable management and research
- 3) Develop conservation and sustainable use strategies for regionally important and threatened tree species
- 4) Strengthen tree seed systems to facilitate ecosystem restoration, support local livelihoods and climate change adaptation and mitigation

APFORGEN is a regional programme for the conservation, restoration and sustainable use of Asia's vast forest genetic resources. It was established in 2003 to enhance networking and collaborative research and strengthen capacities in genetic conservation and sustainable use. APFORGEN's objectives are aligned with the Kunming-Montreal Global Biodiversity Framework [9] of the United Nation's Convention on Biological Diversity and the Global Plan of Action on Forest Genetic Resources [10] by the Food and Agriculture Organisation of the United Nations (FAO). APFORGEN has 15 member countries in South, Southeast and East Asia.

## The approach

The tier-based approach is designed to guide prioritisation in contexts where species diversity is extremely high and resources per species, therefore, limited. By breaking down the process of identifying and designating conservation sites to steps, the approach allows making use of readily available information, setting realistic targets and monitoring and recognising progress. It also allows for flexibility and diversity of implementation approaches appropriate to each context, while enabling comparisons between species and across geographies. For example, finding sufficiently large genetic conservation areas that can be sustained over time may require a combination of protected forest, sustainable management units, community forests, sacred groves and patches of forest in agricultural landscapes. This is particularly relevant in Asian countries where human population densities are often high even in rural areas, and livelihood needs of local communities must be considered in conservation planning.

The guidelines consist of three tiers of tree species conservation sites and seed sources, from confirmed viable populations in protected areas at Tier 3 to officially designated species and genetic conservation units at Tier 1. In addition, criteria are defined for candidate sites to help prioritise conservation efforts. Each site has one or more target tree species. New sites can be entered into the system at any level, depending on which Tier's criteria they best meet (Figure 1). By using environmental variation as an indicator of differently adapted populations, it is possible to identify comprehensive networks of sites even in the absence of genetic

information on the species [11]. These sites can then be targeted for field studies, and if found suitable, they can be flagged for conservation planning, seed source development and designation as genetic reserves where appropriate.

The proposed minimum population sizes are indicative and are based on generic genetic theory and the few available studies on the minimum viable population and breeding unit sizes for tropical Asian tree species [12-17]. Large populations of hundreds of reproductive individuals are needed to avoid the negative impacts of genetic drift (random loss of genetic diversity in relatively small populations) and maintain species' evolutionary potential necessary for their long-term persistence (category 'A' sites). Such populations may already be rare for many threatened and socio-economically valuable tree species in Asian countries that have witnessed a rapid loss of natural forest in the past decades. However, attempts should be made to locate and include such remaining large populations, and conserve them as priority. The criteria for the category A sites are directly aligned with the Headline indicator A.4 of the Global Biodiversity Framework (*The proportion of populations within species with an effective population size >500*), enabling countries to report these sites as contributing to the Target.

Population sizes of approximately 50 reproductive individuals correspond to minimum sizes of *breeding units*, required to avoid inbreeding that can otherwise lead to a rapid loss of productivity and adaptive capacity in just a few generations (category 'B' sites). Although these smaller populations are not sufficient for maintaining species' evolutionary potential over longer term, they still have genetic conservation value in Asia's heavily deforested and fragmented landscapes, and are suitable as sources of genetically diverse seed for forest and landscape restoration and tree planting efforts. Even smaller populations of 15-20 unrelated individuals can have conservation value for rare or severely threatened tree species for which few, if any, large populations remain – however, to be defined as *in situ* conservation sites, specific management actions must be planned for such populations to expand their size and enhance genetic diversity (category 'C' sites).

The proposed minimum population sizes should be reviewed and updated as needed as knowledge on the species' genetic diversity and its distributions accumulates.

Species' populations have adapted to their environments through millennia, and distinct populations harbour unique genetic diversity that may not be found anywhere else. The objective of genetic conservation is to maintain such diversity which forms the foundation of species' capacity to adapt, survive and continue providing ecosystem services in current and changing environments. Therefore, what counts is not only the size of conserved and sustainably managed populations, but also their distribution and representativeness of the diversity of environments where the species is found. *Region of provenance* refers to the area (or group of areas) where ecological conditions are sufficiently uniform and where tree stands or seed sources show similar phenotypic or genetic characters [18]. To avoid potentially useful genetic diversity from being lost, species' populations must be conserved within each region of provenance where they occur. Regions of provenance are ultimately species-specific and have been defined only for a handful of species. Other maps depicting environmental variation, for

example seed transfer zone maps<sup>1</sup> or ecoregion maps<sup>2</sup> can be used as proxies for genetic variation, depending on the available planning resources and needs in each country.

For implementing this guideline, the information on species potential distributions across ecoregions, and potential impacts of climate change on the species are drawn from two regional initiatives. The initiative [APFORGIS – Establishing an Information System for conserving native tree species and their genetic resources in Asia-Pacific](#) was implemented from 2017 to 2019 with funding from the Government of Germany through the Federal Office for Agriculture and Food. The initiative [Strengthening collaborative tree seed supply systems for restoration in Asia](#) is implemented from 2022 to 2024 with funding from the UK Darwin Initiative.

## The guidelines

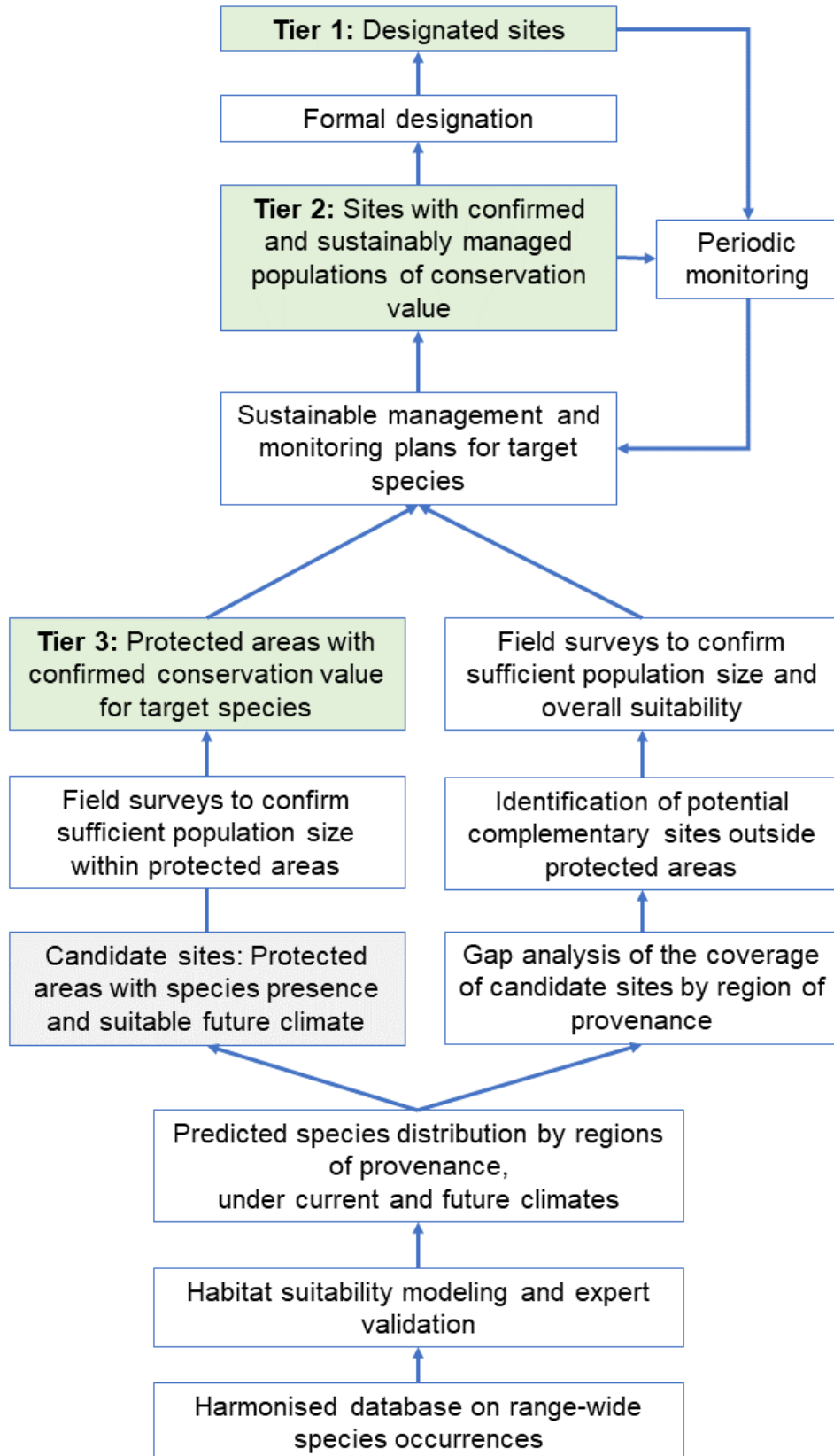
Aspirational targets at the levels of species' ranges, countries and regions of provenance:

- In each region of provenance within each country, there are at least two sites per species in Tiers 1A, 2A or 3A to maintain species' evolutionary potential. At least two sites are required to ensure continuity in case one area is affected by biotic, abiotic or anthropogenic threats.
- Where less than 10% of the species potential distribution within the region of provenance remains, or if the region is predicted to become largely unsuitable for the species under future climates, germplasm collection and *ex situ* conservation are prioritised to avoid permanent loss of genetic diversity. This threshold was selected as a pragmatic target to complement the global target of protecting at least 30% of ecosystems under the Kunming-Montreal Global Biodiversity Framework [9], and to support conservation priority setting in the mega-diverse Asia-Pacific region.

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<sup>1</sup> *Seed zone* or *seed transfer zone* is used as a synonym for region of provenance, and many countries have developed seed zone maps. However, the definitions of seed zones are not necessarily consistent between countries.

<sup>2</sup> Ecoregions are defined as relatively large units of land or water containing a distinct assemblage of natural communities sharing a large majority of species, dynamics, and environmental conditions [19]. Ecoregions may be larger than regions of provenance or seed zones and so not quite as useful as proxies for regions of provenance. However, [a global map of ecoregions](#) exists and so the ecoregion-based approach for zonation can be easily adopted in any country.



**Figure 1.** Process of identifying genetic conservation sites and seed sources.

### **Tier 3: Protected areas with confirmed populations of conservation value**

*Protected area that is predicted to remain suitable for the species under current and future climates and where the target species is confirmed to have at least*

*3A: 500 reproductive individuals (maintaining evolutionary potential) OR*

*3B: 50 reproductive individuals (breeding unit) OR*

*3C: 15 unrelated individuals if the species is rare or threatened*

- **The sites should fall under the IUCN categories for protected areas I or II** (strict nature reserves, wilderness areas or National parks) because species-specific management plans are not available at Tier 3. Small protected areas, with small populations of target species, may require buffer zones to avoid negative impacts on species from land use in surrounding areas.
- **Sufficient regeneration should be present as a sign of population viability**
- Population densities and minimum viable population sizes vary among species depending on their reproductive traits. **The minimum size of a conservation unit can be adjusted based on target tree species** and other considerations as relevant.
- Species that are likely to require relatively larger populations to ensure viability include dioecious species, species that can reproduce vegetatively, species where fecundity varies largely between individuals, and species with strong spatial (genetic) structure.
- Records of field surveys of population sizes are maintained by or accessible to the stakeholder who nominates the site as a conservation unit or seed source.

### **Tier 2: Sites with confirmed and sustainably managed populations of conservation value**

*Protected area, community forest, seed stand or a forest area of otherwise secure tenure where there is a sustainable management plan and monitoring in place for the target species and where the target species is confirmed to have at least*

*2A: 500 reproductive individuals (maintaining evolutionary potential) OR*

*2B: 50 reproductive individuals (breeding unit) OR*

*2C: 15 unrelated individuals if the species is rare or threatened*

- **Other than strictly protected areas can be included** as conservation sites and seed production areas from Tier 2 onwards, because management plans and monitoring are required as a safeguard to ensure sustainability. *Ex situ* conservation sites may also be included under this category. Sites may be prioritised using relevant criteria, including their size, stability, species richness, tenure security, or synergies between conservation and local livelihood needs.
- Sufficient regeneration should be present as a sign of population viability
- Population densities and minimum viable population sizes vary between species depending on their reproductive traits. **The minimum size of a conservation unit can be adjusted based on target tree species** and other considerations as relevant. Depending on the contexts, the unit can also consist of several smaller sub-populations (e.g. forest patches within agricultural landscapes) as long as there is gene flow between them to maintain genetic diversity.
- Where relevant, the **management and monitoring plans should include specific actions to maintain genetic diversity and adaptive capacity** of the target tree species. These may include silviculture techniques such as thinning, selective cutting that

favours random mating, assisted natural regeneration and liberation of regeneration. Management and monitoring plans for Tier 2C sites of rare or threatened species need to include deliberate actions to increase population size to reach the minimum viable population size of 50 reproductive individuals. Early successional species may require specific actions to maintain sufficiently large populations within the landscape as succession of plant communities progresses. Management and monitoring plans are maintained by or accessible to the stakeholder who nominates the site as a conservation unit or seed source.

- For *in situ* conservation sites, natural regeneration should be favoured and assisted where possible. If the site includes artificially regenerated trees of the target species, they should be established using **reproductive material of documented origin that is collected following good seed collection practices**. The reproductive material should be obtained either within the same region of provenance (under similar environmental conditions), or (partly) from a different region of provenance if this is justified to support the population's capacity to adapt to the changing environment.

### **Tier 1: Designated sites with confirmed and sustainably managed populations of conservation value**

*Protected area, community forest, seed stand or a forest area of otherwise secure tenure which is officially designated as a genetic conservation unit, seed source or both, by national or sub-national authorities, and where there is a sustainable management plan and monitoring in place for the target species. The target species is confirmed to have at least*

*1A: 500 reproductive individuals (maintaining evolutionary potential) OR*

*1B: 50 reproductive individuals (breeding unit) OR*

*1C: 15 unrelated individuals if the species is rare or threatened*

- As Tier 2 above, but with a **designated status** (either administrative or legal) as a genetic conservation unit or seed source for the target species.

### **Candidate sites: Protected areas with species presence**

*Protected areas where the target species is confirmed to occur and that are predicted to remain suitable habitat for the species under progressive climate change*

- The purpose of the candidate sites is to allow identification and prioritisation of populations for further analysis so that the sites that fulfil Tier 3 criteria can be more effectively identified.
- Since population sizes of the target species are not known, and sustainable use is not possible without information about population sizes, the considered sites should **fall under the IUCN categories** for protected areas I or II (strict nature reserves, wilderness areas or National parks).
- Identifying and designating *in situ* conservation areas is a long-term effort, and the candidate sites should, therefore, **remain suitable habitat for the species during progressive climate change**<sup>3</sup>. Species populations in protected areas that will likely

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<sup>3</sup> Information on predicted climate change impacts by 2050 is currently available for 63 tree species through project APFORGIS [20].

become unsuitable habitat for the target species in future should be prioritised for *ex situ* conservation.

- After identification of candidate sites, the next step is to conduct field studies to confirm population size that enables moving the sites to Tier 3. Candidate sites may be prioritised for field surveys using relevant criteria, including their size, stability and species richness

## Documentation

A regional, freely and publicly accessible database of genetic conservation sites and seed sources needs to be maintained to enable range-wide assessments of genetic conservation status and appropriate conservation and restoration planning. The database could be directly established and managed by a regional or international entity. In Europe, the European Forest Genetic Resources Network (EUFORGEN) manages such a regional database (<http://www.eufgis.org/>), consisting of information on over 100 tree species across 35 countries and almost 4000 tree populations. Alternatively, since the regional guidelines allow harmonized and comparable information, a regional database could also draw data from national or institutional databases, similarly to the Global Biodiversity Information Facility (GBIF, [www.gbif.org](http://www.gbif.org)). National Coordinators of APFORGEN, forestry authorities, conservation practitioners and other relevant stakeholders who own or manage forest areas can nominate sites for inclusion in the database by submitting relevant documentation. Exact location of sites does not need to be published for sensitive species. However, location and description of sites by region of provenance should be available upon request to support range-wide conservation planning and related research of the target tree species.

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