EUFORGEN
EUROPEAN FOREST GENETIC
RESOURCES PROGRAMME

DYNAMIC AND STATIC *EX SITU* CONSERVATION

MINIMUM REQUIREMENTS, DATA STANDARDS AND INDICATORS FOR MONITORING

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The European Forest Genetic Resources Programme (EUFORGEN) is an instrument based on international cooperation which promotes the conservation and appropriate use of forest genetic resources in Europe. It was established in 1994 to implement Strasbourg Resolution S2 adopted by the first Ministerial Conference of the FOREST EUROPE process, held in France in 1990. EUFORGEN also contribute to the implementation of FOREST EUROPE Madrid Resolution M2 and Bratislava Declaration regarding forest genetic resources and relevant decisions of the Convention on Biological Diversity (CBD). In addition, EUFORGEN contributes to the implementation of regional-level strategic priorities of the Global Plan of Action for the Conservation, Sustainable Use and Development of Forest Genetic Resources (GPAFGR), adopted by the FAO Conference in 2013. The Programme brings together experts from its member countries to exchange information and experiences, analyse relevant policies and practices, and develop science-based strategies, tools and methods for better management of forest genetic resources. Furthermore, EUFORGEN provides input as needed to European and global assessments and serves as a platform for developing and implementing European projects. EUFORGEN is funded by the member countries, and its activities are mainly carried out through working groups and workshops. The EUFORGEN Steering Committee is composed of National Coordinators nominated by the member countries, and the EUFORGEN Secretariat is hosted by the European Forest Institute (EFI). Further information about EUFORGEN can be found at www.euforgen.org.

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PREFACE

The conservation of forest genetic resources (FGR) is the foundation towards the sustainability and resilience of European forests. While *in situ* conservation remains the gold standard for long-term genetic preservation, there is growing recognition that *ex situ* approaches can assist and play a complementary role either in a dynamic or, in certain cases, a static form. Biotic and abiotic threats such as pests, diseases, wildfires, floods, habitat loss, and climate change have been increasingly challenging the survival of the natural populations, thus the need to safeguard genetic diversity outside the native population ranges has become essential.

The European Forest Genetic Resources Programme (EUFORGEN) presents the report "*dynamic and static ex situ conservation*", a report developed through the collective expertise of the EUFORGEN network who are engaged in the conservation of forest genetic resources. Building upon decades of experience, it seeks to clarify terminology, establish minimum requirements and data standards, propose indicators and provide guidance for both dynamic and static *ex situ* approaches, supporting European and national conservation strategies. This report comes at a time when integrating *ex situ* efforts into broader European strategies has become increasingly urgent.

It offers practical insights into the diverse forms of *ex situ* conservation currently implemented across Europe: from living collections and seed orchards to cryopreserved germplasm, and it proposes terminology for genetic conservation units at risk. Through illustrative case studies of different European countries, it highlights national practices and emphasizes the need for European joint strategies that integrate dynamic evolutionary processes with secure long-term storage. These examples demonstrate both the diversity of national contexts and the shared challenges across Europe.

The report also advances the discussion on how *ex situ* conservation can be meaningfully monitored and aligned with pan-European efforts, including the Forest Europe framework of criteria and indicators for sustainable forest management. By proposing harmonized definitions, indicators, and principles, this document contributes to a more coordinated and effective European system for the *ex situ* conservation of forest genetic resources, serving as a complement to the existing *in situ* conservation effort. This alignment supports reporting and policy coherence under European and international frameworks.

This report was prepared by the EUFORGEN Working Group on dynamic and static *ex situ* conservation, following the mandate of the EUFORGEN Steering Committee. The Working Group conceptualised the mandate and drafted, developed and consolidated the main report. The subchapter "Relocation strategy to conserve genetic conservation units at risk" was prepared by another Working Group, whose technical report is included as an annex to this document. The EUFORGEN Steering Committee provided valuable feedback throughout the process and formally adopted the final report.

This document is intended to serve multiple audiences: policymakers developing national conservation strategies, forest managers implementing conservation programmes, researchers advancing the scientific basis for genetic conservation, and technical staff responsible for day-to-day operations of gene banks and genetic conservation units.

It ensures that European forests retain the genetic resilience and sustainability required to adapt to the future challenges and lays the groundwork for future integration of *ex situ* conservation data within EUFGIS and other European systems. The successful implementation of these guidelines will require continued collaboration among European countries, sustained institutional support, and ongoing dialogue between conservation practitioners and the scientific community.

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1. INTRODUCTION

1.1 Background

Forest genetic resources (FGR) are primarily conserved *in situ* because this allows individuals in the population to interact and respond to biotic and abiotic selective pressures over the long term and to adapt to changing environments by means of sexual reproduction and adaptive plasticity. Dynamic *in situ* conservation is most effective for tree species that have a continuous distribution and stand-forming character such as Norway spruce and Scots pine.

However, *ex situ* genetic conservation can be part of an effective FGR conservation programme in cases where *in situ* conservation is either impossible (e.g., when a species does not form natural populations) or is no longer effective (e.g., in case of heavy outbreaks of pests or diseases, habitat loss, or rapid population decline resulting from climate change). *Ex situ* conservation may be the most effective conservation method in the following cases:

- Conserving tree species with **scattered abundance** and **small natural population sizes** such as elms or wild cherry. In such cases, very large genetic *in situ* conservation units would be necessary to capture the diversity of the gene pool.
- **Rapidly changing environments.** This is especially the case where abiotic factors (e.g., droughts) or biotic outbreaks (e.g., ash dieback or Dutch elm disease) are increasingly intense or frequent. Such conditions would result in high levels of mortality and consequent rapid loss of genetic diversity before the population could reach a new adaptive equilibrium state.
- Tree species capable of **hybridization with domestic species** such as wild cherry, wild apple or wild chestnut. In such cases, it would be very difficult to avoid genetic contamination from nearby fruit orchards.

Consequently, *ex situ* conservation methods are already in use in many countries to complement dynamic *in situ* conservation and their importance may significantly increase in the future.

There is a wide range of *ex situ* conservation methods, from stands of a species outside of its natural habitat to seeds stored in a cryo bank or in a seed bank. Because of its versatility, *ex situ* genetic conservation is a complex field and different aspects need to be taken into account before an *ex situ* programme can be started. *Ex situ* conservation requires thorough knowledge, continuous development, and crucial infrastructure so that its full potential can be exploited.

The applicability of *ex situ* conservation has not always been recognized by practitioners, for instance in forest or landscape restoration efforts where genetic knowledge and good record keeping of the origin may be required (e.g., Jalonen *et al.*, 2018; Jones, 2013). As a result, there is a particular need for *ex situ* gene banks that can provide readily available material and conservation stocks to support restoration efforts with autochthonous or locally adapted forest reproductive material (FRM).

Efforts to effectively integrate and combine *in situ* and *ex situ* conservation methods can be fundamental for effective and lasting conservation. While considering costs and benefits of *ex situ* conservation efforts to complement *in situ* conservation, decisions should be guided by evaluating the general threats to the species considered, the threats to each population within the species, any associated risks, the population's significance for overall conservation, the presence of other conserved populations, and the available infrastructure.

1.2 Goals of the report

FGR have been conserved *ex situ* in Europe since the beginning of the twentieth Century. However, there are nearly as many approaches, purposes, and reasons for *ex situ* conservation as there are countries in Europe. Although the general principle is largely the same among all countries (i.e., genetic resources are taken from their natural environment and transplanted or stored in another place), there can be large differences in the ways *ex situ* conservation is considered theoretically and realized in practice.

The overarching goal of this report is to lay out the theoretical foundations and defining principles concerning *ex situ* genetic conservation.

The detailed goals are to:

- give an overview on *ex situ* genetic conservation practices in Europe;
- define important terms and types of *ex situ* genetic conservation;
- address challenges and risks of *ex situ* genetic conservation;
- evaluate existing fundamentals for dynamic *ex situ* genetic conservation;
- develop fundamentals for static *ex situ* genetic conservation;
- develop minimum requirements, data standards, indicators for monitoring; and
- make recommendations for further development and implementation of *ex situ* genetic conservation.

1.3 *Ex situ* conservation justification

Seed is critical to the global food and agriculture system – it is stored and then transported for planting or is eaten as food and used for animal feed. Similarly, clonal plant material is a key element in production of many crops, such as fruit trees. This direct utilization of plant genetic resources depends on material being available for deployment and future breeding.

In this context, *ex situ* conservation is an essential component of agriculture and indeed biodiversity conservation. However, *in situ* genetic conservation is the gold standard for conservation. Only in rare cases is *ex situ* conservation the only option, for example, where there is no longer suitable habitat for a species.

The focus of this report is on wild forest species, some of which are of economic importance while others are not necessarily recognized as economically important. In general, and certainly for seed, the space and resources needed for *ex situ* conservation is much less than that needed for *in situ* conservation. *Ex situ* conservation can thus be used to:

- conserve range wide genetic diversity or marginal and peripheral populations;
- help conserve species/populations threatened by biotic or abiotic outbreaks; and
- conserve clones with specific traits (e.g., special forms or characteristics).

2. CASE STUDIES OF *EX SITU* GENETIC CONSERVATION

2.1 Living collections and cryopreservation in elms (Finland)

Jan-Peter George, Luke, Finland

European white elm (*Ulmus laevis* Pall.) is a broadleaved tree species that is typically rare in Europe and considered endangered in Finland. The core population in Finland is believed to consist of no more than 7 000 trees, including saplings, and is restricted to a small area (20 x 100 km) along a lake and river system in the south of the country (Vakkari *et al.*, 2009). There are also some smaller and more fragmented populations along the Finnish Baltic Sea coast. Molecular analyses suggest that isolation-by-distance has strongly shaped the genetic structure of this marginal white elm population.

Although *Ulmus laevis* is strictly protected by law under the Finnish Nature Conservation Act, there is a clear need for a national programme to safeguard and maintain genetic diversity in this extremely rare species. Currently, *Ulmus laevis* in Finland is conserved *ex situ* in two living collections comprising genotypes that were collected from across the national distribution (Figure 1). The collections consist of 117 grafted clones and 1–10 ramets per clone. The collections serve as a safety back-up for each other. The collections are dynamic, in that they capture a substantial part of the neutral and adaptive diversity of the species, but also strongly enhance gene flow and allow selection to operate within the artificially created living collections. However, since there are also immediate threats to elm populations in Finland (e.g., Dutch elm disease), these dynamic collections are complemented by static cryopreserved collections (Välimäki *et al.*, 2021). This permits a nearly unlimited number of genotypes to be stored and safeguarded over very long time without facing risks of biotic outbreaks or rapid population decline. Nevertheless, a crucial step in cryopreservation of elms is regeneration of genotypes via multiplication. In the Finnish conservation programme more than 80% of the conserved elm genotypes have been successfully regenerated after cryopreservation and the method is under continuous improvement (for details see Välimäki *et al.*, 2021).

2.2 Conservation of germplasm as part of a breeding strategy of *Picea abies* (Norway)

Irena Fundova, NIBIO, Norway

Norway spruce (*Picea abies* (L.) Karst.) is the most commercially significant forest tree species in Norway, accounting for 75% of total timber production. It is also the only species with a comprehensive national breeding programme, run by the Norwegian Forest Seed Center (Skogfrøverket).

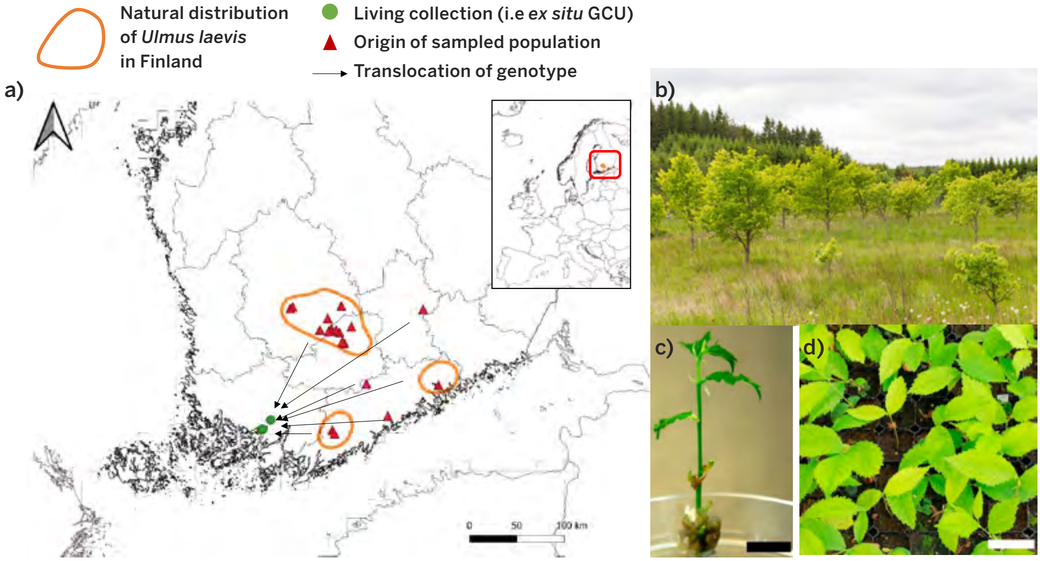

Figure 1. **a) Distribution of European white elm in Finland and location of *ex situ* genetic conservation units (source: Jan-Peter George). b) (source: Erkki Oksanen, Luke). c), and d) pictures extracted from Välimäki *et al*, 2021.**

It aims to supply seeds for establishing new forests with improved growth and wood quality, increased CO_2 sequestration, and higher resilience to climate change and pathogens, without reducing their genetic variation (Edvardsen *et al.*, 2017).

The breeding programme started during 1950s with the selection of phenotypically superior trees, so-called “plus trees”. The plus trees were grafted and planted in first-generation seed orchards to mass-produce seed for reforestation and clonal archives that have served as collections of valuable genotypes. Subsequently, multi-environmental progeny tests were established with the aim of verifying the plus trees’ genetic superiority through the partitioning of their total phenotypic variance into environmental and genetic components, the latter of which is heritable and thus can be passed on to the next generation. Based on the tests’ results (i.e., estimated parental breeding values), a new round of seed orchards was established with refined selections, resulting in so-called 1.5th-generation orchards.

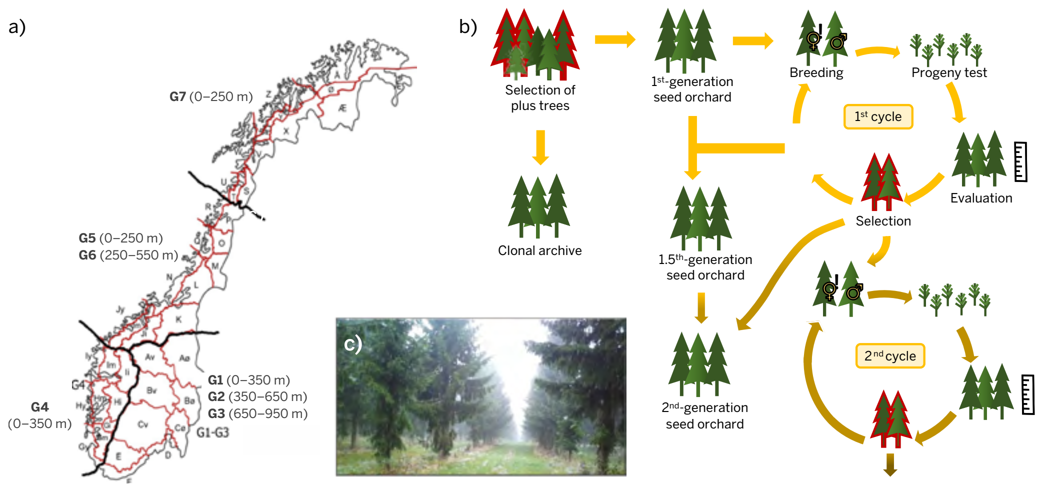

Figure 2. a) Map of Norway spruce breeding and provenance zones (black and red lines, respectively). Note: The breeding zone G0 overlaps with zones G1 and G4 with expected increased temperature by 2°C (Fjellstad & Skrøppa, 2020). b) Diagram of a forest tree breeding programme, adapted from Skogfrøverket (2017). c) Sanderud Norway spruce seed orchard. Photo: Arne Steffenrem.

Second-generation material is now in some cases selected directly from the initial progeny trials. In other cases it is selected from families from controlled crosses among the refined selections of the first generation (Figure 2.).

Around 4 000 plus trees have been tested and the long-term Norway spruce breeding population consists of around 1 100 individuals as parents to each new generation. For a breeding programme to be successful, it is fundamental to maintain a sufficient level of genetic variation, and the breeding population is thus divided into 22 subpopulations, each with 50 unrelated founders (Edvardsen *et al.*, 2017).

To ensure appropriate environmental adaptation of the reproductive material, the country is divided into eight breeding zones (G0 to G7) and further into one or more subzones (Figure 2.) The division follows population history and known climatic variation (Fjellstad & Skrøppa, 2020). Provenance trials encompassing germplasm from different geographic locations help the breeders understand adaptive processes and develop general seed transfer guidelines. Aside from local and other Nordic provenances, some trials also contain provenances from other regions, e.g., Central and Eastern Europe. In light of anticipated climate change, the information they bring is highly relevant.

Seed orchards, clonal archives, and long-term progeny and provenance trials are an integral part of the national breeding programme and represent important *ex situ* gene conservation units. To date, there are 16 Norway spruce seed orchards in Norway with a total area of more than 110 hectares (Myre et al., 2021). Together, these supplied around 95% of all seedlings planted in Norway in 2022. In addition, there are eight Norway spruce clonal archives, 167 operative progeny trials and 20 operative provenance trials (Skogfrøverket, 2021).

The Norwegian Forest Seed Centre also has a seed bank for static *ex situ* conversation. Since 2006, it has stored batches of seeds from various breeding zones and aims at maintaining germination capacity above 89%. Reference samples from older seed lots are also available. The most valuable accessions are kept at the Svalbard Global Seed Vault.

2.3 Seed orchard for conservation of *Malus sylvestris* (Belgium)

Eléonore Scholzen, Public Service of Wallonia, Belgium

The wild or forest apple, *Malus sylvestris* (L.) Mill., is found across most European countries. It is a rare, scattered species that is often found as single individuals or in small groups. Between 2003 and 2006, the Belgian Science Policy Office funded a study of Belgian apple biodiversity to determine the distribution of the wild apple in the country and to evaluate the occurrence of hybridization between wild and cultivated species in order to develop a programme for the long-term conservation of the species. About 700 trees were identified in the Walloon region. These have been analysed using phenotypic and microsatellite classification to distinguish between the wild, hybridized, and cultivated individuals. The wild individuals showed a structuration of their gene pool that corresponded to four different regions of provenance (North of Sambre & Meuse line, Low plateau of the Meuse, Ardenne and Gaume). Between 60 and 70 genotypes have been selected from across each region to represent the genetic variability of the population of origin, resulting in a core collection of 201 genotypes. This core collection has been sampled to be grafted and cloned (Jacques *et al.*, 2003, 2009).

These clones were planted in 2007 in a conservation seed orchard located in Philippeville, on a property belonging to the administration of Walloon region. Five copies of each genotype have been produced and planted randomly to maximize gene flow. All the individuals have been labelled to facilitate the identification of the clones. A full inventory of surviving trees is conducted every year. The orchard is closely monitored for pests and diseases and maintained to maximize the production of fruit and seeds.

2.4 Synthetic population of *Prunus avium* (France)

Aurore Desgroux, INRAE, France

Wild cherry (*Prunus avium* L.) is well spread throughout Europe from Ireland to the Caucasus and from Scandinavia to Spain, although it is rarer in the Mediterranean region and cold areas. Wild cherry is a scattered species where the notion of stand is different from that for social species. In most cases, these are isolated stems, scattered clusters, or edge stands. Clusters are often composed of one or a few genotypes because of its strong suckering ability.

Various threats can affect genetic diversity of wild cherry including: intensive harvesting of adult mature trees for their wood, impacting seed production and regeneration; sylvicultural practices that favour oak or beech trees reducing the number of wild cherry trees; genetic pollution due to transfer of seed from a few areas and/or with dubious origins (e.g., distilleries and jam factories); collection of seeds from a small number of seed stands; phenotypic selection for homogenous stands; hybridization with cultivated sweet cherry; and pests and diseases (Collin *et al.*, 1998; Russel 2003).

Wild cherry is rare in some parts of France (e.g., Britany) and a conservation programme was started in the 1990s (Collin *et al.*, 1998).

New "synthetic populations" were created for Britany and the Occitan region using seeds from multiple sites in each area (Figure 3). The resulting synthetic populations thus represent the genetic diversity of the area. Seeds were collected from one to four mother trees in 25 sites in Britany and 16 sites in the Occitan region. Mother trees selected were at least 50 m apart to avoid suckers and at least 1 km away from any sweet cherry orchards or planted wild cherry stand to avoid hybrids. In 1997, seedlings from 35 families in Britany and 33 families in Occitan, with about 35 seedlings per family (a family comprises descendants from the same mother tree). Since then, plantations have been maintained by weeding in the early years.

Mortality and health surveys were carried out in 2002, 2006, and 2011 to check if all families were still represented in the gene pool. Silvicultural practices have been implemented with the objective of maintaining wild cherry and favouring its regeneration.

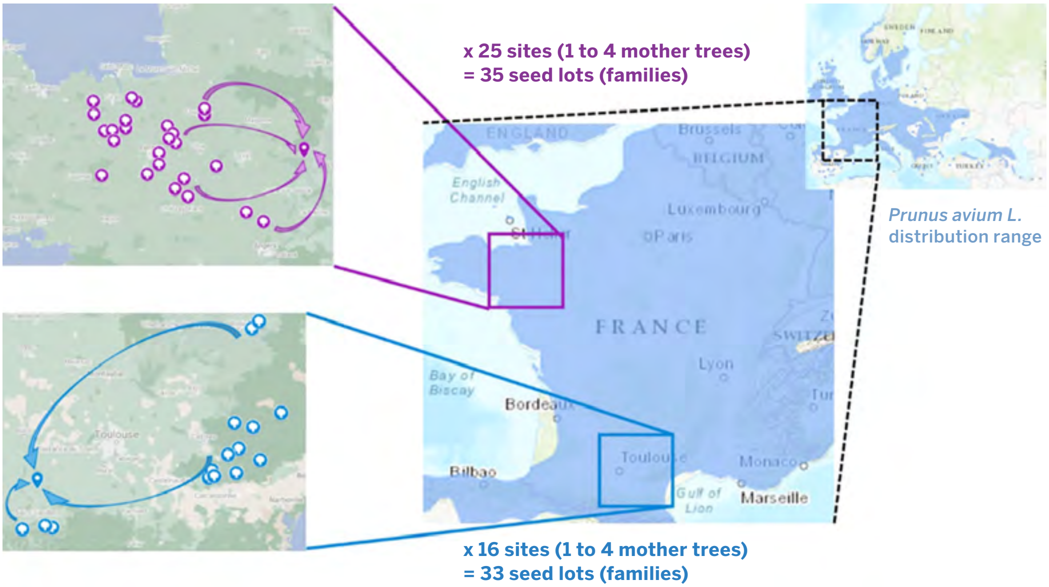

Figure 3. **Sampled sites and planting sites for dynamic *ex situ* conservation of *Prunus avium* in Britany (purple) and in the Occitan region (in blue).** *Source:* Aurore Desgroux (Distribution range map of wild cherry extracted from https://commons.wikimedia.org/wiki/File:Prunus_avium_range.svg).

2.5 Translocation of European larch (*Larix decidua*) from natural mountainous habitats to sites in the lowlands as an example of dynamic ex situ conservation (Switzerland)

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European larch occurs in the Swiss Alps, mostly above 1 400 m a.s.l. The continental climate conditions in the inner Alpine valleys suits its habitat preferences. It is a light-demanding species that regenerates on disturbed sites and on mineral soils. European larch was translocated to the lowlands of Switzerland for forestry purposes. It now grows well and is regenerating naturally where soil conditions, the climate, and forest management suit its habitat preferences. This can be observed in a region of about 150 km^2 in northern Switzerland (500–600 m a.s.l.), where it is believed larch planting started about 150–200 years ago. There, a population outside European larch's natural range has established, is regenerating naturally and is evolving. Although the original provenance of the population is unclear, this stable population may have differentiated by adapting to the lowland site conditions and therefore conserve valuable genetic variation. This case is on the limit of *in situ* conservation and shows that the delimitation between *in situ* and *ex situ* conservation has a transition range.

2.6 Living collections in botanic gardens and arboreta (United Kingdom and Ireland)

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Living collections of trees in botanic gardens can perform multiple functions for conservation. For example, they can be used to maintain the genetic diversity of living material for safe-keeping and propagation and the material can also be utilized for education and awareness purposes. Botanic gardens often have limited space and thus maintain limited numbers of individuals. However, conservation of individuals or small populations might be the only option, particularly with rare species.

One stand-out example of conservation in botanic gardens and arboreta is the *ex situ* work undertaken by the International Conifer Conservation Programme (ICCP), which is based at the Royal Botanic Garden Edinburgh (Gardner, 2021). The ICCP aims to broaden the genetic base for a selection of threatened conifer species. A key element in the *ex situ* component of the ICCP is to set up so-called “safe sites”. These sites must have a secure future and sufficient space for planting replicates of the material. The result of the ICCP is a network of sites across the UK and Ireland with a suite of endangered conifer species. One aspect of the ICCP stresses the importance of keeping records of provenance of the material (Maunder *et al.*, 2001).

An important finding of the ICCP work is that emphasis needs to be put on aftercare of the plants. Setting up an *ex situ* collection alone does not guarantee success. These collections need to be maintained and assessed on a regular basis. One target species is the rare conifer *Fitzroya cupressoides* (Mol.) Johnst., which is rare and restricted to temperate rainforests in northern Patagonia (Premoli *et al.,* 2000). Although this species was growing in isolated *ex situ* collections in Britain and Ireland, the material was shown to be from a single female clone. To increase the value of these *ex situ* collections, more than 100 genotypes were collected and distributed across multiple sites (Figure 4), thus bolstering the potential of this *ex situ* collection (Gardner, 2021).

Figure 4. **A map showing the locations of the ICCP *Fitzroya cupressoides* “safe sites” across Britain and Ireland.** *Source:* Modified from Gardner, M.F. (2021).

2.7 Ex situ conservation of genetic diversity in ash (*Fraxinus excelsior L.*) (United Kingdom)

Jan-Peter George, Luke, Finland

Ash (*Fraxinus excelsior* L.) is a stand-forming tree widespread across Europe. However, in the past 15 years in particular, populations have been impacted by the spread of ash dieback, which is caused by the fungal pathogen *Hymenoscyphus fraxineus*. As an economically important species, and with the onset of the threat from this fungal pathogen, there has been an increased focus on this species to try to halt the progress of the disease and to try to select for resistant genotypes. In addition, there is a need to capture the genetic diversity of this species before it is decimated by the disease.

There are a number of sampling options to capture genetic diversity. Direct measurements of genetic or phenotypic diversity can be used if they are known, but often this is not known, and an alternative is to use geographic or environmental proxies. As an example, environmental proxies were used to establish a core network of conservation units for forest trees across Europe (De Vries *et al.*, 2015).

The UK National Tree Seed Project aimed to develop a representative collection of *Fraxinus excelsior* seed in the UK by using simulations and geographic data to guide sampling protocols (Hoban *et al.*, 2018). The approach taken was to build a demographic-genetic model based on forest inventory data, run a simulation model to produce a distribution of trees and their genes from which to select populations across the range based on allele frequencies, and to compare the selected populations with the overall dataset. The simulations and tests calculated that the sampling strategy would capture 90% of all alleles.

The UK has 24 seed zones, characterized based on biogeography and environmental variables, and the national protocol aims to collect seed from all 24 zones. The local sampling protocol aims to capture genetic diversity of autochthonous material in local populations or "target collections", which may represent fragmented populations. The protocol for local populations/target collections is to collect from at least 15 trees, with sampled trees being at least 50 m apart. The number of trees sampled is a compromise between maximizing genetic capture and physical effort. Seed is taken from across the entire canopy, with the goal being to collect 10 000 viable seed per population, sufficient for seed storage and experimentation. The simulations were also used to test the "return" in collecting additional seed from an individual versus collecting from an additional mother tree (see Figure 5). Collecting from additional mother trees gives a greater return than collecting more seed from an individual tree. The overall approach highlights the use of simulations in developing sampling strategies, in particular where limited resources are available to undertake regional genetic characterization.

2.8 *Ex situ* conservation of *Abies nebrodensis* (Italy)

Written by **Fulvio Ducci, CREA, Italy**

Abies nebrodensis Lojac. Mattei, also known as the Sicilian fir, is a species at very high risk of extinction, being represented by only a single very small relict population of about 30 individuals spread over about 150 hectares at 1600–1800 m altitude on the Madonie mountain range in northern Sicily (IUCN, 2017). It is classified as CR-D, Critical Danger, in the IUCN (International Union for Conservation of Nature) Red List of Endangered Species.

This small population has been systematically inventoried and monitored since the early 1960s, and this has continued with the establishment of a regional park and an integral reserve.

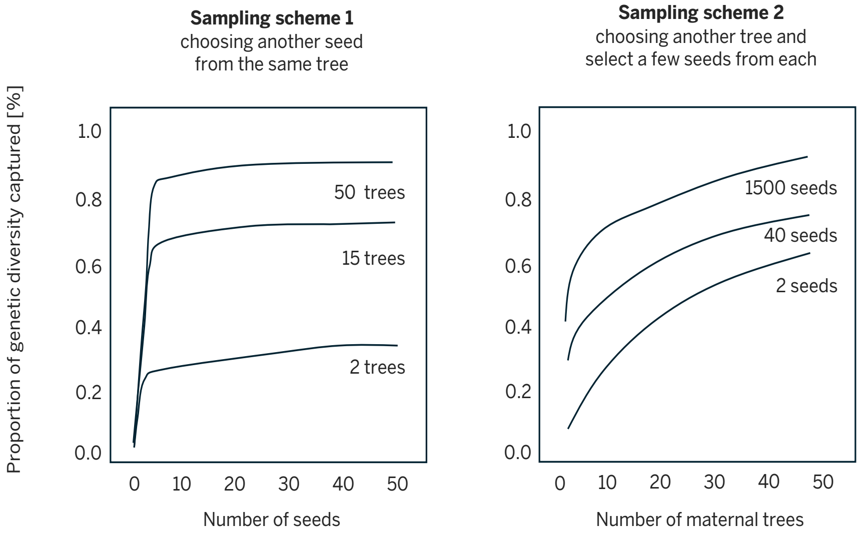

Figure 5. **Graphs used to show the diminishing returns of gathering additional seeds versus additional maternal trees.** *Source:* Based on results of Hoban, S., Kallow, S., & Trivedi, C. 2018.

Since this establishment, grazing has been suspended, and the plants have been individually protected and have started to grow again and produce cones. However, there are serious problems *in situ*. Natural regeneration is almost absent or very limited due to adverse environmental conditions linked above all to soil degradation, reduced seed germination, and intense autogamy phenomena determined by the spatial and genetic structure of the population. Moreover, the local microclimate is also changing rapidly and does not favour the survival of seedlings. Despite these adverse factors, the original population still has good levels of genetic variability, albeit with high homozygosity. This offers hope for restarting the evolutionary genetic dynamics in potentially favourable conditions. The difficult conditions *in situ*, which strongly suggest worsening chances of survival for the fir, have convinced the scientific world to start research, experiments, and *ex situ* conservation programmes.

A long-term experiment of assisted migration was started in 1993 by the CREA Research Centre for Forestry and Wood of Arezzo. The experiment is structured in various phases. The first, initiated after the initial genetic studies, was the establishment in the northern Apennines of an arboretum from clonal seed created with grafted copies of all the genotypes of the original population. The aims are to create conditions tending to panmixia, reducing the originally high levels of homozygosity, to produce seed to be reintroduced in Sicily, to conserve the original gene pool *ex situ*, and to create a dynamic population in a specially chosen site. The genetic structure, the adaptive traits, and any epigenetic phenomena are being monitored in the new site. At the same time, the possible genetic contribution of collections of Sicilian fir seedlings created *ex situ* in the past is being studied.

Around the beginning of the 2000s, a similar programme was started in Sicily by the Department of Botany of the University of Palermo. This subsequently led to a collaboration with the CNR-IBE Institute for BioEconomy in developing controlled crosses between the original genotypes, testing methods of somatic embryogenesis, and creating a cryopreserved pollen and tissue germplasm bank.

It is hoped that in subsequent phases the two lines of research and experimentation can proceed in close connection.

The species seems to be slowly recovering, thanks also to intense dissemination and interaction efforts with the local communities.

Mast cone production in a grafted genotype of *Abies nebrodensis* →

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3. *EX SITU* GENETIC CONSERVATION

3.1 Definitions

The following terms are defined for the purposes of this report:

An **arboretum** is a collection of tree or shrub species, their varieties, and/or growth forms. These are typically represented by only a small number of specimens, as arboreta are primarily established for education purposes.

A **clonal archive** is a collection of vegetatively propagated accessions that is maintained *in vitro* or *in vivo* for the purpose of genetic conservation and/or breeding. An *in vivo* archive is usually created by grafting scions collected from mother trees (ortets) onto appropriate root stocks and typically consists of several copies of the same accession (ramets).

A **family archive** is a collection of generatively propagated mother trees from which open- or control-pollinated seeds were collected and thus represent half- or full-sib progenies, respectively. The offspring can further be replicated *in vitro* or *in vivo* to ensure the survival of each new accession.

Autochthony refers to adaptedness to local environmental conditions and genetic distinctiveness. It is most likely realized by long-term local genealogical continuity (Kleinschmidt *et al.*, 2004).

A **gene bank** is a repository whose purpose is to conserve genetic materials. It consists of a set of individuals or populations and can exist in several forms, such as living collections of individuals or clones, *in vitro* collections on agar or in cryopreservation, dormant seed collections, and pollen collections.

A **seed bank** is a category of gene bank in which the genetic diversity is preserved in the form of dormant seed.

A living collection is an individual or a group of individuals-maintained *ex situ* that retains the capability of generating and providing biologically active genetic material in the future.

Cryopreservation is a specific conservation technique where cells or tissues are dehydrated, frozen, and conserved at very low temperature (typically at -196°C in liquid nitrogen).

Germplasm refers to any type of genetic material such as plants (or their parts), seeds, pollen, or cultured tissue. In the context of genetic conservation, it comprises forest genetic resources that are maintained to preserve the existing genetic variability within and among populations.

***Ex situ* accession** refers to a forest genetic resources sample with known origin stored in a stand (e.g., non-native genotypes in planted conservation stands), a gene bank (e.g., seed, pollen, dormant bud, any other form of germplasm), or a living collection of genotypes (e.g., conservation orchards, clonal archives).

***Ex situ* conservation of FGR** refers to the conservation of FGR outside their natural habitats or away from their population origins. It consists of stands and clone collections established with collected or multiplied genetic material.

***Ex situ* conservation unit** generally refers to a combination of an *ex situ* accession and the place where it is being conserved, stored, or maintained (i.e., the location of the gene bank, the location of the living collection). The name of the unit serves as a unique identifier, which is used at national or international level for data reporting.

Dynamic *ex situ* conservation permits evolutionary processes to operate over time according to environmental conditions, leading to changes in the genetic structure of populations from one generation to the next. Dynamic *ex situ* conservation can prepare populations/species for adaptation to predicted future conditions, and for non-native species in particular it can promote evolutionary adaptation to a new environment. Examples of dynamic *ex situ* conservation include “living collections” and “*ex situ* conservation stands,” which may consist of a defined minimum number of unique and representative individuals (see minimum requirements) from each origin or accession transplanted to another site within the country or to another country. The populations composed of a single origin may include translocated populations, seed orchards, or other conservation methods. Populations composed of several origins may be represented by synthetic populations, seed orchards, or other approaches.

Static *ex situ* conservation aims to conserve the allelic, genotypic, or phenotypic diversity existing at the time of collection but does not permit population genetic processes to happen. This can be achieved through various methods, such as long-term storage of seeds, pollen, tissues, or by vegetative propagation.

National (or subnational) *ex situ* conservation programme/system/framework for FGR refers to a higher-level conservation programme comprising one or several species and coordinated by a national institution. Such a programme is often based on a combination of several *ex situ* conservation stands, gene banks, and collections.

Origin is the precise location where the genetic material was collected.

A **population** is a group of individuals from a species which are geographically isolated from other populations, leading to reproduction between the individuals of that population being favoured relative to individuals of neighbouring populations. Therefore, a population has its own properties such as genotypic and allelic frequencies.

A **synthetic population** is a population created with several accessions originating from several different locations that are planted together with the aim of creating a new population with multiple origins. This can be applied, for example, if there are only a few remaining trees in each population or if trees are too far away from each other to be able to mate.

A **subpopulation** is a distinct, localized group of individuals within a larger population that experiences limited gene flow with other groups, often due to geographical or ecological barriers. These subpopulations act as local interbreeding units, meaning they share a common gene pool, but genetic differences can arise over time.

A **translocated population** is a population created from several accessions sampled within the same population of origin but planted at another site. It can be applied, e.g., if the population is threatened by biotic or abiotic factors.

3.2 *Ex situ* conservation methods and characteristics

Table 1 lists the dynamic and static *ex situ* conservation methods and their characteristics considered in this document.

Table 1. Dynamic and static *ex situ* conservation methods and their characteristics considered in this document

Ex situ conservation methods	Reference One population	Reference Several populations	Dynamic	Static
Translocated population	x		x	
Seed orchard	x	x	x	x
Synthetic population		x	x	
Seed lot/seed gene bank	x	x		x
Clone/family archives *in vivo/vitro*	x	x		x
Pollen archive	x	x		x
Arboreta/Botanical gardens	x	x	x	x

Additionally, other *ex situ* conservation efforts are ongoing at the national and international levels, maintained by different communities such as Botanic Gardens Conservation International. These efforts include botanic gardens, arboreta, and individual tree conservation in parks and gardens.

3.3 Challenges and risks of *ex situ* genetic conservation

Challenges (What should we think of before we start a new *ex situ* genetic conservation programme or revise an ongoing programme?)

Technical challenges

Technical challenges include all challenges related to feasibility and implementation of *ex situ* conservation. They occur for both dynamic and static *ex situ* conservation approaches and include, for example, missing or unsuitable infrastructure, lack of suitable land, inadequate financial resources, etc. Dynamic *ex situ* conservation requires knowledge of species biology and reproduction systems and also depends on the available infrastructure (e.g., greenhouses) and skills (e.g., skilled nursery staff.). Static *ex situ* conservation faces similar challenges, but the technical requirements are often even higher than for dynamic conservation: If and how long seeds can be stored, for instance, depends on whether the species is considered recalcitrant (e.g., oaks) or orthodox (e.g., European ash). Whether a species can be preserved by means of cryopreservation depends also on anatomical issues of the species itself: for example, if the plan is to collect dormant buds it should be determined beforehand whether anatomical features of the species could create problems (e.g., woolly filaments of the bud leading to fungal contamination). Existing literature provides information on such technical problems for many tree species and should be consulted before the conservation programme starts.

Conceptual challenges

Conceptual challenges are related to the general objective(s) of the planned *ex situ* conservation programme. It is always possible to conserve something somewhere, but the efficiency and effectivity of the planned conservation activities should be considered in relation to specific conservation goals. Important questions include why *ex situ* genetic conservation was chosen and whether available financial resources allow long-term maintenance of the programme.

Conceptual challenges can be formulated as simple general questions:

What is the target of the *ex situ* conservation programme?

- → An entire species (throughout its distribution range)?
- → Several populations?
- → A single population?
- → A few individuals?

What type of genetic diversity is addressed in the programme?

- → Neutral diversity?
- → Adaptive diversity?
- → Phenotypic diversity?
- → Rare alleles?
- → Rare forms or ecotypes?

These are just a few questions that may help to better define the desired conceptual *ex situ* conservation framework. For instance, capturing mainly rare alleles in a species requires different sampling strategies to those for preserving the average allelic composition of a species across its distribution. Other conceptual challenges can relate to the long-term genetic integrity and maladaptation of populations or subspecies when conserved dynamically *ex situ* (e.g., gene swamping, introgression, or pollen contamination).

Risks (What can affect the success rate of an ongoing *ex situ* genetic conservation programme?)

Technical risks

Technical risks can determine the success of both dynamic *ex situ* conservation (e.g., clones die after a short time because of wrong grafting techniques) and static *ex situ* conservation (e.g., the cryotank runs out of cooling media). Technical risks usually have a big impact, because they often affect the entire conservation unit. Technical risks can be minimized, when the infrastructure is well organized and when required skills are continuously available.

Abiotic/biotic risks

Abiotic and biotic risks most often refer to the environment in which the *ex situ* conservation unit is situated. Optimal site conditions are crucial for dynamic *ex situ* conservation because they largely determine whether mortality could occur or if reproduction success is guaranteed in a conservation unit. Intensive browsing by deer, moose, hares, etc. can reduce the long-term viability of a conservation unit but can be avoided by fencing and proper site management such as mowing, single-tree protection, and application of rodent repellent. Fungal contaminations of *in vitro* stored seed, buds, or other germplasm can heavily affect static *ex situ* conservation methods. Optimal storage conditions (e.g., temperature, moisture, light, airflow) and regular checks on the stored material help avoid such risks.

Conceptual risks

Conceptual risks can be seen as similar to conceptual challenges, but they are more relevant when an already defined conservation goal changes during the lifetime of a conservation programme. These risks may occur when institutional or political circumstances change in such a way that the original conservation objective becomes irrelevant or loses its financial support. *Ex situ* conservation programmes often last for several decades and be directed and managed by one person or only a few people. Once institutional responsibilities change (e.g., retirement), ongoing programmes may lose direction and lack active management. Conceptual risks can be minimized by thorough documentation of actions, plans, and databases of the conservation programme so that the work can easily be continued once responsibilities change.

To avoid conceptual risks, it is important to carefully examine the lifetime of the *ex situ* conservation programme and its long-term funding and make sure that the conservation goals are well-defined and reachable.

Another key conceptual consideration is how big is big enough when it comes to conserving a sufficient level of genetic diversity *ex situ*. Answering this question requires critical decisions on when *ex situ* conservation is required and what type of *ex situ* conservation, along with knowledge of availability of funding and trained staff.

A common challenge facing *ex situ* conservation is to effectively utilize seed orchards or living collections that were not primarily established for conservation and restoration purposes. Since seed orchards can be artificial populations of individuals representing wider geographic areas, there is a potential risk of outbreeding depression (OD), which could affect the long-term survival and adaptability of populations (or species) in the wild. The probability of OD largely depends on the rate of historic and contemporary gene flow among mating partners (i.e., the more gene flow, the less the probability of OD) and the environmental differences between the origins of breeding individuals (the smaller the differences, the smaller the probability of OD) (Frankham *et al.,* 2011). Decisions on how to design or utilize *ex situ* conservation units for restoration purposes will consequently depend on species-specific and country-specific features such as the number of environmental zones in a country and connectivity among natural populations. Furthermore, as seed orchards may be composed of individuals selected primarily for breeding purposes based on specific selection criteria such as volume production, wood quality, or stem straightness, they may possess a non-random component of genetic diversity within the species, leading to potential issues with inbreeding and consequent reduced adaptability. Some potentially important alleles may even be eliminated from a population or species if selective breeding unintentionally alters the genetic composition of loci that are tightly linked to those controlling selection traits.

To minimize the risk, the establishment of seed orchards and the utilization of their seed follows geographical zonation that is carefully designated based on the most recent scientific research.

Another risk associated with the utilization of seeds from seed orchard is that seed orchards are commonly established far from their trees' locations of origin with the aim of phenologically isolating the trees from undesired pollen sources and increasing their fecundity and in turn seed yield. When the isolation is not perfect, the trees may be fertilized by ambient pollen with unsuitable genetic constitution, and their seeds may thus no longer be suitable for the original locations.

Other challenges can come from more technical aspects, such as the risk associated with management activities both in the field or lab involved in maintaining and propagating the preserved species, or the potential for misuse or breakdown of the equipment. These activities can introduce risks to the genetic integrity and health of the collection.

Lastly, a significant challenge lies in a philosophical bias, which could bring the community to overly rely on *ex situ* conservation once established and neglect *in situ* conservation or the regular maintenance of the existing *ex situ* conservation collections.

3.4 Relocation strategy to conserve genetic conservation units at risk

This section was developed by the EUFORGEN Working Group on "Evacuation of threatened material and tracking of movements," consisting of **Joan Cottrell (United Kingdom), Delphine Grivet (Spain), Katharina Liepe (Germany), An Vanden Broeck (Belgium), Berthold Heinze (Austria), Andrea Piotti (Italy), Brynja Hrafnkelsdóttir (Iceland) and Ülo Niinemets (Estonia).** The group formulated a concept on the replication of *ex situ* genetic conservation units. The full concept is available in Annex C.

When a genetic conservation unit (GCU) is at risk, its long-term survival in its current environment may be uncertain. Where the loss of a GCU is considered to be unavoidable, immediate action is required to conserve its genetic material. One strategy involves relocating or replicating the genetic material of entire populations from their original, threatened habitats to safer locations. This relocation is generally seen as a last resort when *in situ* conservation efforts fail but plays a critical role in maintaining the genetic diversity and adaptability of species under threat from environmental changes. The

Within and outside-range *ex situ* Genetic Conservation Unit (GCU) Replication

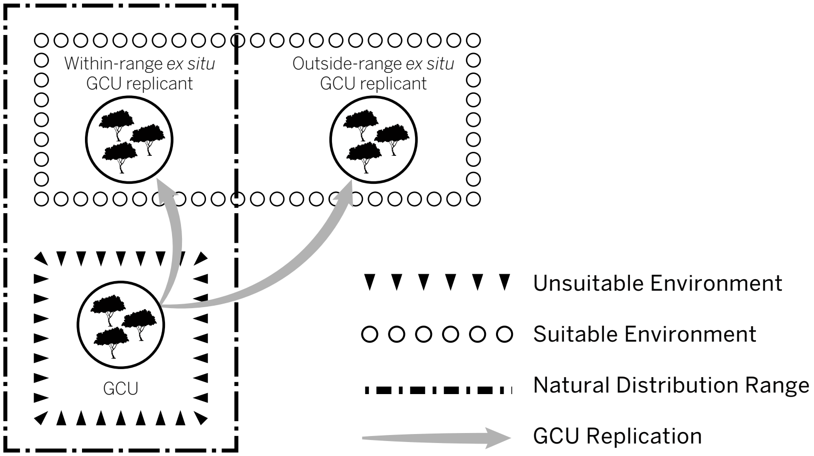

Figure 6. Replication of a genetic conservation unit within or outside the natural range of the species

replication of the GCU can be either within or outside the natural distribution range of the species (Figure 6).

Within-range *ex situ* GCU replication

- This refers to a dynamic *ex situ* replication of the GCU, established within the natural distribution range of species in the GCU.
- The replication of the GCU is achieved by collecting FRM from the original GCU and using it to establish a new GCU in another suitable location **inside** the natural distribution range of the species, allowing the new population to be exposed to evolutionary forces.

Outside-range *ex situ* GCU replication

- This refers to a dynamic *ex situ* replication of the GCU, established beyond the natural distribution range of species in the GCU.

- This is achieved by collecting FRM from the original GCU and using it to establish a new GCU in another suitable location **outside** the natural distribution range of the species, allowing the new population to be exposed to evolutionary forces.

The process of relocating or replicating genetic material begins with collecting seeds or cuttings from a diverse selection of individuals (genets) in the population at risk. Information on individual genotypes and assessment of the genetic diversity present in the collected material can help to minimize genetic relatedness within the GCU replicant and maximize allelic richness. Once propagated, the material is used to establish a GCU replicant at a suitable location, with careful attention paid to spatial arrangement of individuals within the site to promote random mating and natural regeneration. Genetic monitoring is necessary to ensure the survival of individual genotypes and maintain genetic diversity, with additional genetic material introduced as needed to supplement any losses. This approach helps to ensure that evolutionary processes continue in the GCU replicant, securing the species' adaptive potential.

Where appropriate, *ex situ* conservation through GCU replication is a valuable tool, but it should complement rather than replace *in situ* approaches. Its success depends on clear objectives, technical preparedness, institutional support, and long-term vision. While GCU replicants can secure genetic material that would otherwise be lost and provide sources for restoration or breeding, their establishment outside the original environment entails risks. These include ecological mismatch, maladaptation, reduced representativeness of the collected material, the absence of co-evolved organisms, contamination or unwanted gene flow, and failures related to infrastructure or management. Moreover, exposure to novel environmental conditions can alter the genetic trajectory of the population, potentially compromising its evolutionary integrity.

Long-term success therefore requires careful design, representative sampling, and continuous management, monitoring, and evaluation to ensure that genetic diversity and evolutionary processes are maintained. Complementary measures such as provenance and species mixture trials and sentinel plantings across different environments can provide early warnings and guidance on where specific genetic materials are most likely to persist under changing climate scenarios.

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4. CRITICAL EVALUATION AND HANDLING OF DYNAMIC *EX SITU* GENETIC CONSERVATION

The EUFGIS information system offers geographically referenced data concerning the conservation of FGR in Europe, along with access to comprehensive information about GCUs for forest trees in various countries. The data is sourced from the EUFGIS national focal points and is regularly updated to adhere to pan-European minimum requirements (Annex A) and data standards (Annex B) for these units.

Examples of dynamic *ex situ* conservation are given in section 2 of this report. This part of the report evaluates if the minimum requirements and data standards remain relevant for dynamic *ex situ* conservation.

In general, minimum requirements and data standards must be met before any dynamic *ex situ* GCU is established.

4.1 Minimum requirements

The minimum requirements for dynamic conservation (Annex A) were originally developed mainly to serve *in situ* conservation. For taking better into account some *ex situ* aspects, an additional requirement is needed: the precise location of the origin, in point or polygon form.

4.2 Data standards

In assessing dynamic *ex situ* conservation practices, certain deviations from and gaps in the existing data standards for dynamic *in situ* conservation (see Annex B) have been identified. Deviations will be addressed through modifications to fields in EUFGIS, while gaps will be addressed by adding additional fields for use when entering dynamic *ex situ* conservation units. These fields are described in the Table 2.

Table 2. Fields to be modified and added to EUFGIS for dynamic *ex situ* conservation units

No.	Field name in database	Data standards (*indicates that this information is mandatory) and brief description	Data type (and options if appropriate)	Example
35. ex	**PopulationOrigin**	**Origin of the material*** *This is a deviation from the* in situ *data standards since an ex situ unit cannot be autochthonous*	2) Introduced 3) unknown	2
XX	**ExSituCategory**	**Category of dynamic *ex situ* conservation***	1) Single-origin population (i.e., a single population collected) 2) Multiple-origin population (i.e., several populations were collected) 3) Unknown 4) Other, specify	1
XX	**PreciseLocation**	**Precise location of the material origin** Countries ideally should report the precise location (coordinates or GCU number) of the origin of the material. If not possible, province, country, or other admin info should be indicated.	Coordinates GCU number Province Country Other	

DEVELOPMENT OF FUNDAMENTALS/ PRINCIPALS OF STATIC *EX SITU* GENETIC CONSERVATION

This section of the report explores the minimum requirements and data standards essential for conserving FGR *ex situ*. Static *ex situ* conservation involves the storage and preservation of germplasm (seed, pollen, tissue, whole plants, etc.), outside their natural habitats, providing an additional layer of security against loss of genetic diversity in case of rapid population decline. This can be achieved through various methods, such as the long-term storage of germplasm, or by vegetative cloning. In some cases, there may be hybrid forms between dynamic and static *ex situ* conservation (e.g., clonal archives), and the decision of whether the method is considered dynamic or static depends on the purpose of the programme.

Minimum requirements and data standards must be met before any static *ex situ* GCU is created.

5.1 Minimum requirements

To be included into the EUFGIS information system, a seed or cryopreservation lot must adhere to the following minimum requirements for static *ex situ* in terms of sample size.

Consistent with the minimum requirements for dynamic *in situ* conservation (Koskela *et al.,* 2013), we propose different minimum requirements depending on the conservation objectives.

1) To preserve genetic diversity of a single population:

- collect >15 unrelated individuals[1]
- If the population has fewer than 15 unrelated individuals, collect as many unrelated individuals as possible.

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[1] Unrelated individuals: Unrelated here does not strictly refer to genetic relatedness in the narrower sense (e.g., co-ancestry, kinship coefficient, etc.) but is intended to mean that certain standards are maintained in the field in order to avoid close genetic relationships. This can be achieved, for example, by maintaining minimum distances between sampled trees.

2) To preserve genetic diversity of a fraction/subset of populations or if the total number of populations in the country is fewer than 20:

- collect >15 unrelated individuals per population/subpopulation
- If the populations have fewer than 15 unrelated individuals, collect as many unrelated individuals as possible.

3) To capture and preserve nationwide genetic diversity of a species on a defined geographical area (assuming that >20 populations still exist):

- collect at least one individual per population on a maximum number of populations and at least on 20 populations (Gallais & Lefèvre, 2021)

5.2 Data standards

Table 3 outlines the essential data standards for static *ex situ* conservation of FGR. These standardized fields and attributes can assist documentation, monitoring, and strategic decision-making, contributing to the conservation of FGR.

Table 3. Essential data standards for static *ex situ* conservation of forest genetic resources

No.	Field name in database	Data standards (*indicates that this information is mandatory) and brief description	Data type (and options if appropriate)	Example
1.	**GeneBank**	**Location or name of the genebank***	Text	Millenium Seed bank
2.	**ConservedSpecies**	**Species conserved *ex situ* in seed lots*** Give full Latin name (genus, species, subspecies, variety) (if applicable)	In Latin, separate names with semicolon Multiple choice	*Pinus sylvestris*
3.	**GermplasmOriginCoordinates**	**GCU-code or accurate coordinates of the germplasm origin*** Centre, polygon, or approximate location	Text Coordinates (Decimal Degree WGS84) ESRI shapefile	FIN00024 60.871661, 27.658081
4.	**SampleSize**	**Actual number of samples included*** In Categories. The system will allow to report 1–14 (i.e., less than the recommended number of individuals) but this will not appear publicly	Drop-down List 1) 1–14 (not to appear publicly) 2) 15–50 3) >50 4) precise number (if available)	e.g. 1: >15 2: (15–20) or 4: 534
5.	**SeedWeight**	**Weight or count of seeds sampled (estimate)**	Free text	5 kg
6.	**GermplasmCollectionYear**	**Year of collection of the germplasm data entered*** Year when the germplasm was collected. Indicate ripening year in a parenthesis (if known) in case of deviation	Number	2023(2022)

No.	Field name in database	Data standards (*indicates that this information is mandatory) and brief description	Data type (and options if appropriate)	Example
7.	**SeedRipeningYearDeviation**	**(Year of collection)-(Ripening Year)** <0 (-1 seed collected one year before the ripening year) 1) =0 (0 collected at the ripening year) 2) >0 (+1 seed collected one year after the ripening year)	Number	-1
8.	**GermplasmCollectionRationale**	**Germplasm collection rationale*** Examples: (with examples in the description and/or drop-down menu)	Drop-down menu 1) Conservation/ genetic diversity 2) Genetic gain/breeding (e.g., plus tree selection, provenance test) 3) Other	1
9.	**GermplasmStorage**	**Germplasm storage*** The temperature at which the germplasm is stored	Drop-down menu: 1) Room temperature 2) 0–+4 C 3) <0 C 4) Cryopreservation 5) Unknown	3
10.	**GermplasmIndividualsCollection**	**Number of unrelated individuals of each (sub)population*** The number of unrelated individuals from each (sub)population of which germplasm was collected	Number If there is more than one subpopulation indicated, the numbers should be divided by a semicolon	25;16;30

6. INDICATORS FOR MONITORING

Within the Forest Europe framework of criteria and indicators for sustainable forest management (CI-SFM project), the proposed revised indicator 4.6 aims to support FGR conservation strategies at the pan-European level. It is based on common standard indices of conservation provided at national levels and comprises verifiers to quantify the conservation efforts and assess the conservation strategies. The purpose of the indicators is to effectively monitor FGR conservation at pan-European level and to support harmonized and coordinated FGR conservation at national levels. Indicators need to fulfil several requirements as they should be:

- *reliable:* based on commonly defined minimum requirements
- *specific*: purpose is to monitor conservation of FGR and not anything else
- *simple:* indicators can be easily calculated from EUFGIS data input and are defined as ratios with possible values between 0 (no conservation effort) to 1 (fully achieved conservation effort)
- *relevant*: the indicators should be related to general conservation effort, neutral -, and adaptive genetic diversity conserved
- *useful*: indicators are capable of monitoring conservation efforts at pan-European and national level.

6.1 Dynamic *ex situ* genetic conservation

Verifiers designed to monitor and report on dynamic *in situ* conservation for native and non-native tree species (Tables 4 and 5) have also been used to monitor dynamic *ex situ* efforts. The applicability of these verifiers to dynamic *ex situ* depends on the *ex situ* conservation approach used.

Table 4. Applicability of verifiers to dynamic *ex situ* conservation at the species

Index name	Calculation	Applicable to dynamic *ex situ* conservation
Country-involvement index	N countries≥1GCU/N countries in range	Yes
Ecozone diversity index	N ecozones≥1GCU/N ecozones in range	Yes, but depending on *ex situ* method
Insurance index	N ecozones≥2GCU/N ecozones in range	Yes, but depending on *ex situ* method

Table 5. Applicability of verifiers to dynamic *ex situ* conservation at the country-level

Index name	Calculation	Applicable to dynamic *ex situ* conservation
Conservation effort	Total N of GCUs	Yes
Species diversity index	N species≥1GCU/N species in country	Yes, but could be modified/extended to any species that is not currently conserved as dynamic *in situ*
Ecozone diversity index	N ecozones≥1GCU/N ecozones in country	Yes, but the number of origins may be of greater interest than the number of GCUs
Insurance index	N ecozones≥2GCU/N ecozones in country	Same as above. In addition: the inclusion of static *ex situ* back-ups can complement this indicator (see section 3.3)

6.2 Static *ex situ* genetic conservation

Until now, indicators and verifiers were formulated for dynamic conservation only (*in situ* and to a minor degree for *ex situ*). The reason for this is that minimum requirements for static *ex situ* conservation were missing. Generally, species-level verifiers for static *ex situ* conservation could be formulated in analogy to those for dynamic *in situ* conservation, but their interpretation would not always be straightforward. For instance, the fact that a seed bank or a clonal archive exists for a given species in a country or ecozone (in analogy to the existence of an *in situ* GCU) does not add much information from a genetic perspective nor is it likely that the number of such units will change over time. Hence, it is questionable whether the indicator would be specific, relevant, and sufficiently useful for monitoring. It will remain a general question for static *ex situ* conservation whether the site of a GCU or the origins of the materials are conserved within the GCU is more important for calculating indicators. Similarly, a large number of seed banks in a given ecozone, a large number of origins of materials from within an ecozone, or any *ex situ* back-up of an existing *in situ* unit (e.g., when germplasm is taken for long-term storage from an *in situ* GCU that is under threat) may be considered an indicator of insurance. Box 1 shows how these different interpretations would translate into different numerical indicators. It is therefore of utmost importance to develop frameworks that are able to define when and if static *ex situ* efforts are equivalent or complementary to dynamic *in situ* conservation (see section 6.3).

Box 1: Numerical indicators used for dynamic *in situ* conservation and how they would change by integrating *ex situ* measures

Example: A species occurs in four ecozones. Two ecozones have >2 dynamic *in situ* GCUs for this species and the ecozone diversity index is 2/4=0.5. The insurance index would also be 0.5, because there are two replicates in each of the two ecozones. If a seed lot with >15 unrelated individuals is created from a GCU in one of the other two ecozones as a static *ex situ* back-up, the ecozone diversity index would change to 3/4=0.75, while insurance would remain 0.5. The same calculation would apply to country-level indicators. This would assume that dynamic *in situ* and static *ex situ* are completely equivalent measures of genetic conservation. However, it could be worth knowing to what extent a species is “insured” by means of static *ex situ* conservation (e.g., in case of rapid population decline across the entire range). This would speak in favour of a complementary indicator where static *ex situ* efforts are either counted under the exiting insurance index or under a separate one (e.g., *ex situ* insurance).

In the example above, the numbers would remain the same (0.5/0.5), because the *ex situ* seed lot was created in an ecozone which has as yet no dynamic *in situ* unit.

At country-level, however, it could be useful to monitor static *ex situ* in analogy to dynamic *in situ*, but with modified stand-alone indicators. The reason for this is that some countries prefer static *ex situ* over dynamic conservation, in particular when national gene banks or clonal archives exist in a country. The formulation of analogous verifiers is summarized in Table 6.

Level	Indicator	Conservation type	Complementarity/ Equivalence*	Conservation objective	Could be realized in...
Country level	Species diversity	Dynamic *ex situ*	Equivalent	Species which cannot be conserved dynamically *in situ*/Genetic rescue of existing dynamic *in situ* GCUS Living collection or synthetic	Living collection or synthetic population/ translocated population
	Ecozone diversity		Equivalent	Conservation of several origins sampled over environmental gradients	Multiple-origin population/translocated population
	Insurance		Equivalent/ Complementary	Establishing *ex situ* archive of existing *in situ* GCU	Equivalent: translocated population copied several times in one environmental zone; Complementary: synthetic populations or multiple-origin populations with a 1:1 back-up or partial back-up
Species level	Country involvement		Equivalent	Rangewide conservation of species genetic diversity	Synthetic population
	Ecozone diversity		same as country level	same as country level	same as country level
	Insurance		same as country level	same as country level	same as country level

Figure 7. Overview of the complementarity/equivalence decision for dynamic *ex situ* conservation measures. *Complementarity or equivalence always refers to an existing hypothetical conservation objective already in place. This overall objective might differ among countries or species, but the broad objectives as defined in the Forest Genetic Resources Strategy for Europe[2] can serve as a general benchmark.

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[2] EUFORGEN. (2021). *Forest Genetic Resources Strategy for Europe*. European Forest Institute (EFI). https://www.euforgen.org/fileadmin/templates/euforgen.org/upload/Publications/Thematic_publications/FGR_Strategy-4Europe.pdf

Level	Indicator	Conservation type	Complementarity/ Equivalence*	Conservation objective	Could be realized in...
Country level	Species diversity	Static *ex situ*	Equivalent/ Complementary	Conserving rare species/populations with orthodox seed	Seed bank, cryotank, Aboretum
	Ecozone diversity		Complementary	Rangewide conservation of adaptive/neutral genetic diversity	Seed bank, pollen bank, cryotank
	Insurance		Complementary	Backing-up genetic diversity from existing/threatened/small *in situ* GCUs; Conserving valuable or rare phenotypes from existing *in situ* GCUs	Seed bank, pollen bank, cryotank
Species level	Country involvement		Complementary	Conserving rangewide genetic diversity at continental scale	Seed bank, European network of clonal archives
	Ecozone diversity		Complementary	same as country level	same as country level
	Insurance		Complementary	same as country level	same as country level

Figure 8. Overview of the complementarity/equivalence decision for static *ex situ* conservation measures. *Complementarity or equivalence always refers to an existing hypothetical conservation objective already in place. This overall objective might differ among countries or species, but the broad objectives as defined in the Forest Genetic Resources Strategy for Europe[3] can serve as a general benchmark.

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[3] EUFORGEN. (2021). *Forest Genetic Resources Strategy for Europe*. European Forest Institute (EFI). https://www.euforgen.org/fileadmin/templates/euforgen.org/upload/Publications/Thematic_publications/FGR_Strategy4Europe.pdf

Table 6. Proposed verifiers for static *ex situ* conservation

Index name	Calculation	Comment
Conservation effort	Total N of origins sampled with >15 unrelated inds	Possibly together with viability/germination information
Species diversity index	N species>1origin with >15 unrel. inds/N species in country	This could be modified/extended to vulnerable species (IUCN categories, Cost action FP1202 list of marginal species)
Ecozone diversity index	N ecozones>1 origins with > 15 unrel. inds/N ecozones in country	
Insurance index	N ecozones≥2 origins with 15 unrel inds/N ecozones in country	To be discussed and improved

The main difference between indicators for dynamic and static *ex situ* conservation is that for static *ex situ* the number of origins may be more important than the number of GCUs. The insurance index for static *ex situ* conservation needs further research and discussion.

6.3 Equivalency versus complementarity

As outlined in the previous section, it needs to be decided whether *ex situ* conservation efforts are equivalent or complementary to *in situ* conservation measures. If all *ex situ* efforts are unconditionally considered equivalent to *in situ* efforts, the existing indicators could be inflated, because *ex situ* conservation cannot replace dynamic *in situ* conservation in all cases. There are situations where the two types of conservation do essentially different things (e.g., adaptation to climate). On the other hand, if *ex situ* efforts are generally seen as complementary measures only, there is the risk that many *ex situ* conservation efforts will not or barely become visible and therefore monitorable in the future, although they play a significant role in conservation efforts in many countries and for numerous tree species.

Whether *ex situ* conservation efforts are equivalent to *in situ* conservation efforts depends mainly on the defined conservation objective for a certain species (see section 5.1). Equivalency is generally given when a certain conservation objective cannot be achieved by means of dynamic *in situ* conservation and *ex situ* conservation is the only possible alternative. An example of this would be a tree species that does not form populations in the forest large enough to be conserved *in situ*. In this case, *ex situ* living collections can, under certain circumstances, achieve a desired conservation goal such as long-term adaptation to climate or minimizing effects of genetic drift and should be counted in the same way as any *in situ* effort, such as established gene reserve forests.

Another example would be the establishment of dynamic *ex situ* units for species that will have part of their current range outside their ecological optimum in the future as a result of climate change. Since the maintenance of all *in situ* units for such species would become difficult or impossible under future climate scenarios, dynamic *ex situ* conservation could be a flexible and equivalent alternative. Complementarity, on the other hand, is given when static *ex situ* conservation efforts are aiming to safeguard genetic diversity in rare cases of biotic outbreaks. The overall objective of long-term adaptation to gradually changing environments may be still achievable by means of dynamic *in situ* conservation in such a situation, but static *ex situ* conservation efforts serve the purpose in a complementary way (e.g., through cryopreservation or long-term seed storage). These are fairly simple examples and there will be cases in which it is more difficult to decide whether the measures should be considered equivalent or complementary. It is the scope of this report to solve this issue entirely, but further discussion within the community is strongly advised at this point. Nevertheless, Figures 7 and 8 give a general overview of how the equivalence/complementarity decision could be guided in the near future.

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RECOMMENDATIONS

The creation of a FGR conservation programme is essential for the survival of some species and for helping to maintain the genetic diversity of others, but it requires careful and thorough planning to be effective and efficient. Carrying it out also demands knowledge, time, financial resources, and qualified professionals. In most cases, *in situ* conservation is preferable to *ex situ* conservation, but it is not always achievable as a stand-alone solution. In such cases, *ex situ* conservation is a vital component for achieving the desired conservation goals, and it should be justified why *in situ* conservation cannot be applied.

The following recommendations, in sequential steps, help in deciding whether to pursue *ex situ* conservation:

1. The first step is to define a clear conservation objective: Which species is or are concerned, and for what purpose? Is the overall goal long-term preservation of genetic diversity (both neutral and adaptive) or genetic rescue of populations at risk? Is it important to preserve certain traits adapted to environmental cues, or is it more important to conserve the widest diversity possible?

2. Once the objective is set, planning of the programme can begin. It is important to know before starting what budget is available for the whole duration of the *ex situ* conservation programme. The budget will determine what will or will not be possible to implement.

3. The method chosen for the conservation (living collection, seed bank, gene bank) depends on the biological characteristics of the species considered, the goal of the conservation programme (long-term storage, reintroduction, restoration or breeding, etc.), the risks and challenges (Section 3.2), and on the available resources (equipment, facilities, human resources, etc.).

4. The collection and sampling of materials to be conserved should be based on a thorough knowledge of the distribution of genetic diversity within and among populations, as well as on the conservation method and objectives.

Other recommendations

- → The possibility of recording back-up seed collections of *in situ* GCUs should be added to EUFGIS (as a yes/no closed-ended question) and/or a database for recording *ex situ* collections should be developed.
- → Each country should maintain a list of species conserved *ex situ* in Europe, reflecting their respective efforts in the conservation of FGR.
- → Each country should undertake an assessment of the potential for *ex situ* conservation under its particular circumstances.
- → A risk management plan for the *ex situ* conservation programme should be developed.
- → *Ex situ* conservation should not substitute for *in situ* conservation but rather complement it.
- → When monitoring *ex situ* conservation efforts, equivalence with or complementarity to *in situ* conservation should be defined.
- → For monitoring *ex situ* conservation efforts, existing, adapted, and new indicators suggested in this report should be used, depending on the conservation method.
- → The minimum requirements and data standards for dynamic and static *ex situ* conservation proposed in this report should be included in EUFGIS.

REFERENCES

Collin, E., Bilger, I., & Héois, B. (1998). Conservation des ressources génétiques du merisier. *Forêt Entreprise*, *120*, 59–64.

De Vries, S., Alan, M., Bozzano, M., Burianek, V., Collin, E., Cottrell, J., Ivankovic, M., Kelleher, C., Koskela, J., Rotach, P., Vietto, L. & Yrjänä, L. (2015). *Pan-European strategy for genetic conservation of forest trees and establishment of a core network of dynamic conservation units*. European Forest Genetic Resources Programme (EUFORGEN), Bioversity International.

EUFORGEN. (2021). *Forest Genetic Resources Strategy for Europe*. European Forest Institute (EFI). https://www.euforgen.org/fileadmin/templates/euforgen.org/upload/Publications/Thematic_publications/FGR_Strategy4Europe.pdf

Fjellstad, K.B., & Skrøppa, T. (2020). *State of forest genetic resources in Norway 2020*. NIBIO Report, 6(167). Norwegian Institute of Bioeconomy Research.

Frankham, R., Ballou, J. D., Eldridge, M. D. B., Lacy, R. C., Ralls, K., Dudash, M. R., & Fenster, C. B. (2011). Predicting the Probability of Outbreeding Depression. *Conservation Biology*, *25*(3), 465–475. https://doi.org/10.1111/j.1523-1739.2011.01662.x

Gallais, A., & Lefèvre, F. (2021). ANOVA for estimating Nei's diversity and related parameters in a fixed set of populations with an application in genetic resources conservation. *Euphytica*, *217*(10), 192. https://doi.org/10.1007/s10681-021-02904-x

Gardner, M.F. (2021). Managing botanic garden collections of high conservation value. *Sibbaldia*, *20*, 81–94. https://doi.org/10.24823/Sibbaldia.2021.360

Hoban, S., Kallow, S. & Trivedi, C. (2018). Implementing a new approach to effective conservation of genetic diversity, with ash (*Fraxinus excelsior*) in the UK as a case study. *Biological Conservation*, 225, 10–21. https://doi.org/10.1016/j.biocon.2018.06.017

IUCN (International Union for Conservation of Nature). (2017). *Abies nebrodensis.* IUCN: The Top 50 Mediterranean Island Plants – Update 2017. https://top50.iucn-mpsg.org/species/1

Jacques, D., Lateur, M., Watillon, B., Lemaire, S., Coart, E., Roldan Ruiz, I., Vander Mijnsbrugge, K., Vanwynsberghe, L., & Keulemans, W. (2003). Développement d'un programme de gestion de la diversité génétique du pommier sauvage (*Malus sylvestris* Mill.) en Belgique: application en Région wallonne. *Les Naturalistes Belges*, *84*(2–3–4), 149–161.

Jacques, D., Vander Mijnsbrugghe, K., Lemaire, S., Antofie, A., & Lateur, M. (2009). Natural distribution and variability of wild apple (*Malus sylvestris*) in Belgium. *Belgian Journal of Botany*, *142*, 39–49.

Jalonen, R., Valette, M., Boshier, D., Duminil, J., & Thomas, E. (2018). Forest and landscape restoration severely constrained by a lack of attention to the quantity and quality of tree seed: Insights from a global survey. *Conservation Letters*, *11*(4), e12424.

Jones, T.A. (2013). When local isn't best. *Evolutionary Applications*, *6*(7), 1109–1118

Kleinschmit, J.R., Kownatzki, D., & Gregorius, H.R. (2004). Adaptational characteristics of autochthonous populations—consequences for provenance delineation. *Forest Ecology and Management*, *197*(1–3), 213–224. https://doi.org/10.1016/j.foreco.2004.05.037

Koskela, J., Lefèvre, F., Schueler, S., Kraigher, H., Olrik, D. C., Hubert, J., Longauer, R., Bozzano, M., Yrjänä, L., Alizoti, P., Rotach, P., Vietto, L., Bordács, S., Myking, T., Eysteinsson, T., Souvannavong, O., Fady, B., De Cuyper, B., Heinze, B., … Ditlevsen, B. (2013). Translating conservation genetics into management: Pan-European minimum requirements for dynamic conservation units of forest tree genetic diversity. *Biological Conservation*, *157*, 39–49. https://doi.org/10.1016/j.biocon.2012.07.023

Maunder, M., Higgens, S., & Culham, A. (2001). The effectiveness of botanic garden collections in supporting plant conservation: a European case study. *Biodiversity and Conservation*, *10*: 383–401. https://doi.org/10.1023/A:1016666526878

Myre, M.F., Steffenrem, A., Edvardsen, Ø.M., & Hjorth, F. (2021). *Prognoser for granfrøproduksjon i norske frøplantasjer fra 2020*. [Forecasts of spruce seed production in Norwegian seed plantations from 2020.]. Stiftelsen Det norske Skogfrøverk.

Premoli, A.C., Kitzberger, T., & Veblen, T.T. (2000). Conservation genetics of the endangered conifer *Fitzroya cupressoides* in Chile and Argentina. *Conservation Genetics*, *1*, 57–66. https://doi.org/10.1023/A:1010181603374

Skogfrøverket. (2021). *Årsmelding 2021*. [Annual report 2021]. Stiftelsen Det norske Skogfrøverk.

Skogfrøverket. (2017). *Skogfrøverkets strategi for skogplanteforedling 2010-2040 (revidert 2017)*. [Breeding strategy for 2010-2040 at Skogfrøverket, (revised 2017)]. In Edvardsen, Ø. M., Steffenrem, A., Johnskås, O. R., Johnsen, Ø., Myking, T., & Kvaalen, H. (Eds.), *Skogfrøverket* (pp. 22). Hamar: Stiftelsen det norske Skogfrøverk.

Vakkari, P., Rusanen, M., & Kärkkäinen, K. (2009). High genetic differentiation in marginal populations of European white elm (*Ulmus laevis*). *Silva Fennica*, *43*(2). https://doi.org/10.14214/sf.205

Välimäki, S., Rusanen, M., Pečínková, D., Tikkinen, M., & Aronen, T. (2021). Cryopreservation and micropropagation methods for conservation of genetic resources of *Ulmus laevis* and *Ulmus glabra*. *Forests*, *12*(8), 1121. https://doi.org/10.3390/f12081121

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ANNEXES

ANNEX A

Pan-European minimum requirements for dynamic genetic conservation units of forest trees

November 2008

Summary

The purpose of these minimum requirements is to define what "a dynamic genetic conservation unit" is and to increase awareness of how such units should be managed so that they contribute to long-term genetic conservation, i.e., maintenance of evolutionary processes within tree populations. This document also serves as a checklist for national focal points before they start entering data into the EUFGIS information system.

The units should have a designated status as genetic conservation areas of forest trees at national level. The units can be located in forests managed for multiple uses, protected areas, or seed stands.

The minimum size of a unit depends on tree species and conservation objectives as follows; 1) 500 or more reproducing trees (when the objective is to conserve gene diversity of widely occurring and stand-forming conifers or broadleaf species), 2) 50 reproducing trees (when the objective is to conserve adaptive or other traits in marginal or scattered tree populations) or 50 seed bearing trees (scattered tree species with sexual dimorphism), and 3) 15 unrelated reproducing trees (when the objective is to conserve remaining populations of rare or endangered tree species).

One or more tree species should be recognized as target tree species for each unit. This means that the management efforts for the purpose of genetic conservation are being carried out to equally favour these species. If a unit has several target species, each target species must meet the appropriate minimum population size, as indicated above.

The management of the units should aim to maintain and enhance the long-term evolutionary potential of tree populations. This means that management measures and silvicultural techniques are applied, as needed, to favour genetic processes that maintain the long-term viability of target tree populations.

The monitoring of the units should be carried out by visiting them regularly to observe that they still serve their purpose and that they have not been damaged or destroyed. A comprehensive assessment of the units should ideally be carried out through systematic field inventories conducted every 5 or 10 years.

Introduction

This document provides common minimum requirements for "*a dynamic genetic conservation unit*" of forest trees in Europe. These pan-European minimum requirements were developed as part of the EUFGIS project (Establishment of a European Information System on Forest Genetic Resources, April 2007-September 2010) which is one of the 17 actions co-funded by the European Commission through the Council Regulation (EC No 870/2004) on genetic resources in agriculture. The EUFGIS project is being implemented in close collaboration with the European Forest Genetic Resources Programme (EUFORGEN) which is a collaborative effort to promote conservation and sustainable use of forest genetic resources in Europe with over 30 participating countries. A large group of scientists, experts, managers, and policy-makers in these countries contribute to the work of EUFORGEN via the Conifers, Scattered Broadleaves, Stand-forming Broadleaves, and Forest Management Networks. Both EUFORGEN and the EUFGIS project are coordinated by Bioversity International.

Previously, the EUFORGEN Networks have developed requirements for genetic conservation units of different groups of tree species (conifers, scattered broadleaves, and stand-forming broadleaves). The EUFGIS project aims to harmonize these species-specific requirements and develop pan-European minimum requirements for the units that could be applied to any tree species. The purpose of the pan-European minimum requirements is also to serve as a first-level check of what kind of units can be included into the EUFGIS information system. Furthermore, the EUFGIS project is developing common data standards for the information that will be compiled on the units and included into the information system. The drafting work was done by a small expert group established as part of the EUFGIS project.

The pan-European minimum requirements and the data standards contribute to sustainable use of forests as conservation of forest genetic resources is one component of the pan-European criteria and indicators for sustainable forest management. They will also increase synergies between FGR conservation and the overall biodiversity conservation. By making available georeferenced data on the existing genetic conservation units of forest trees across their entire distribution range in Europe, the EUFGIS information system will facilitate development of truly pan-European genetic conservation strategies or action plans, and sharing of responsibilities in FGR conservation among European countries.

Dynamic genetic conservation units

Dynamic genetic conservation emphasizes the maintenance of evolutionary processes within tree populations to safeguard their potential for continuous adaptation. This means either managing tree populations at their natural sites within the environment to which they are adapted (*in situ*), or artificial, but dynamically evolving populations, elsewhere (*ex situ*). Climate change makes it even more important to apply the concept of the dynamic genetic conservation to manage the genetic resources of forest trees for the long-term sustainability of forests and forestry in Europe.

Assessment of the state of genetic conservation and development of genetic conservation strategies for forest trees at pan-European level have been hampered by a lack of harmonized and comparable data across different countries. This is mainly due to the fact that there is no common, widely agreed definition for a genetic conservation unit. In addition, there is no clear understanding of the level of management required in order to declare an area for genetic conservation purposes at pan-European level. Scientific definitions for *in situ* and *ex situ* conservation are clear but operational definitions have been more difficult to develop and subsequently countries apply a range of definitions while implementing and reporting their genetic conservation efforts for forest trees.

Due to the lack of common minimum requirements, a wide range of protected and production forests are presently declared as genetic conservation areas in addition to more clearly defined gene reserve forests. However, most protected areas are established solely for species or habitat conservation and their suitability for long-term genetic conservation of forest trees has rarely been assessed prior to their establishment. Furthermore, genetic conservation often has a low priority in the management of the protected areas and in most cases any active silvicultural measures, which are often needed for managing the genetic resources, are not allowed in the protected areas. In the case of production forests, it is often assumed, without any documentation available, that seemingly natural forests consist of autochthonous, genetically diverse tree populations. However, historical records show that forest reproductive material has been traded and distributed across Europe for hundreds of years. Unfortunately, the use of this material was and still is poorly documented in practical forestry operations.

Dynamic genetic conservation can be integrated with other management goals of forests. Thus it does not prevent forests from being used for forestry nor biodiversity conservation. The existing genetic conservation units in European countries are typically located in forests managed for multiple uses, protected areas, or seed stands. The reasons for establishing the genetic conservation units can be classified into the following categories; 1) to maintain genetic diversity in large tree populations, 2) to conserve adaptive or other traits in marginal or scattered tree populations which are often relatively small, and 3) to conserve rare or endangered tree species with populations consisting of a low number of remaining individuals. Seed stands also contribute to genetic conservation and they can be classified into the first or second category, depending on tree species.

The EUFGIS information system will include data on genetic conservation units which are established for these reasons, have a designated status as genetic conservation areas of forest trees at national level, and which are also managed for this purpose. Only those seed stands which meet the minimum requirements can be included in the information system. The EUFGIS project does not attempt to include all seed stands as there are other ongoing efforts to document seed production stands and tree breeding material in Europe (e.g., TREEBREEDEX).

The expert group recommended that the minimum size of a genetic conservation unit can be adjusted according to tree species and specific conditions. The minimum size and other specific requirements are described in detail in the following chapters.

Minimum size of a genetic conservation unit

Each unit should have a sufficient number of effectively mating and reproducing trees to fulfil the objectives (e.g., the above-mentioned categories), to prevent reduction of genetic diversity through demographic bottlenecks and consanguineous mating, and to maintain genetic diversity. The sufficient number of reproducing trees is dependent on the biology of a given species, density and spatial arrangement of trees, as well as biotic and abiotic conditions. The number of trees should be high enough to reasonably assume that sexual reproduction takes place randomly and that the level of relatedness among the next generation of trees is as low as possible. However, it is often very difficult to determine the number of reproducing trees and their sexual function in the field.

To be included into the EUFGIS information system, a genetic conservation unit must meet one of the following minimum requirements in terms of population size.

- **Case 1:** If the purpose of the unit is to maintain genetic diversity of widely occurring and stand-forming conifers or broadleaf species, the unit must consist of 500 or more reproducing trees.
- **Case 2:** If the unit was established to conserve adaptive or other traits in marginal or scattered tree populations (both scattered conifers and broadleaf species), the unit must harbour a minimum of 50 reproducing trees or, in the case of dioecious tree species with sexual dimorphism, 50 seed bearing trees.
- **Case 3:** If the unit is aiming to conserve remaining populations of rare or endangered tree species, it must harbour a minimum of 15 unrelated reproducing trees.

Some tree species are capable of vegetative reproduction through root sprouts or partially buried shoots, for example. Efforts should be made, when feasible, to check if there are identical genotypes (clones) of such tree species present within a unit and take this into consideration when estimating the number of reproducing trees.

In Cases 1 and 2, the minimum number of reproducing trees within a unit can be temporarily lower than what is indicated above if it is necessary to thin the original tree population within the unit (or stands within the unit) or to create gaps to promote natural regeneration. The prerequisite is that enough reproducing trees have contributed to mating (and seeding depending on the species) before the regeneration process has been initiated with silvicultural measures. Furthermore, it is expected that the number of reproducing trees will recover to the minimum level or above in the near future.

Genetic conservation units established for maintaining the remaining populations of rare or endangered tree species (Case 3) can only be included in the EUFGIS information system if it can be demonstrated that they contribute to dynamic genetic conservation. A national focal point should contact the EUFORGEN Secretariat and make a special request to include such units into the information system.

Target tree species and populations

In each genetic conservation unit, there should one or more tree species which are recognized as "*target tree species*". This means that the management efforts for the purpose of genetic conservation are being carried out to equally favour these species. If a genetic conservation unit has several target species, each target species must meet the appropriate minimum population size, as indicated above.

The units should be ideally located in autochthonous tree populations[4]. Additional *ex situ* units can also be included if they represent well-adapted forests. The *ex situ* genetic conservation units are artificially established and transplanted tree populations that are managed for genetic conservation and/or seed production purposes within or outside of the natural distribution range of a given species.

Units of introduced tree species (i.e., species introduced to new areas from within Europe or from other regions outside Europe) will also meet the minimum requirements if they are established to conserve well identified and differentiated characteristics compared to their original source populations (landraces) and managed following the concept of dynamic genetic conservation.

The genetic conservation units can consist of pure and/or mixed-species stands. No unknown or non-adapted genetic material should be present within a unit, but natural interspecific hybrids are allowed.

Management of the genetic conservation units

The management of the units should aim to maintain and enhance the long-term evolutionary potential of tree populations. This means that any management measures and silvicultural techniques applied should primarily aim to favour genetic processes that maintain the long-term viability of tree populations. The management of the units should favour all tree species which have been recognized as target species. It is a prerequisite that the conservation units are secured for the future.

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[4] A tree population which has been continuously regenerated by natural regeneration.

Silvicultural techniques should be applied in such a way that they support reproductive processes and result in adequate regeneration of the target tree species. Natural regeneration should be favoured as a regeneration method, but stands within a unit can also be regenerated by planting or seeding. If stands are regenerated artificially, the reproductive material should originate from the same genetic conservation unit, or, if not available, from another autochthonous stand nearby. Silvicultural techniques applied within a unit should also be adapted to protect the tree population(s) against strong environmental changes and extreme weather events. For example, different selective cutting and regeneration techniques could be used within and among the units to promote variability in mating patterns (e.g., clustered, random, and regular spacing of seed trees).

The EUFGIS information system will only include genetic conservation units which have a designated status as long-term genetic conservation areas or stands, recognized by the appropriate authorities or agencies in a country. The designated status does not necessarily mean that such units should have a legal status; an administrative status or other similar arrangement is enough. The genetic conservation units should have a basic management plan and genetic conservation should be recognized as a major management goal. All management efforts carried out within a unit should be documented in detail. The records of management efforts will not be included into the EUFGIS information system, but they should be maintained either by the landowner, the organization responsible for the management of the unit or a relevant national authority.

Monitoring genetic conservation units

Monitoring of the units is highly recommendable in order to evaluate the regeneration success and to ensure the maintenance of reproductive capacity of trees over time. The genetic conservation units should be visited regularly to observe that they still serve their purpose and that they have not been damaged or destroyed by storms or insect outbreaks, for example. At the country-level, there should also be a communication mechanism in place to ensure that a local forest manager is able to alert the national focal point of the EUFGIS information system about such damages or other changes in the state of a unit.

A comprehensive assessment of the units should ideally be carried out through systematic field inventories conducted every 5 or 10 years, as indicated by the management plan. The field inventories should focus on assessing the success of natural regeneration and the effective population size. The EUFGIS information system will facilitate future monitoring efforts by storing old data records on the units and thus building time series of the data. Furthermore, when countries join the information system (through a memorandum of understanding), they agree to update the data they provide at reasonable intervals.

The most intensive and expensive level of monitoring is genetic monitoring of tree populations using specific genetic criteria and indicators (C&I) or even molecular markers. There are various efforts under way to improve genetic C&I, including the work of the EUFORGEN Networks. In the future, further guidance on this type of monitoring will become available for those countries that have resources for it.

ANNEX B

Data standards for dynamic genetic conservation units of forest trees to be included into the EUFGIS information system

November 2008

UNIT LEVEL

No	Field name in database	Data Standards (*indicates that this information is mandatory) and brief description	Data type (and options if appropriate)	Example
1.	**UnitCountry**	**Country of the unit*** Country in which the unit is located	Text	FIN
2. key	**UnitNumber**	**Unit number* (XXXNNNNN)** This number is the unique identifier of the unit described. This number should not be duplicated or reassigned to another unit	Text	FIN00001
3.	**UnitGeneNumber**	**National genetic conservation unit number*** Unit number from the national registry	Free text	GR 19
4.	**UnitProvince**	**Province or state** Name of the primary administrative subdivision of the country where the unit is located	Free text	
5.	**UnitDepartment**	**Department or county** Name of the secondary administrative subdivision (within a province or state) of the country where the unit is located	Free text	

No	Field name in database	**Data Standards** (*indicates that this information is mandatory) **and brief description**	**Data type** (and options if appropriate)	**Example**
6.	**UnitMunicipality**	**Municipality** Name of the lowest administrative subdivision	Free text	Rovaniemi
7.	**UnitLocalName**	**Local name** Local name of the area or forest	Free text	Koiravaara
8.	**UnitLatitude**	**Latitude*** The latitude of the centre of the unit	3 separate numerical fields + 1 filed for N or S If data will be provided in centesimal degrees, the database will automatically convert to sexagesimal	66˚ 31' 32.34" N
9.	**UnitLongitude**	**Longitude*** The longitude of the centre of the unit	3 separate numerical fields + 1 filed for E or W If data will be provided in centesimal degrees, the database will automatically convert to sexagesimal	25˚ 31' 06.66" E
10.	**UnitCoordinatesRestriction**	**Restriction in making the geographical coordinates publically available** If "Yes" the accuracy of the geographic data will be modified when making the information available.	Yes-No Only one choice possible	Yes
11.	**UnitGeodeticDatum**	**Datum** Indicate the Datum of the projection used to obtain the coordinates. If not provided "WGS 1984" will be used. A horizontal geodetic datum based on an ellipsoid that has its origin at the earth's centre of mass. Examples are the World Geodetic System of 1984, the North American Datum of 1983, and the Geodetic Datum of Australia of 1994. The first uses the WGS84 ellipsoid; the latter two use the GRS80 ellipsoid.	From list Only one choice possible	WGS84

No	Field name in database	Data Standards (*indicates that this information is mandatory) and brief description	Data type (and options if appropriate)	Example
12.	**UnitPolygon**	Polygon coordinates (if available) A series of coordinate points describing the vertices of the polygon. (The projection to be used will be defined later)	Memo field – A series of numbers can be entered indicating the vertex of the polygon	
13.	**UnitMinimumElevation**	**Minimum elevation*** The minimum elevation of the unit expressed in metres above mean sea level. Negative values are allowed.	number	129
14.	**UnitMaximumElevation**	**Maximum elevation*** The maximum elevation of the unit expressed in metres above mean sea level. Negative values are allowed.	number	180
15.	**UnitArea**	**Surface area of the unit*** Total surface area of the unit in hectares accuracy of 0.1 ha.	Number with accuracy of 0.1	36.1
16.	**UnitOwnership**	**Ownership of the unit**	Public/Private/others Only one choice possible	Private
17.	**UnitType**	**Type and function of the unit**	1) Gene reserve forest 1) Biodiversity conservation (habitats and/or species) 2) Seed stand 3) Protective forest area (soil, water, timber line, etc) 4) Forest area managed for wood production and / or multiple uses and services Multiple choice Separate elements with semicolon	1;3;5
18.		**Monthly temperature (°C)** [min, max, mean x 12]	OBTAINED FROM WorldClim	OBTAINED FROM WorldClim

No	Field name in database	**Data Standards** (*indicates that this information is mandatory) **and brief description**	**Data type** (and options if appropriate)	Example
19.		**Total annual mean precipitation (mm)**	OBTAINED FROM WorldClim	OBTAINED FROM WorldClim
20.		**Heat sum and/or length of the growing season (in days)**	OBTAINED FROM WorldClim	OBTAINED FROM WorldClim
21.		**Accumulated moisture deficit**	OBTAINED FROM WorldClim	OBTAINED FROM WorldClim
22. key	**UnitDataCollectionYear**	**Year of collection of the field data entered*** Year when the data on the unit was collected in the field	Number	2004
23.	**UnitLastVisitYear**	**Year of the most recent visit***	Number	2005
24.	**UnitSoilRemarks**	**Remarks on specific soil characteristics**	Free Text	Calcareous
25.	**UnitRemarks**	**Remarks on other specific characteristics of the unit**	Free Text	Very low temperature during summer
26.	**UnitSpecies**	**All tree species growing in the unit*** List of target and non-target species growing in the unit, give full Latin name (genus, species, subspecies as appropriate)	In Latin, separate names with semicolon Multiple choice	*Pinus sylvestris; Betula pendula*

SPECIES LEVEL

No	Field name in database	Data Standards (Descriptor) (*indicates that this information is mandatory)	Data (and options if appropriate)	type
27. key	**PopulationTargetSpecies**	**Target species*** Give full Latin name (genus, species, sub species as appropriate)	In Latin, separate names with semicolon Multiple choice	*Pinus sylvestris*
28. key	**UnitNumber**	**Unit number* (XXXNNNNN)** This number is the unique identifier of the unit described. This number should not be duplicated or reassigned to another unit	From Unit table This field is needed to link the species table to the unit table, is a repetition of the field in the unit table – field No 2	FIN00001
29. key	**UnitDataCollectionYear**	**Year of collection of the field data entered*** Year when the data on the unit was collected in the field	From Unit table This field is needed to link the species table to the unit table, is a repetition of the field in the unit table – field No 22	2004
30.	**PopulationUnitNumber**	**National population unit number if existing**	Free Text	GR 19 Unit 3334TTT6-2
31.	**PopulationEstablishmentYear**	**Year of Establishment of the GCU for the species** Year when the genetic conservation activities for the given species have started in the unit	Number	2001
32.	**PopulationLastVisitYear**	**Year of the most recent visit***	Number	2005
33.	**PopulationStatus**	**Status of the target tree population regarding the EUFORGEN common action plans**	1) Included 2) Not included 3) Pending Only one choice possible	3
34.	**PopulationSitu**	**Category of the population***	1) *In situ* 2) *Ex situ* Only one choice possible	1

No	Field name in database	Data Standards (Descriptor) (*indicates that this information is mandatory)	Data (and options if appropriate)	type
35.	**PopulationOrigin**	**Origin of the material***	1) Autochthonous 2) Introduced 3) Unknown Only one choice possible	2
36.	**PopulationSystem**	**Predominant silvicultural system**	1) Coppice 1) Clear-cutting with artificial regeneration (planting or seeding) 2) Clear-cutting with natural regeneration (seed trees or strips) 3) Shelterwood systems 4) Close-to-nature forestry (continuous cover forest, selective logging) 5) No silviculture Only one choice possible	6
37.	**PopulationManagement**	**Level of management allowed to favour the target species**	1) No intervention allowed 2) Minimum intervention allowed 3) Conservation through active intervention carried out. Only one choice possible	3
38.	**PopulationJustification**	**Main reason for carrying out genetic conservation for this species***	to maintain genetic diversity in large tree populations 1) to conserve specific adaptive and/or phenotypic traits in marginal or scattered tree populations which are often relatively small 2) to conserve rare or endangered tree species with populations consisting of a low number of remaining individuals Only one choice possible	1

No	Field name in database	Data Standards (Descriptor) (*indicates that this information is mandatory)	Data (and options if appropriate)	type
39.	**PopulationReproducingTrees**	**Total number of reproducing trees per unit***	1) 15–50 2) 51–500 3) 501–5 000 4) > 5 001 Only one choice possible	3
40.	**PopulationSexRatio**	**Sex ratio, if appropriate**	1) Predominately males 2) Even sex ratio 3) Predominately females Only one choice possible	
41.	**PopulationRegeneration**	**Status of long-term viable regeneration**	1) Continuous 2) Sporadic 3) Requires management intervention Only one choice possible	1
42.	**Population Distribution**	**Distribution of the reproducing trees in the unit (multiple choice)**	1) In stands 2) Scattered 3) In groups Multiple choice Separate elements by semicolon	1;3
43.	**Population Share**	**Estimated share of the total area within the unit in which the species is occurring (%)***	Number	30.0
44.	**Population Remarks**	**Remarks on the population**	Free text	

ANNEX C

Ex situ conservation of genetic conservation units at risk

This annex was developed by the EUFORGEN Working Group on “Evacuation of threatened material and tracking of movements,”. Authors: **Joan Cottrell (United Kingdom), Delphine Grivet (Spain), Katharina Liepe (Germany), An Vanden Broeck (Belgium), Berthold Heinze (Austria), Andrea Piotti (Italy), Brynja Hrafnkelsdóttir (Iceland), Ülo Niinemets (Estonia), Michele Bozzano (EUFORGEN Secretariat), Anna-Maria Farsakoglou (EUFORGEN Secretariat)**.
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Introduction

European countries are currently active in conserving their forest genetic resources (FGR) through a network of genetic conservation units (GCUs). These are forest areas formally designated for the protection of FGR of one or more tree species. They are established to support the full cycle of natural processes, with the primary objective of dynamically conserving the evolutionary potential of forest populations. GCUs can be located in protected areas, managed forests, or seed stands, and support genetic conservation *in situ* (in the species' natural habitat) or *ex situ* (following replication in a different location).

However, in the face of accelerating ecological changes and the increasing frequency of extreme climatic events, this traditional conservation approach may no longer suffice for all GCUs. To ensure the effective preservation of genetic diversity, it is essential to identify GCUs that are particularly at risk of being lost and to anticipate the need for conserving FGR by replicating them in more ecologically suitable locations while continuing to support and respect the natural evolutionary trajectories of these populations.

FGR comprise material that is of current or future social, scientific, or environmental interest, and contain the genetic diversity that exists within and between species and populations. Actions to support dynamic genetic conservation employ management approaches that retain both the genetic diversity and the evolutionary potential of species, and GCUs are a key component of this approach in forest tree species. Individual GCUs consist of mapped populations of single or several target tree species.

In this Annex, we focus specifically on the conservation and sustainable use of the within-species diversity of FGR.

At the European level, GCUs are coordinated through the European Forest Genetic Resources Programme (EUFORGEN) and listed and characterized in the European Forest Genetic Resources Information System (EUFGIS), forming a continent-wide network that supports a shared conservation strategy. For each species, a core network of GCUs ensures broad genetic coverage. The aim of the network of GCUs is to conserve, with the minimum of effort and at a socially accepted level, the within-species diversity of FGR across the European distribution range of the target species.

There are two criteria that distinguish a GCU from other unregistered forests. First, to qualify for registration and inclusion in EUFGIS, a GCU must include genetic conservation as a key objective in its management plan. Second, the management plan must state that the GCU will be regularly monitored to assess whether this objective is being met.

The current genetic diversity of a species and its geographic pattern of distribution is the product of complex historical events. Therefore, EUFORGEN's pan-European approach to the management of GCUs is key to conserving the full evolutionary potential of a species. Although European forests generally harbour most of their genetic diversity within, as opposed to between populations, there is evidence of geographic differentiation between populations. In terms of neutral diversity, populations originating from glacial refugia (corresponding to hotspots of genetic diversity) are typically more differentiated than are populations from secondary contact zones/recolonization crossroads (corresponding to melting pots of diversity; e.g., Petit. *et al.,* 2003). Populations are also differentiated in terms of adaptive genetic diversity. This is demonstrated using common garden experiments which reveal pan-European geographic gradients in adaptive traits such as growth, timing of bud break, and leaf senescence.

With ongoing climate change, GCUs at the rear edge, or in any areas that are currently under extreme environmental pressure, may harbour genes that may become adaptively relevant to survival of populations in other areas in the future and this underpins the concept of assisted gene flow. Conserving this basic material is therefore vitally important. Some of these key populations are currently at risk and taking action now to replicate and relocate them in less-threatened locations (either within or outside the natural distribution range) may secure this essential resource so that it can later serve as a source of useful genetic diversity to support the survival of other populations.

Minimum requirements of GCU establishment

To be recognised by EUFORGEN/EUFGIS, a GCU must meet minimum requirements regarding its designation, size, target species, management, and monitoring. These criteria help to ensure that each unit effectively supports the long-term conservation of forest genetic resources across Europe.

Minimum requirements for a GCU (based on EUFORGEN [2008] and Hubert and Cottrell [2014]) define what a dynamic genetic conservation unit is and increase awareness of how such units should be managed to optimize their contribution to long-term genetic conservation, i.e., maintenance of evolutionary processes within tree populations. The minimum requirements also serve as a checklist for national focal points before they start entering data into the EUFGIS information system.

A population must meet the following minimum requirements to be registered as a GCU in EUFGIS:

1) **The minimal number of reproducing trees**

   In terms of population size, a population must conform to one of the criteria below:

   - For widely occurring and stand-forming tree species (e.g., oak, beech, birch), the GCU should contain a minimum of 500 mature or reproducing trees.
   - For scattered tree species that occupy fragmented habitat patches (e.g., wild service-tree [*Sorbus torminalis*]) and tree species that propagate vegetatively (e.g., aspen [*Populus tremula*]), the GCU should contain a minimum of 50 mature or reproducing trees.

2) **A basic management plan** with conservation of one or more target tree species stated as a key goal. Genetic conservation units must be managed to mitigate threats such as climate change, invasive species, pests, diseases, and overharvesting and must be monitored at regular intervals.

3) The units should have a **designated status as genetic conservation areas** of forest trees at national level. The units can be located in forests managed for multiple uses, protected areas, or seed stands.

4) One or more tree species should be recognized as target tree species for each unit. This means that the management efforts for the purpose of genetic conservation are being carried out to favour these species equally.
5) The monitoring of the units should be carried out by visiting them regularly to ensure that they continue to serve their purpose as a GCU and that they have not been damaged or destroyed.

Define genetic conservation units "at risk"

Categories of GCUs at risk

In this document, we stress the importance of taking action on those GCUs that can be considered "at risk" as they have a high probability of extinction for demographic and genetic reasons. The categories of "at risk" GCUs can be defined as follows:

1) **A population of a native target tree species that is located (and has been for centuries) at the edge of the species' distribution range** (marginal populations). These populations have a high probability of extinction for demographic and genetic reasons. Conservation actions are urgently needed because these populations may contain individuals that can tolerate more extreme conditions compared with those in the centre of the natural distribution range. Species distribution models can be informative to identify marginal populations and where climatic changes are forecast.
2) **A population of a native target tree species that represents a specific evolutionary lineage** within the species and therefore justifies conservation. Genetic diversity is generally geographically structured and is not evenly distributed across the species' distribution range. Different genetic lineages arise from demographic processes experienced by these populations. Historic isolation of some populations during glacial periods leads to differentiation and the presence of unique alleles that may be important for adaptation.
3) **Isolated populations of native target species** have a high extinction risk **and are at risk in the long term.** Some tree species have a naturally scattered distribution and are rare and endangered. They are often represented by only a few relict individuals or small populations. Natural or artificially established populations (e.g., planted populations, seed orchards, gene banks) of such "at risk" target species can play an important role in the conservation of these species.

4) A population of one species whose **relative dominance is threatened by replacement of individuals from another species**.

5) A population whose **persistence is at risk following mortality from stress or/and disturbances**.

6) A population whose **persistence is threatened by low reproductive success** and a lack of establishment of individuals in successive generations.

What "measurable" indicators do we have to define a GCU "at risk"?

When a GCU has been identified to be "at risk" based on the categories defined above, indicators may be used to quantify the likelihood of it being lost and to prioritize actions on those GCUs that are particularly "at risk". The indicators vary in the degree of complexity involved in applying them.

→ **Population dynamics:** this indicator could be used by monitoring and estimating demographic parameters from inventory data (e.g., survival and recruitment; involves long-term monitoring) or from genetic data (e.g., contemporary effective population size; however, this not reliable for large and connected populations).

→ **Intraspecific neutral and adaptive genetic diversity:** prioritizing populations with specific characteristics in terms of gene flow, hybridization, degree of differentiation, inbreeding, genetic drift, rare/private alleles, and genetic irreplaceability, and estimating the adaptive potential of populations (e.g., outlier tests and environmental association studies; Allendorf *et al.*, 2010, Andrello *et al.*, 2022).

→ **Projected species distribution:** predicted future species distribution based on species distribution models (basic ones using presence-absence of the species or more sophisticated and realistic ones incorporating plasticity and genetic adaptation).

→ **Population viability analyses:** species-specific method of risk assessment that determines the probability that a population will go extinct within a given number of years (not very realistic as it assumes that the system will not change).

- **Population genomic offset**: combining genomic and environmental data from different time points and/or locations to assess the degree of possible maladaptation to new environmental conditions.

- **Genetic load:** combining genomic and fitness data to assess whether any change in genetic diversity will likely impact a population's viability.

Overview of similar existing terminology

According to Hällfors *et al.* (2014) assisted migration generally describes the concept of "moving organisms in response to climate change." Over the last decade this relatively broad definition has been subdivided by various authors on the basis of transfer distance between original and new locations and purpose of movement, e.g., *assisted population migration* refers to "the movement of species within a species' established range" and *assisted range expansion* is defined as "the movement of species to areas just outside their established range." *Assisted colonization* (also termed *assisted long-distance dispersal*) has been used to describe "the movement of species to areas far outside their established range."

In the context of operational forestry, these terms are generally **target oriented**, with the focus on planting forests with trees that are adapted to the climate of their planted environment as being fundamental to establishing resilient and productive ecosystems. In contrast, from the perspective of genetic conservation, the emphasis is **source oriented**, i.e., the motivation is focused on rescuing species and populations that are at risk of extinction or extirpation as a result of climate change and/or other disturbances.

When referring specifically to moving material from a GCU to another currently more-suitable planting location in order to conserve the genetic diversity contained in this material, specific terms comparable to those used in the target-oriented forestry context are lacking. For the source-oriented conservation activity, the general term "*ex situ* conservation" per se is not appropriate nor is it sufficiently specific since this term also includes strategies of static preservation.

Within and outside-range *ex situ* Genetic Conservation Unit (GCU) Replication

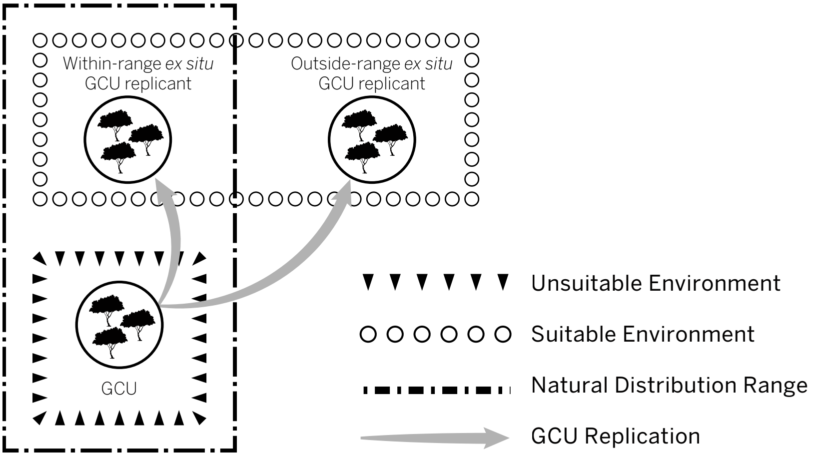

Figure C1. Replication of a genetic conservation unit within or outside the natural range of the species

In general, the following terms and definitions are frequently used:

- **Assisted migration/assisted population migration/assisted species migration/ assisted range expansion:**
  The intentional translocation or movement of populations, seed sources, or species outside of their natural geographical ranges to mitigate actual or anticipated biodiversity losses caused by anthropogenic climate change. It aims to maintain ecosystems and biological diversity that are at risk. “Moving seed sources or populations to new locations within the historical species range.” (Handler *et al*. 2018)

- **Assisted colonization**
  Improve status (of the focal species) or restore natural ecosystem functions or processes outside indigenous species range to avoid population extinction of focal species at any scale.

- **Assisted gene flow/assisted evolution**
  Moving organisms, resilient individuals, or forest reproductive material (FRM) between populations within a species’ existing range to preserve genetic diversity, as well as

moving species beyond their historical range. Populations are then left to undergo evolution in their natural habitat.

- ***Ex situ* conservation**
  The conservation of an endangered species outside its natural habitat, being the movement of plant material or populations outside, off site, or away from the natural location to easily manageable environments such as gardens. The aim is to support conservation by ensuring the survival of threatened species and the maintenance of associated genetic diversity, aiding recovery or reintroduction.

- ***In situ* conservation**
  Conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural habitats.

- **Translocation conservation/conservation translocations/plant translocation OR deliberate movement of genetic material**
  The deliberate transfer of plant material into currently depleted populations or sites where populations were known or were assumed to have been found historically, with the aim of re-establishing self-sustainability. Deliberately moving and releasing organisms where the primary goal is a conservation benefit.

Proposal new terminology

For an “at risk” GCU, long-term maintenance at its current site and within its adapted environment is not guaranteed to be sufficient to conserve it. In some cases, the existing management regime is no longer adequate and the loss of a GCU is considered to be unavoidable unless urgent action is taken to conserve its genetic material. Conserving the genetic material of a GCU is important for the maintenance of evolutionary processes within a focus tree species. The following strategy aims to conserve genetic diversity of an “at risk” GCU whose loss, in the absence of supportive action, is inevitable.

In the context of conserving genetic diversity, the process of rescuing genes or populations involves the replication and relocation of representative genetic material or entire populations from their original, threatened habitats to more secure locations. Such action is generally seen as a last resort when *in situ* measures to conserve them are insufficient or impracticable. However, replication and relocation play a critical role in ensuring the conservation of overall genetic diversity and the resilience of species which are experiencing rapid environmental changes and other threats. The adaptive potential of a species can be safeguarded by replicating and relocating genetic material from a GCU which is considered to be “at risk” (source population).

The ultimate goal of replication of an “at risk” GCU is to establish a self-sustaining GCU replicate in a new and more-suitable environment to optimize the potential for evolutionary processes to continue (Figure C1). The replication of an “at risk” GCU constitutes a dynamic *ex situ* conservation strategy. To avoid confusion, the following terms are used to define two specific forms of GCU replicates.

1) **Within-range *ex situ* GCU replicate**: a dynamic *ex situ* replication of the GCU, established within the natural distribution range.

   This is achieved by collecting FRM from the original GCU where the climate/environment is becoming unsuitable and using it to establish a new GCU in another suitable location **inside** the species natural distribution range, allowing the new population to be exposed to evolutionary forces.

2) **Outside-range *ex situ* GCU replicate:** a dynamic *ex situ* replication of the GCU, established beyond natural distribution range.

   This is achieved by collecting FRM from the original GCU where the climate/environment is becoming unsuitable and using it to establish a new GCU in another suitable location **outside** the species natural distribution range, allowing the new population to be exposed to evolutionary forces.

How to establish a GCU replicate

The life-history traits of the target tree species in the “at risk” GCU influence the ways in which the material for a GCU replicate can be obtained, e.g., by seeds or cuttings.

The first step consists of taking material (cuttings or seeds) from a selected number of individuals (genets) from the source population (a subset of the “at risk” GCU) and using this material to propagate these individuals, for example in a nursery or a greenhouse. Ideally, the adult individuals of the source population should be genotyped to avoid duplications of genotypes and to optimize the genetic diversity by the selection of individuals to be propagated. This information is also helpful to determine the optimal number of individual genotypes or offspring families to include in the GCU replicate to conserve most (e.g., 95%) of the common and private alleles. If a target species is propagated by cuttings, each genet should be represented by several ramets. For a target species that is propagated by seeds, the number of mother trees from which progeny are collected should be as large as possible (e.g., 30) and distributed throughout the stand.

The second step is to establish a GCU replicate at an appropriate location using plants derived from the cuttings or seeds from the source population. The aim is to promote seed production and natural generation in the GCU replicate. The spatial arrangement of the genotypes in the GCU replicate may influence subsequent seed production by individual genotypes and ramets. Optimization of this spatial arrangement depends on the reproduction biology of the target species (pollination and genetic compatibility system).

Finally, the GCU replicate should be characterized and a management plan drawn up, after which it should be entered into the EUFGIS information system and monitored. Survival rates of individual ramets and genotypes should be recorded, and any loss of genetic diversity should be replaced with additional ramets and genotypes.

Challenges and risks

Where appropriate, *ex situ* conservation is a valuable tool, but its success hinges on **clear objectives**, **technical preparedness**, **ongoing support**, and **integration with *in situ* efforts**. Strategic planning, careful implementation, and long-term vision are essential if genetic diversity is to be preserved effectively.

Ex situ genetic conservation presents several challenges and risks that must be carefully considered before launching or revising a programme. Technically, it requires appropriate infrastructure, skilled staff, and species-specific knowledge – whether for living collections or seed storage. Conceptually, programmes must have clear, realistic goals: a clear vision of the reasons why genetic diversity is being conserved, and for how long.

Causes of failure of *ex situ* conservation include equipment breakdown, environmental threats, and biological issues such as contamination of local FGR or maladaptation of relocated FGR.

Long-term success depends on stable institutional support – programmes can falter if priorities shift or leadership changes.

Moreover, using resources such as seed orchards originally meant for breeding can introduce genetic risks such as reduced diversity or unwanted gene flow. There is also a broader risk of over-reliance on *ex situ* methods and neglecting the essential role of *in situ* conservation.

When a GCU is replicated and relocated, it is effectively exposed to a new set of environmental conditions, such as climate, soil, and biotic interactions, that introduce novel selection pressures. These pressures can alter the genetic trajectory of the population, potentially favouring traits that are adaptive in the new environment but no longer representative of the original genetic composition. Over time, this may compromise the conservation goal of maintaining the evolutionary potential and integrity of the source population.

To buffer against this, establishing species and provenance mixture trials can provide valuable support in guiding future *ex situ* conservation efforts, especially since *ex situ* sites are expected to persist for many years in new locations while retaining as much of the original genetic diversity as possible.

Additionally, "sentinel" plantings – experimental plantings across different environments – can help to identify where particular genetic materials are most likely to thrive or face risk. These proactive trials serve as early warning systems, helping guide decisions on where to establish GCUs or restoration projects, especially under changing climate scenarios.

Case study on *Picea omorika*

One of the most threatened tree species hosted within the Balkan biodiversity hotspot is Serbian spruce [*Picea omorika* (Panč.) Purk.]. Serbian spruce has an exceptionally narrow distribution, with few, small and fragmented populations that are highly susceptible to disturbance (Ivetić and Aleksić, 2016, 2019), a biogeographic feature which has influenced the genetic layout of its populations (e.g., Aleksić *et al.*, 2017; Mataruga *et al.*, 2020). The combination of frequent wildfires and scarce natural regeneration severely constrain survival of Serbian spruce despite the relatively high levels of genetic diversity of its populations (Kuittinen *et al.*, 1991; Aleksić and Geburek, 2010, 2014; Aleksić *et al.*, 2017; Mataruga *et al.*, 2020).

Serbian spruce is one of only few IUCN red-listed European conifers. However, current rigid conservation measures, which forbid any intervention in the ~30 remnant populations, and the extant network of genetic conservation units (GCUs) (four natural populations and three planted stands from the western part of the species range, in the Republic of Srpska, Bosnia and Herzegovina) might be ineffective in preserving the species' genetic diversity (Mataruga *et al.*, 2020, Aleksić *et al.*, 2022).

Recent findings on post-disturbance gene flow patterns in the only Serbian spruce GCU with reportedly abundant regeneration showed that fire disturbance triggered the regeneration process and boosted pollen immigration (Aleksić *et al.*, 2022). However, seed immigration was still absent after fire in the studied GCU, as might be expected for natural, undisturbed populations. Gene flow into the studied Serbian spruce population was thus accomplished exclusively through pollen immigration, apparently at a rate sufficient to counteract genetic drift, at least in the short term. The authors concluded that such incoming gene flow would obviate the need for urgent intervention but calls for genetic diversity levels to be constantly monitored. There is a risk that genetic diversity could be reduced as a result of seedling mortality and genetic impoverishment in the near future can not be excluded, in particular considering the lack of seed immigration.

→

The marked genetic structure of Serbian spruce at both regional (Aleksić and Geburek, 2014; Mataruga *et al.*, 2020) and local scale (Aleksić *et al.*, 2017), the highly fragmented distribution of the few remnant populations, as well as the reportedly difficult gamete exchanges, highlight the need to monitor temporal trends in genetic diversity in this threatened species. Complementary conservation measures, such as the creation of static *ex situ* collections or assisted migration and assisted gene flow, should be considered if connection is insufficient and genetic diversity becomes impoverished (Schueler *et al.*, 2014; Aitken and Bemmels, 2016). In the particular case of GCUs at risk, the proposed concept of "GCU replication" should be applied.

Sources

Aitken, S.N., & Bemmels, J.B. (2016). Time to get moving: assisted gene flow of forest trees. *Evolutionary Applications*, *9*(1), 271–290. https://doi.org/10.1111/eva.12293

Aleksić, J.M., & Geburek, T. (2010). Mitochondrial DNA reveals complex genetic structuring in a stenoendemic conifer *Picea omorika* [(Panč.) Purk.] caused by its long persistence within the refugial Balkan region. *Plant Systematics and Evolution*, *285*, 1–11. https://doi.org/10.1007/s00606-009-0250-0

Aleksić, J.M., Piotti, A., Geburek, T., & Vendramin, G.G. (2017). Exploring and conserving a "microcosm": whole-population genetic characterization within a refugial area of the endemic, relict conifer *Picea omorika*. *Conservation Genetics*, *18*, 777–788. https://doi.org/10.1007/s10592-017-0926-x

Aleksić, J.M., Mataruga, M., Daničić, V., Cvjetković, B., Milanović, Đ., Vendramin, G.G. Avanzi, C. & Piotti, A. (2022). High pollen immigration but no gene flow via-seed into a Genetic Conservation Unit of the endangered *Picea omorika* after disturbance. *Forest Ecology and Management*, *510*, 120115. https://doi.org/10.1016/j.foreco.2022.120115

Ivetić, V., & Aleksić, J.M. (2016). Response of rare and endangered species *Picea omorika* to climate change: The need for speed. *Reforesta*, *1*(2), 81–89.

Ivetić, V., & Aleksić, J.M. (2019). Serbian spruce and climate change: Possible outcomes and conservation strategy. In M. Šijačić-Nikolić, J. Milovanović, & M. Nonić, M. (Eds.), *Forests of southeast Europe under a changing climate* (pp. 353–371). Springer. https://doi.org/10.1007/978-3-319-95267-3_30

Kuittinen, H., Muona, O., Kärkkäinen, K., & Borzan, Ž. (1991). Serbian spruce, a narrow endemic, contains much genetic variation. *Canadian Journal of Forest Research*, *21*(3), 363–367. https://doi.org/10.1139/x91-044

Mataruga, M., Piotti, A., Daničić, V., Cvjetković, B., Fussi, B., Konnert, M., Vendramin, G.G., & Aleksić, J.M. (2020). Towards the dynamic conservation of Serbian spruce (*Picea omorika*) western populations. *Annals of Forest Science*, *77*, 1. https://doi.org/10.1007/s13595-019-0892-1

Schueler, S., Falk, W., Koskela, J., Lefèvre, F., Bozzano, M., Hubert, J., Kraigher, H., Longauer, R., & Olrik, D.C. (2014). Vulnerability of dynamic genetic conservation units of forest trees in Europe to climate change. *Global Change Biology*, *20*(5), 1498–1511. https://doi.org/10.1111/gcb.12476

Key issues to address for an effective implementation

Further key issues need to be defined and addressed to ensure the effective implementation of the concept presented in this report. These may include, but are not limited to, the following:

- What are the criteria and processes for selecting suitable sites for transferring the plant material from original GCUs?
- What legal instruments apply at both the European Union and national levels, and how can they be aligned to support these efforts?
- If a suitable site is identified, what can be the hurdles in terms of clearing or managing existing vegetation?
- Who are the key stakeholders (e.g., forest managers, landowners, local communities) and how can their support be secured?

References

Allendorf, F.W., Hohenlohe, P.A., & Luikart, G. (2010). Genomics and the future of conservation genetics. *Nature Reviews Genetics*, *11*(10), 697–709. https://doi.org/10.1038/nrg2844

Aleksić, J.M., & Geburek, T. (2010). Mitochondrial DNA reveals complex genetic structuring in a stenoendemic conifer *Picea omorika* [(Panč.) Purk.] caused by its long persistence within the refugial Balkan region. *Plant Systematics and Evolution*, *285*, 1–11. https://doi.org/10.1007/s00606-009-0250-0

Aleksić, J.M., Piotti, A., Geburek, T., & Vendramin, G.G. (2017). Exploring and conserving a "microcosm": whole-population genetic characterization within a refugial area of the endemic, relict conifer *Picea omorika*. *Conservation Genetics*, *18*, 777–788. https://doi.org/10.1007/s10592-017-0926-x

Aleksić, J.M., Mataruga, M., Daničić, V., Cvjetković, B., Milanović, Đ., Vendramin, G. G.,... & Piotti, A. (2022). High pollen immigration but no gene flow via-seed into a Genetic Conservation Unit of the endangered *Picea omorika* after disturbance. *Forest Ecology and Management*, *510*, 120115. https://doi.org/10.1016/j.foreco.2022.120115

Andrello, M., D'aloia, C., Dalongeville, A., Escalante, M.A., Guerrero, J., Perrier, C., Torres-Florez, J.P., Xuereb, A., & Manel, S. (2022). Evolving spatial conservation prioritization with intraspecific genetic data. *Trends in Ecology & Evolution*, *37*(6), 553–564. https://doi.org/10.1016/j.tree.2022.03.003

EUFORGEN. (2008). *Pan-European minimum requirements for dynamic genetic conservation units of forest trees*. EUFORGEN. https://www.euforgen.org/fileadmin/templates/euforgen.org/upload/Publications/Other_PDFs/EUFGIS_Minimum_requirements.pdf

Handler, S., Pike, C., St. Clair, B., Abbotts, H., & Janowiak, M. (2018). *Assisted Migration*. USDA Forest Service Climate Change Resource Center. https://doi.org/10.32747/2018.6893746.ch

Hällfors, M. H., Vaara, E. M., Hyvärinen, M., Oksanen, M., Schulman, L. E., Siipi, H., & Lehvävirta, S. (2014). Coming to terms with the concept of moving species threatened by climate change - A systematic review of the terminology and definitions. *PLOS ONE*, *9*(7), e102979. https://doi.org/10.1371/journal.pone.0102979

Hubert, J., & Cottrell, J. (2014). *Establishing and managing genetic conservation units*. Practice Note. Forestry Commission. https://cdn.forestresearch.gov.uk/2014/03/fcpn021.pdf

Petit, R.J., Aguinagalde, I., de Beaulieu, J.L., Bittkau, C., Brewer, S., Cheddadi, R., Ennos, R., Fineschi, S., Grivet, D., Lascoux, M., Mohanty, A., Mu̇ller-Starck, G., Demesure-Musch, B., Palmé, A., Martîn, J.P., Rendell, S. & Vendramin, G.G. (2003). Glacial refugia: hotspots but not melting pots of genetic diversity. *Science*, *300*(5625), 1563–1565. https://doi.org/10.1126/science.1083264

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