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Evaluation and adaptation of the current strategy

**Jan Peter George, Leena Yrjänä, Egbert Beuker and
Mari Rusanen**

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Executive Summary

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Natural Resources Institute Finland (LUKE)

The objectives and methods of conservation of forest genetic resources in Finland are defined in the National Genetic Resources Program for Agriculture, Forestry and Fishery. While dynamic *in situ* conservation is the preferred type of conservation for most of the economically important tree species, Finland also manages and maintains genetic resources for nine tree species in *ex situ* conservation units. This document is a revision of the current national *ex situ* strategy and tries to unravel knowledge and conservation gaps, shows where conservation progress has been made to reach the defined conservation goals, and gives recommendations for the creation of a new action plan. The revision of the current *ex situ* framework also considers the global context of international treaties, conventions, and strategies aiming at improving genetic conservation in forest trees and monitoring conservation efforts more thoroughly. Due to its versatile applicability, *ex situ* genetic conservation has the potential to serve conservation needs in a multifunctional way and can make a significant contribution for short-term and long-term protection of forest genetic resources in response to abiotic and biotic threats.

Ex situ conservation progress has been made for the highly endangered white elm population in Finland (*Ulmus laevis*) for which a significant part has been conserved in dynamic and static clonal archives covering the entire natural distribution range in Finland. Conservation progress has also been made for some other noble hardwood species: Oak (*Quercus robur*), Norway maple (*Acer platanoides*), and rowan (*Sorbus aucuparia*).

Conservation gaps, on the other hand, do exist for wych elm (*Ulmus glabra*), linden (*Tilia cordata*), and in European ash (*Fraxinus excelsior*). This is mainly because of current biotic threats, which have the potential to drastically reduce the population sizes in these species.

In the **short-term** (3–5 years from now) we recommend conservation plans for European ash, white elm, and wych elm that include the following actions:

- **Inventory and rescue** of resilient European ash clones/families from the 4 existing archives into one dynamic conservation unit.
- Development of **static *ex situ*** conservation methods (e.g., cryopreservation, seedlots) in European ash for fast rescue into long-term *ex situ* repositories.
- Identification of **new conservation units** for white elm and wych elm with more favorable site conditions to replace the currently existing units in Paimio.
- Achieving a **conservation goal** in white elm and wych elm of **270 and 425 unrelated individuals**, respectively.

In the **long-term** (10–15 years from now) we recommend achieving the following conservation goals for species which are not under immediate threat:

- Norway maple (*Acer platanoides*): 600 unrelated individuals
- Linden (*Tilia cordata*): 1,200 unrelated individuals
- Oak (*Quercus robur*): 400 unrelated individuals
- Rowan (*Sorbus aucuparia*): 400 unrelated individuals
- Juniper (*Juniperus communis*): 400 unrelated individuals
- Bird cherry (*Prunus padus*): 400 unrelated individuals

In addition, Luke strongly emphasizes to make use of already existing and novel data resources to improve the genetic monitoring and population genetic analyses of forest genetic resources. Such resources should encompass:

- DNA markers & genetic simulation tools
- Climate data
- Biodiversity databases
- Novel sensing technologies for monitoring

A detailed **implementation plan** with budgetary considerations will be prepared by LUKE during **2024** to achieve the conservation targets.

Keywords: *ex situ* conservation, genetic resources, forest trees

Tiivistelmä

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Luonnonvarakeskus (Luke)

Suomen metsägeenivarojen säilyttämisen tavoitteet ja menetelmät on määritelty maa-, metsä- ja kalatalouden geenivaraohjelmassa. Vaikka dynaaminen *in situ* -suojelu on suosituin suojelumuoto useimmille taloudellisesti tärkeille puulajeille, Suomessa hoidetaan ja ylläpidetään myös yhdeksän puulajin geenivaroja *ex situ* -suojeluyksiköissä. Tämä asiakirja on nykyisen kansallisen *ex situ* -strategian evaluaatio ja pyrkii osoittamaan tietämyksen ja suojelun puutteita, sekä kartoittamaan, missä määrin suojelussa on edistytty asetettujen suojelutavoitteiden saavuttamisessa. Todetun perusteella annetaan suosituksia uuden toimintasuunnitelman laatimiseksi. Nykyisen *ex situ* -kehiksen uudistamisessa huomioidaan myös yhteys kansainvälisiin sopimuksiin ja strategioihin, joiden tavoitteena on parantaa metsäpuiden geneettistä suojelua ja seurata suojelun edistymistä. Monipuolisen sovellettavuuden ansiosta *ex situ* -geenisäilytyksellä on edellytykset palvella suojelutarpeita monella tapaa ja sillä voi olla merkittävä panos metsägeenivarojen lyhyen ja pitkän aikavälin suojeluun vastauksena abiottisiin ja bioottisiin uhkiin.

Suomessa erittäin uhanalaisen kynäjalavan (*Ulmus laevis*) *ex situ* -suojelussa on edistytty, kun merkittävä osa luontaisista esiintymistä on säilytyksessä dynaamisissa ja staattisissa kloonar-kistoissa, jotka kattavat koko Suomen luonnollisen levinneisyysalueen. Myös joidenkin muiden lehtipuulajien suojelussa on edistytty: tammi (*Quercus robur*), vaahtera (*Acer platanoides*) ja pihlaja (*Sorbus aucuparia*).

Sen sijaan säilytys ei ole kattavaa vuorijalavalla (*Ulmus glabra*), lehmuksella (*Tilia cordata*) ja saarnella (*Fraxinus excelsior*). Tämä johtuu pääasiassa nykyisistä bioottisista uhista, jotka voivat pienentää näiden lajien populaatioiden kokoa merkittävästi.

Lyhyellä aikavälillä (3–5 vuoden kuluessa) suosittelemme saarnelle kynäjalavalle ja vuorijalavalle suojelusuunnitelmia, jotka sisältävät seuraavat toimenpiteet:

- Saarnen kloonien/perheiden kartoitus ja pelastaminen neljästä olemassa olevasta kokoelmasta yhdeksi dynaamiseksi säilytysyksiköksi.
- Staattisten *ex situ* -säilytysmenetelmien kehittäminen (esim. kylmäsäilytys, siemenen varastointi) saarnelle ja nopea pelastaminen pitkäaikaisiin *ex situ* -varastoihin.
- Kynäjalavan ja vuorijalavan uusien kokoelmien perustaminen olosuhteiltaan suotuisammalle alueelle nykyisten Paimion yksiköiden tilalle.
- Saavutetaan 270 ja 425 riippumattoman yksilön suojelutavoite kynä- ja vuorijalavalla.

Suosittelemme pitkällä aikavälillä (10–15 vuoden kuluessa) seuraavien suojelutavoitteiden saavuttamista lajeille, jotka eivät ole välittömässä vaarassa:

- Vaahtera (*Acer platanoides*): 600 yksilöä, jotka eivät ole sukulaisia keskenään
- Lehmus (*Tilia cordata*): 1 200 yksilöä, jotka eivät ole sukulaisia keskenään
- Tammi (*Quercus robur*): 400 yksilöä, jotka eivät ole sukulaisia keskenään
- Pihlaja (*Sorbus aucuparia*): 400 yksilöä, jotka eivät ole sukulaisia keskenään
- Kataja (*Juniperus communis*): 400 yksilöä, jotka eivät ole sukulaisia keskenään
- Lehtotuomi (*Prunus padus*): 400 yksilöä, jotka eivät ole sukulaisia keskenään

Lisäksi Luke painottaa vahvasti jo olemassa olevien ja uusien tietoresurssien vai tietoineistojen ja menetelmien hyödyntämistä metsägeenivarojen geneettisen seurannan ja populaatio-geneettisten analyysien parantamiseksi. Tällaisten resurssien tulisi sisältää:

- DNA-markkerit ja geneettiset simulointityökalut
- Ilmastotiedot
- Biologista monimuotoisuutta koskevat tietokannat
- Uudet mittaustekniikat seurannoissa

LUKE laatii vuoden 2024 aikana yksityiskohtaisen toteutus suunnitelman budjetinäkökohti-
neen suojelutavoitteiden saavuttamiseksi.

Avainsanat: *ex situ* -suojaus, geenivarat, metsäpuut

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1. The Finnish conservation program for forest genetic resources

Among all countries within the European Union Finland is the one with the highest ratio of forested area. With a standing wood volume of 2.5 billion cubic meters Finland has at the same time the fifth largest wood production in Europe. A long tradition in forestry, forest management, as well as in industrial timber production makes it possible that a considerable part of the population creates either direct or indirect financial income from forest resources. In 2015 the forest sector in Finland accounted for 4% of the gross domestic product (GDP) which is the highest relative contribution among the EU member states.

Such intensive use of natural forest resources in combination with global change¹ makes long-term conservation and sustainable use of forest genetic resources indispensable. In fact, genetic diversity is the basis for natural selection, adaptation, and tree breeding. Because of this Finland has laid out its long-term conservation strategy of forest genetic resources under the umbrella of the National Genetic Resources Program for Agriculture, Forestry and Fishery mandated by the Ministry of Agriculture and Forestry and coordinated by Natural Resources Institute Finland (Pehu et al. 2020).

The overall aim of this program is to conserve and enhance genetic variation in forest tree species to support future selection and adaptation processes and to avoid long-term erosion of gene pools due to overexploitation or rapid population decline as a result of biotic or abiotic stress. The main method to reach the goals of the program is selecting *in-situ* genetic conservation units (GCU) where genotypes are thriving and reproducing within their natural environments as natural or managed populations. This is currently realized for a 8 tree species in 44x so-called gene reserve forests which are established on a total of 7,218 ha in Finland. However, *in situ* conservation cannot be applied for tree species which do not occur in continuous populations with sufficient mating partners in close adjacency to each other. For such species *ex situ* genetic conservation is applied, by creating artificial populations in a small to realize and enhance gene flow among otherwise highly scattered individuals. *Ex situ* genetic conservation can be dynamic within or outside the natural distribution of the target species and can also be complemented with static methods such as cryopreservation or any other form of gene bank where germplasm of forest trees is stored for very long time and when necessary rejuvenated. Dynamic *ex situ* genetic conservation in the Finnish program is currently applied for 9 species with a total of 19 collections (see paragraph 5). For two of these species (*Ulmus laevis* & *U. glabra*) dynamic *ex situ* conservation is complemented by cryopreservation.

This report covers the future strategy for *ex situ* genetic conservation, further development and extension of *ex situ* conservation towards other tree species, as well as changing perceptions regarding its functional versatility (e.g., conservation seed orchard).

¹ We define here the term global change which comprises climate change, but also other important threats such as invasive biotic agents and altered land use.

2. The role of *ex situ* genetic conservation in the current national conservation program

The importance of *ex situ* genetic conservation has been mainly recognized for species which are characterized by scattered and discontinuous occurrence. Finland is the northern range margin for many of those tree species and marginal populations are consequently characterized by a high degree of fragmentation and isolation among subpopulations. Inbreeding and drift load would likely occur in these species in the long-term without *ex situ* conservation efforts. Consequently, *ex situ* genetic conservation (mostly dynamic and to a minor degree static) has been adopted by the Finish National Genetic Resources Program (2020) as a justified conservation measure. There are mainly four criteria considered for the decision to conserve the national genetic make-up of tree species dynamically *ex situ*: i) extent and continuity of the distribution area, ii) abundance of flowering and seed production, iii) efficiency of pollen and seed dispersal and iv) the abundance/rarity of the species in Finland. These are criteria relating mainly to the biology and ecology of the species. However, to decide how to plan and design future *ex situ* genetic conservation units, these criteria shall be complemented with novel information such as the projected future distribution under climate change, projected degree of habitat fragmentation, future utilization potential, value for biodiversity, adaptation to local environments and available research resources. Each species will have a distinct population genetic fate within the next century and attention should be paid to this when managing existing and establishing new *ex situ* genetic conservation units.

There are currently 9 tree species in the Finish National Genetic Resources Program (see chapter 5) which are conserved *ex situ* and they all differ in terms of biology, abiotic and biotic threat exposure, as well as in knowledge availability. In addition, there are also tree species in Finland for which the need of *ex situ* genetic conservation had not been identified in the past but will have importance in the future because of a rapidly changing environment. Clonal breeding collections of economically more important tree species in Finland (e.g., Norway spruce, Scots pine, Silver birch), are not part of the ongoing national program for genetic conservation and therefore not part of this report.

3. National forest policies and programs addressing rare tree species

Many rare hardwood species which are currently conserved *ex situ* mutually occur in similar environments and forest types. Some of these forests need special protection because they harbor significantly more biodiversity than other forest types. Herb-rich forests in Finland are the most prominent example as they are home to 6 of the 9 tree species which are currently in the *ex situ* program (Heikkinen 2002). Genetic diversity is vital for tree populations and the protection and management of forest genetic resources in rare tree species has therefore to be seen in a bigger legislative and strategic context. While the National Genetic Resources Program for Agriculture, Forestry and Fishery lays out the main principles and conservation guidelines for tree species in Finland, there are many more policies, strategies, and programs which provide links to the use and management of genetic resources of rare tree species. Figure 1 gives a brief, yet not exhaustive overview of relevant policies, strategies, and programs. Many of these links were included for the further development of the national strategy of *ex situ* genetic conservation in forest trees to pay more attention to specific global threats and future opportunities regarding rare tree species in Finnish forestry.

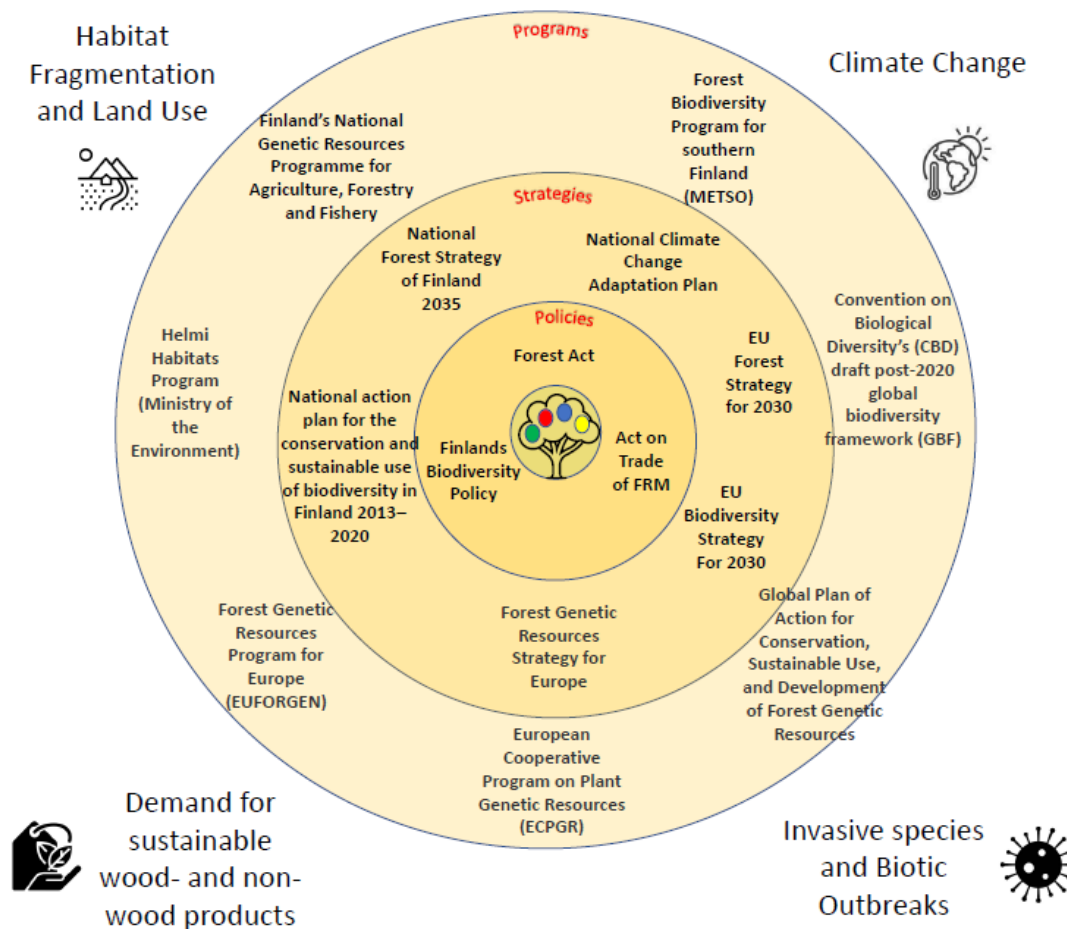


Figure 1. National and international programs, strategies, and policies which have relevance for *ex situ* genetic conservation in forest trees. The strategies are to be seen in the field of tension between sustainable timber production, invasive species, habitat loss and climate change.

4. Finland's contributions to international networks and conventions for *ex situ* conservation of forest genetic resources

Finland is strongly engaged and involved in international cooperation and networks for further developing the concept of genetic conservation. Within the Convention on Biological Diversity (CBD) Finland is committed to the objectives and targets that were formulated under the Aichi Biodiversity Targets (www.cbd.int/sp/targets#GoalC). Target 13 under the strategic goal C specifically addresses the need for maintaining levels of genetic diversity in wild and cultivated plants and for developing and implementing strategies which help to minimize genetic erosion in populations by 2020. In addition, the global plan of action for the conservation, sustainable use, and development of forest genetic resources (FAO 2014) identified 4 areas with strategic priorities. Area 2 defines strategic priorities at international and national level regarding conservation of forest genetic resources (*in situ* and *ex situ*). Particularly, strategic priority 6 (SP6) promotes the establishment and development of efficient and sustainable *ex situ* conservation programs. Strategic priority 6 underpins the need for *ex situ* conservation as being (partly) the only available option for conserving genetic diversity in peripheral populations and in populations which are seriously threatened by changes in land use and other abiotic and biotic environmental conditions. Objectives of *ex situ* GCUs as defined under the FAO Global Action Plan contain:

- to serve as back-up measures in case *in situ* genetic conservation actions will fail.
- to ensure that the range-wide genetic make-up of a species is conserved.
- to manage the regeneration of a species outside its natural environment in a more controlled way.

Actions under SP6 comprise the establishment of collections (clonal or non-clonal), applying representative sampling strategies, maintaining quality of seed before and after *ex situ* conservation, involvement of the private sector in conservation actions, and promoting and encouraging research on conservation of recalcitrant-seed species such as *Quercus robur*. Furthermore, the establishment of collections with improved seeds or germplasm is of utmost importance because it addresses the need for genetic rescue in species which are under immediate threat such as *Fraxinus excelsior* in Finland and Europe in general.

Similar, yet less detailed objectives were formulated at the World Conservation Congress in 2016 as part of the IUCN Resolution on autochthonous forest genetic diversity as the following statement: „*The WCC ask the states, governmental and non-governmental organisations involved in nature conservation to encourage and facilitate the creation, expansion, monitoring and documentation of genetic resources both **ex situ** and close to the sites, through seed banks, orchards, provenance trials and other in vivo collections of different trees;...*” (<https://portals.iucn.org/library/node/46521>).

At European level Finland is strongly engaged as contributor to the EUFORGEN program for further developing *in situ* and *ex situ* genetic conservation frameworks and information systems. EUFORGEN was established in 1994 as a result of the first Ministerial Conference of the Forest Europe process and has ever since worked as a pan-European program for promoting the conservation and use of forest genetic resources. The Forest Genetic Resources Strategy

for Europe (EUFORGEN, 2021) lays out the guidelines for European coordination a level above national strategies to achieve genetic conservation goals as outlined in the Convention on Biological diversity (CBD) as well as in the new Forest Strategy 2030 of the European Union. A key commitment outlined in the strategy regarding *ex situ* genetic conservation of forest genetic resources is to develop pan-European minimum requirements and indicators for establishing and monitoring dynamic and static *ex situ* genetic conservation units. In addition, a European platform for storing *ex situ* conservation data of each country shall be developed under the new strategy².

² Finland has been mandated together with six other countries (Belgium, France, Ireland, Norway, Slovenia, Switzerland) to actively develop these minimum requirements and indicators until the end of 2024 for the EUFORGEN program.

5. Population genetic risks and opportunities for *ex situ* conserved tree species in the near and far future

5.1. Climate change

Climate change and the occurrence of extreme climatic events will remain the biggest challenge for European forestry in the next decades. Specifically, the increasing frequency of climatic extremes will further threaten tree populations in Europe as they are able to boost large-scale tree mortality and reduce population sizes. As Finland constitutes the northern range margin for many of these tree species, a general assumption is that gradual warming could accelerate survival and growth for some of those species due to longer vegetation periods and milder winters: For example, Dyderski et al. (2018) predict range expansion for oak and ash (*Quercus robur* and *Fraxinus excelsior*) in Finland due to more favorable climate conditions until the year 2100 even under the most pessimistic representative concentration pathway (RCP 8.5). In contrast, Mauri et al. (2022) predict little to no range expansion (e.g. *Acer platanoides*, *Tilia cordata*, *Prunus padus*, *Sorbus aucuparia*, *Quercus robur*) or even population contraction (*Ulmus laevis*, *Ulmus glabra*) under both optimistic (RCP4.5) and pessimistic (RCP8.5) climate scenarios. The models by Mauri et al. (2022) also take into account dispersal constraints and available habitat and can be seen as more realistic compared to models which consider solely climate parameters. We can hence assume that the combined effects of climate change, availability of suitable habitat and dispersal capacity at the northern distribution margin will likely accelerate population fragmentation for rare tree species. This assumption will hold stronger for species which have their main distribution in southern Finland compared to species which occur further north. For other species such as *Juniperus communis* milder winters such as the one in 2019/2020 can constitute a threat, because they can reduce germination rates and natural regeneration potential (Forestry Commission Scotland 2009).

5.2. Pests & diseases

Pests and pathogens have the potential to reduce population sizes in short time and consequently reduce future adaptation potential. Some of them are novel as a consequence of increasing global trade with plant and seed material and are especially harmful as is the case for the Dutch elm disease or ash dieback. The distributions of elms and European ash in Finland, as an example, could be further fragmented by invasion of new vectors or pests in the next years, although it is still not clear if temperature conditions and host availability in Finland constitute a natural expansion barrier for these. In any case, European ash is already experiencing a severe population genetic bottleneck and immediate actions are required to avoid further loss of genetic diversity (see chapter 7 for more details on recommendations). What is more, European ash is a keystone species in herb-rich forests in southern Finland (Heikkinen 2002) where its population decline will likely cause loss of genetic diversity in more than 100 associated taxa (Hultberg et al. 2020).

Similarly, both naturally occurring elms (*Ulmus glabra*, *Ulmus laevis*) could be exposed to higher mortality rates in the near future, since the vectors carrying the Dutch elm disease are expanding northward and have already reached neighbouring countries (Jürisoo et al. 2021).

There is also evidence that outbreaks of native insect species will occur more frequently in the future as a consequence of climate change (e.g., after drought stress), although they are not expected to cause rapid population decline. For example, increased outbreaks of *Apiognomonina errabunda* have been already observed in *Tilia cordata* populations in southern Finland and *Yponomeuta* spp. in *Prunus padus* populations and *Limantria* spp. in *Sorbus aucuparia* populations are expected to increase (Räty et al. 2016, Vanio et al. 2017, Uusitalo 2004).

There will be also a need to carefully monitor new occurrences of fungal and other diseases across Europe before they arrive in Finland, in order to allocate resources for genetic conservation in due time. Acute oak decline (AOD) is an emerging disease affecting both *Quercus robur* and *Quercus petraea* in the UK and can kill trees within a few years similarly to ash dieback (Denman et al. 2010). Additionally, *Phytophthora austrocederii* has been imported from south America to the UK where it locally threatens *Juniperus* populations and it may become invasive to Finland in the Future (Donald et al. 2020).

5.3. Land use

Finland has the highest rate of forest covered land within the European Union and the fifth largest amount of growing stock on forest land (Finnish Statistical Yearbook of forestry 2022). Finnish forests will therefore play an important role in mitigating climate change impacts and for achieving greenhouse gas reductions. Goals for this have been defined in accordance with the LULUCF regulations and will determine how forests will be managed and utilized in the future to optimize decarbonizing of the atmosphere. At the same time, international and national programs increasingly promote multiple forest ecosystem services and biodiversity (FESB). Therefore, it is essential to halt biodiversity loss due to habitat fragmentation. Many of the species which are currently conserved *ex situ* are either late-successional or light-demanding such as *Fraxinus excelsior*, *Quercus robur*, *Tilia cordata*, and *Acer platanoides*. These species harbor only modest growth and yield potential under Finnish climate conditions. It is not surprising that suitable habitat has become increasingly rare in the past due to other land use preferences. Population genetic risks increase due to progressive isolation of populations which are anyway characterized by small census size and infrequent flowering and seed production. Reduction of gene flow among populations due to habitat fragmentation and loss of connectivity will accelerate drift load and segregating load (i.e., inbreeding) in the long-term. Even if long-distance transfer of seeds and pollen can partially compensate for the negative effects of loss of connectivity, it has been empirically shown that populations at the northern edge of the distribution range are more strongly affected by the loss of connectivity compared to core populations. These effects can have a substantial long-term impact on survival ability and population fitness (e.g., Nielsen & Kjaer 2010).

5.4. Forestry and use of noble hardwoods in the boreal climate zone: a prospect for forward genetic conservation of rare tree species

The threats induced by loss of biodiversity have been addressed by international and national policies and their implementation has started at national and European level. Very recently, the European Commission has launched the EU Biodiversity Strategy for 2030 aiming to put Europe's biodiversity back on the path to recovery. In March 2023, the commission published two new sets of guidelines on forestry which contain specific guidelines on planting, monitoring and protection of forests: i) Guidelines of biodiversity-friendly afforestation, reforestation, and tree-planting and ii) Guidelines for defining, mapping, monitoring and strictly protecting primary and old-growth forests within the EU. Both guidelines are relevant for the future conservation and use of forest genetic resources, since the use of underutilized and rare species as well as the connectivity and protection of isolated old-growth forests are key targets. For instance, the guidelines mention that „... *Natural genetic adaptability should also be promoted...*“ (SWD(2023) 61 final, p. 15) and that „... *It is recommended to choose species which support others (e.g., endangered, rare, umbrella species, etc.) and the nearby communities...*“ (SWD(2023) 61 final, p. 15). Already existing *ex situ* genetic conservation strategies and frameworks may be more widely utilized in the near future to actively support these goals. As an example, genetically diverse forest reproductive material for afforestation could be provided from the existing *ex situ* units for rare and endangered species (see for instance the PUUVA project under <https://www.metsakeskus.fi/fi/hankkeet/puuva>). Those seed sources may be used to restore highly fragmented ecosystems and old growth forests. Trees planted in the open landscape can work as stepping stones for connecting populations.

At national level, the Helmi Habitats Programme and the Forest Biodiversity Programme for southern Finland (METSO) are examples of how rare tree species could serve as umbrella species for restoration of fragmented populations and ecosystems. The METSO Programme is a collaborative effort between the Ministry of the Environment, the Ministry of Agriculture and Forestry and different stakeholders, in particular private forest owners who wish to dedicate part of their property to voluntary protection of biodiversity. Restoration (including planting of rare tree species) is carried out under the program and seed obtained from *ex situ* genetic conservation units would be a safe and easy way to ensure that genetically diverse and autochthonous planting material will be utilized for these purposes.

6. Recommendations for long-term use and protection of forest genetic resources in rare tree species in Finland

6.1. From *ex situ* units to *ex situ* frameworks (GCFs)

A common approach to conserve genetic diversity *ex situ* is to establish collections of either clonally replicated material or seed-propagated offspring gathered from natural stands. Size, location, and geographic coverage of these genetic conservation units (hereafter referred to as **GCU**) depend on availability of land, conservation priority of the target species and resources available for sampling, propagation, and maintenance. Dynamic *ex situ* GCUs are supposed to create recombinant genotypes via sexual reproduction and these genotypes - when deployed as forest reproductive material- will be exposed to natural selection potentially featuring adaptation to new environmental conditions. In contrast, static *ex situ* archives established in form of seed or germplasm banks do not inhabit this feature, but they require less space and maintenance work. While dynamic preservation should be preferred in most cases, static preservation can make an important contribution in cases where populations are exposed to high mortality (e.g., biotic outbreaks) or if the conservation of genetic resources is to be achieved systematically over large geographical areas. Hence and as a very first recommendation we propose to combine dynamic and static *ex situ* approaches in the future by shifting conservation paradigms from *ex situ* genetic conservation units (GCUs) to *ex situ* genetic conservation frameworks (hereafter referred to as **GCFs**). Future GCFs may consist of a single clonal collection (similar to current GCU) or they constitute a more complex combination of dynamic and static *ex situ* units, depending on the conservation goal, species-specific needs, and available infrastructure and monetary resources. In any case, the added value of using GCFs instead of multiple stand-alone GCUs must be clear and can, for instance, relate to:

- Higher conservation efficiency (conserving more diversity at lower costs).
- Higher conservation effectivity (conserving more diversity in general - e.g., sampling more populations, conserving higher allele copy numbers for backup purposes).
- Genetic rescue of populations and avoiding immediate loss of diversity (e.g., during biotic outbreaks).

Another feature of GCFs in comparison with GCUs is that they are easily extendable towards more complex systems so that changes in environmental frame conditions would not require termination of the existing framework, but rather complementation whenever the situation requires it. An example could be a tree pandemic, which would require rescue of resilient or surviving genotypes. In this case, a combination of dynamic and static conservation would ensure that population resilience can still evolve (assuming moderate to high heritability) via breeding, while range wide genetic diversity will be rescued by means of static *ex situ* conservation (e.g., in seed banks or cryopreservation of germplasm) over long time.

An example of three different GCFs is illustrated in Fig. 2 for a hypothetical tree species consisting of several populations.

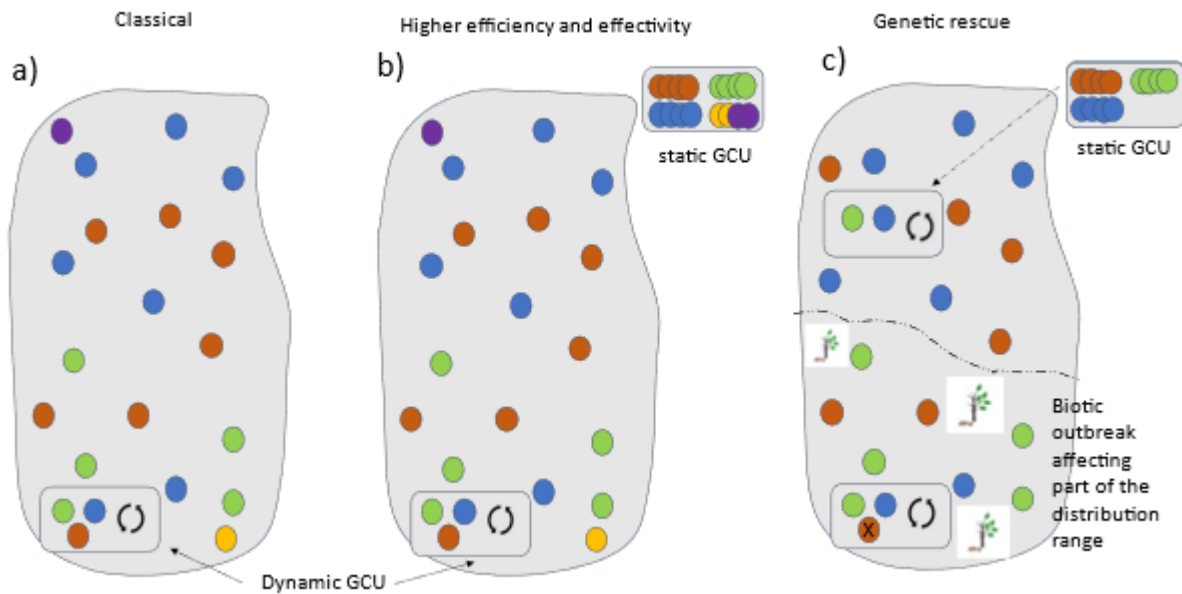


Figure 2: Illustrative examples of GCU vs. GCFs. a) A classical dynamic *ex situ* unit which captures a considerable part of the allele spectrum (colored circles). However, to sample alleles with low frequency (yellow, lilac) an exhaustive sampling effort and space requirement would be necessary. b) A GCF combining dynamic and static conservation is capable of conserving higher copy numbers and more alleles in total either through seed storage or other germplasm. a static repository can also be used to restore dynamic units as well as for research purposes, in particular when micropropagation allows for clonal replication. c) In a case of a biotic outbreak during which the existing dynamic GCU is severely affected, moving naturally resilient genotypes into a new dynamic collection outside the pathogen/agents range and complementing it with a static long-term repository can be an immediate conservation management strategy. The dashed arrow implicates that the static repository may be used to temporarily move genotypes from static to dynamic units in to increase population size.

6.2. Definition of functions and tasks of GCFs

A changing world requires to rethink originally defined aims, objectives, and tasks of *ex situ* collections and frameworks. This has environmental, political, and societal reasons: climatic extremes and biotic outbreaks, for instance, can cause that existing *ex situ* units cannot fulfill or only partly fulfill their tasks in the future. In addition, market-oriented conservation actions will require a higher number of seed with sufficient levels of genetic diversity for rare tree species than currently provided. Finally, societal awareness is not only raising for biodiversity themes in general, but also increasingly visible for genetic diversity in particular as reflected in the post-2020 Global Biodiversity Framework. This places *ex situ* genetic conservation into a novel frame requiring thoughtful and cost-efficient decisions. New functions and tasks may be therefore added under the global framework in order to meet the defined goals and targets.

We generally define a **function** as the future type a GCF may represent (e.g., clonal archive) and its associated **task** as the desired conservation aim (e.g., adaptation to new environmental conditions). The most commonly identified functions and tasks which were found to be plausible under Finnish conditions are listed in Fig. 3 and are sorted by increasing complexity level.

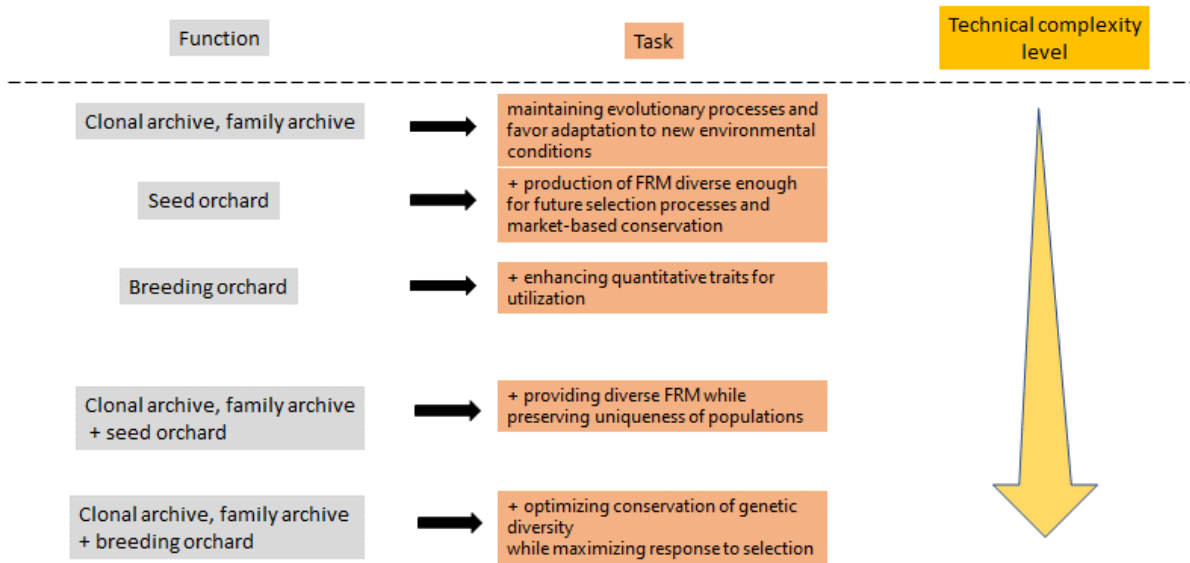


Figure 3: Possible functions and tasks of future GCFs. The + symbol in task boxes indicate additional tasks below the main task, which is to maintain evolutionary processes and favor adaptation to new environmental conditions.

In the simplest case the desired function is a clonal archive or family archive consisting of a certain number of clonal copies or families. These may originate from several natural stands across the natural distribution and the archives are situated within or outside species ranges depending on site availability and size requirements (i.e., plant spacing). Archives are often realized in so-called living collections, but with the possibility of static *ex situ* back-up. The technical complexity level is low, but regular maintenance work, fencing, and temporary inventory is necessary.

A seed orchard has a different function, different task, and different requirements (see section 7.3) compared with a clonal/family archive. Seed orchards are more complex regarding its maintenance and management, but they can be a powerful element within a GCF in order to promote the use of FRM of underutilized tree species. One of the key elements is that seed orchards within a GCF can produce FRM with higher levels of genetic diversity compared with the original populations from which they originate. This can be achieved by optimization of spatial arrangements between adjacent trees which increases panmixia (e.g., Chaloupkova et al. 2016).

In analogy to seed orchards, breeding orchards could add value to GCFs if the task would be to enhance certain traits for marketing (e.g., fruit quality if the fruits are edible or wood quality in certain species). This will be currently only plausible for a very small number of species, but examples from the past are, for instance, conservation and breeding of *Sorbus aucuparia* genotypes for enhanced fruit production and medical purposes (e.g., Letzig & Handschack 1963).

We also identify two mixed forms of GCFs, which combine tasks of clonal/family archives and orchards. Their architecture is similar to their pure counterparts, but they are designed for better accounting for within- and among population diversity while providing enhanced

forest reproductive material. A combined clonal archive – seed orchard would be able to provide diverse FRM, while preserving uniqueness of subpopulations, if desirable. This could be the recommended GCF if significant subpopulation structure exists within a species (e.g., presence of several postglacial recolonization lines). While the technical complexity level in terms of maintenance and site conditions are very similar to orchards, the resulting GCF will consist of more units to avoid mixing of subpopulations during seed production. However, whether conservation of unique subpopulations should be favored over intra-specific lineage mixing is under debate and especially relevant for oak (*Quercus robur*) in Finland (see results for oak below).

A combined clonal/family archive – breeding orchard has the additional feature that conservation of genetic diversity needs to be balanced against genetic gain when additional subpopulation structure exists. It has the highest technical complexity among all functions, because it requires mathematical optimization procedures and the assessment of heritabilities (e.g., Mullin 2017). However, this function has been currently not identified being plausible for any of the species in the Finnish conservation program and will be therefore not discussed further throughout this report.

6.3. Necessary requirements, decision tools, and indicators for *ex situ* conservation of rare tree species in a changing world

Different **requirements** need to be given for each species in order to decide which function would serve as the optimal and most suitable way to conserve genetic resources. In addition, requirements will determine the complexity of a GCF (that is: how many units?, where to place the units? etc.). **Requirements** relate to past, present, and future characteristics of a species and take into account existing knowledge and data as well as information on existing genetic conservation units. Requirement levels can refer to relatively simple questions such as *Does the clonal archive cover the species distribution well?* when the desired function is a clonal archive, but requirements can also address more complex questions such as existing vs. needed estimates of effective population size when the desired function will be a seed orchard. **Decision tools**, on the other hand, are specific tools to determine whether requirements are fulfilled. Decision tools describe the way in which requirements can be evaluated, but they are flexible in a way that new data and knowledge can always be integrated. Decision tools can range from literature review, review of policy aspects up to numerical assessments and genetic marker analysis (if possible and feasible). Most importantly, requirements and decision tools need to be complemented by **indicators**, which constitute a pseudo-numerical threshold and benchmark for deciding if requirements are fulfilled and if the desired function can be fulfilled by the GCF. **Indicators** will be mainly based on population genetic metrics and constitute the scientific implementation of the *ex situ* conservation genetic program. Indicators can be relatively simple, for instance measuring how much of the geographic distribution of a species is covered in a GCF, but they can be also more demanding in terms of data input (e.g., assessment of flowering asymmetry or effective population size). In any way, thresholds for indicators as well as the way they are assessed are not static and under steady development and discussion. In total, 25 criteria were applied for the Finnish *ex situ* long-term strategy, which will serve as guidelines for definition of indicator thresholds. These can be found in Appendix 1 of this report. Among these 25 indicators are metrics

which can assess i) the current status of existing GCUs (geographic coverage and damage), ii) abiotic and biotic future threats, iii) estimates of effective population size, iv) assessments of adaptive clines, v) assessments of neutral genetic diversity within and among populations, vi) species overall impact on forest biodiversity, vii) estimate on the future desired use of the species, viii) special policy and conservation aspects (if any), ix) information on availability of genomic resources, and x) general information on reproductive system, pollination, and propagation methods. Figure 4 gives an overview of requirements, decision tools, and (possible) indicators for each identified GCF function.

6.4. Technical implementation and evaluation of the long-term strategy

Multifunctional genetic conservation requires different thinking compared with traditional conservation efforts. The increasing complexity level from clonal/family archives to seed orchards, breeding orchards, and combined frameworks is related to site conditions (e.g., soil, climate, infrastructure), data requirements (e.g., flowering assessments, pedigrees), thinning and pruning, rotation period, and many more. Suboptimal growing and management conditions may cause that one or more of the desired functions cannot be fulfilled and counteract conservation success. A particular challenge will be the establishment of new genetic conservation units, because of the high competition for suitable land between conservation, agriculture and forestry. Careful cost-benefit analysis is required to decide whether the selection of easily available but poor land does not result in higher costs (e.g., through repeated replanting) and lower conservation success compared to an investment in more fertile land. Poor site conditions (e.g., clay with intermittent waterlogging and troughs) should be avoided in any case, because they hinder flowering and fruiting success and will require costly remedial work because of high plant losses. When the same conservation function is identified for several species, establishing *ex situ* conservation centers (e.g., seed orchard and breeding orchard centers) can be beneficial. In such a case it would be ensured that site conditions are homogenous, and the shared infrastructure will reduce costs for maintenance and management (e.g., labor cost for weed control, fencing, transport, etc.).

Different types of data and data assessment tools will be required in the future in order to monitor conservation success in the proposed *ex situ* genetic conservation frameworks. Finland is a country with well-developed information resources which are often publicly available (see also next paragraph). Such resources should be deployed, for instance, for GIS-based and remotely sensed population monitoring and identification of target populations for complementing existing *ex situ* units or for the establishment of new ones. However, seed orchards, breeding orchards, and combined genetic conservation frameworks require data which often goes beyond publicly available data: the accurate assessment of flowering, seed viability assessments, estimates of effective population size, and pedigrees among trees are some of these required data types and they usually come at considerably higher costs. Nevertheless, the future action and implementation plan will exploit technical advancement whenever possible and as cost-effective as possible. Automated flowering and fruiting assessments (e.g., Mann et al. 2022) and novel genetic resources with markers in very high density across the genome for comparably low costs are just some of the resources which can help to make *ex situ* genetic conservation more effective in the future. Static *ex situ* methodologies are already applied in the national program in form of cryopreservation of dormant buds (for *Ulmus laevis* and *Ulmus glabra*) and will be further developed for other species such

as European ash (*Fraxinus excelsior*). Because cryopreservation is currently not applicable for every species in the program, we recommend also further professional exchange with experts on long-term seed conservation. The Millennium Seed Bank in the UK holds currently 2.4 billion seed for long-term conservation and has profound knowledge in static *ex situ* conservation of seed for almost all tree species in the Finnish program (e.g., Hoban et al. 2018). Hence, the national program could significantly benefit from knowledge transfer between countries. Table 1 gives an overview of some (yet not all) technical aspects which are important to be considered for the implementation of the long-term strategy.

Table 1: Technical aspects of different functions of a particular GCF.

Objective	Requirement for optimal site conditions	Data requirement	Technical complexity	Rotation period	Min. number of units	Static <i>ex situ</i>	protection from wild pollen contamination
clonal/family archive (CA)	low-moderate	low	low	high	1 (either dynamic or static or both)	obligatory	no
seed orchard (SO)	high (seed orchard centers?)	high (seed orchard centers?)	moderate-high	low (10-15 years)	1	not obligatory	no
CA + SO	high	high	moderate-high	moderate (15-20 years)	2	not obligatory, but beneficial	yes
CA + SO + BO	high	high	high	low (10-15 years)	2	not obligatory, but beneficial	yes

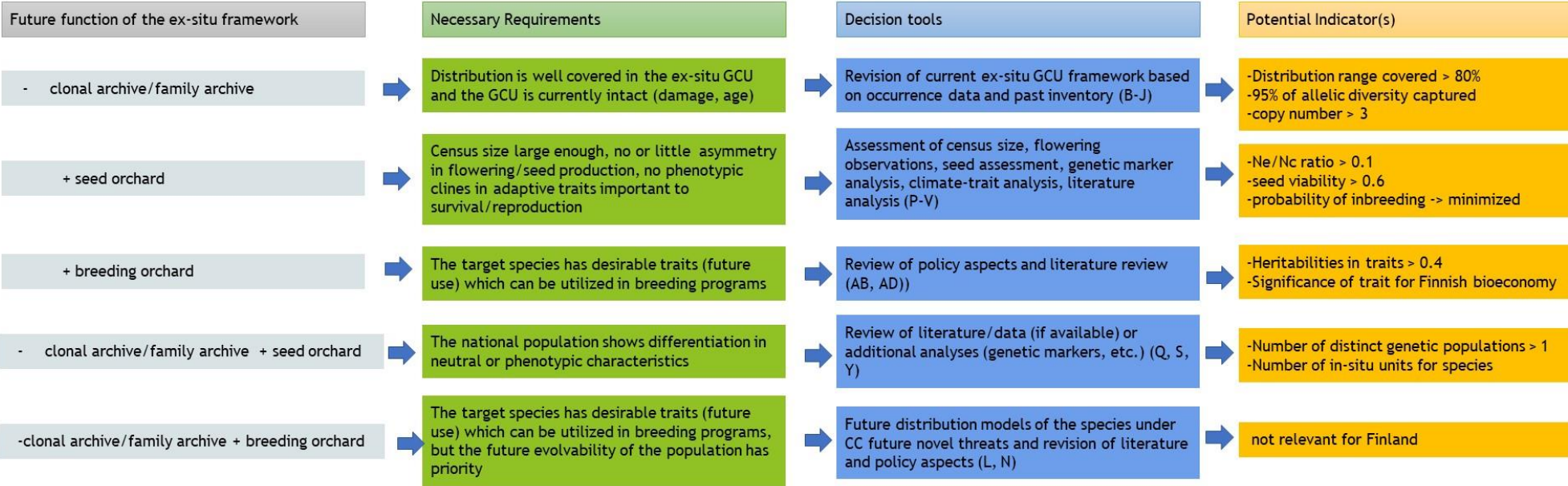


Figure 4: Functions and their corresponding requirements, decision tools, and indicators for monitoring progress and success of the future *ex situ* genetic conservation Action plan in Finland. The list of indicators is not exhaustive and under permanent development.

Defining and monitoring indicators for the primary conservation function (clonal archive/family archive) and its associated task (“maintaining evolutionary processes and favor adaptation”) is essential to meet conservation goals and to develop meaningful guidelines for species-specific conservation plans. These goals must be, however, identifiable (which species and where?), measurable (how much and until when?), and most importantly achievable (yes or no). During its fourth meeting in Nairobi in June 2022, the working group on the post-2020 Global Biodiversity Framework defined specific goals relating to the 2050 Vision for Biodiversity (CBD 2022, Hoban et al. 2023). Under Goal A Option 1 it is written that, **The genetic diversity and adaptive potential of [all] [known] [wild and domesticated] species is safeguarded and [all genetically distinct populations are] maintained [by 2030, at least [95] per cent of genetic diversity among and within populations of [native] [wild and domesticated] species is maintained by 2050.**”

In particular, the last part of Goal A provides at least pseudo-numerical guidelines of what should be achieved and until when. The corresponding target of Goal A further specifies that. **“[and] [to] [maintain and restore] the [genetic diversity] [within and between populations] of [all species] [[all] [native] wild and domesticated species]] [[to] [and] maintain their adaptive potential] including through in situ and *ex situ* conservation,...”**.

Although the finally adopted agreement sounds much softer, we used the CBD goal A for benchmarking and evaluating the current *ex situ* conservation program and for guidance of the long-term strategy of *ex situ* genetic conservation of forest genetic resources. Despite that the goal of 95% conservation goal sounds very ambitious and may not be reachable by applying dynamic *ex situ* conservation alone, it will serve as a benchmark for identifying conservation gaps in the present *ex situ* program.

Delineating genetically distinct populations, metapopulations and estimating population sizes will be of utmost importance to evaluate how far the current strategy offsets from the 95% maintenance goal. While genetic and genomic analysis would be the appropriate tool, their use for evaluating the current strategy would be simply too exhaustive both in terms of labor and financial resources. Hence, we propose and recommend making use of data resources, which are already available (either publicly or within LUKE) and which would allow to circumvent costly genomic analyses at this point. A possible and illustrative workflow is shown in Figure 5 and the results of this analysis will be outlined for each species in the following chapter. Briefly, geographical information resources are merged for each species. These resources comprise layers referring to the species natural occurrences in Finland, locations of stands which are already conserved, species observational records from the Finnish Biodiversity Atlas, Finnish major regions, as well as the Multi-Source National Forest Inventory of Finland. If necessary, observational bias in species observations and evenness of sampling across environments can be assessed by additional data such as from the National Land Survey of Finland (NLS) and the Finnish Meteorological Institute. Numbers and sizes of populations will be determined by means of density-based population clustering using published data on gene flow capabilities (if available). Finally, Hoban (2019) published guidelines on population sampling for optimizing *ex situ* genetic conservation both for capturing 95% of theoretical allelic composition and optimal copy number for back-up conservation. These guidelines are drawn from simulated population genetic parameters and conservation goals can be approximated with the determined population number and average sizes for defining the minimum number of individuals needed for establishing the *ex situ* genetic conservation framework. The step can be seen as a benchmarking process and will be the basis for final recommendations on how many stands should be sampled and how many dynamic and static units should be established to achieve the conservation goal.

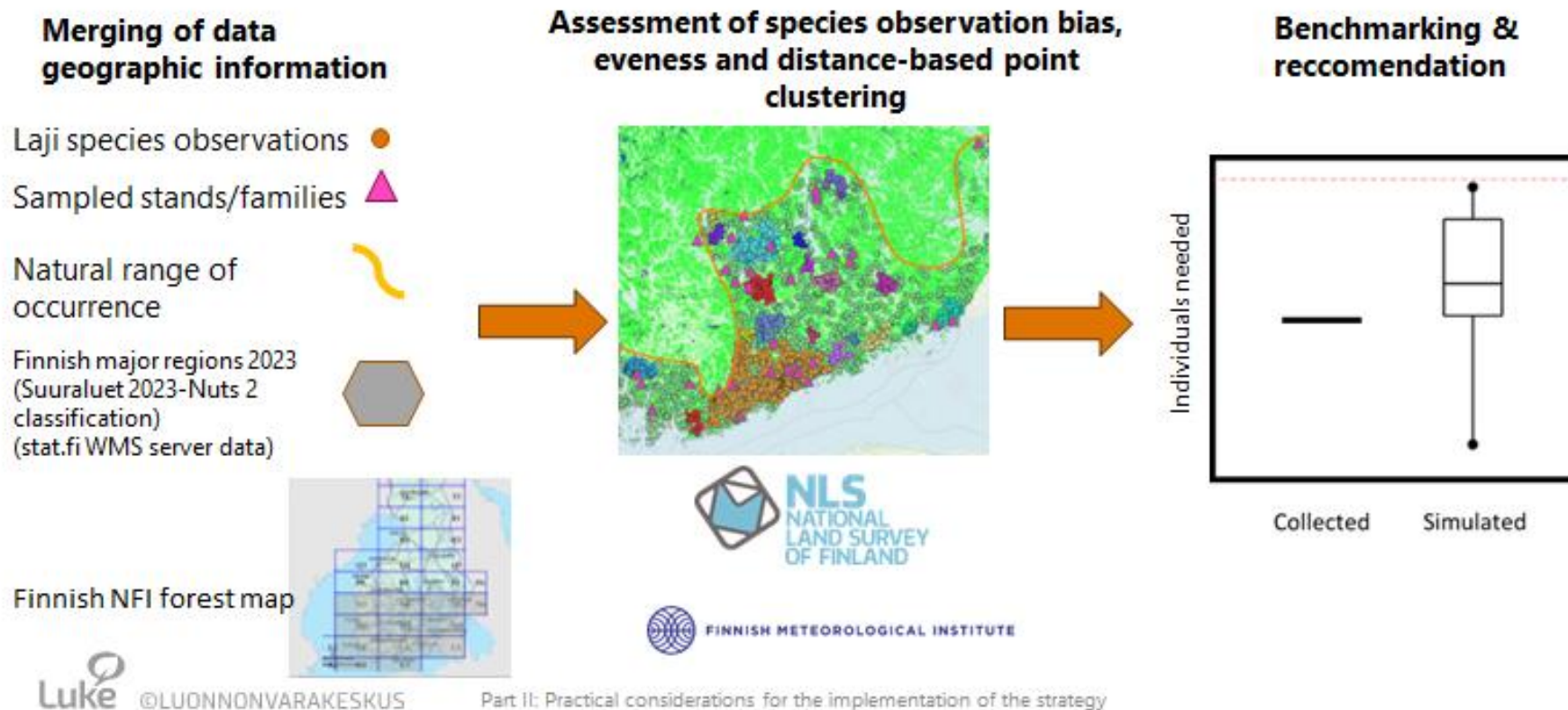


Figure 5: The general scheme for evaluation of conservation success in existing and future GCFs. The first step will be to merge available geographic information sources for each species. Second, observational bias and sampling evenness can be assessed by including additional data resources. Species observations will be clustered to infer the approximate number of populations and mean population size in Finland. Lastly, the collected number of distinct individuals will be compared to a theoretical minimum number required to capture 95% of allelic diversity (red dashed line).

6.5. Extension of the current *ex situ* program: additional tree species needing attention

The current *ex situ* program covers nine tree species which are conserved in 19 dynamic units in Finland. While the current program has mainly given priority to species which are forest trees, we also examined all other wooden species in Finland to be potentially conserved in the program (see Appendix 8.3 for details). Since genetic knowledge for many of these species is scarce or even completely absent, we developed a four-criteria scheme to determine whether some of these species are eligible for the *ex situ* program in the future. These criteria comprised the current distribution, degree of scatteredness, level of threat (according to the Web Service of Red List for Finnish Species), and potential for future use. All criteria were assessed by a maximum of four points where a higher number of points indicate higher necessity for genetic conservation. A final weighted sum was calculated across all four criteria (30% weight on the first three criteria and 10% on future use potential). High conservation priority was defined for all species which had a weighted sum ≥ 3.5 and details for these species can be found in Table 2 further below. According to table 2, we identified *Crataegus monogyna* (tylppöorapihlaja), *Malus sylvestris* (Metsäomenapuu), *Crataegus rhipidophylla* (Suippuorapihlaja), *Scandosorbus intermedia* (Ruotsinpihlaja), *Prunus spinosa* (Oratuomi), and *Taxus baccata* (Marjakuusi) as species with very high *ex situ* conservation priority. Four of the six species are already listed as “critically endangered”, “endangered”, or “vulnerable” and further population decline could have severe consequences for long-term population viability. Nearly all prioritized species have their very limited distribution in south-west Finland and in the Åland islands so that sampling could be possibly streamlined to a few field visits at relatively low costs. Yet, knowledge on planting, grafting, maintenance and optimal site selection for these species need to be acquired before definite conservation actions can start.

It needs to be stressed that the four criteria strongly emphasize biological reasons for conservation, while other reasons may be important though. *Alnus glutinosa*, *Alnus incana* and *Populus tremula* are not short-listed in table 2, although they are publicly more important or better known. It will be hence important to find consensus in the future about further indicators and criteria which make *ex situ* conservation comprehensive and plausible. Another example is mountain birch (*Betula pubescens* var. *pumila* (L.)), which is growing only under arctic and sub-arctic conditions. The species could be threatened by increasing outbreaks of insects due to climate change (Ryde et al. 2021), but due to the lack of data for this rare hybrid, a current inclusion in the national *ex situ* program should be more thoroughly discussed. Finally, there remains the important question under which responsible authority these identified species will fall.

Table 2: Assessment of genetic conservation priority for tree and shrub species in Finland. Shown are the six species with a weighted sum ≥ 3.5 and the four species with lower genetic conservation priority. More details on the criteria can be found in Appendix 8.3. Note that higher values indicate higher conservation priority.

Species	Distribution	Scatteredness	Degree of Threat	Potential for future use	weighted sum	Category
<i>Crataegus monogyna</i>	4	4	4	3	3.9	high priority
<i>Malus sylvestris</i>	4	4	4	2	3.8	high priority
<i>Crataegus rhipidophylla</i>	4	4	4	1	3.7	high priority
<i>Scandosorbus intermedia</i>	4	4	3	1	3.7	high priority
<i>Prunus spinosa</i>	4	4	3	3	3.6	high priority
<i>Taxus baccata</i>	4	4	1	2	3.5	high priority
<i>Alnus glutinosa</i>	2	3	1	3	2.1	no priority
<i>Salix caprea</i>	1	2	1	1	1.3	no priority
<i>Populus tremula</i>	1	1	1	4	1.3	no priority
<i>Alnus incana</i>	1	1	1	1	1.0	no priority

7. Specific recommendations for species currently conserved *ex situ*

7.1. *Acer platanoides*

Current state of conservation:

Acer platanoides is currently conserved in two *ex situ* units, one is located in Preitilä (Kok185) and one in Punkaharju (Kok186). The units have a size of 1.19 ha and contain together 647 seedlings from 235 families originating from 39 stands across Finland. Kok185 was established in 1999-2002 and Kok186 in 1999. Trees in Preitilä thrive well but occasionally show stem cracks due to sun-induced thawing in spring. Families are assembled in rows (Punkaharju) and clusters (Preitilä), respectively. Both units have been thinned during 2023. In Preitilä the thinning was light, removing only 23 % of trees, but in Punkaharju removal was 77 % of the trees thus leaving predominantly only one tree per family. The current status of *A. platanoides* in Finland according to IUCN is *least concern* (LC).

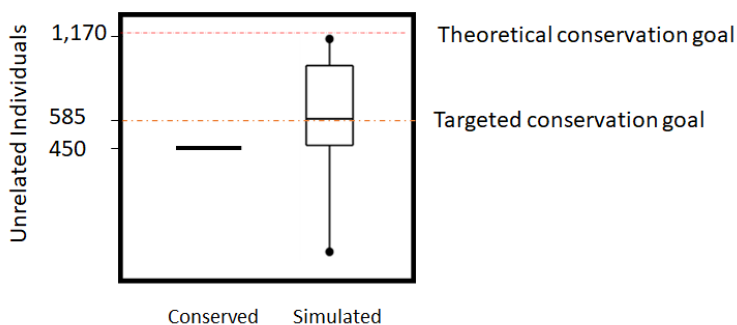
Threats:

There are no novel threats known. Future climate conditions in Finland would potentially allow northward expansion of the species.

Use:

Acer platanoides is an important host species for many other taxa and part of the herb-rich forests in southern Finland. There is, however, no immediate potential for economic use of the species.

Conservation goal (10 years):



Proposed *ex situ* framework(s) and action plan:

We propose to conserve *A. platanoides* in form of family archives with the option of functioning as a seed orchard. At least Kok 185 shows sufficient flowering and seed production. Status numbers (as a surrogate for genetic diversity) were assessed in 2021 and 2022 and showed plausible results ($N_{r\ 2021}$: 27.9% and $N_{r\ 2022}$: 33.8%).

Further recommendations:

Currently none.

Note: There are currently 647 seedlings in the collections. Since these were collected from 235 families, the status number (rather than the census number) should be considered for benchmarking. Hence, the number of collected individuals is given as 450 instead of 647. The status number according to Kang et al. (2005) is used throughout the report.

7.2. *Fraxinus excelsior*

Current state of conservation:

Fraxinus excelsior is currently conserved in 4 *ex situ* GCUs (Kok162, Kok193, Kok195, Kok231) in form of family archives. Kok162, 193 and 195 are approximately 25 years and Kok231 is 5 years old. Most of the GCUs are located in southern Finland (Sipoo, Raasepori), but Kok195 is located in Savonlinna. The number of families varies between 44 and 58 among GCUs and families were collected from 10–15 stands across southern Finland. All GCUs are severely impacted by ash dieback (see below) and the remaining number of families is expected to be much lower compared to current records. The GCU in Sipoo (Kok162) has been largely abandoned and is partly overgrown by willow. *Fraxinus excelsior* is currently not protected in Finland, but its IUCN status has changed to *near threatened*.

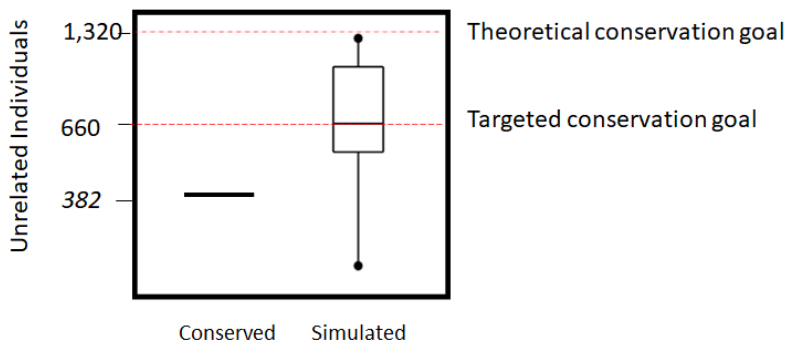
Threats:

The biggest threat for *Fraxinus excelsior* is ash dieback, an aggressive and lethal fungal disease imported from Asia. The fungus has entered Finland approximately 20 years ago and caused an immediate and rapid decline of ash trees. The decline is still ongoing and supposed to be more lethal at wet sites compared to dry sites. A moderate, but significant genetic component causes that a small fraction (~5%) of trees is surviving the disease. Another important threat for ash is the Emerald ash borer, which is just about to enter Europe from Russia in the very next years.

Use:

There is no potential of commercial use of *Fraxinus excelsior* in Finland.

Conservation goal (3 years):



Proposed *ex situ* framework(s) and action plan:

Rapid population decline caused by ash dieback is posing a significant challenge for dynamic *ex situ* conservation in ash. As an immediate action we recommend exploiting the natural variation in resistance against the disease within the existing collections (that is: examination of numbers of healthy/surviving families). The resulting assembly of families should be vegetatively propagated by producing cuttings and graftings. Drier sites are less prone to the disease and should be favored for establishing one new second generation clonal archive. In addition, protocols for in-vitro conservation techniques must be developed for static conservation. These are immediate actions and should be realized within the next 3 years. A long-term goal for genetic conservation of *Fraxinus excelsior* is difficult to formulate given the uncertainty about remaining populations in Finland. Nevertheless, sampling campaigns in natural ash stands should be undertaken in order to safeguard valuable and healthy trees via seed

conservation. Inventories of the existing *ex situ* GCU's should be done as some of the data on material included is fairly old and some of the families may have disappeared.

Further recommendations:

Populations from the Åland islands are currently not included in the *ex situ* conservation framework. We hence recommend extending the current framework towards these valuable island populations.

Note: There are currently 965 seedlings in the collections. Since these were collected from 136 families, the status number (rather than the census number) should be considered for benchmarking. Hence, the number of collected individuals is given as 382 instead of 965. The status number according to Kang et al. (2005) is used throughout the report.

7.3. *Juniperus communis*

Current state of conservation:

Juniperus communis is currently conserved in two clonal archives. Kok220 is located in Paimio and contains 785 ramets from 177 clones. Kok221 is located in Suonenjoki and contains 526 ramets from 129 clones. Clones were sampled from across 60 and 47 stands, respectively and cover the entire Finnish distribution range. Archives were established in 2007 (Paimio) and 2008 (Suonenjoki) and have sizes of 0.26 and 0.18 ha. It is worth to mention that both archives express notable phenotypic variation among provenances. The current conservation status of *J. communis* in Finland is *least concern* (LC).

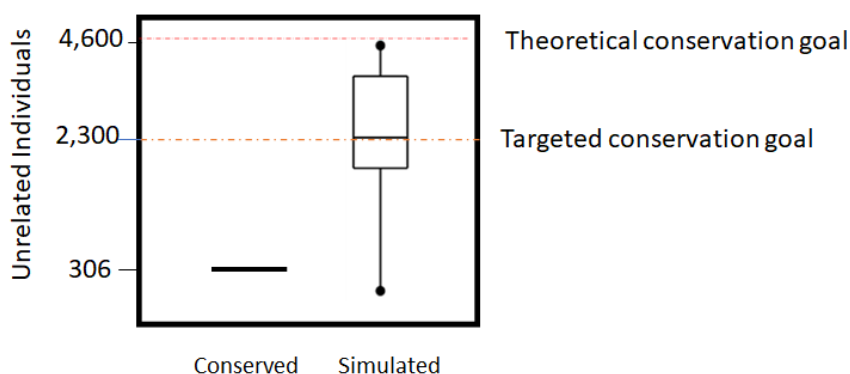
Threats:

There are no immediate threats known, but *Phytophthora austrocederii* (imported from south America) is already present in the UK and may become invasive in Finland in the near future (Flora et al. 2020). Other studies suggest that milder winters can be a threat for seed viability and germination success (Forestry Commission Scotland, 2009).

Use:

There is limited potential for *Juniperus communis* as a non-wood forest product. Juniper berries contain many compounds with biological activity and medical purpose. As such, alpha-pinene is used in form of therapeutical oils and essences (Albrecht & Madisch, 2022). There may be also usage for ornamental purposes given the notable phenotypic variation among provenances. However, more information on the future Finnish demand on Juniper berries would be needed before discussing the possibility of breeding orchards, etc.

Conservation goal (10 years):



Proposed *ex situ* framework(s) and action plan:

We recommend to conserve *Juniperus communis* in a form of a clonal archive with two units. The two existing units in Paimio and Suonenjoki can barely be extended, and we hence recommend to conserve *Juniperus* seed collected from natural stands in order to reach the targeted conservation goal. *Juniperus* seed are orthodox and can be stored for several years in dried condition.

Further recommendations:

None.

7.4. *Prunus padus*

Current state of conservation:

Prunus padus is currently only conserved in one *ex situ* GCU (Kok 214 in Savonlinna). The family archive was established in 2001 and contains 72 seedlings from 11 families. These families originate all from a relatively small area and were collected from 6 different stands in southern Finland. The current status of *P. padus* in Finland according to IUCN is *least concern* (LC).

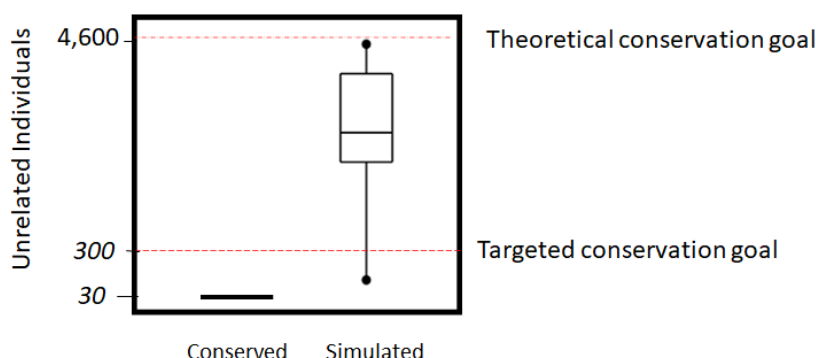
Threats:

There are currently no immediate threats for *Prunus padus*. Small ermine moth and bird cherry-oat aphids can cause temporal defoliation in some years, but are usually harmless in the long-term (Uusitalo, 2004)

Use:

Prunus padus was widely used in the past for ornamental, nutritional and medical purposes. However, it is rarely used any more for commercial purposes except than in some far-eastern Asian countries. However, there are several cultivars and subspecies in Scandinavia, which are partly conserved in botanical gardens. According to Uusitalo (2004), there are 62 rare varieties in Finland and some of them are kept in the University of Oulu Botanical garden.

Conservation goal (10 years):



Proposed *ex situ* framework(s) and action plan:

We recommend to conserve *Prunus padus* in form of a clonal/family archive in two units (south and north). The number of rare varieties would, however, suggest extending the actual sampling effort in order to include more genotypes from different regions. A holistic sampling such as for *Ulmus laevis* is not cost-effective, because *Prunus padus* occurs all over Finland and is not protected or endangered. Clones from rare genotypes are currently conserved

in Oulu at the Botanical garden facilities and we recommend knowledge-exchange between Luke and the University of Oulu in order to synergize conservation efforts.

Further recommendations:

None.

7.5. *Quercus robur*

Current state of conservation:

Quercus robur is conserved in one family archive in Kalvdal (Kok182). There are in total 602 seedlings from 127 families, which were collected in 40 stands across southern Finland. The archive is 0.46 ha in size. The current status of *Q. robur* in Finland according to IUCN is *least concern* (LC).

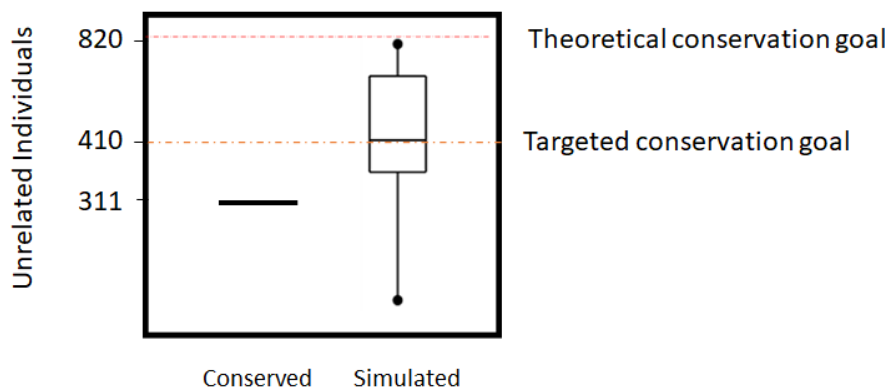
Threats:

Currently none, but acute oak decline (AOD) could become an issue in the future (Denman et al. 2010).

Use:

Oak is the rare broadleaf with potential for use in forestry (MMM 2023). Limited economic use as ornamental tree sold in nurseries.

Conservation goal (10 years):



Proposed *ex situ* framework(s) and action plan:

We propose to conserve *Q. robur* in form of two family archives with the option of functioning as a seed orchard. Although effective family numbers were low and showed significant asymmetry due to overrepresentation of a few families in 2021-2023, the establishment of a second archive with optimal site conditions and spatial randomization would allow for production of genetically very diverse seed for commercialization. Thinning should be done by removing approximately a third of the trees to promote flowering.

Further recommendations:

Because oak is difficult to conserve via seed, we recommend to conserve exclusively in a dynamic fashion via the proposed family archives. Development of automatic flower and seed assessment (e.g., cameras, drones) is recommended for annual seed forecasting and diversity assessment.

Note: There are currently 602 seedlings in the collections. Since these were collected from 127 families, the status number (rather than the census number) should be considered for

benchmarking. Hence, the number of collected individuals is given as 311 instead of 603. The status number according to Kang et al. (2005) is used throughout the report.

7.6. *Sorbus aucuparia*

Current state of conservation:

Sorbus aucuparia is currently conserved in three *ex situ* GCUs in Finland. Kok222 is located in Paimio and was established in 2010. There are currently 484 seedlings from 155 families which were sampled from across 46 stands. Kok223 is located in Suonenjoki and was also established in 2010; Kok223 comprises 781 seedlings from 161 families. Kok230 in Kaarina is the smallest of the three GCUs and contains 236 seedlings from 89 families. Kok222 and kok230 are partial copies of Kok223, meaning that they do not contain any unique families, but only subsets of families in Kok223. The current status of *S. aucuparia* in Finland according to IUCN is *least concern* (LC).

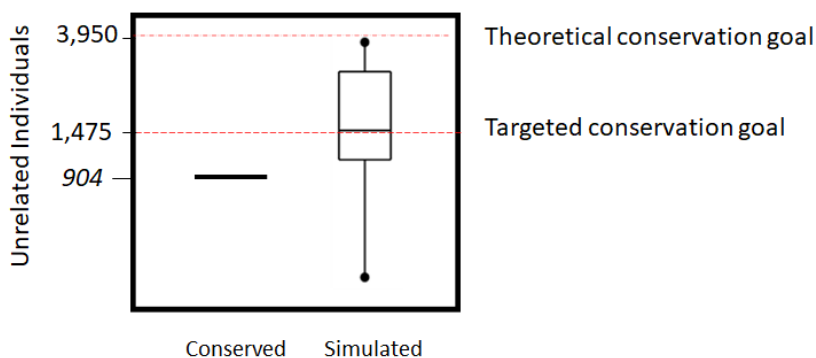
Threats:

There are no immediate threats. However, *Sorbus aucuparia* is natural host to *Limantria spec.* which is supposed to increase its virulence under climate change in southern Finland (Räty et al. 2016).

Use:

There is some potential for *Sorbus aucuparia* to be used as non-wood forest product. *Sorbus aucuparia* fruits are edible and known for their nutritional and medicinal properties. Extracts are potent antioxidants. In Austria and the eastern part of Germany *Sorbus aucuparia* was for a long time subject to tree breeding in order to improve Vitamin-C content of fruits for nutritional purposes (Rutkowska et al. 2021).

Conservation goal (10 years):



Note: There are currently 1,501 seedlings in the collections. Since these were collected from 413 families, the status number (rather than the census number) should be considered for benchmarking. Hence, the number of collected individuals is given as 904 instead of 1,501. The status number according to Kang et al. (2005) is used throughout the report.

Proposed *ex situ* framework(s) and action plan:

We propose to conserve *S. aucuparia* in form of family archives with the option of functioning as a seed orchard. This would require the definition of seed employment zones for *Sorbus aucuparia* and the design of at least two new *ex situ* GCUs, because the current three GCUs contain genotypes from all over Finland, which could lead to outbreeding depression once the seed will be used for afforestation or restoration purposes. A preliminary study on

present and future seed demand in Finland will also be necessary in order to prove the usefulness and cost-effectiveness for *S. aucuparia* seed orchards.

Further recommendations:

We recommend to extend sampling of genotypes further to the north, since this area is currently underrepresented in the living collections. A breeding program and the establishment of breeding orchards for *Sorbus aucuparia* fruit traits is a possible extension of the proposed framework, but the societal demand and political framework needs to be integrated in such a decision. We therefore recommend setting up a pilot study on usage potential together with the respective institutions (e.g., Ministry for Agriculture & Forestry) within the next three years.

7.7. *Tilia cordata*

Current state of conservation:

Tilia cordata is currently conserved in two *ex situ* GCUs. Kok 183 is located in Preitilä and was established in 1998. It contains currently 363 ramets from 259 clones (After replanting in 2023). Kok 190 is located in Punkaharju and contained originally 167 seedlings from 20 families. It was established in 1999. After several thinnings between 1999 and 2023 the number of seedlings in Kok 190 was reduced to 20 (1 per family). The status of *Tilia cordata* in Finland is *least concern* (LC) according to IUCN.

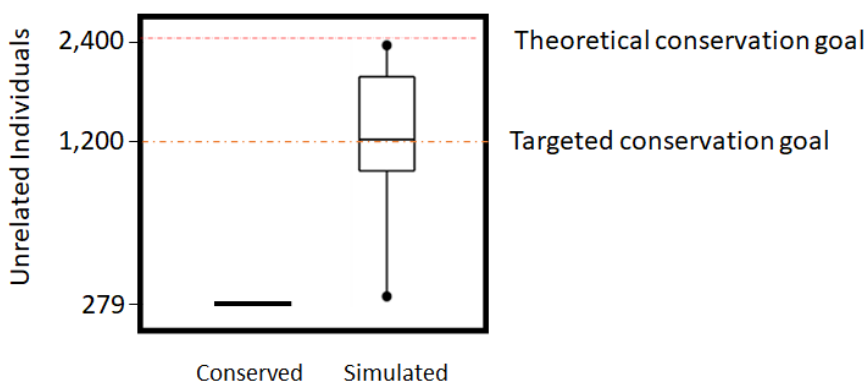
Threats:

Currently none, but sporadic outbreaks of *Apiognomonia errabunda* have been observed in the last years in southern Finland (Vainio et al. 2017).

Use:

Tilia cordata has some potential for commercialization of non-wood products such as linden flowers and linden honey for medical purposes.

Conservation goal (10 years):



Proposed *ex situ* framework(s) and action plan:

We recommend to conserve *Tilia cordata* in form of a seed- and breeding orchard. At least Kok 183 shows very good flowering and seed production in recent years. Status numbers (as a surrogate for genetic diversity) were assessed in 2021 and 2022 and showed plausible results ($N_{r\ 2021}$: 60.1% and $N_{r\ 2022}$: 50.8%). A project on heritability of flower traits for medical purposes could be beneficial for laying the foundation for a future breeding orchard.

Further recommendations:

We recommend to extend sampling for conservation of further individuals towards the north-eastern part of its current distribution, since this part is currently underrepresented in the collections. Conservation of seed in long-term repositories is also recommended.

7.8. *Ulmus glabra*

Current state of conservation:

Ulmus glabra is currently conserved in two *ex situ* GCUs in Finland. Kok184 is located in Paimio and was established in 1998. There are currently 18 ramets from 17 clones which were sampled from across 14 stands growing in Kok184. Kok192 was established in 1969 and has only a size of 0.7 ha. The last inventory has been done in 1997 and there were 73 ramets from 6 clones to that time. Kok184 is located on a site with sub-optimal growing conditions (transient waterlogging) and many clones have therefore ceased during the years. *Ulmus glabra* is threatened in Finland and its status according to IUCN is *vulnerable* (VU).

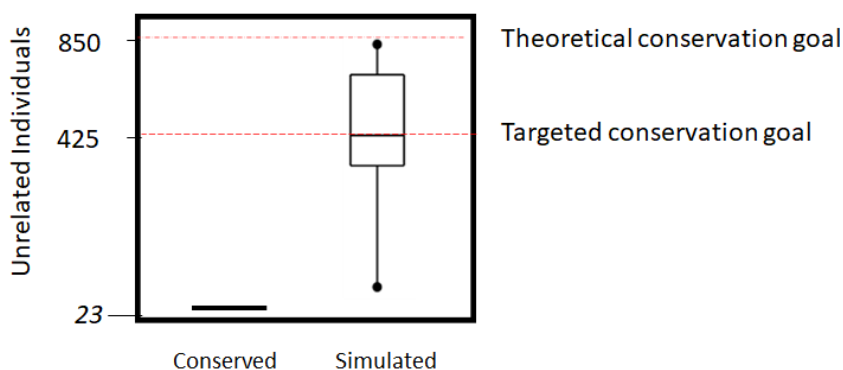
Threats:

The most current threat to *Ulmus glabra* is the Dutch Elm Disease (DED), which will accelerate in the near future due to migrating vectors from neighboring countries (Estonia, Russia).

Use:

There is no potential for future use of *Ulmus glabra* in Finland.

Conservation goal (3 years):



Proposed *ex situ* framework(s) and action plan:

We recommend conserving genetic diversity in *Ulmus glabra* in a dynamic clonal archive with static *ex situ* backup via cryopreservation. The current archive located in Preitilä should be moved within the next 3 years to a location with more suitable and homogenous site conditions to promote flowering and fructification. As an indicator for conservation success, we estimate that an N_{median} of 425 individuals should be reached through dynamic and static *ex situ* conservation. In addition, a static back-up is highly recommended either via cryopreservation or long-term seed storage.

Further recommendations:

No further recommendations.

7.9. *Ulmus laevis*

Current state of conservation:

Ulmus laevis is currently conserved in two *ex situ* units located in south-west Finland (Preitilä: 22 years old and Piikkiö: 5 years old) with a total of 117 clones from 19 natural stands. Site conditions among sites are not homogenous and prone to late-frost occurrence. Particularly, the GCU in Preitilä is characterized by transient waterlogging. Trees in Preitilä flower occasionally, but fructification is strongly limited due to site conditions. *Ulmus laevis* is protected in Finland (NCD 1997/160, Appendix 3a 2021/521) and its status according to IUCN is *vulnerable*.

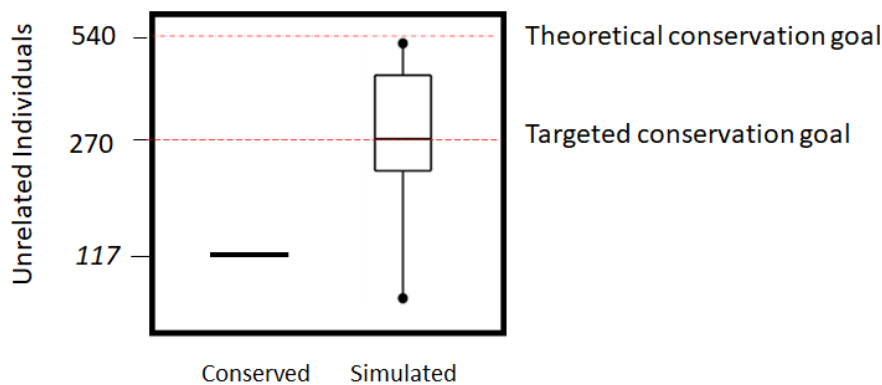
Threats:

Ulmus laevis has a very small and scattered distribution in southern Finland. Future natural population expansion is unlikely due to the low dispersal capacity and availability of suitable habitat. Gene flow is strongly limited among existing populations.

Use:

There is no potential for future use of *Ulmus laevis* due to its protected status in Finland.

Conservation goal (3 years):



Proposed *ex situ* framework(s) and action plan:

We recommend conserving genetic diversity in *Ulmus laevis* in a dynamic clonal archive with static *ex situ* backup via cryopreservation. The current archive located in Preitilä should be moved within the next 3 years to a location with more suitable and homogenous site conditions to promote flowering and fructification. As an indicator for conservation success, we estimate that an N_{median} of 270 individuals should be reached through dynamic and static *ex situ* conservation.

Further recommendations:

Sampling and conservation should be extended towards identified target populations. These are located in the Åland islands, Turku region, and close to Suoniemi.

References

- CBD 2022. Report of the open-ended working group on the post2020 global biodiversity framework on its fourth meeting. CBD/ WG2020/4/4. UNEP.
<https://www.cbd.int/doc/c/3303/d892/4fd11c27963bd3f826a961e1/wg2020-04-04-en.pdf>
- Chaloupková, K., Stejskal, J., El-Kassaby, Y.A. & Lstibůrek, M. 2016. Optimum neighborhood seed orchard design. *Tree Genetics & Genomes* 12: 1–7.
- Commission Guidelines for Defining, Mapping, Monitoring and Strictly Protecting EU Primary and Old-Growth Forests. Commission staff working document. Brussels, 20.03.2023
- Denman, S., Kirk, S. & Webber, J. 2010. Managing acute oak decline. Farnham: Forestry Commission.
- Donald, F., Green, S., Searle, K., Cunniffe, N.J. & Purse, B.V. 2020. Small scale variability in soil moisture drives infection of vulnerable juniper populations by invasive forest pathogen. *Forest Ecology and Management* 473: 118324.
- Dyderski, M.K., Paż, S., Frelich, L.E. & Jagodziński, A.M. 2018. How much does climate change threaten European forest tree species distributions? *Global Change Biology* 24(3): 1150–1163.
- EUFORGEN 2021. Forest Genetic Resources Strategy for Europe. 2021. European Forest Institute.
- Finland's Forests 2020 in a European context demonstrated with selected FOREST EUROPE Criteria and Indicators of Sustainable Forest Management. Natural Resources Institute Finland
- Food and Agriculture Organization (FAO) 2014. Global Plan of Action for the Conservation, Use, and Development of Forest Genetic Resources. Commission on Genetic Resources for Food and Agriculture, Rome.
- Forestry Commission Scotland 2009. Action for juniper.
- Guidelines on Biodiversity-Friendly Afforestation, Reforestation and Tree Planting. Commission staff working document. Brussels, 20.03.2023
- Heikkinen, R.K. 2002. Complementarity and other key criteria in the conservation of herb-rich forests in Finland. *Biodiversity & Conservation*, 11:1939–1958.
- Hoban, S., Bruford, M.W., da Silva, J.M., Funk, W.C., Frankham, R., Gill, M.J., ... & Laikre, L. 2023. Genetic diversity goals and targets have improved but remain insufficient for clear implementation of the post-2020 global biodiversity framework. *Conservation Genetics* 1–11.
- Hoban, S. 2019. New guidance for *ex situ* gene conservation: Sampling realistic population systems and accounting for collection attrition. *Biological Conservation* 235: 199–208.
- 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.

- Hultberg, T., Sandström, J., Felton, A., Öhman, K., Rönnerberg, J., Witzell, J. & Cleary, M. 2020. Ash dieback risks an extinction cascade. *Biological Conservation* 244: 108516.
- Jürisoo, L., Süda, I., Agan, A. & Drenkhan, R. 2021. Vectors of Dutch elm disease in northern Europe. *Insects* 12(5): 393.
- Kang, K.S., El-Kassaby, Y.A., Han, S.U. & Kim, C.S. 2005. Genetic gain and diversity under different thinning scenarios in a breeding seed orchard of *Quercus acutissima*. *Forest ecology and management* 212(1–3): 405–410.
- Kremer, A., Ronce, O., Robledo-Arnuncio, J.J., Guillaume, F., Bohrer, G., Nathan, R., ... & Schueler, S. 2012. Long-distance gene flow and adaptation of forest trees to rapid climate change. *Ecology Letters* 15(4): 378–392.
- Letzig, E. & Handschack, W. 1963. Vergleichende Untersuchungen über einige Inhaltsstoffe bitterer und süßer Ebereschenfrüchte während des Reifens. *Food/Nahrung* 7(8): 591–605.
- Mann, H.M., Iosifidis, A., Jepsen, J.U., Welker, J.M., Loonen, M.J. & Høye, T.T. 2022. Automatic flower detection and phenology monitoring using time-lapse cameras and deep learning. *Remote Sensing in Ecology and Conservation* 8(6): 765–777.
- Mauri, A., Girardello, M., Strona, G., Beck, P.S., Forzieri, G., Caudullo, G., ... & Cescatti, A. 2022. EU-Trees4F, a dataset on the future distribution of European tree species. *Scientific Data* 9(1): 37.
- Mullin, T.J. 2017. OPSEL 2.0: a computer program for optimal selection in tree breeding. Arbetsrapport från Skogforsk 954-2017.
- Nielsen, L.R. & Kjær, E.D. 2010. Gene flow and mating patterns in individuals of wych elm (*Ulmus glabra*) in forest and open land after the influence of Dutch elm disease. *Conservation Genetics* 11: 257–268.
- Pehu, T., Kiviharju, E., Rusanen, M., Kantanen, J. & Heinimaa, P. 2020. Finland's National Genetic Resources Programme for Agriculture, Forestry and Fishery: Summary of the Finland's National Genetic Resources Programme for Agriculture.
- Räty, M., Caudullo, G. & de Rigo, D. 2016. *Sorbus aucuparia* in Europe: Distribution, habitat, usage and threats. In San-Miguel-Ayán, J., de Rigo, D., Caudullo, G., Houston Durrant, T. & Mauri, A. (Eds.). *European Atlas of Forest Tree Species*: 176–177.
- Rusanen, M., Beuker, E., Yrjänä, L., Haapanen, M. & Paanukoski, S. 2021. Finland's forest genetic resources, use and conservation. *Natural resources and bioeconomy studies* 4/2021. Natural Resources Institute Finland. Helsinki. 35 p.
- Uusitalo, M. 2004. European bird cherry (*Prunus padus* L.)-a biodiverse wild plant for horticulture. MTT.
- Vainio, E.J., Velmala, S.M., Salo, P., Huhtinen, S. & Müller, M.M. 2017. Defoliation of *Tilia cordata* trees associated with *Apiognomonia errabunda* infection in Finland. *Silva Fennica*.

Appendix

Criteria list and explanation of the decision tool

The following criteria were considered for the decision which conservation genetic framework will be best suited for each species:

1. Is the distribution of the species well covered in the existing GCUs? [categorical answer: 1-insufficient; 2-sufficiently covered; 3-well covered]
2. Are the existing units damaged or impacted by any abiotic or biotic agent? [binary answer: yes/no]
3. Have the existing units been thinned? [binary answer: yes/no]
4. Are there any threats known for the conserved species which could have an impact for future conservation or population size? [free text after literature review]
5. What is the future projected distribution of the species under climate change in Finland? [free text after literature review]
6. Has phenological data such as flushing or flowering been assessed and analysed in the conserved species? [binary yes/no]
7. Has adaptive clinal variation been observed in the conserved species within its distribution and particularly in Finland? [free text after literature review]
8. Has neutral genetic diversity/differentiation been assessed/observed in the conserved species within its distribution and particularly in Finland? [free text after literature review]
9. Has tree-wise data such as growth, DNA samples, phenology, etc. been collected from existing GCUs? [binary: yes/no]
10. What is the overall impact of the conserved species on biodiversity in Finland (i.e., potential for co-conservation)? [free text after literature review]
11. Are classical or novel genomic resources available for the conserved species (e.g., DNA markers, reference genome, etc.)? [free text after literature review]
12. Are there any genomic resources/genetic data for the conserved species available at Luke? [free text after database review]
13. What is the future desired utility of the conserved species in Finland? [categorical: 1-primary wood production; 2-fuel and energy wood; 3-non-timber forest product; 4-biodiversity; 5-no use]
14. Are there any special policy aspects related to the conservation of the species? [free text after policy review]
15. Is static conservation (e.g., cryopreservation, seed storage) possible in the conserved species? [free text after literature review]
16. What is the mating and reproduction system of the conserved species like? [free text after literature review]
17. What is the pollination type of the conserved species? [free text after literature review]
18. What are the average distances for seed and pollen dispersal? [free text after literature review]

Information sources for population delineation and benchmarking

The analytical process of population delineation and benchmarking can be briefly summarized into three steps:

1. Gathering and merging geospatial information for each species.
 2. Applying a distance- and density-based clustering algorithm.
 3. Comparing the number of unrelated individuals which currently is in the collections to a theoretical number which would be necessary to capture a certain fraction of the intraspecific allelic diversity.
- 1) Species presence data was obtained from the Finnish Atlas of Biodiversity (laji.fi) for each of the nine species and merged with administrative boundary data for Finland at different levels (GISCO database available under <https://ec.europa.eu/eurostat/web/gisco/overview>). Additionally, species occurrence margins and the Finnish Forest map were added as shape- and raster files respectively. The Finnish forest map is available under <https://kartta.luke.fi/opendata/valinta-en.html>. We chose the thematic layer "Land Class 2021" which distinguishes between three forest types (forest land, poorly productive forest land, and unproductive land). Species occurrences were subsequently clipped to observations within the natural range margins and which were made on forest land only (all three categories). The species presence data have not been adjusted for observational bias.
 - 2) We applied the DB-Scan (Density-based spatial clustering of applications with noise) algorithm in order to group species presence points into homogenous groups of pseudo-populations. The DB-scan algorithm requires two parameters: i) the minimum number of points clustered together for a region to be considered dense, ii) the maximum distance allowed between clustered points. For pragmatic reasons, we used uniform parameters of 5 points and 5000m for all species except oak (5/1000). We are aware that the obtained number of populations strongly varies with the above parameters changing, but the chosen parameter combination yielded biologically plausible results. Number of populations and average population size as well as variance in population size and minimum population size were obtained by running a short R-script over the exported point features.
 - 3) Hoban (2019) provided guidelines for sampling of populations for *ex situ* genetic conservation. Briefly, the number of unrelated individuals needed to capture a certain fraction of the theoretical allelic diversity is a function of the number of populations, population size, migration rate, and -most importantly- the type of alleles one intends to capture. For the current report it was assumed that the aim of conservation is to capture all alleles in a population regardless of the minimum frequency. This would mean that even singletons would be subject to conservation and sampling strategies. Data which was obtained from step 2) described above was then used to calculate the theoretical number of individuals needed and this number was compared to the number of unrelated individuals which are currently in the collection.

It must be noted here that the data and calculations may be improved in the future: the species observations are to some extent biased and constitute presence-only data without detailed absence information. It is also important to consider copy numbers

in the future, which will increase the size of collections and may call for stronger static *ex situ* efforts to reach the necessary number of unrelated individuals. The methodology will constantly be improved within Luke and conservation targets will be accordingly adjusted whenever necessary.

Decision tool for identifying tree species to be conserved *ex situ* in the future

A simple weighted sum of four criteria was applied to all species. The four criteria were: i) degree of scatteredness (1-4: with 1 indicating low scatteredness and 4 very high scatteredness), ii) distribution (1-4 with 1 indicating a wide distribution and 4 a very narrow distribution in Finland), iii) degree of threat (1: least concern, 2: data deficiency, 3: nearly threatened, 4: threatened), and iv) potential for future use (1-4 with 1 indicating no use at all and 4 indicating potential for use at high scale). 30% weight was put on each of the first three criteria and 10% on the potential for future use criterion. The reason for this weighting scheme is that the first three criteria are based on the current and known population conditions, while the potential for future use is speculative and was derived from a literature review. Data sources for criteria 1-3 were taken from the Finnish Biodiversity atlas and the Red List of Finnish species. Below is an example for *Crataegus monogyna* (Hawthorn).

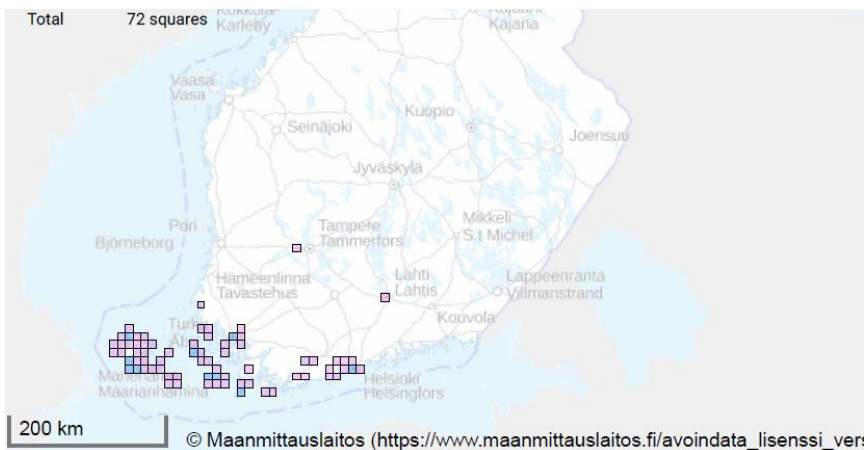


Figure A.1: The map shows observations for hawthorn in Finland. The colors of the squares refer to number of individuals which were mapped. Purple: 1-9 individuals, blue: 10-99 individuals. (Score=4 for both scatteredness and distribution).

The current status of *Crataegus monogyna* in Finland is *critically endangered* (i.e. Threatened). (Score=4)

There is some potential for future use for *Crataegus monogyna* due to its medical purposes. Particularly, flowers and berries are known for their bioactive and antibacterial characteristics. However, it is unlikely that hawthorn will be used at high scale because of its medical purposes alone in Finland. Hence, potential for use at low economic scale can be probably expected. (Score=3)

Example source: Caliskan, O. (2015). Mediterranean hawthorn fruit (*Crataegus*) species and potential usage. In *The mediterranean diet* (pp. 621-628). Academic Press.

The overall score is calculated as: $(0.3 \times 4) + (0.3 \times 4) + (0.3 \times 4) + (0.1 \times 3) = 3.9$



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