In Situ and *Ex Situ* Conservation Measures

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Abies alba seed orchard managed by AWG. (Photo: T. Hase, StMELF)

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Abstract

The effects of climate change and biodiversity loss are global and not limited by national borders, with forest ecosystems, in particular, suffering under increasing pressure. To preserve and maintain species genetic diversity, well-considered *in situ* and *ex situ* measures are needed. We present a step-by-step guide outlining the key processes for structuring, performing, and selecting appropriate sustainable use and conservation measures for forest genetic resources (FGR). Two case studies focusing on European white elm (*Ulmus laevis* Pall.) and wild service tree (*Sorbus torminalis* (L.) Crantz), for which the guide was followed, demonstrate that differences in the regional genetic pattern should be followed when designing FGR sustainable use and conservation efforts. The fact that seed orchards can maintain high genetic diversity and provide high-quality, genetically diverse seed material makes them an optimal supplement to *in situ* genetic conservation units. Especially for scattered or threatened tree species, *ex situ* measures are of utmost importance. In light of a severe pest outbreak, i.e., ash dieback, preserving less susceptible ash trees (*Fraxinus excelsior* L.) is crucial to enable their reproduction and facilitate gene flow among them to prevent crucial loss of genetic diversity and eventually the species itself. Therefore, forest genetic monitoring should be used more intensively to observe, measure, and assess the long-term FGR conservation efforts as genetic variation is an integral part of biological diversity, which requires special attention.

Keywords

Forest genetic resources · Sustainable use of FGR · Genetic diversity · Conservation · GCU · Disease resistance · Gene flow · Forest genetic monitoring · FGM

Introduction

The effects of climate change and biodiversity loss are global and not limited by national borders, with forest ecosystems, in particular, suffering under increasing pressure (European Green Deal 2019; Lefevre et al. 2024). According to the New EU Forest Strategy for 2030, the adaptation of forests to climate change will require large quantities of appropriate forest reproductive material (FRM) from *in situ* and *ex situ* forest genetic resources/conservation units. Therefore, coordinated efforts following “best practice” examples will be needed to conserve and sustainably use forest genetic resources (FGR) on which more climate-adapted forestry depends. Furthermore, to increase the production and availability of such FRM, policymakers will need to raise support for research to develop principles and application methods for *in situ* and *ex situ* conservation as well as for assisted forest species migration where needed (New EU Forest Strategy for 2030).

Box 11.1 Definition of In Situ and *Ex Situ*
By definition, *in situ* conservation means "the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticated or cultivated species, in the surroundings where they have developed their distinctive properties," while *ex situ* conservation is defined as the conservation of components of biological diversity outside their natural habitats (Convention on Biological Diversity, Art. 2; https://www.cbd.int/convention/articles/?a=cbd-02).

Thus, conservation of FGR can be *in situ* dynamic, allowing evolutionary forces such as selection, mutation, recombination, and gene flow to act; *ex situ* dynamic when species or populations are moved and planted outside of their original habitats or even outside of their natural distribution range (*ex situ* conservation stand and seed orchards); or static (*ex situ*) when genetic material (seed, pollen, or plant tissues) is stored in gene banks (Forest Genetic Resources Strategy for Europe, 2021). Following the Forest Genetic Resources Strategy for Europe (2021), *in situ* conservation should be a priority and the primary conservation strategy for FGR since it enables evolution and local adaptation.

However, effective conservation of FGR requires a combination of both *in situ* and *ex situ* (dynamic and static) methods to be applied, as outlined in the Forest Genetic Resources Strategy for Europe (2021). This strategy is integrated, for example, into the concept for the conservation and sustainable use of FGR in Bavaria (Generhaltungskonzept 2015), which is based on the "Concept for the Conservation of Forest Genetic Resources in the Federal Republic of Germany" (Paul et al. 2000). Coordination of forest genetic resources selection, use, and conservation efforts in the Federal Republic of Germany has been led by a federal state working group (BLAG-FGR) since 1985. With the development of the "Recommendations for the Designation of Gene Conservation Units, Taking Minimum Criteria into Account," the procedure for recording and designating *in situ* gene conservation was defined (BLAG-FGR, status 01/2017). These recommendations align with the guidelines set forth by the European Forest Genetic Resources Conservation Programme (EUFORGEN).

Both *ex situ* and *in situ* conservation measures require decisions on which populations to select or sample (Ledig 1986). To optimize the conservation network and its management activities, it is important to accumulate relevant knowledge on species ecology, biology, distribution, and patterns of genetic variation (Ledig 1986 and references therein). According to Neel and Cummings (2003), if a selection of gene conservation units (GCU) is made without data on genetic variation, then larger sample sizes within each population and larger numbers of populations are needed to ensure the conservation of genetic diversity and representation of rare and common alleles. Thus, following Ledig (1986), a common method to select GCUs without genetic information would be to select populations representing different

environments or habitats, which are most likely to contain most of the species' genetic variation. However, this type of conservation requires intensive selection of larger conservation units from different environments, and the consent of different forest owners is often necessary. In addition, the protection of individual trees as well as small and marginal populations of scattered tree species should also be considered in the process of selection for conservation since they can possess specific genetic variants and are needed to ensure connectivity among population fragments (Ledig, 1986; Bednorz 2007).

Since biotechnologies including various genotyping techniques have become cheaper and more efficient, DNA analysis after systematic sampling from different environments can be used to map the patterns of spatial genetic structure (gene pools) across a species' natural distribution range. Collected information and genetic diversity measures provide information on genetic variability within and among populations, allowing the optimized choice of populations for species conservation and the use of FGR to be optimized (Marshall and Brown 1975; Ledig, 1986; Hettemer 1995; Petit et al. 1998; Rajora and Mosseler 2001; Caballero et al. 2010; Koskela et al. 2013; Schueler et al. 2014; de Vries et al. 2015). Extensive sampling combined with DNA analysis can thus lead to a well-supported number and selection of populations needed for actual conservation measures (Ledig 1986 and references therein). There are numerous such examples for various tree species in Europe, like *Sorbus torminalis* (Demesure et al. 2000; Hoebee et al. 2006; Bednorz and Kosiński 2006; Bednorz 2007; Kučerova et al. 2010; Kavaliauskas et al. 2021; etc.), *Ulmus laevis* (Collin and Bozzano 2015; Collin et al. 2020; Kavaliauskas et al. 2022a; etc.), *Taxus baccata* (Šeho et al. 2022; Komárková et al. 2022; Linares 2013; Klumpp et al. 2011; Dubreuil et al. 2010), *Pinus* spp. (González-Martınez et al. 2004; Dzialuk et al. 2014; Pyhäjärvi et al. 2020; Kavaliauskas et al. 2022b; etc.), *Fagus sylvatica* (Lefevre et al. 2013; von Wuehlisch 2008; Vornam et al. 2004), and *Quercus* spp. (de Dato et al. 2018; Lefevre et al. 2013; Ducousso and Bordacs 2004).

IUCN has formulated different management categories for protected areas to comply with the purpose of protection (IUCN 1994; Dudley et al. 2010). Several conservation programs exist for forest trees (White et al. 2007). However, the selection of conservation strategies and GCUs for specific tree species depends on many factors such as species biology (e.g., pollination type), ecology (e.g., species rarity and scatteredness), genetic structure (e.g., genetic variation within and among populations), and external factors including forestry policies, ownership, economic importance, risk of extinction, etc. The Forest Genetic Resources Strategy for Europe (2021) underlines that GCUs (*in situ* and *ex situ* together) are the key elements in the pan-European network for the dynamic conservation of FGR and that the distribution and coverage of GCUs must be expanded to cover as many species and their genetic diversity as possible, including rare tree species and marginal populations at the boundaries of natural distributions. Furthermore, active GCU monitoring and maintenance through management, if necessary, must maintain evolutionary processes and increase the adaptability of selected tree populations. Regular genetic monitoring is needed to assess the effective population size and

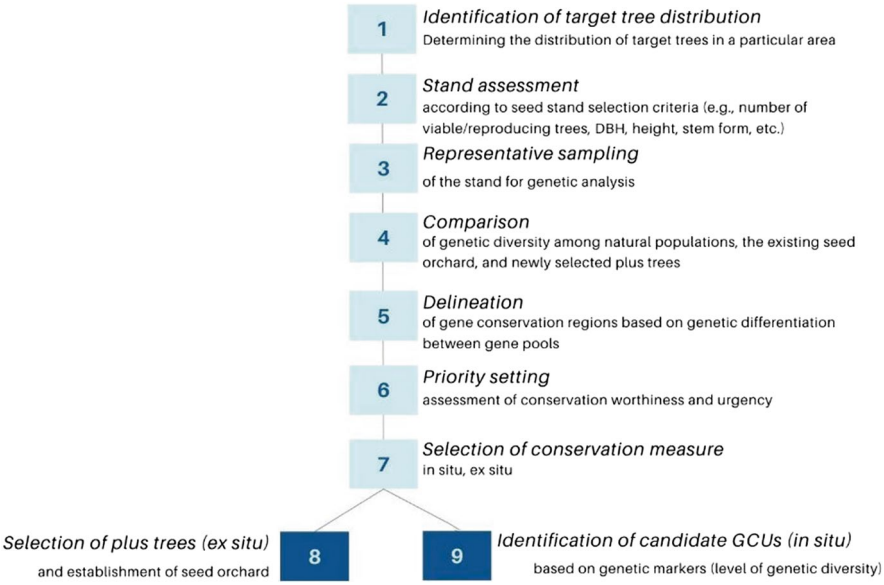


Fig. 11.1 A step-by-step guide to conservation of FGR including the choice of measure (*in situ* or *ex situ*)

reproduction capabilities of GCUs and their ability to adapt under changing environmental conditions (Fussi et al. 2016; Bajc et al. 2020, Liesebach et al. 2024, Forest Genetic Resources Strategy for Europe 2021). In the following, we will discuss *in situ* and *ex situ* conservation measures with examples for dominant and scattered tree species (Fig. 11.1).

Anthropogenic disturbances have negative consequences for genetic diversity and the adaptive potential of species (Aravanopoulos 2018; Kavaliauskas et al. 2018; Gautam et al. 2021, Lefevre et al. 2024). A high level of genetic diversity is the basis for the adaptation and adaptability of FGR and must therefore be maintained for the future. Conservation of FGR aims to improve the genetic diversity and adaptability of forest stands over time, and forest genetic monitoring (FGM) provides us with information on the conditions and changes in the forest genetic system (Fussi et al. 2016, Bajc et al. 2020). Modern forestry is based on the prudent use of FGR. The basis of silvicultural activity is the conservation and improvement of the various forest functions and the conservation of biological diversity at all levels. Assignment of a forest stand as a seed stand can enhance the usage and spread of a species, thereby increasing its distribution and preventing further fragmentation of its range.

Following the flowchart in Fig. 11.1, certain steps should be taken prior to making decisions on species conservation. First, information on the existing populations of the target species should be gathered. Species distribution maps, data from forest inventories, and surveys among forest owners can help collect all the relevant details on the species in a certain area. Based on the collected data, stands should be sorted

according to minimum requirements and then visited and evaluated using a predesigned routine. Photographs of the potential stands facilitate comparison between them. Stand size and tree numbers depend on the tree species and the conservation objectives. Koskela et al. (2013) suggested minimum sizes of the GCUs to be set at 500, 50, or 15 reproducing individuals for stand-forming scattered and endangered tree species, respectively. Potential stands should be vital and possess good to very good quality (e.g., height growth, form, and vigor), and a minimum of 50 individuals of the target species should be present in each stand or within gene flow distance. These 50 trees should be of reproductive age. If flowering or fructification cannot be assessed directly, the DBH or crown size can serve as a proxy (DBH > 20 cm for most tree species). The more reproducing trees are present, the higher the potential for new genetic genotypes/combinations. Gene conservation for forestry purposes may also include attributes like the ability to harvest seeds from the stand or a minimum distance to poor phenotypes of 400 m (recommendations according to German FoVG, 2003). Information on the autochthony of the origin of the populations is also beneficial. Following this initial evaluation of the stands, populations to be sampled for genetic analysis should be preselected. In addition, species distribution should be considered for representative sampling. Sampling for genetic analysis should ideally be systematic to cover the entire population and include at least 50 reproducing trees with a minimum distance of 30 m between sampled individuals. The genetic analysis provides an overview of the species' genetic variation and spatial genetic structure and can help identify hotspots of genetic diversity. Several genetic diversity parameters can be used for comparison and prioritization of different populations. Following Marshall and Brown (1975), Petit et al. (1998), Rajora et al. (2000), Rajora and Mosseler (2001), and Caballero et al. (2010), we consider the allelic richness (Ar) value (number of different alleles segregating in the population) to be of key importance in conservation programs, especially for subdivided and scattered tree species. Therefore, we suggest Ar as the main parameter for GCU selection. In addition, the measure of effective population size (Ne) is a critical verifier in the selection and conservation of forest genetic resources (Lande and Barrowclough 1987, Santos-del-Blanco et al. 2022, Hoban et al. 2023, Liesebach et al. 2024, etc.). Estimates of contemporary effective population size (Ne) can provide valuable information for genetic conservation and monitoring, pinpointing populations at higher risk of genetic erosion, decreased fitness, maladaptation, and ultimately, demographic decline (Santos-del-Blanco et al. 2022 and references therein). In conservation genetics, Ne is important because it influences the rate at which genetic diversity is lost (e.g., due to genetic drift). Thus, small populations of scattered and threatened tree species are susceptible to genetic drift, leading to a faster loss of genetic diversity and an increased risk of inbreeding depression and the accumulation of deleterious mutations. Therefore, Ne should serve as a crucial measure for FGR selection and is essential for preserving genetic diversity, ensuring the long-term viability of populations, and formulating necessary action plans (Santos-del-Blanco et al. 2022, Pérez-Pereira et al. 2022 and references therein, Hoban et al. 2023).

The required number of populations to conserve as GCUs within a species depends on how diversity is divided within and among populations, which measure of diversity is chosen, and how much of the total diversity is considered sufficient (Neel and Cummings 2003). According to Neel and Cummings (2003), a greater number of populations is required to conserve genetic diversity if GCUs are selected without genetic information. The selection of GCUs should therefore be based on collective data of genetic diversity, environmental data, and tree/population distribution in certain regions to ensure gene flow among populations and sufficiently high genetic diversity. Moreover, genetic differentiation among populations may be used as one of the measures for GCU selection, even if some populations do not exhibit the required level of genetic diversity, since some of them may possess rare alleles and genotypes (Bednorz 2007; Jost et al. 2018). However, due to the high costs of genetic analysis, target areas and species might be prioritized and selected.

Species and population prioritization consider endangerment status and allow decisions regarding the urgency of conservation measures. From an ecological or economic point of view, valuable populations of a species that are adapted to their site conditions and harbor high genetic variability should be the focus for genetic conservation. For dominant tree species, in addition to vitality and the presence of natural regeneration, above-average stem quality and growth characteristics can also be considered important criteria for selection for conservation. An assessment of conservation necessity should be conducted for populations at high risk of extinction or decline. Within the group of rare and ecologically important tree species, the focus lies on the assessment of conservation urgency at the species level. For example, the guideline for the conservation and sustainable use of forest genetic resources in Bavaria (Germany) defines three priority levels:

1. Species of high priority—gene conservation measures are urgently needed.
2. Species of medium priority—gene conservation measures are needed but not urgent.
3. Species of low priority—gene conservation measures are currently not needed.

The endangerment of a population can be determined by estimating the following risk factors, some of which mutually influence each other or increase multiple risks when they coincide:

– Actual population size, minimum viable population size, and effective population size: For example, the minimum size for a viable population often has been used as a crucial measure in conservation practice to determine the extinction risks of populations and species. An effective population size of at least 50 unrelated and reproducing individuals (Ne = 50) is needed to minimize the risk of extinction due to inbreeding depression, and Ne of 500 individuals is required for a population's long-term survival (Pérez-Pereira et al. 2022 and references therein). The smaller the population, the higher the risk of extinction through drift effects (e.g., natural disaster and disease incidence).
– Deviation from the potential natural vegetation: The further the current population is from the optimal distribution (suitable ecological niche) for its species, the higher the risk of extinction (Aitken et al. 2008; Gougherty et al. 2021, etc.).

- Weakness in competition: Competition from precocious, more competitive species increases the risk of decline.
- Disposition to diseases/disasters: Species whose existence is threatened by diseases/disasters are at increased risk.
- Hybridization with cultivars: Plantations of cultivars in the immediate vicinity of gene conservation objects pose a threat to the gene resource through introgression (e.g., wild cherry, wild apple, wild pear, small-leaved lime, etc.).
- Loss of forest areas leads to a reduction in effective population size, as well as making gene flow more difficult due to habitat fragmentation.
- Browsing of natural regeneration limits the genetic preservation of GCU since establishing new tree generations becomes challenging.

Following the prioritization of populations, the appropriate conservation measures must be chosen. These can be *in situ* or *ex situ* measures or a combination of both depending on the circumstances; possible approaches are described in the following.

In Situ Conservation Measures

Species with an adequate number of viable populations within their natural distribution range can be considered for *in situ* conservation. The objective should be to conserve the genetic variation, facilitate the natural regeneration of the GCU, or conduct artificial regeneration with reproductive material taken from the same population. In situ measures offer the advantage that they can be integrated into regular forest management (forest management planning corresponding to GCU conservation aims).

By contrast, rare tree species should generally be completely protected from exploitation, with only minor exceptions granted if populations meet specific criteria, which ensures population continuity, such as the presence of natural regeneration, compliance with viable population size standards, etc. Different populations of a rare species often have unique genetic compositions, making the loss of any population an irreparable genetic loss (e.g., because of lost locally adapted genetic variation, interrupted connectivity, and gene flow). For most rare species, GCUs are an absolute necessity to protect the FGR, and additional *ex situ* preservation is also required to reduce the risk of sudden loss through drift effects (e.g., catastrophic events like fire or landslides). Common tree species are often genetically variable but are generally exploited more intensively, and population-specific (rare and private) alleles can therefore be lost if management methods do not consider the species' genetic peculiarities (Danusevičius et al. 2016; Kavaliauskas et al. 2018, Danusevičius et al. 2023, etc.). Certain forest areas with populations of target tree species should be set aside to allow natural evolutionary processes to act (natural regeneration is mandatory, harvest techniques enhancing genetic diversity, reproduction, selection, etc.). GCUs may be influenced by undesirable pollen flow from surrounding plantations regenerated with seedlings of off-site parentage. However,

geneticists disagree strongly on the impact of pollen contamination (Nienstaedt, 1980). While some reports show that wide buffer zones are necessary (Yeatman, 1973), thus making GCUs impractically large, others report that pollen migration will be ineffectual if immigrants carry maladapted genes since proper harvesting can assure dense regeneration, and natural selection can be relied upon to eliminate unfit progeny (Adams and Burczyk 2000). On the other hand, if migration introduces selectively advantageous genes, then contamination poses no problem for the preservation of adapted populations (Fitzpatrick et al. 2015, Tigano and Friesen, 2016). The substitution of neutral alleles may be a problem if the management unit is so small that pollen influx swamps the local pollen contribution. However, many management alternatives can be devised to reduce the problem of pollen contamination; they include surrounding the management unit with plantations of different species, resorting to mass pollination with appropriate pollen, or controlled pollination, and artificial regeneration with progeny known to have originated from crossing among native trees (Ledig, 1986). Trees tend to have high levels of heterozygosity, but it is not clear whether they have the evolutionary potential to withstand climate change and whether their phenotypic plasticity enables them to respond to short- and medium-term climate shifts (Kelleher, 2018). Since only 1% of all tree species have been genetically analyzed, the use of indicators (e.g., allelic richness and effective population size) is needed to obtain a more comprehensive picture of global forest genetic resources. In any case, the best practice for the conservation of large, long-lived organisms like trees is a dynamic or near-natural in situ conservation approach facilitating evolution (Kelleher, 2018).

Ex Situ Conservation Measures

In some specific cases, established *in situ* GCUs may not survive, particularly in areas where environmental conditions are changing rapidly. Moreover, there are species exhibiting highly fragmented populations like *Sorbus torminalis, Sorbus domestica,* or *Pyrus pyraster*, where traditional *in situ* conservation approaches might be ineffective because of low target tree species densities in certain areas (Forest Genetic Resources Strategy for Europe 2021). Thus, for such species with a low number of viable populations and low tree density per population, *ex situ* measures should be favored. *Ex situ* measures include the establishment of populations outside a species' natural surroundings, conservation seed orchards, clone collections, *ex situ* conservation stands, storage of seeds and pollen, storage of plants and plant parts, and permanent vegetative and in vitro propagation.

Ex situ conservation is appropriate when a tree species is rare and grows only in small patches, when the habitat is threatened, or when natural regeneration is impeded (e.g., by game browsing or occurrence of clones). The principal method for *ex situ* conservation of forest tree species is the establishment of various tree collections (e.g., seedling or clonal seed orchards, clonal tree archives, *ex situ* conservation stands, and other tree collections). Individual trees are either propagated by grafting and the grafts moved to clone collections or by collecting seeds from the



Fig. 11.2 Long-term seed storage at AWG Teisendorf. (Photo: AWG/ Muhidin Seho)

original trees to establish so-called family collections with seedlings. In these family collections, several seedlings of one family are planted near each other, and thinning is carried out so that only one tree representing the family is ultimately left growing. The families representing the same forest are distributed within the collection so that they can also be used for seed production after thinning. One of the benefits of such tree collections is that a certain amount of selection takes place within them. They produce well-adapted and genetically variable seeds that can be used in forest regeneration or landscaping (Koskela et al. 2007).

In addition to *ex situ* conservation in living collections, mentioned in the paragraph above, static *ex situ* conservation in gene banks is an important method among gene conservation measures. Thus, long-term seed storage is an effective tool for ex situ conservation, especially for conifer tree species and for most small-fruited deciduous tree species. For example, in Bavaria (Germany) this form of gene conservation has been practiced in a forestry gene bank at the Bavarian Office for Forest Genetics (AWG) since 1989. AWG gene bank is structured into two storage facilities; in one of them, the temperature is −10 °C and in the other, −20 °C, with a total storage area of 55 m^2 (Fig. 11.2**,** Generhaltungskonzept 2015). Currently (data from 2024), AWG gene bank stores 158 seed lots of 24 tree species and 53 provenances, out of which 23.8 million plants can be produced, if necessary, in case of an emergency.

However, to reach the most effective gene conservation aims, both *in situ* and *ex situ* conservation methods must be combined and used depending on the threats to each population or species overall (Forest Genetic Resources Strategy for Europe 2021).

Box 11.2 Forest Genetic Monitoring

Forest genetic monitoring (FGM) is used as a tool to measure and observe the long-term conservation of FGR. Safeguarding the sustainability of forest ecosystems with their habitat variability and all their functions is of the utmost importance, and the long-term adaptability of forest ecosystems to a changing environment must therefore be secured, for example, through sustainable forest management. High adaptability is based on biological variation starting at the genetic level of each species. Monitoring of biological diversity over time allows changes that threaten biological resources to be detected. Genetic variation as an integral part of biological diversity requires special attention, and its monitoring can ensure effective conservation (Pearman et al. 2024). FGM is an important module of biodiversity monitoring and has been defined as the assessment of a forest population's capacity to survive, reproduce, and persist in the long term despite rapid environmental changes (Fussi et al. 2016).

Long-term genetic monitoring of specific tree species in selected areas (so far, priority has been given to silver fir, beech, ash, and spruce in Germany) allows changes in the formation, preservation, and transmission of genetic information to the next generation to be assessed (Kätzel et al. 2005; Konnert et al. 2011). A recent Germany-wide study reports on the transmission of genetic diversity to the offspring in 12 German beech and ten spruce stands (Liesebach et al. 2024). Effective population size values showed clear differences between the stands and generations studied. Natural regeneration was similar to adult trees, while seed samples revealed a clear bottleneck effect. Seeds were harvested from only 20 trees, which points to the fact that this number is too small to represent the genetic diversity of the stand. From these results, conclusions can be drawn for sustainable natural regeneration management in forest stands for the approval of seed stands and appropriate seed harvesting.

These observations fulfill the function of an "early warning system" for ecosystem changes at higher levels (e.g., stand composition, vitality, and regeneration success), which only occur much later but are determined by the genetic system. In Bavaria, multiple assessments are currently being conducted at regular intervals (bud break and flowering intensity every year, seed testing every 5 years, and genetic analysis every 10 years) on four FGM plots (two beech, one silver fir, and one Norway spruce) (Fig. 11.3).

Several genetic monitoring concepts have been proposed during the past decade, with a major step forward being achieved within the LIFEGENMON project, in which a comprehensive manual for forest genetic monitoring and detailed practical guidelines for seven species have been developed (Bajc et al. 2020). Within the project, several indicators and verifiers for forest genetic monitoring on three levels (basic level, standard level, and intensive level) have been defined, and the appropriate level can be applied depending on capacity and financial support.

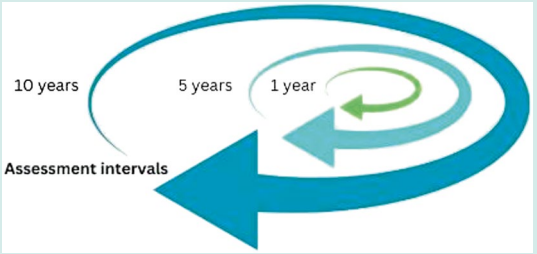


Fig. 11.3 Assessment intervals of forest genetic monitoring in Bavaria

Case Study of Species Genetic Conservation and Sustainable Use

In the following chapter, we are presenting two case studies focusing on the European white elm (***Ulmus laevis***) and wild service tree (*Sorbus torminalis)* in Bavaria (Germany), where a step-by-step guide outlining key processes for structuring, performing, and selecting appropriate forest genetic resources (FGR) for conservation and sustainable use is introduced. Field inventories and DNA-based results on *U. laevis* and *S. torminalis* revealed distinct genetic clusters in each species, guiding both *in situ* and *ex situ* FGR use and conservation strategies. In addition, our results are emphasizing the critical role of seed orchards in generating high-quality seed material due to the observed higher genetic diversity in seed orchards compared to natural populations.

Ulmus laevis

The European white elm (*U. laevis*) has a large natural distribution range in Europe, extending from the Pyrenees in the west to their eastern limit of distribution in the Urals (Fig. 11.4). In Germany, the largest populations are concentrated in the northeast of the country; in Bavaria, however, *U. laevis* is an ecologically important rare tree species. The main natural distribution of the species in Bavaria is along the main river systems (Main, Danube, and Isar). The preferred European white elm habitats are groundwater-affected soils, riparian forests, floodplain soils, and boggy soils.

In Bavaria, *U. laevis* covers only a small distribution area; its economic importance for timber production is low to medium, and its vulnerability is likewise medium. The European white elm is assessed as a tree species with high priority, with gene conservation measures rather urgently needed. However, until now, there has been a lack of knowledge on the genetic structure and diversity of European white elm populations in Bavaria. Kavaliauskas et al. (2021) designed a study to assess this genetic structure and diversity and select putative seed stands and gene

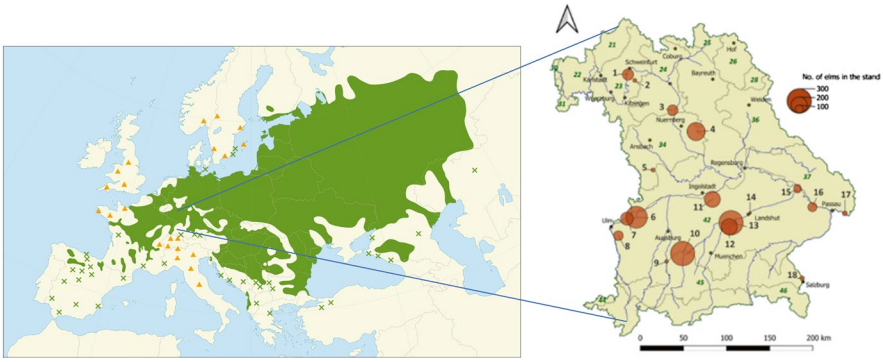


Fig. 11.4 Distribution map of *U. laevis* (European white elm) according to Caudullo et al. (2017). Legend: *filled green area*: Native range. *Filled green X*: Isolated population. *Filled yellow triangle*: Introduced and naturalized (synanthropic). Magnified (right): Distribution of sampled populations of European white elm in Bavaria. The size of each circle corresponds to the respective population size. (Kavaliauskas et al. 2021)

conservation units (GCU) for European white elm. Studies on the genetic variation of European white elm across Europe show a relatively low genetic variation (Venturas et al. 2013), and the 18 populations analyzed in Bavaria confirm this moderate-to-low genetic diversity, e.g., mean expected heterozygosity He = 0.343, the mean number of effective alleles Ne = 1.77, and rarified allelic richness Ar = 2.72 (Kavaliauskas et al. 2021).

Analysis of molecular variance (AMOVA) showed that 89% of the total genetic variation exists within populations and 11% between populations. This can be viewed as an indication of the isolation of individual populations when compared to other tree species (e.g., 4% for *Sorbus torminalis*). Bayesian cluster analysis using the STRUCTURE software revealed a possible structure of four genetic clusters (the highest delta K of 6.5 was K = 4, indicating four genetic groups) within the investigated European white elm populations in Bavaria (Fig. 11.5). One cluster follows the Main River basin (cluster K1) with the highest proportion of green. The other clusters (one main cluster and two subclusters) dominate the central part of Bavaria, following the basin of the Danube River and its tributaries. However, in all studied populations, an admixture with other genetic clusters was observed (Fig. 11.5).

In situ conservation is the favored protection measure for the European white elm. Due to the decline of suitable habitats, its natural distribution area became fragmented. The two identified main clusters should be considered for the future so that the existing gene pool can be retained. Different studies recommend using the allelic richness value (Ar) as the primary parameter for GCU selection (Petit et al. 1998; Foulley et al. 2006), and Ar has therefore become the main value for GCU selection up to now. We suggest dividing European white elm populations into three categories. Populations with a value of Ar > 3 are recommended for *in situ* conservation (populations 1, 2, 11, 14, and 18 in Fig. 11.5.). For these most precious

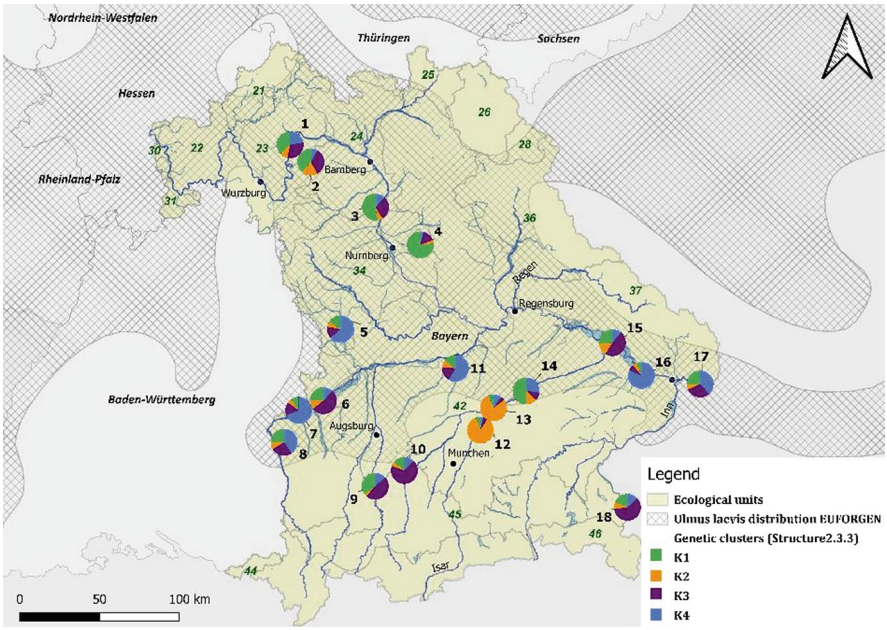


Fig. 11.5 Population genetic structure of *U. laevis* populations in Bavaria based on STRUCTURE clusters

populations, regeneration should only be carried out with their respective own reproductive material. Within the second category with Ar > 2.6, which is worthy of conservation in terms of forest genetics, the same procedure should be applied to populations 6 and 17 in Fig. 11.5. With this selection of GCUs, all relevant genetic conservation zones in Bavaria are represented. For populations, which are at the lower limit of this value, enrichment planting by introducing forest reproductive material (FRM) from suitable source populations should be considered. In addition to the genetic diversity parameters, gene flow between populations is particularly important. For this reason, the establishment of stepping-stone populations should be considered in the long term. Furthermore, additional GCUs should be registered at the European level; only two German populations of *U. laevis* are included in the European Information System on Forest Genetic Resources database (EUFGIS, http://portal.eufgis.org/). These data fill existing gaps regarding the sustainable use and conservation of rare and scattered tree species by providing insights into the genetic variation and genetic structure of these species, thereby allowing us to better plan genetic conservation measures and select GCU in Bavaria. We, therefore, suggest that all gene conservation units should go through all the steps in Fig. 11.2. As *ex situ* measures, the establishment of conservation seed orchards, which can simultaneously be used for conservation and the production of high-quality reproductive material, are planned. Therefore, at least 80–100 clones should be selected and a seed orchard established to maintain a large effective population size.

Sorbus torminalis

Ongoing changes in environmental conditions and climate are prompting forest owners to reconsider their methods of forest management and enhance the adaptation and resilience of their forest stands through the establishment of mixed forests (Dorren et al. 2004; Knoke et al. 2008; Bauhus et al. 2017). In recent years, the wild service tree (*Sorbus torminalis* (L.) Crantz) has been one of the species of increasing interest among forest owners in Europe owing to its highly valuable wood, high tolerance for drought and pathogens, and relatively fast growth. Despite its wide distribution, it is considered a rare forest tree species; it is light-demanding and has low competitive capability (Demesure-Musch and Oddou-Muratorio 2004; Bednorz 2007; Hemery et al. 2010; Welk et al. 2016). The wild service tree is a post-pioneer tree that colonizes disturbed areas and forest edges and can grow on all types of soil (Demesure et al. 2000; Welk et al. 2016). Many researchers (Spiecker 2006; Angelone et al. 2007; Paganova 2007; Pyttel et al. 2013 and references therein) claim that the formation of high forests and the transformation of coppice forests into high forests are reasons for continuing species loss. Overall, there is a lack of knowledge on the distribution and genetics of scattered broadleaves such as the wild service tree. Furthermore, there is a lack of legal guidelines for the sustainable use and protection of rare and scattered tree species such as *Sorbus torminalis* in the FRM regulations in Germany based on the German Act on Forest Reproductive Material (FoVG, 2003).

Therefore, in 2016, the AWG implemented a project on the wild service tree in southern Germany (Bavaria [BY] and Baden-Württemberg [BW]), which aimed to analyze the genetic structure and diversity of the species, delineate provenance regions, identify and propose new seed stands, and discuss GCU selection based on its distribution as well as the structure and extent of its genetic variation. The workflow for FGR selection and conservation for other rare tree species (see Fig. 11.2) was followed.

During the project, 998 trees from 34 natural wild service tree populations were sampled in BY and BW (Fig. 11.6). In addition, natural wild service tree populations were compared with a seedling seed orchard of 93 trees in Neudorf (BY) and a cohort of 56 plus trees (e.g. Fig. 11.6) selected from the 34 natural populations (46 plus trees in BY and ten in BW; Kavaliauskas et al. (2021)).

The results for the wild service tree populations in Southern Germany revealed medium differentiation among studied populations ($F_{ST} = 4\%$), probably because of the fragmented distribution across the sampled area. The level of overall genetic diversity within stands was comparatively high (He = 0.782) (Kavaliauskas et al. 2021). Other studies also found relatively high genetic diversity within wild service tree populations in the species' main distribution range in Western and Central Europe, but certain populations may be endangered due to spatial isolation and low connectivity resulting in a lack of gene flow between them (Demesure et al. 2000; Bednorz 2007; Angelone et al. 2007). Therefore, active conservation measures should be considered to protect and maintain the level of genetic diversity among natural wild service tree populations.

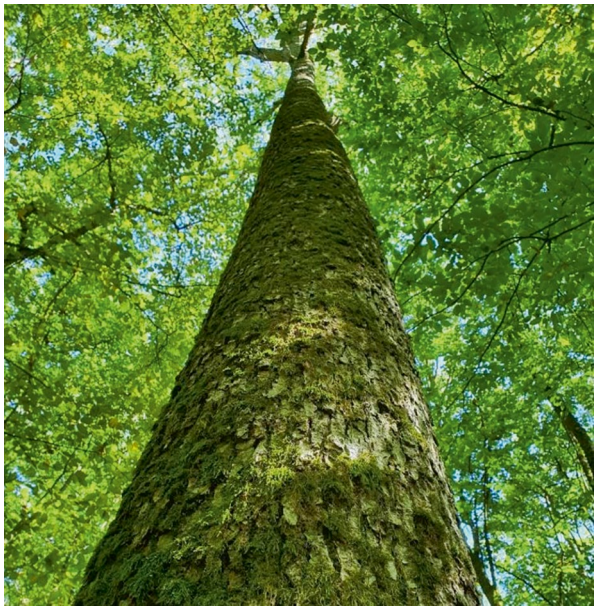


Fig. 11.6 Selected plus tree of *Sorbus torminalis* in Bavaria. (Photo: AWG/ Muhidin Šeho)

Half of the sampled populations (nine in BY and eight in BW) exhibit higher than average allelic richness (Ar ≥ 9.2) and were thus considered potential GCUs. We ultimately proposed approving the five populations with the highest allelic richness (Ar ≥ 10.0) as GCUs.

Further analysis of our data showed evidence of isolation by distance (IBD) based on the Mantel test, which is in line with other studies conducted in Poland (Bednorz and Kosiński 2006), Switzerland (Angelone et al. 2007), and France (Demesure et al. 2000). The Bayesian clustering method implemented in STRUCTURE 2.3.3 (Evanno et al. 2005) revealed the existence of four genetic clusters within the 34 studied wild service tree populations in Southern Germany (Fig. 11.7). We used genetic data based on genetic markers to infer population clustering and delineated four regions of provenance for the wild service tree in Southern Germany. The final decision regarding the number and distribution of provenance regions resulted from a synthesis of species distribution, genetic differentiation, and clustering and geographical proximity in Southern Germany. Thus, our results and identified provenance regions enabled us to select seed stands in a similar way as for the species regulated under the FoVG (2003), following the distribution of genetic diversity and phenotypic quality in a representative manner within a given provenance region. A total of 12 forest stands (three in BW and nine in BY) fulfilling genetic diversity and phenotypic quality selection parameters were proposed as potential seed stands. In addition, a comparison of genetic variation among natural wild service tree populations (34 populations) with the already existing Neudorf seedling seed orchard and the newly selected cohort of plus trees (56 trees) revealed a higher genetic diversity in the seed orchard and the cohort of plus trees than in natural populations (Kavaliauskas et al. 2021). In *Tilia platyphyllos,* the comparison

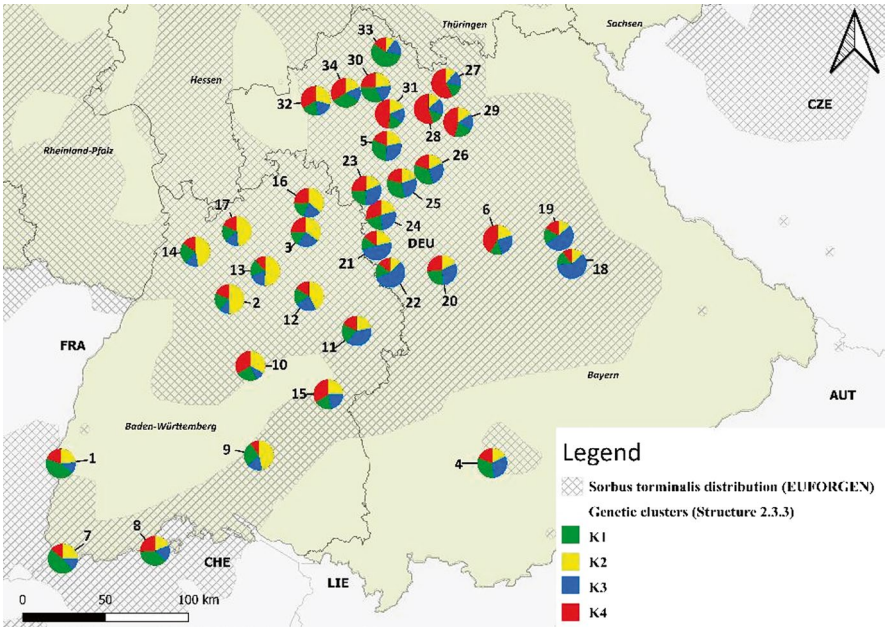


Fig. 11.7 Population genetic structure based on Bayesian clustering (STRUCTURE 2.3.3). The pie charts show the relative proportions of the four genetic clusters within the studied wild service tree populations. (Kavaliauskas et al. 2021)

of genetic variation of natural stands and seed orchards revealed that all parameters of genetic diversity were higher in seed orchards (Rau et al. 2023, Kavaliauskas et al. 2024). This confirms that seed orchards are highly important as an *ex situ* measure for ensuring high genetic diversity in wild service tree seeds. A new seed orchard including 93 selected plus trees to ensure high-quality FRM production and use in Southern Germany was established in 2022. Our study thus provides a straightforward approach for FGR selection from the delineation of provenance regions to the selection of seed stands, GCUs, and plus trees, enabling us to create a network of *in situ* and *ex situ* sites for wild service trees in different environments as a basis for further FGR use and conservation. The sustainable use of GCUs for moderate seed harvest allows the species' distribution to be increased and economic, as well as ecological goals to be reached.

Case Study of Species Genetic Conservation After Pathogen Outbreak

Fraxinus excelsior

The common ash (*Fraxinus excelsior* L.) is an important component of mixed forest ecosystems in Europe and can be found across a wide range of growing conditions from nutrient-rich floodplain forests to calcareous drier sites (Pautasso et al. 2013;



Fig. 11.8 Long-term observation plot with ash trees of varying susceptibility levels. (Photo: AWG/B. Fussi)

Kölling and Walentowski, 2002). It was therefore considered a promising tree species under climate change. Ash trees account for 1–2% of the forest area in Europe, with higher densities in some regions (Enderle et al. 2019). In Bavaria, more than 120 ash seed stands are registered, which confirms the high relevance of the species. Seeds were harvested regularly until ash dieback (caused by the pathogen *Hymenoscyphus fraxineus* introduced from Eastern Asia) appeared; disease impact nearly resulted in the loss of this economically and ecologically valuable tree species (Enderle et al. 2017). As an ecological keystone species in floodplain forests, loss of ash would mean a loss of habitat for several other species and, potentially, the extinction of species dependent on ash trees (Pautasso et al. 2013); e.g., larvae of *Euphydryas maturna* feeds exclusively on ash leaves. Ash trees are hosts to a wide range of taxa: in the UK, it was estimated that 953 species are associated with European ash and that the 69 most strongly associated species might rapidly become extinct if the ash populations were to decline (Mitchell et al. 2014).

In recent decades, ash populations in Europe have been threatened by ash dieback caused by the fungus *Hymenoscyphus fraxineus* (T. Kowalski) (Baral et al. 2014). The disease has already led to massive salvage felling and mortality and endangers the future utilization of ash in European forestry as a whole (Enderle et al. 2017). A comprehensive survey with a pan-European perspective (data from ICP Forests Level I) found a substantial increase in defoliation and mortality over time, indicating that crown defoliation has almost doubled during the past three decades; the study forecasts that the overall mean defoliation will likely reach 50% as early as 2030 (George et al. 2022). However, lower susceptibility toward ash dieback has been found to be present in a small fraction of ash individuals, which exhibit few symptoms, possibly providing a solution to sustaining the species in European forests (e.g., McKinney et al. 2014; Rigling et al. 2016; Enderle, 2019) through intensive selection and breeding efforts. Observations in a clonal and a progeny trial in Bavaria since 2014 (Fig. 11.8) have revealed that about 30 percent

of all offspring showed high resilience to ash dieback (Seidel et al. 2025). The genomic basis of ash dieback tolerance in *F. excelsior* is more and more understood and can complement phenotypic selection and breeding efforts. Found SNPs with the highest predictive power located within genes related to plant defense and phenology and provided insights into a multifaceted defense response, according to which a combination of direct defense mechanisms and phenological avoidance of pathogen spread constitutes tolerance to ash dieback.

Resistance can be controlled by only a few genes, but it more often involves numerous genes, each with a small effect (White et al. 2007). Low-frequency alleles unevenly distributed across the species range are a major challenge for conservation considerations (White et al. 2007). Less susceptible genotypes need to be tested under heavy disease pressure in the field or with artificial inoculations and planted together in seed orchards or artificial populations (gene reserves). In natural populations, less susceptible genotypes should be conserved and their reproduction and natural regeneration stimulated. The overall goal is to maintain several forms of resistance as well as high genetic diversity to withstand the disease in the long term (Jump et al. 2009). Static *ex situ* conservation measures like cryopreservation of genetically diverse and less susceptible genotypes (tissue, seed, and pollen) might complement conservation efforts (Mirjani et al. 2022).

In Southern Germany, genetic variation between damaged and undamaged subpopulations was compared to see whether genetic differences between these two collectives exist (Fussi and Konnert, 2014). The authors detected higher proportions of heterozygotic individuals (observed heterozygosity) among less susceptible trees compared to susceptible ones, indicating that heterozygotic individuals might be able to withstand ash dieback better than homozygotic individuals. This means a higher variability at the individual level for heterozygotic individuals, which might therefore possess higher plasticity and responsiveness against the disease. Namkoong et al. (1998) and Tessier du Cros et al. (1999) have previously also suggested that heterozygotic individuals could be more resistant to environmental stresses.

Several studies based on genetic markers have revealed high genetic variation within stands (e.g., for Italy: Ferrazzini et al. 2007; for Germany: Höltken et al. 2003; Heuertz et al. 2004a, 2004b; Hebel et al. 2006; Fussi and Konnert, 2014; and for Austria: Heinze and Fussi, 2017), and a generally higher level of genetic variation was detected in Central and Western Europe than in Southeastern Europe (Heuertz et al. 2004a). By contrast, genetic differentiation was greater among populations in Southeastern Europe than in Central Europe (Heuertz et al. 2004a). Levels of genetic differentiation in Austria were low, with some clustering of stands along the Danube River compared to two stands in the Alps (Heinze and Fussi, 2017) and higher in Germany (Hebel et al. 2006b; Fussi and Konnert, 2014). Different gene flow intensities during postglacial recolonization likely explain these patterns (Heuertz et al. 2004a).

Using chloroplast haplotypes, distinct regions within Europe were identified, with certain haplotypes found to be typical for different regions (Heuertz et al. 2004b). Higher chloroplast variation with four haplotypes was detected in Southern Germany (Heuertz et al. 2004b), especially in populations from southeastern

Bavaria (Fussi and Konnert, 2014); this is caused by historical contact between chloroplast lineages from different refugia in Italy, the eastern Alps, and the Balkan Peninsula (Heuertz et al. 2004b).

Habitat fragmentation can reduce the genetic connectivity of plant populations. Therefore, pollen and seed dispersal patterns must be studied to understand and prevent the consequences of reduced habitat size and spatial isolation (Sork and Smouse, 2006). Ash has wind-dispersed pollen and seeds. Studies on *Fraxinus pennsylvanica* estimated mean seed dispersal distances between 47 and 60 m, with long-distance dispersal reaching up to 150 m (Schmiedel et al. 2013). Semizer-Cuming et al. (2017) examined the genetic connectivity of ash trees in an isolated forest area where only individual ash trees occurred within a radius of 5 km around the study site. It was found that most analyzed seeds and seedlings descended from local ash trees (no seed transport beyond 100 m) (Semizer-Cuming et al. 2017).

Pollen was found to be more mobile, with 50% of pollen dispersed within approximately 270 m, while 10% can be dispersed further than ca. 1400 m and 1% can reach distances of more than 4400 m (Semizer-Cuming et al. 2017). Landscape structure and wind speed influenced this pattern more strongly for ash seed than for pollen dispersal (Semizer-Cuming et al. 2017). However, the cardinal wind direction associated with the highest pollen impaction was also identical to the predominant wind direction (Eisen et al. 2022).

Pollen flow studies using pollen traps in two seed orchards revealed that 50% of pollen was found within 200 m and more than 10% at 500 m (Eisen et al. 2022). To ensure the cross-pollination of healthy ash trees, the distance between ash individuals or stands should not be too great, and barriers like large conifer stands should be avoided. In years with little flowering, more intensive gene flow from outside trees to the seed orchard was detected (Eisen et al. 2022), and it is thus recommended to conduct seed harvesting from ash trees in the orchards preferentially in full-mast years. Based on parentage analyses in a seed orchard and a floodplain forest, pollination success decreased substantially with increasing distance to the mother tree (mean distance of 76 m and 166 m, respectively) (Eisen et al. 2023). However, despite the dense tree cover in the floodplain forest, pollen was transported over long distances there as well (greater than 550 m), suggesting that nonlocal sources also play a role in pollination. This is supported by the amount of foreign pollen input identified in the seed orchard (66.5%) (Eisen et al. 2023).

Heuertz et al. (2004a) indicated that from a historical perspective, effective seed dispersal occurred mainly over short distances, whereas pollen dispersal seemed to be effective over longer distances as well. In some cases, gene flow by pollen into fragmented populations can be extensive; 46–95% were detected in each of the three remnant populations (Bacles et al. 2005) with a very localized and restricted part and another part extending over long distances, with dispersal occurring over several kilometers (Bacles et al. 2005). Effective dispersal distances (average: 328 m) were greater for fragmented populations than the values reported for contiguous populations (Bacles et al. 2005).

Self-pollination was detected only to a very small extent, with no major influence on reproduction (Eisen et al. 2023). Common ash trees with low susceptibility to

ash dieback have higher reproductive fitness compared to highly susceptible trees, as determined for males (Eisen et al. 2023), and in an even more pronounced fashion for female success (Semizer-Cuming et al. 2019). Overall, this leaves healthy ash trees overrepresented as seed and pollen parents for next-generation seedlings (Semizer-Cuming et al. 2021). Long-distance pollen transport contributes to the connectivity between ash trees in the landscape. Additionally, both healthy and slightly diseased fathers/pollinators provide a greater contribution to pollination, thus potentially improving the health of the next generation of ash trees. Moreover, gene flow between stepping-stone populations is necessary to ensure a positive impact on the genetic diversity of ash populations in the future. However, the ash dieback disease itself causes major loss of ash (through natural death and active withdrawal), leading to declining populations with restricted effective gene flow between the remaining—and possibly less susceptible—trees.

European ash usually regenerates very successfully and can be very competitive on suitable sites. This should be considered for *in situ* conservation when silvicultural management options are developed with the aim of increasing resistance against ash dieback in future ash populations. Once there is enough natural ash regeneration, basically, no further management actions are necessary for the next 10–15 years. Regular thinning of older stands is still strongly recommended, along with the promotion of complementary tree species and sound-looking ash individuals (Enderle et al. 2019). Individual tree vigor, crown defoliation, and epicormic shoots as measures of individual vitality are the most important criteria in the selection of ash trees for thinning. Foresters tend to clear-cut heavily affected stands because they look for ash trees without any symptoms; however, such trees rarely exist. Instead, the focus should be on less affected individuals (Fig. 11.9), and these should be maintained as it is essential for the long-term conservation of ash to allow these trees to reproduce. Otherwise, fragmentation of ash populations and a crucial loss of genetic diversity must be expected.

Selection against the most susceptible genotypes at generation turnover represents good news for the potential recovery of ash forests, facilitating the establishment of dieback-resistant ash and—together with substantial gene flow over longer distances—generating hope for the species' future in European forests (Semizer-Cuming et al. 2019, 2021; Eisen et al. 2022, 2023). However, removing trees that appear less affected and eliminating natural regeneration will promote the ongoing fragmentation of ash populations caused by ash dieback and eventually could lead to the loss of the species. As an *ex situ* measure, healthy and less damaged plus trees are being collected in Germany to be grafted and planted as gene banks in several places (FraxGen-Project, https://www.fraxforfuture.de/). Overall, around 600 trees have been collected. Compared to the total area of ash in Germany, however, this can only be a first step, and further efforts will need to be undertaken to secure as many healthy ash trees as possible. The overall goal is to establish seed orchards of healthy ash trees to produce high-quality seeds and restore healthy ash forests. This must be considered in the light of potential new threats. For a few years, *Agrilus planipennis* (emerald ash borer, EAB), a wood-boring beetle native to East Asia, has been on its way from Russia toward Eastern Europe (Valenta et al. 2017). All ash



Fig. 11.9 Less susceptible plus tree grafted for the newly established seed orchard in Bavaria. (Photo: AWG/H. Seidel)

species native to Europe and North America are known to be susceptible to EAB attacks, which cause high tree mortality even among formerly healthy trees. Given current expansion rates, EAB is expected to reach Central Europe within 15–20 years (Valenta et al. 2017). Most likely, EAB will become a major pest in Europe; therefore, early and dedicated response is needed to reduce the level of ash mortality and cope with this new pest in the future.

Conclusion and Outlook

Both foresters and society, policymakers, conservation actors, and the scientific community need to be concerned about *in situ* and *ex situ* conservation of FGR due to environmental and climatic changes that may increase forest susceptibility to pests and stochastic events. It is crucial to recognize that forest genetic diversity and variability are vital because of their importance for adaptation and fulfilling ecological and economic forest functions now and in the future. The increasing loss of biological and genetic diversity threatens the stability of entire forest ecosystems. These concerns can promote efforts to evaluate, monitor, and conserve genetic variability (*in situ* and *ex situ*) and protect endangered species and their genetic

resources. The examples provided in this chapter offer insights into the development of *in situ* and *ex situ* conservation measures for different species groups, such as rare species or those suffering from diseases.

References

Adams WT, Burczyk J (2000) Magnitude and implications of gene flow in gene conservation reserves. In: Young AG, Boshier D, Boyle TJB (eds) Forest conservation genetics: principles and practice. CABI Pub, New York, pp 215–244

Aitken SN, Yeaman S, Holliday JA, Wang T, Curtis-McLane S (2008) Adaptation, migration or extirpation: climate change outcomes for tree populations. Evol Appl 1(1):95–111

Angelone S, Hilfiker K, Holderegger R, Bergamini A, Hoebee SE (2007) Regional population dynamics define the local genetic structure in *Sorbus torminalis*. Mol Ecol 16(6):1291–1301. https://doi.org/10.1111/j.0962-1083.2006.03202.x

Aravanopoulos FA (2018) Do silviculture and forest management affect the genetic diversity and structure of long-impacted forest tree populations? Forests 9(6):355

Bacles CFE, Ennos RA (2008) Paternity analysis of pollen-mediated gene flow for Fraxinus excelsior L. in a chronically fragmented landscape. Heredity 101:368–380. https://doi.org/10.1038/hdy.2008.66

Bacles CF, Burczyk J, Lowe AJ, Ennos RA (2005) Historical and contemporary mating patterns in remnant populations of the forest treefraxinus excelsior L. Evolution 59(5):979–990

Bajc M, Aravanopoulos F, Westergren M, Fussi B, Kavaliauskas D, Alizoti P et al (2020) Manual for forest genetic monitoring. Slovenian Forestry Institute, Silva Slovenica Publishing Centre, Ljubljana. https://doi.org/10.20315/SFS.167

Baral HO, Queloz V, Hosoya T (2014) Hymenoscyphus fraxineus, the correct scientific name for the fungus causing ash dieback in Europe. IMA Fungus 5(1):79–80

Bauhus J, Forrester DI, Gardiner B, Jactel H, Vallejo R, Pretzsch H (2017) Ecological stability of mixed-species forests. In: Mixed-species forests. Springer, Berlin, Heidelberg, pp 337–382

Bednorz L (2007) Conservation of genetic resources of Sorbus torminalis in Poland. Dendrobiology 58:3–7

Bednorz L, Kosiński P (2006) Genetic variability and structure of the wild service tree (*Sorbus torminalis* (L.) Crantz) in Poland. Silvae Genet 55(1–6):197–202. https://doi.org/10.1515/sg-2006-0027

Caballero A, Rodríguez-Ramilo ST, Avila V, Fernández J (2010) Management of genetic diversity of subdivided populations in conservation programmes. Conserv Genet 11(2):409–419. https://doi.org/10.1007/s10592-009-0020-0

Danusevičius D, Kerpauskaitė V, Kavaliauskas D, Fussi B, Konnert M, Baliuckas V (2016) The effect of tending and commercial thinning on the genetic diversity of Scots pine stands. Eur J For Res 135(6):1159–1174. https://doi.org/10.1007/s10342-016-1002-7

Danusevicius D, Rajora OP, Kavaliauskas D, Baliuckas V, Augustaitis A (2023) Genetic diversity and fine-scale spatial genetic structure of unmanaged old-growth versus managed second-growth populations of Scots pine (*Pinus sylvestris* L.) in Lithuania. Eur J For Res:1–21. https://doi.org/10.1007/s10342-023-01556-x

De Dato G, Teani A, Mattioni C, Marchi M, Monteverdi MC, Ducci F (2018) Delineation of seed collection zones based on environmental and genetic characteristics for *Quercus suber* L. in Sardinia, Italy. iForest 11(5):651

Demesure B, Le Guerroué B, Lucchi G, Prat D, Petit RJ (2000) Genetic variability of a scattered temperate forest tree: *Sorbus torminalis* L. (Crantz). Ann For Sci 57(1):63–71. https://doi.org/10.1051/forest:2000101

Demesure-Musch B, Oddou-Muratorio S (2004) EUFORGEN technical guidelines for genetic conservation and use for wild service tree (*Sorbus torminalis*). Bioversity International

Doonan JM, Budde KB, Kosawang C, Lobo A, Verbylaite R, Brealey JC et al (2023) Multiple, single trait GWAS and supervised machine learning reveal the genetic architecture of Fraxinus excelsior tolerance to ash dieback in Europe. Plant Cell Environ 48(5):3793–3809

Dorren LK, Berger F, Imeson AC, Maier B, Rey F (2004) Integrity, stability and management of protection forests in the European Alps. For Ecol Manag 195(1–2):165–176. https://doi.org/10.1016/j.foreco.2004.02.057

Dubreuil M, Riba M, Gonzalez-Martinez S, Vendramin GG, Sebastiani F, Mayol M (2010) Genetic effects of chronic habitat fragmentation revisited: strong genetic structure in temperate tree, *Taxus baccata (Taxaceae*), with great dispersal capability. Am J Bot 97(2):303–310. https://doi.org/10.3732/ajb.0900148

Ducousso A, Bordacs S (2004) EUFORGEN technical guidelines for genetic conservation and use for pedunculate and sessile oaks (*Quercus robur and Q. petraea*). International Plant Genetic Resources Institute, Rome. 6 pages

Dudley N, Parrish J, Redford K, Stolton S (2010) The revised IUCN protected area management categories: the debate and ways forward. Oryx 44(4):485–490. https://doi.org/10.1017/S0030605310000566

Eisen AK, Fussi B, Šikoparija B, Jochner-Oette S (2022) Aerobiological pollen deposition and transport of *Fraxinus excelsior* L. at a small spatial scale. Forests 13(3):424

Eisen AK, Semizer-Cuming D, Jochner-Oette S et al (2023) Pollination success of *Fraxinus excelsior* L. in the context of ash dieback. Ann For Sci 80:22. https://doi.org/10.1186/s13595-023-01189-5

Enderle R, Fussi B, Lenz HD, Langer G, Nagel R, Metzler B (2017) Ash dieback in Germany: research on disease development, resistance and management options. In: Vasaitis R, Enderle R (eds) Dieback of European Ash (*Fraxinus* spp.): consequences and guidelines for sustainable management. SLU, Uppsala, pp 89–105

Enderle R, Stenlid J, Vasaitis R (2019) An overview of ash (*Fraxinus* spp.) and the ash dieback disease in Europe. CABI Rev 2019:1–12

European Union (EU) directive 1999/105/CE of 22 December (1999) Marketing of forest reproductive material. Access to European Union law web. https://eur-lex.europa.eu/eli/dir/1999/105/oj. Accessed 26 Oct 2021

European Union (EU) communication from The Commission to the European Parliament, The European Council, The Council, The European Economic And Social Committee and The Committee of the Regions December (2019) The European Green Deal. Access to European Union law web. https://eur-lex.europa.eu/legal-content/EN/TXT/?uri. Accessed 28 Jan 2025

Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Mol Ecol 14:2611–2620. https://doi.org/10.1111/j.1365-294X.2005.02553.x

Ferrazzini D, Monteleone I, Belletti P (2007) Genetic variability and divergence among Italian populations of common ash (*Fraxinus excelsior* L.). Ann For Sci 64(2):159–168

Fitzpatrick SW, Gerberich JC, Kronenberger JA, Angeloni LM, Funk WC (2015) Locally adapted traits maintained in the face of high gene flow. Ecol Lett 18(1):37–47

Foulley JL, Ollivier L (2006) Estimating allelic richness and its diversity. Livest Sci 101(1–3):150–158

FoVG (2003) Forstvermehrungsgutgesetz (FoVG) (The German Act on Forest Reproductive Material) 01.01.2003. https://www.ble.de/DE/Themen/Wald-Holz/Forstliches-Vermehrungsgut/forstliches-vermehrungsgut_node.html. Accessed 27 Oct 2021

Fussi B, Konnert M (2014) Genetic analysis of European common ash (Fraxinus excelsior L.) populations affected by ash dieback. Silvae Genetica 63(1–6):198–212

Fussi B, Westergren M, Aravanopoulos F, Baier R, Kavaliauskas D, Finzgar D, Alizoti P, Bozic G, Avramidou E, Konnert M, Kraigher H (2016) Forest genetic monitoring: an overview of concepts and definitions. Environ Monit Assess 188(8):493. https://doi.org/10.1007/s10661-016-5489-7

Gautam S, Timilsina S, Shrestha M (2021) The effects of forest management activities on genetic diversity of forest trees. Indones J Soc Environ Issues (IJSEI) 2(2):110–118

Generhaltungskonzept (2015) Konzept zur Erhaltung und zur nachhaltigen Nutzung forstlicher Genressourcen in Bayern. (Concept for the conservation and sustainable use of forest genetic resources in Bavaria). https://awg.bayern.de/mam/cms02/asp/bilder/generhaltungskonzept_bayern.pdf. Accessed 29 Jan 2024

George JP, Sanders TG, Timmermann V, Potočić N, Lang M (2022) European-wide forest monitoring substantiate the neccessity for a joint conservation strategy to rescue European ash species (*Fraxinus* spp.). Sci Rep 12(1):4764

Gougherty AV, Keller SR, Fitzpatrick MC (2021) Maladaptation, migration and extirpation fuel climate change risk in a forest tree species. Nat Clim Chang 11(2):166–171

Hebel I, Haas R, Dounavi A (2006) Genetic variation of common ash (*Fraxinus excelsior* L.) populations from provenance regions in southern Germany by using nuclear and chloroplast microsatellites. Silvae Genetica 55(1):38–43

Heinze B, Fussi B (2017) Pre-disease levels of genetic diversity and differentiation among common Ash (*Fraxinus excelsior* L.) Seedlots in Austria. Balt For 23(1):198–208

Hemery GE, Clark JR, Aldinger E, Claessens H, Malvolti ME, O'connor E et al (2010) Growing scattered broadleaved tree species in Europe in a changing climate: a review of risks and opportunities. Forestry 83(1):65–81. https://doi.org/10.1093/forestry/cpp034

Heuertz M, Hausman JF, Hardy OJ, Vendramin GG, Frascaria-Lacoste N, Vekemans X (2004a) Nuclear microsatellites reveal contrasting patterns of genetic structure between western and southeastern European populations of the common ash (*Fraxinus excelsior* L.). Evolution 58(5):976–988

Heuertz M, Fineschi S, Anzidei M, Pastorelli R, Salvini D, Paule L et al (2004b) Chloroplast DNA variation and postglacial recolonization of common ash (*Fraxinus excelsior* L.) in Europe. Mol Ecol 13(11):3437–3452

Hoban, S., Bruford, M., 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. Conserv Genet, 24, 181–191. https://doi.org/10.1007/s10592-022-01492-0

Höltken AM, Tahtinen J, Pappinen A (2003) Effects of discontinuous marginal habitats on the genetic structure of common ash (*Fraxinus excelsior* L.). Silvae Genetica 52(5–6):206–211

IUCN (1994) Guidelines for protected area management categories. IUCN, Gland/Cambridge

Jost L, Archer F, Flanagan S, Gaggiotti O, Hoban S, Latch E (2018) Differentiation measures for conservation genetics. Evol Appl 11(7):1139–1148

Jump AS, Marchant R, Peñuelas J (2009) Environmental change and the option value of genetic diversity. Trends Plant Sci 14(1):51–58

Kavaliauskas D, Fussi B, Westergren M, Aravanopoulos F, Finzgar D, Baier R, Alizoti P, Bozic G, Avramidou E, Konnert M, Kraigher H (2018) The interplay between forest management practices, genetic monitoring, and other long-term monitoring systems. Forests 9(3):133. https://doi.org/10.3390/f9030133

Kavaliauskas D, Šeho M, Baier R, Fussi B (2021) Genetic variability to assist in the delineation of provenance regions and selection of seed stands and gene conservation units of wild service tree (*Sorbus torminalis* (L.) Crantz) in southern Germany. Eur J For Res 140(3):551–565

Kavaliauskas D, Fussi B, Rau B, Šeho M (2022a) Assessing genetic diversity of European white elm (*Ulmus laevis* Pallas) in Bavaria as an indicator for *in-situ* conservation and sustainable use of the species genetic resources. Eur J For Res 142(1):145

Kavaliauskas D, Danusevičius D, Baliuckas V (2022b) New insight into genetic structure and diversity of Scots pine (*Pinus sylvestris* L.) populations in Lithuania based on nuclear, chloroplast and mitochondrial DNA markers. Forests 13(8):1179

Kavaliauskas D, Fussi B, Šeho M (2024) Strong genetic differentiation and diversity of highly fragmented *Tilia platyphyllos* populations in Bavaria. Eur J For Res. (In preparation)

Kelleher CT (2018) Evolution and conservation of trees – a review of salient issues. In: Roberts JA (ed) Annual plant reviews. https://doi.org/10.1002/9781119312994.apr0621

Kleinschmit JR, Kownatzki D, Gregorius HR (2004) Adaptational characteristics of autochthonous populations—consequences for provenance delineation. For Ecol Manag 197(1–3):213–224. https://doi.org/10.1016/j.foreco.2004.05.037

Klumpp R, Dhar A (2011) Genetic variation of *Taxus baccata* L. populations in the Eastern Alps and its implications for conservation management. Scand J For Res 26(4):294–304. https://doi.org/10.1080/02827581.2011.566888

Knoke T, Ammer C, Stimm B, Mosandl R (2008) Admixing broadleaved to coniferous tree species: a review on yield, ecological stability and economics. Eur J For Res 127(2):89–101. https://doi.org/10.1007/s10342-007-0186-2

Kölling C, Walentowski H (2002) Die Rolle der Esche (*Fraxinus excelsior*) in einheimischen Waldgesellschaften. Berichte aus der LWF 34:6–20

Komárková M, Novotný P, Cvrčková H, Máchová P (2022) The genetic differences and structure of selected important populations of the endangered *Taxus baccata* in The Czech Republic. Forests 13(2):137. https://doi.org/10.3390/f13020137

Lande R, Barrowclough GF (1987) Effective population size, genetic variation, and their use in population management. In: Viable populations for conservation, vol 87. Cambridge University Press, Cambridge, pp 87–124

Lefevre F, Koskela J, Hubert J, Kraigher H, Longauer R, Olrik DC, Schuler S, Bozzano M et al (2013) Dynamic conservation of forest genetic resources in 33 European countries. Conserv Biol 27(2):373–384

Lefevre F, Bojkovski D, Bou Dagher Kharrat M, Bozzano M, Charvolin-Lemaire E, Hiemstra SJ, Kraigher H, Laloe D, Restoux G, Sharrock S, Sturaro E, van Hintum T, Westergren M, Maxted N, Gen Res Bridge Expert Panel (2024) European genetic resources conservation in a rapidly changing world: three existential challenges for the crop, forest and animal domains in the 21st century. Genet Res 5(9):13–28. https://doi.org/10.46265/genresj.REJR6896

Liesebach H, Eusemann P, Höltken AM, Tröber U, Kuchma O, Karopka M et al (2024) Effective population size of adult and offspring cohorts as a genetic monitoring tool in two stand-forming and wind-pollinated tree species: *Fagus sylvatica* L. and *Picea abies* (L.) Karst. Conserv Genet:1–15

Linares JC (2013) Shifting limiting factors for population dynamics and conservation status of the endangered English yew (*Taxus baccata L., Taxaceae*). For Ecol Manag 291:119–127. https://doi.org/10.1016/j.foreco.2012.11.009

Marshall DR, Brown AHD (1975) Optimum sampling strategies in genetic conservation. In: Frankel OH, Hawkes JG (eds) Crop genetic resources for today and tomorrow, vol 2. CUP Archive, pp 53–80

McKinney LV, Nielsen LR, Collinge DB, Thomsen IM, Hansen JK, Kjaer ED (2014) The ash dieback crisis: genetic variation in resistance can prove a long-term solution. Plant Pathol 63:485–499. https://doi.org/10.1111/ppa.12196

Mirjani L, Ghamarizare A, Spahbodi K (2022) Preservation of the genetic resources of Fraxinus excelsior L. in cryopreservation. Iran J Rangelands Forests Plant Breed GenetRes 30(1):108–117. https://doi.org/10.22092/ijrfpbgr.2022.357696.1409

Mitchell RJ et al (2014) Ash dieback in the UK: a review of the ecological and conservation implications and potential management options. Biol Conserv 175:95–109

Namkoong G (1998) Forest genetics and conservation in Europe. Conservation of forest genetic resources in Europe. International Plant for Genetic Resources Institute, Rome, pp 3–10

Neel MC, Cummings MP (2003) Effectiveness of conservation targets in capturing genetic diversity. Conserv Biol 17(1):219–229. https://doi.org/10.1046/j.1523-1739.2003.01352.x

Paganová V (2007) Ecology and distribution of *Sorbus torminalis* (L.) Crantz. in Slovakia. Hortic Sci 34(4):138–151

Paul M, Hinrichs T, Janssen A, Schmitt H-P, Soppa B, Stephan BR, Doerflinger H (2000) Konzept zur Erhaltung und nachhaltigen Nutzung forstlicher Genressourcen in der Bundesrepublik Deutschland. Sächsische Landesanstalt für Forsten. 66 S

Pautasso M, Aas G, Queloz V, Holdenrieder O (2013) European ash (*Fraxinus excelsior*) dieback–a conservation biology challenge. Biol Conserv 158:37–49

Pérez-Pereira N, Wang J, Quesada H, Caballero A (2022) Prediction of the minimum effective size of a population viable in the long term. Biodivers Conserv 31(11):2763–2780

Petit RJ, Elmousadik A, Pons O (1998) Identifying populations for conservation on the basis of genetic markers. Conserv Biol 12(4):844–855. https://doi.org/10.1111/j.1523-1739.1998.96489.x

Pyttel P, Kunz J, Bauhus J (2013) Growth, regeneration and shade tolerance of the Wild Service Tree (*Sorbus torminalis* (L.) Crantz) in aged oak coppice forests. Trees 27(6):1609–1619. https://doi.org/10.1007/s00468-013-0908-7

Rajora OP, Mosseler A (2001) Challenges and opportunities for conservation of forest genetic resources. Euphytica 118(2):197–212. https://doi.org/10.1023/A:1004150525384

Rajora OP, Rahman MH, Buchert GP, Dancik BP (2000) Microsatellite DNA analysis of genetic effects of harvesting in old-growth eastern white pine (*Pinus strobus*) in Ontario, Canada. Mol Ecol 9(3):339–348. https://doi.org/10.1046/j.1365-294x.2000.00886.x

Rau B, Kavaliauskas D, Fussi B, Šeho M (2023) Bewertung von Erntebeständen der Sommerlinde in Bayern. AFZ DerWald 8(2023):18–21

Rigling D, Hilfiker S, Schöbel C, Meier F, Engesser R, Scheidegger C et al (2016) Ash dieback: biology, disease symptoms and recommendations for control. Merkblatt für die Praxis 57

Santos-del-Blanco L, Olsson S, Budde KB, Grivet D, González-Martínez SC, Alía R, Robledo-Arnuncio JJ (2022) On the feasibility of estimating contemporary effective population size (Ne) for genetic conservation and monitoring of forest trees. Biol Conserv 273:109704

Schmiedel D, Huth F, Wagner S (2013) Using data from seed-dispersal modelling to manage invasive tree species: the example of *Fraxinus pennsylvanica* Marshall in Europe. Environ Manag 52:851–860

Šeho M, Fussi B, Rau B, Kavaliauskas D (2022) Conservation and sustainable use of forest genetic resources of English yew (*Taxus baccata* L.) in Bavaria. SilvaWorld 1(1):52–68. https://doi.org/10.29329/silva.2022.462.06

Seidel H, Šeho M, Fussi B (2025) Hope for ash conservation and propagation—single individuals can be highly resistant to an invasive pathogen. J Plant Dis Prot 132(1):1–15

Seidel H, Šeho M, Fussi B (submitted) Few resilient individuals as the potential key for tree breeding towards tolerance against an invasive pathogen, submitted to Journal of Plant Diseases and Protection

Semizer-Cuming D, Kjær ED, Finkeldey R (2017) Gene flow of common ash (*Fraxinus excelsior* L) in a fragmented landscape. PLoS One 12:e0186757. https://doi.org/10.1371/journal.pone.0186757

Semizer-Cuming D, Finkeldey R, Nielsen LR et al (2019) Negative correlation between ash dieback susceptibility and reproductive success: good news for European ash forests. Ann For Sci 76:16. https://doi.org/10.1007/s13595-019-0799-x

Semizer-Cuming D, Chybicki IJ, Finkeldey R et al (2021) Gene flow and reproductive success in ash (*Fraxinus excelsior* L.) in the face of ash dieback: restoration and conservation. Ann For Sci 78:14. https://doi.org/10.1007/s13595-020-01025-0

Sork VL, Smouse PE (2006) Genetic analysis of landscape connectivity in tree populations. Landsc Ecol 21(6):821–836

Spiecker H (2006) Minority tree species–a challenge for multi-purpose forestry. Nature based forestry in central Europe. Alternative to industrial forestry and strict preservation. Studia Forestalia Slovenica 126:47–59

Tessier du Cros E, Màtyàs C, Kriebel H (1999) Contribution of genetics to the sustained management of global forest resources—conclusions and recommendations. In: Màtyàs C (ed) Forest genetics and sustainability, forestry sciences, vol 63. Kluwer, Dordrecht, pp 281–287

Tigano A, Friesen VL (2016) Genomics of local adaptation with gene flow. Mol Ecol 25(10):2144–2164

Valenta V, Moser D, Kapeller S, Essl F (2017) A new forest pest in Europe: a review of Emerald ash borer (*Agrilus planipennis*) invasion. J Appl Entomol 141(7):507–526

Venturas M, Fuentes-Utrilla P, Ennos R, Collada C, Gil L (2013) Human-induced changes on fine-scale genetic structure in *Ulmus laevis* Pallas wetland forests at its SW distribution limit. Plant Ecol 214(2):317–327

von Wuehlisch G (2008) EUFORGEN technical guidelines for genetic conservation and use for European beech (*Fagus sylvatica*). Biodiversity International, Rome. 6 pages

Vornam B, Recarli N, Gailing O (2004) Spatial distribution of genetic variation in a natural beech stand (*Fagus sylvatica* L.) based on microsatellite markers. Conserv Genet 5:561–570

Welk E, De Rigo D, Caudullo G (2016) *Sorbus torminalis* in Europe: distribution, habitat, usage and threats. In: San-Miguel-Ayanz J, De Rigo D, Caudullo G, Durrant TH, Mauri A (eds) European atlas of forest tree species. Publ. Off. EU, Luxembourg, p e01090d+

White TL, Adams WT, Neale DB (eds) (2007) Forest genetics. Cabi

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