forests

MDPI

Review

Forest Genetic Monitoring: A Global Review on Methods, Results and Consequences of Genetic Studies and Long-Term Monitoring Projects

Ágnes Gál-Babicz [1], Klára Cseke [2], Beáta Pintér [1] and Sándor Bordács [1,*]

[1] Department of Botany, Institute of Agronomy, Hungarian University of Agriculture and Life Sciences, Villányi út 29-43, 1118 Budapest, Hungary
[2] Department of Tree Improvement, Forest Research Institute, University of Sopron, Várkerület 30/A, 9600 Sárvár, Hungary
* Correspondence: bordacs.sandor@uni-mate.hu

Abstract

Numerous publications on forest genetic monitoring (FGM) and related topics in genetics and gene conservation have been published over the past three decades. This paper reviews the methods used in FGM and, more broadly, related scientific findings published to date, of which general conclusions can be applied worldwide in FGM. In the strict sense, long-term FGM projects have been established only in a few regions in Europe. The methodological basis (guidelines) for FGM has already been developed, specifically for European tree species and forest communities. In genetic analyses, traditional SSR markers are predominantly used, but SNP markers from new-generation sequencing are increasingly available. Nonetheless, there is a high level of variation in monitoring activities such as biodiversity, forest health, and forest genetics, likely due to the efforts of national (governmental) and international professional organizations. Early evaluation of the first FGM projects has already been published. Scientific evidence for FGM has been limited because of the low number of projects that represent a few geographic regions and species.

Keywords: forest genetic monitoring; genetic markers; forest genetic resources; monitoring methods; manuals and guidelines; genetic criteria; overall value of FGM

Check for updates

Academic Editor: Nevenka Ćelepirović

Received: 12 December 2025
Revised: 21 January 2026
Accepted: 23 January 2026
Published: 27 January 2026

1. Introduction

Forest ecosystems have been monitored for several decades and for various purposes. In many countries, forest reserves have been monitored to record natural processes within a forest stand and to collect data on changes in various biotic and abiotic factors. Forest health monitoring began in earnest worldwide when the most severe diebacks were observed across Europe due to industrial air pollution and acid deposition, beginning in the last quarter of the 20th century [1–5].

In addition to forest health monitoring projects, forest reserves have also been widely assessed in many countries to record natural processes within a forest stand and to collect data on changes in various biotic and abiotic factors. The diversity of plant, animal, and fungal species is a key focus worldwide [6,7]. However, most projects, especially in tropical and subtropical regions, are limited to inventorying species diversity by listing the biological components of forest ecosystems [8,9].

Forest genetic monitoring (FGM) is a novel and fundamental approach for the long-term conservation and sustainable management of forest genetic resources [10–12]. Basi-

https://doi.org/10.3390/f17020165

cally, FGM projects aim to monitor relevant changes in a forest ecosystem, especially the demographic, phenotypic, and genotypic changes in dominant and character tree species within a forest community [10]. Forest genetic monitoring is a suite of methods to track genetic diversity, phenotypic variation, and demographic structure of the major tree species growing within a monitoring plot [12,13]. In conclusion, forest genetic monitoring is an early warning system for assessing the tree species responses to environmental change at a long-term time scale [13].

Phenotypic traits and phenological characteristics can be used as monitoring tools, such as the timing of budburst [14], flowering, fruit ripening, and even autumn coloration and leaf fall in deciduous tree species [10,13]. Phenotypic and phenological traits have been used in provenance trials of forest tree species to evaluate the phenotypic variation within and among provenances for more than 70 years [15–17]. Variation in phenotypic traits is usually linked to specific adaptive genes and can be evaluated by establishing field trials [17–21]. Reductions in genetic diversity and alterations in phenotypic traits within a population may reflect adaptation, fixation in the population’s gene pool, or indicate the intensity or direction of the modification. Consequently, phenotypic traits can be used to monitor adaptive changes in population genetic diversity [13,20].

First population genetic studies of forest tree species began in the 1970s, when techniques for protein and isozyme markers were available [22–24]. Firstly, gymnosperm taxa were investigated when pine forests were severely damaged by acid rain and industrial air pollution [1,25–30]. In general, population genetic studies at that time focused on population differentiation, specifically on the correlation between resistance (vs. susceptibility) and various genetic markers [31–33]. The isozyme markers were also used for deciduous tree species, either to detect resistant and tolerant populations which had similar genetic constitutions [34] or to highlight differences or similarities among populations in provenance trials [10]. Later, at the end of the 20th century, DNA techniques replaced isozyme-based methods, creating new opportunities for population studies.

Recently, the development of molecular genetic techniques has accelerated. Exploring the genetic structure of forest species populations, even on a large scale and in previously unexpected detail, is an achievable goal today. As the volume of genetic information on forest tree species has increased, the population genetic functions of forest ecosystems have become increasingly relevant. Any alterations in the genetic structure of stand-forming forest tree species can, in a direct or indirect way, provide useful information on the adaptiveness of tree populations [35–37]. Consequently, monitoring changes within the gene pool of tree populations can also help in understanding adaptive responses to environmental changes or alterations that affect populations.

Since the end of the last century, more and more studies have focused on forest tree populations as complex ecosystems. Specific ecological factors, such as soil characteristics, hydrology, and climatic parameters, are synthesized with the results of the genetic analyses [38,39]. Principally, among abiotic ecological factors, changing climatic parameters affected forest stands across all forest zones (temperate, Mediterranean, tropical, and subtropical). For a few decades, rising air temperatures, fluctuating precipitation, and climatic extremes have caused significant damage to forest ecosystems. In the context of climate change, the use of genetic markers might be a useful tool for monitoring the adaptability of the populations of forest tree species [40,41].

The challenges of the rapidly changing environment forced the forestry sector to reconsider the general rules and requirements of forest management practices. In the context of climate change, the forestry policies have particularly focused on the sustainability of forest management. Sustainable forest management (SFM) was defined by the FAO, and the concept has been well documented in various aspects of sustainable [42]. To a more precise definition of SFM, an expert team of the Center for International Forestry Research (CIFOR) formulated a new criteria set, including genetic aspects as well [11]. This was later accepted by the FAO [43].

The concept of forest genetic monitoring (FGM) was formulated about 20 years ago in Germany [43–45]. The basis of the concept was laid down at the global level and previously published by CIFOR and FAO [11,43], which included four essential indicators. The four indicators include: (i) level of genetic variation, (ii) directional changes in gene or genotypic frequencies; (iii) changes in mating system processes, and (iv) gene migration between populations. Simultaneously, the first pilot studies were also started in Germany to test principles of the concept, specifically, the genetic criteria and indicators adapted to a few pilot tree species, such as *Fagus sylvatica* and *Prunus avium* [46,47].

Ten years after the publication of the FAO working paper [43], an early evaluation was made on the results of FGM pilot projects in Germany [10], and the authors summarized the most important outputs of the 'German monitoring concept'. The essential verifiers were also summarized for each indicator, primarily the commonly used genetic parameters and values (e.g., F-value, number of alleles). The phenotypic traits and morphological characteristics were also evaluated and listed, which can be measured and observed on site and have an important role in the mating system of tree populations. The authors also discussed and evaluated site and demographic parameters, e.g., optimal plot design and size, minimum number of trees, etc., for two pilot species (*Fagus sylvatica* and *Prunus avium,* anemogamous vs. zoogamous taxa) distributed across Europe [10].

EUFORGEN is a Pan-European platform for discussing and summarizing scientific results and evidence in forest genetics, with a focus on the dynamic conservation of forest genetic resources. In Phase IV (2010–2014), the EUFORGEN established a specific working group dedicated to forest genetic monitoring [48]. A science-based discussion started on various aspects of the different forest genetic monitoring approaches and concepts, primarily focusing on the effectiveness of monitoring projects, including economic efficiency, rentability, and sustainability, and, nevertheless, the general expediency of the forest genetic monitoring methods. The working group discussed and evaluated the existing monitoring methods and specific approaches of various pilot projects. The working group's experts proposed and identified regions in Europe for genetic monitoring, along with the genetic monitoring units within these areas. Furthermore, the most applicable indicators and verifiers for genetic monitoring were selected and summarized, along with the technical requirements for the practical implementation of FGM plots, e.g., design and minimum size [49]. The EUFORGEN experts emphasized that the FGM recommendations were specified for Europe and implemented for European forests, but the outputs and conclusions of the FGM projects can also be used at the global level.

Simultaneously, the FORGER project [50] (*Towards the Sustainable Management of Forest Genetic Resources in Europe*) aimed to integrate and extend existing knowledge on the management and sustainable use of forest genetic resources, particularly to develop a standard protocol for measuring and monitoring the genetic diversity of forest tree species. A couple of practice-based recommendations were published as scientific results of the project, e.g., results from field trials measuring and evaluating phenotypic traits such as bud bursting, crown parameters, and flowering phenology [14,51].

Based on EUFORGEN results and recommendations [49] and further synthesis papers [12,52,53], a regional Life project (LIFEGENMON) was launched in Europe to integrate genetic monitoring into conservation programs and sustainable forest management. Based on the indicators and verifiers, genetic monitoring is an effective tool for assessing changes in adaptive and neutral genetic variation in tree species and populations over time. LIFEGENMON experts prepared manuals for forest genetic monitoring of seven tree genera

(*Abies*, *Fagus*, *Fraxinus*, *Pinus*, *Populus*, *Prunus*, and *Quercus*) and, in addition, a decision-support system for decision-makers to establish forest genetic monitoring systems across different countries and regions in Europe [13].

The relevance of forest genetic monitoring was recognized and emphasized in the FAO Second Report on the State of the World's Forest Genetic Resources [54]. The progress made on FGM projects was briefly reported since the first FAO Report (SoW-FGR1) was published [55]. Besides Germany and the LIFEGENMON project-leading countries (Slovenia and Greece), one European country (Lithuania) reported establishing a pilot FGM project, and another (Sweden) reported starting discussions about potential FGM projects [54]. Nevertheless, the FAO report concluded the importance of forest genetic monitoring and recommended 'expanding genetic monitoring and characterization system at national level' [56].

In the current paper, the authors aimed to survey global levels of FGM:

(i) How the genetic concepts were implemented into the management of forest genetic resources and consequently, developed forest genetic monitoring methods;
(ii) How forest genetic monitoring methods were adapted to local or regional circumstances and prospects;
(iii) Which kinds of genetic markers and phenotypic or morphological traits can be used for genetic monitoring of forest trees and populations;
(iv) Which kinds of scientific evidence or practical consequences are summarized by publications in the context of forest genetic monitoring.

2. Materials and Methods

Literature Review Methodology

The literature review was conducted using a range of international scientific databases and scholarly search engines, including Google Scholar, Web of Science, Scopus, ScienceDirect, SpringerLink, Wiley Online Library, and MDPI, as well as specialized forestry repositories such as FAO, EUFORGEN, FOREST EUROPE, and UNECE/FAO. During the preparation of this manuscript, both regular search (large-scale inclusion) and Boolean search (fine-scale exclusion) were used. Searches were performed using targeted keywords, including forest genetic monitoring, FGM, genetic diversity, provenance trials, adaptive variation, molecular markers (e.g., SSR, SNP), forest biodiversity monitoring, climate adaptation, genetic conservation, and assisted migration, in addition to species-specific terms (e.g., *Liquidambar orientalis*, *Fagus sylvatica*, *Quercus* spp.) For more details, see Table S1 in the Supplementary. The searching timeframe was set from the 1970s to the present day, with a closing date of 31 October 2025.

The search process yielded more than 100 relevant publications, comprising peer-reviewed journal articles, books and book chapters, international technical reports, conference proceedings, and methodological guidelines. First, publications were screened by removing duplicates, then reviewing titles and abstracts for relevance to forest genetic monitoring, empirical data availability, English-language proficiency, and journal publication; ineligible items (e.g., non-empirical reviews, book chapters, or off-topic ecological studies) were excluded. Final inclusion required full-text assessment for methodological rigor and contribution to key themes, with quality evaluated as high or moderate by expert consensus on criteria like data robustness and peer-review status, prioritizing contemporary (post-2000) and foundational works. The inclusion or exclusion of specific references was decided separately by consensus among the authors. In the comparative analysis of the referenced papers, the FGM publications (*sensu stricto*) were the primary focus. In the case of specific aspects related to FGM topics *sensu lato*, e.g., molecular markers, surveys by geographic region, comparison of forest monitoring approaches, many other 'topic-specific' publications were also assessed. The publications included for the specific analyses were referenced for each specific part.

To evaluate the applicability of genetic markers, a single SWOT analysis was conducted to assess the **S**trengths, **W**eaknesses, **O**pportunities, and **T**hreats of the markers for genetic analyses intended for monitoring purposes.

3. Results

3.1. A Review of Methods of Forest Genetic Monitoring Published and Referenced at the Global Level

In this part, the reviewed publications were assessed and clustered, focusing on the questions below:

1. What principles and methods are used for the field work of FGM studies, such as the selection criteria and minimum size of monitoring plots, geographic location of the plot, morphological and phenological parameters measured on trees, etc.?
2. What principles and methods are used in the molecular genetic analyses, specifically, the types of genetic markers?
3. What principles and methods are used for measuring and recording the ecological factors and parameters, e.g., soil types, hydrology, exposure, or others?
4. What principles and methods are used for the complex data evaluation (statistical evaluation, descriptive models, algorithms, AI-based software, etc.)?

The most general and relevant information was summarized separately into paragraphs and subparagraphs, depending on the context.

3.1.1. Forest Genetic Monitoring

The first and most critical step in FGM is identifying and selecting the monitoring plots. These plots must reliably represent both the genetic resources of the target region and the full natural distribution range of the species, to the extent possible.

The selection process for monitoring plots should integrate gene–ecological criteria, typically including ecological zoning, biogeographical regions, and species distribution patterns, to ensure that all major environmental and evolutionary contexts are included [12,49].

Whenever possible, monitoring units should be located within existing conservation, management, or long-term monitoring areas, as these sites offer logistical advantages, established infrastructure, and complementary ecological or demographic datasets. Furthermore, monitoring networks should capture all ecological conditions in which the species occurs, with particular emphasis on areas known for elevated genetic diversity—such as range margins, refugial zones, and environmentally heterogeneous regions [10].

3.1.2. Design of Monitoring Units and Sampling Strategy

Monitoring units are spatially delineated areas that include a sufficiently large population to allow reliable genetic assessment, typically comprising both reproductively mature individuals and natural regeneration [49]. The appropriate sampling strategy depends on the species' reproductive biology. For monoecious species, sampling generally requires at least 50 unrelated mature trees, whereas dioecious species—such as *Fraxinus excelsior*—necessitate the collection of genetic material from a minimum of 25 reproductively mature males and 25 females [10,49].

To reduce the risk of sampling closely related individuals and thus avoid kinship bias, a minimum spacing of approximately 30 m between sampled trees is recommended [49]. Monitoring units should also incorporate natural regeneration areas, as these enable the assessment of recruitment patterns, gene flow, and ongoing evolutionary processes within the population [12].

3.1.3. Morphological, Demographic, and Phenological Parameters

Forest genetic monitoring relies on systematic, long-term recording of morphological, demographic, and phenological traits to detect selective pressures and assess the adaptive potential of tree populations [10,12]. Mortality and survival of permanently tagged individuals are recorded at decadal intervals or after major climatic disturbances, enabling the identification of genetic and environmental stress responses.

The density of natural regeneration—typically expressed as the number of seedlings per unit area—serves as a key indicator of reproductive success and the strength of selective forces acting on early life stages [49]. Population structure is described using age and size-class distributions, often quantified with measurements such as diameter at breast height (DBH) and total height, which provide insight into past disturbance regimes and long-term recruitment patterns [10].

Reproductive performance is evaluated using metrics such as fructification intensity, seed fill percentage, and germination rate [49]. Phenological monitoring encompasses observations of flowering abundance, the onset and duration of flowering, budburst timing, and leaf senescence—all traits known for their high sensitivity to climatic variation [49]. More advanced assessments, such as monitoring flowering synchrony, provide valuable information on mating dynamics and potential shifts in gene flow patterns under changing environmental conditions. In general, phenological and phenotypic traits are often species-specific and are encoded by highly variable adaptive loci. Therefore, the monitoring manuals focus on species-specific parameters, and general rules for forest tree species are rarely formulated [13].

3.1.4. Genetic Marker Types and Applications

FGM uses a broad spectrum of molecular markers, generally selected based on the required resolution and specific monitoring objectives. Earlier monitoring programs commonly employed biochemical markers, particularly isozymes, due to their low cost and ease of use in large-scale assessments [10]. In modern applications, however, DNA-based markers have become standard. As stated in the Introduction, a small number of FGM projects have been established, and the number of tree species in these projects is also limited; therefore, the use of genetic markers was surveyed broadly, including various studies on the genetic diversity of forest tree species.

Cytoplasmic markers, including chloroplast SSRs and mitochondrial variants, enable differentiation of maternal and paternal gene movement, offering insights into sex-specific dispersal patterns [57]. Nuclear microsatellites (nSSRs)—typically involving around 20 loci—remain widely used for detecting genetic drift, assessing population structure, and quantifying gene flow [49,57]. Single-nucleotide polymorphisms (SNPs) provide higher genomic resolution. They are particularly effective for reconstructing demographic history and identifying genomic regions under selection, especially when SNPs occur within or near functional genes [12].

Next-generation sequencing (NGS) technologies have significantly expanded FGM capabilities by enabling the analysis of thousands of loci simultaneously and the detection of signatures of adaptive variation at genome-wide scales [12,58]. The emerging RNA-based approaches and molecular techniques—such as exon-primed intron-crossing (EPIC) markers—can also offer considerable potential for future adaptive genetic monitoring, particularly for linking gene expression patterns to environmental selection pressures [59–61].

Nevertheless, the applicability of the most frequently used molecular markers is different, and the accelerating development of molecular techniques can rapidly replace some of the recently used genetic markers. Therefore, the 11 most relevant marker types were analyzed using SWOT factors (**S**trengths, **W**eaknesses, **O**pportunities, and **T**hreats), detailed and summarized in Table 1, including brief descriptions and references.

Table 1. The list of molecular markers commonly used for FGM analyses and in population genetic studies to monitor the genetic diversity of forest tree species. All the markers were described and assessed by SWOT factors. As a source of information, the most relevant publications were referred to the given markers and to tree taxa distributed in Europe.

Genetic Marker	Name/ Synonyme	Short Description	SWOT Factors (Strengths, Weaknesses, Opportunities, Threats)	Species Investigated in FGM Projects	References
isozyme	isoenzyme, allozyme	"first-generation" biochemical marker; mostly neutral for evaluating broad-scale genetic patterns	**S:** Very low cost; requires minimal equipment; codominant markers enable estimation of heterozygosity; historically comparable datasets across decades. **W:** Limited genome coverage; low polymorphism reduces resolution; requires fresh or well-preserved tissues; sensitive to enzyme degradation; cannot detect fine-scale structure. **O:** Useful for long-term baseline monitoring in low-income regions; suitable for training and rapid assessments. **T:** Largely displaced by DNA-based markers; lack of standardization across labs threatens comparability.	*Quercus robur*; *Quercus petraea*; *Fagus sylvatica*; *Abies alba*; various tree species	[62–66]
cpSSR	chloroplast microsatellite (syn. Simple Sequence Repeat)	uniparental marker type for broad-scale phylogeographical analyses	**S:** Maternal inheritance allows seed-dispersal inference; useful for reconstructing colonization routes; low cost; suitable for cpDNA haplotype studies. **W:** Typically low polymorphism in conifers; limited power for fine-scale diversity; dominant scoring possible. **O:** Integration with cp-genome sequencing; complementary to nuclear markers in landscape genetics. **T:** Declining use due to complete plastome sequencing becoming affordable.	*Fagaceae* spp. universal for various tree families	[67–69]
nSSR	nuclear microsatellite (syn. Simple Sequence Repeat)	genetic fingerprinting; neutral marker type for evaluating both fine- and broad-scale genetic patterns	**S:** High polymorphism; codominant; excellent resolution for population structure, gene flow, relatedness, and hybridization; widely validated in forest trees; moderate lab cost. **W:** Requires primer development; allele scoring can be subjective; capillary electrophoresis instruments required; potential scoring inconsistencies across labs. **O:** Strong candidate for long-term forest genetic monitoring (FGM) time series; harmonizable reference loci; cross-country comparability. **T:** Being gradually replaced by genome-wide SNP assays; PCR stutter and allele dropout may affect datasets.	*Quercus* spp.; *Fagus sylvatica*; *Pinus sylvestris*	[49,70–73]

Table 1. *Cont.*

Genetic Marker	Name/ Synonyme	Short Description	SWOT Factors (Strengths, Weaknesses, Opportunities, Threats)	Species Investigated in FGM Projects	References
EST-SSR	expressed sequence tag SSR	potentially linkage to adaptive traits	**S:** Targets (linked to) expressed genes; highly transferable across related species; informative for functional diversity and stress response. **W:** Lower polymorphism compared to genomic SSRs; dependence on EST database quality; locus dropout possible. **O:** Linking genetic diversity to phenotypic traits and adaptive potential. **T:** EST resources are disappearing with the shift to full transcriptome sequencing (RNA-seq).	*Quercus* spp.; *Picea abies*; *Fagus sylvatica*	[74–76]
ISSR	inter simple sequence repeat	highly polimorhic marker; detects polymorphisms in inter-microsatellite DNA regions	**S:** Simple; no prior genomic information required; more stable than RAPD. **W:** Dominant scoring, moderate reproducibility; limited genome coverage; moderate resolution **O:** Practical for rapid screening of variability in understudied species. **T:** Limited use in high-quality genetic monitoring due to lack of comparability across studies.	*Quercus suber*; *Fagaceae*; *Pinus sylvestris*	[77–79]
RAPD	randomly amplified polymorphic DNAs	simple PCR-based marker type producing dominant pattern	**S:** Very low cost; simple workflow; no sequence information needed; useful for initial exploratory studies. **W:** Extremely poor reproducibility; dominant marker; highly sensitive to primer and PCR conditions; limited scientific acceptance. **O:** Educational purposes or low-budget preliminary variability scans. **T:** Considered obsolete; nearly fully replaced by modern sequencing-based methods.	*Fagus sylvatica*; *Quercus* spp.; universal for various tree species	[66,80,81]
AFLP	amplified fragment length polymorphism	dominant molecular marker combining restriction enzyme digestion and selective amplification steps	**S:** Genome-wide representation without prior sequence; high reproducibility when standardized; suitable for species delimitation and broad-scale assessments. **W:** Dominant markers; high sensitivity to lab conditions; requires fluorescent capillary systems; limited repeatability across labs. **O:** Useful for rapid pre-screening of diversity; applicable to understudied species. **T:** Superseded by next-generation sequencing (SNP-based) methods; inter-lab comparability issues limit long-term monitoring use.	*Prunus avium*; *Fagus sylvatica*;	[10,82,83]

Table 1. *Cont.*

Genetic Marker	Name/ Synonyme	Short Description	SWOT Factors (Strengths, Weaknesses, Opportunities, Threats)	Species Investigated in FGM Projects	References
SNP array	type of DNA microarrays	studying subtle variations between whole genomes; used for genome-wide association studies	**S:** Highly standardized; extremely reproducible; low missing data; ideal for long-term monitoring series. **W:** Limited to predefined SNPs; ascertainment bias affects diversity estimates; arrays age quickly. **O:** Creation of international reference SNP panels for FGM. **T:** Obsolescence as genomic resources expand; may miss novel adaptive variants.	*Quercus robur*; *Pinus sylvestris*	[84–86]
KASP	Kompetitive allele specific PCR	SNP genotyping platform	**S:** Extremely cost-efficient per SNP; high-throughput; highly reproducible across labs; excellent for targeted genotyping panels. **W:** Only evaluates known loci; requires pre-designed assays; unsuitable for discovery. **O:** Routine monitoring. **T:** Less informative than sequencing when genome-wide variation is needed.	*Fagus sylvatica*; *Quercus suber*; *Quercus ilex*; *Pinus sylvestris*	[87–89]
ddRA-Dseq	Double digest restriction-site associated DNA	generates a large set of SNP markers; can be used to infer very precisely the genetic diversity and population structure	**S:** Reproducible reduced-representation sequencing (genome complexity reduced by restriction enzyme digestion); strong SNP density; good for population structure and gene flow. **W:** Sensitive to enzyme selection; moderate missing data; requires consistent lab workflow. **O:** Comparative and multi-species monitoring. **T:** Protocol inconsistency reduces long-term comparability across labs.	*Fagus sylvatica*; *Quercus robur*; *Quercus petraea*; *Pinus sylvestris*	[90–94]
GBS	Genotyping by sequencing	using next-generation sequencing (NGS) for genotyping; a screening method for discovering novel SNPs	**S:** Genome-wide SNP discovery without reference genome; reduced-representation sequencing method; cost-effective; high data density; suitable for non-model species. **W:** High missing-data rate; batch effects common; requires harmonized pipelines; sensitive to DNA quality. **O:** Monitoring adaptive variation, species-wide scans. **T:** Comparability across years/labs may be reduced by library prep variation.	*Fagus sylvatica*; *Quercus robur*; *Alnus glutinosa*	[90,91,95, 96]

3.1.5. Genetic Metrics and Data Analysis

FGM relies on a suite of standard population-genetic metrics to quantify genetic diversity, structure, and evolutionary processes within monitoring units. Core diversity indicators include the number of alleles (Na), the effective number of alleles (Ne), Shannon's diversity index (I), observed heterozygosity (Ho), and expected heterozygosity (He). The

Latent Genetic Potential (LGP) index, which emphasizes the contribution of rare alleles to evolutionary resilience, is particularly valuable for long-term monitoring [10].

Population differentiation is typically measured using FST, while deviations from random mating are assessed using inbreeding coefficients (FIS) [12]. Characterization of the mating system and estimation of gene flow commonly involve multilocus outcrossing rates (tm) and the effective number of migrants (Nm), metrics frequently computed with dedicated software such as MLTR [10,12].

Genetic datasets are processed using a range of specialized tools, including GSED, PopGene, MacGen, GenAlEx, FSTAT, NEESTIMATOR, MLTR, and STRUCTURE, the latter of which supports Bayesian clustering and admixture inference [12]. These analytical capabilities are increasingly complemented by R-based packages such as adegenet and poppr, which facilitate flexible and reproducible data analysis workflows.

Temporal comparisons of genetic or phenotypic traits employ statistical models suited to the data structure: linear regression for continuous traits, ordinal or non-parametric tests for ranked or categorical variables, and Poisson regression for count-based datasets [12].

3.1.6. Integration of Environmental and Ecological Data

Integrating environmental and ecological variables into FGM is essential for interpreting patterns of genetic variation and assessing the adaptive capacity of forest populations. Key environmental factors include climatic variables, soil properties, hydrological conditions, site exposure, and geographic coordinates, all of which shape selective pressures across the species' range [13,49,52].

Comprehensive ecological characterization—encompassing forest community composition, stand age structure, regeneration dynamics, and management history—provides critical context for understanding observed genetic patterns. These ecological descriptors support the evaluation of long-term demographic trends, disturbance regimes, and the influence of habitat on genetic diversity and evolutionary processes [97].

3.2. A Review of Results Published at the Global Level by Continents or by Geographic Regions

In this part, the reviewed publications were analyzed and clustered by geographic regions. Firstly, publications related to specific keywords, such as genetics and genomics, monitoring of any kind of diversity, and economically important tree species by geographic region, were assessed in terms of the bullet-point paragraphs detailed in the previous parts. Secondly, the main elements and potential synergistic factors of FGM projects were listed and evaluated, with those already in action or essential for future FGM activities. For the most comprehensive evaluation, historical perspectives were also considered, e.g., the general status of forest genetic resources, especially the state of conservation of FGRs; furthermore, the findings and scientific evidence of recent genetic studies on forest tree species, and additionally, the level of national policies or initiatives of international organizations and platforms.

3.2.1. Europe & Turkey

The monitoring of European forests primarily aims to conserve forest ecosystems, ensure the sustainable use of resources, and implement adaptive management strategies in response to environmental change [10,49,98]. A key component of this framework is forest genetic monitoring, which functions as an early-warning system by detecting genetic changes that may signal declining population viability, biodiversity shifts, or increasing vulnerability to climate impacts [11,12,49,99]. Across the continent, forests—covering approximately 215 million hectares—face diverse pressures, including climate change, air pollution, unsustainable management, invasive species, land-use conversion, and habitat fragmentation [98,100].

These monitoring efforts build on long-standing initiatives such as ICP Forests, launched under the Convention on Long-range Transboundary Air Pollution. ICP Forests developed harmonized pan-European protocols for assessing forest condition, crown health, deposition, and soil chemistry, forming the backbone of environmental and genetic monitoring in European forest ecosystems [101,102].

Monitoring encompasses many ecologically and economically important species. Deciduous taxa frequently included are *Fagus sylvatica*, *Quercus robur*, *Quercus petraea*, *Fraxinus excelsior*, *Populus nigra*, and *Prunus avium.* Coniferous species include *Picea abies*, *Abies alba*, *Pinus sylvestris*, and *Pinus nigra* [10,103]. Sampling is stratified across diverse biogeographic and climatic zones to capture the full spectrum of adaptive and ecological variation across Europe [49].

Complementary to phenotypic monitoring, a continent-wide network (EUFORGEN) of Genetic Conservation Units (GCUs) supports dynamic in situ conservation. These units are designed based on species-specific ecological requirements and evolutionary processes, enabling the maintenance of genetic diversity and evolutionary potential under changing environmental conditions [49].

Europe has also established large-scale provenance trials, which provide essential insights into adaptive genetic variation and climate-related responses. A notable example is the Hucking Provenance Trial in the United Kingdom, testing multiple provenances of *Quercus robur*, *Prunus avium*, *Castanea sativa*, and *Corylus avellana* from across the UK, France, and Italy. Analyses reveal strong provenance effects for survival, growth, phenology, and biotic resilience, with Mediterranean provenances showing enhanced drought tolerance—findings that align with assisted migration and climate-matching strategies [53,104].

Similarly, the BeechCOSTe52 network comprises one of Europe's most extensive sets of *Fagus sylvatica* provenance trials, involving 217 provenances across 38 sites. Results demonstrate pronounced population differentiation in traits such as budburst phenology, drought resistance, and growth plasticity, highlighting the species' adaptive capacity and sensitivity to climatic variation [105,106].

Additional evidence comes from the UK Native Tree Species Provenance Trials, which examine species such as *Pinus sylvestris*, *Sorbus aucuparia*, and *Fraxinus excelsior*. These trials show strong local adaptation—particularly in cold tolerance, budburst timing, and photosynthetic efficiency—emphasizing the importance of regionally appropriate seed sourcing for restoration and afforestation initiatives [103].

In the eastern Mediterranean, the relict tree *Liquidambar orientalis*, native primarily to southwestern Turkey, is increasingly threatened by habitat loss, fragmentation, and land-use pressures such as overgrazing, tourism, and agricultural expansion. Climate change poses additional risks: recent modeling indicates a significant contraction of climatically suitable habitat, with limited potential northward or upward expansion despite warming trends [107]. Habitat degradation remains a primary threat, and conservation strategies emphasize strict habitat protection, in situ management, and safeguarding seed sources within GCUs [108,109].

3.2.2. North America (USA & Canada)

North America's forest monitoring programs cover approximately 677.5 million hectares and place strong emphasis on maintaining forest health, productivity, and resilience to both biotic and abiotic stressors [100,110]. In the United States, the Forest Health Monitoring (FHM) program represents one of the central frameworks for long-term forest assessment. The program includes targeted evaluations of high-elevation conifer species, as well as systematic monitoring of insects, diseases, and climatic stressors, to support early detection and management of emerging threats [110].

Canada employs an integrated forest monitoring system that combines national forest inventories with a National Early Warning System, enabling the detection of anomalies in temperature, pest outbreaks, and regeneration dynamics across vast boreal ecosystems. This system provides key insights into disturbance regimes and forest ecosystem responses to environmental change [6].

Genetic and provenance assessments in North America focus on ecologically and economically critical temperate and boreal tree species, including *Acer saccharum*, *Fraxinus americana*, *Quercus rubra*, and *Populus tremuloides* [111]. These assessments align with international sustainability frameworks such as the Montreal Process, which emphasize biodiversity conservation, ecosystem integrity, and long-term productive capacity [Montreal Process, 2010].

A large number of provenance trials have been established in the region since the mid-20th century. In general, economically important tree species in the northern regions were in focus, such as *Pinus strobus* [112,113], *Pseudotsuga menziesii* [23], or *Quercus rubra* [114]. Subsequently, provenance research on southern pines, e.g., *Pinus taeda*, *Pinus elliotti*, was also initiated [15], taxa that were widely planted not only in the USA but also in other continents (South America, Africa) [115,116]. A continent-wide synthesis by Risk et al. [111] evaluated results from 773 provenances across 62 test sites for seven major species, including *Picea glauca*, *Picea mariana*, *Pinus banksiana*, *Pinus strobus*, *Larix laricina*, *Quercus rubra*, and *Betula alleghaniensis*. The results reveal strong adaptive population differentiation and clinal adaptation in phenotypic traits, which is common in most species. In specific cases, e.g., *Picea glauca*, provenances from southern Ontario demonstrated a higher survival rate and height growth when transferred northward. On the contrary, underperformance was recorded for the provenances from colder and drier continental regions. The trend can be explained by integrating the effects of different postglacial migration routes and, consequently, by the diverse genetic background of *Picea glauca* [117].

Long-term experiments involving *Pinus ponderosa*, *Pinus contorta*, and *Pseudotsuga menziesii* highlight the potential of assisted migration, showing that populations originating from warmer climates often outperform local genotypes. These results underscore the potential role of genetic transfer and assisted migration in climate adaptation strategies for North American forests [118].

3.2.3. Central Asia

Countries in temperate Asia demonstrate extensive efforts to monitor forest biodiversity and genetic resources, integrating ecological and genetic approaches to support conservation and sustainable forest management strategies.

Within Central Asia, countries such as Azerbaijan, Turkey, and Uzbekistan face severe anthropogenic pressures, including unsustainable logging, overgrazing, and habitat degradation. These challenges have prompted the development of regional guidelines to improve forest monitoring capacities and reinforce genetic conservation systems [49,97,109,119]. Conservation priorities focus on threatened tree species with fragmented populations and declining genetic diversity, such as *Liquidambar orientalis* and *Pistacia atlantica* [120]. Contemporary forest monitoring frameworks in countries in temperate Asia emphasize not only biodiversity assessments but also evaluations of management effectiveness, integrating ecological and genetic data to support adaptive responses to environmental change [8,120].

Asia also hosts several notable provenance trial programs, many of which were historically coordinated by FAO and UNEP. The global provenance trials initiated by FAO during the 1970s and 1980s for species such as *Eucalyptus camaldulensis*, *Eucalyptus tereticornis*, *Acacia auriculiformis*, and *Prosopis* spp., spanned 17 countries and revealed substantial adaptive variation in traits, including drought tolerance, growth performance, and pest resistance. For *Eucalyptus camaldulensis*, provenances originating from arid interior regions of Australia consistently outperformed coastal provenances in drought-prone plantation environments in India, Thailand, and Sudan.

In Central Asia, provenance trials for *Liquidambar orientalis* demonstrated that western Turkish populations exhibit enhanced growth and survival under heat and water stress, indicating strong suitability for climate change–oriented restoration efforts [121].

3.2.4. Countries in Tropical & Subtropical America

Tropical forests in the Americas exhibit exceptionally high species diversity, which poses significant challenges for biodiversity monitoring due to taxonomic complexity and the difficulty of accurately identifying species [122,123]. Monitoring programs across South America predominantly address key threats such as deforestation and climate change, with studies indicating that more than 70% of ecogeographic range segments for priority species are considered threatened [123,124]. Conservation efforts focus on biodiversity hotspots such as the Atlantic Forest and the Amazon Basin, where habitat fragmentation and land-use pressures heighten the risk of genetic erosion [123]. Plantation forestry is one of the threats to the degradation of the biodiversity of the region's natural forests. Therefore, provenance trials of non-native tree species are often in the focus of regional breeding programs, such as in the case of *Eucalyptus urophylla* originating from Flores Island, Indonesia [125]. The use of non-native tree species in plantations, however, minimizes the risks of hybridization with native woody taxa and closes out the introgression or degradation in the gene pool of native species.

3.2.5. Countries in Tropical & Subtropical Africa

In Africa, community-based forest monitoring approaches blend indigenous knowledge systems with formal biodiversity assessments to address region-specific threats such as unsustainable harvesting and climatic variability [9]. Climatic zones in the region are predicted to be intensively modified due to desertification from the Saharan region. *Prunus africana* is among the most critically threatened species, with overexploitation and habitat loss driving the need for targeted conservation and monitoring initiatives [126]. Forest monitoring frameworks span a broad range of ecological zones—from savannah landscapes to montane forests—and prioritize genetic conservation within community-managed areas [127].

Provenance trials of *Prunus africana* in Cameroon, Kenya, and Ethiopia indicate that montane populations exhibit superior survival under extreme temperature fluctuations, supporting their use in climate-resilient restoration and assisted population management, probably for the Sub-Saharan region as well [128]. Similar to other tropical and subtropical regions, the biodiversity of natural forests is also threatened by plantation forestry. Most of the provenance trials are in the focus of breeding programs, including many introduced species [116].

3.2.6. Countries in Tropical & Subtropical Asia

Tropical Asia benefits from regional collaborations such as the APFORGEN network, which coordinates conservation and sustainable management of forest genetic resources across Southeast Asia, with special emphasis on dipterocarp species that dominate many lowland forests [97,120]. However, extensive deforestation driven by agricultural expansion, logging, and urbanization underscores the need for integrated in situ and ex situ conservation strategies, including seed banking and ecological restoration [97].

In Malaysia and Indonesia, provenance trials, involving dipterocarp species such as *Shorea leprosula* and *Shorea parvifolia*, documented strong population differentiation in drought responses, offering practical guidance for regionally tailored conservation actions [120]. Tropical provenance trials have played a central role in understanding the adaptive traits of fast-growing tree species. FAO-coordinated international provenance trials involving *Eucalyptus* and *Acacia* species have revealed substantial genetic variation in drought tolerance, salinity resistance, and stem form across tropical and subtropical populations [129,130].

In China, the Chinese Forest Biodiversity Monitoring Network (CForBio) conducts systematic assessments across a broad latitudinal gradient spanning tropical to boreal biomes. Its studies evaluate the influence of topography, historical climate variability, and environmental heterogeneity on forest community composition [8]. Subtropical evergreen species, including *Quercus* spp., receive substantial attention in genetic conservation due to their ecological importance and sensitivity to climate change [58,131]. Similarly, provenance trials in China for subtropical oak species have identified pronounced elevational clines in drought and heat tolerance, with high-elevation populations showing greater resilience to temperature extremes. These findings underscore the importance of provenance trails and the use of the results in genetic conservation and in climate-resilient forestry [132].

3.2.7. North and Sub-Saharan Africa

Sub-Saharan Africa's forests face severe pressures from deforestation and climate change, with over 2000 tree species at risk and many genetically uncharacterized. SAFORGEN, launched in 1999 after Dakar 1997 and Ouagadougou 1998 consultations, targets 302 priority species through genetic diversity assessments, conservation tools, and exchange via four Working Groups (Food, Medicinal, Fodder, Wood/Fibre Species).

To improve the management of forest genetic resources, achievements, which are usually managed and coordinated by international organizations and NGOs, include workshops (Burkina Faso 1998; Kenya 1999; Ethiopia 2008), fellowships or local projects involving assessments of endangered species such as *Prunus africana* [128]. Mediterranean tree species also play an important role in the countries across the region, such as *Quercus suber*. An international provenance trial of *Quercus suber* was organized by EUFORGEN in 1997 and established in Tunisia to test the adaptability of the provenances representing the whole distribution area [133]. Recently, populations of *Cedrus atlantica* were tested to evaluate the spatial genetic structure of provenances from their natural distribution range in North Africa [134].

These pan-African efforts emphasize coordinated provenance testing and genetic monitoring to preserve diverse, threatened tree resources amid global change. SAFORGEN has not been mentioned in ongoing projects, events, or funding as of 2025. Recent discussions of forest genetic resources focus on European networks such as EUFORGEN's Phase VII (2025–2029), suggesting that SAFORGEN may be dormant or integrated into broader FAO/Bioversity efforts [134,135].

3.2.8. Australia & New-Zealand

Australia's forest monitoring is embedded within national sustainability frameworks that emphasize biodiversity conservation, ecosystem health, and adaptive management measures designed to address climate change impacts [136]. The country contains approximately 134 million hectares of forested land, dominated by *Eucalyptus* and *Acacia* species. Major threats to these ecosystems include invasive species, pest outbreaks, pathogenic diseases, and increasingly frequent, high-intensity wildfires driven by climatic variability.

Genetic structuring in Australian tree species is strongly shaped by biotic pollination systems mediated by animals and insects, differing from the predominantly anemogamous (wind-driven) pollination systems of many Northern Hemisphere taxa [10]. This reliance on biotic vectors influences gene flow, maintains high genetic diversity, and contributes to the adaptive potential of native species.

Australia has a long-established tradition of tree improvement and breeding programs, particularly for economically and ecologically important genera such as *Eucalyptus* and

Araucaria. These initiatives aim to strengthen adaptive capacity, enhance resilience in both plantation and native forests, and support sustainable resource management [136].

The country also maintains provenance trial networks. Provenance trials of *Eucalyptus globulus* reveal pronounced adaptive differentiation: Tasmanian populations exhibit strong cold tolerance, while Victorian mainland provenances display rapid early growth but reduced drought resistance [137]. Similarly, trials of *Eucalyptus camaldulensis* across semi-arid regions have consistently demonstrated the superior heat and drought tolerance of inland populations [138]. For *Araucaria cunninghamii*, provenance evaluations indicate that northern Queensland populations possess greater tolerance to thermal stress and nutrient-poor soils, informing seed transfer and deployment decisions for plantations in climatically vulnerable regions [139,140].

3.3. Comparison

Comparative analysis of forest monitoring practices across world regions reveals a shared emphasis on sustainable forest management and forest genetic conservation. Provenance trials constitute a central component of these efforts by elucidating adaptive genetic variation fundamental to long-term ecosystem resilience. However, region by region, a high level of variation was observed in the approaches and programmes related to forest genetic resources. For better comprehensibility, the geographic regions were classified according to three criteria: ‘type of biological monitoring’, ‘mode of conservation and use of forest genetic resources’, and ‘organizational impacts’, which are considered relevant to recent or future forest genetic monitoring activities. The three main criteria were further divided into subgroups, and the geographic regions were assessed across 11 aspects in total. For this comparison, all publications on FGM, sensu stricto or sensu lato, referenced in previous parts were assessed. The classification by region is presented in Table 2, and the overall results are visualized in a color-coded map (Figure 1). The criteria were summarized but not ranked.

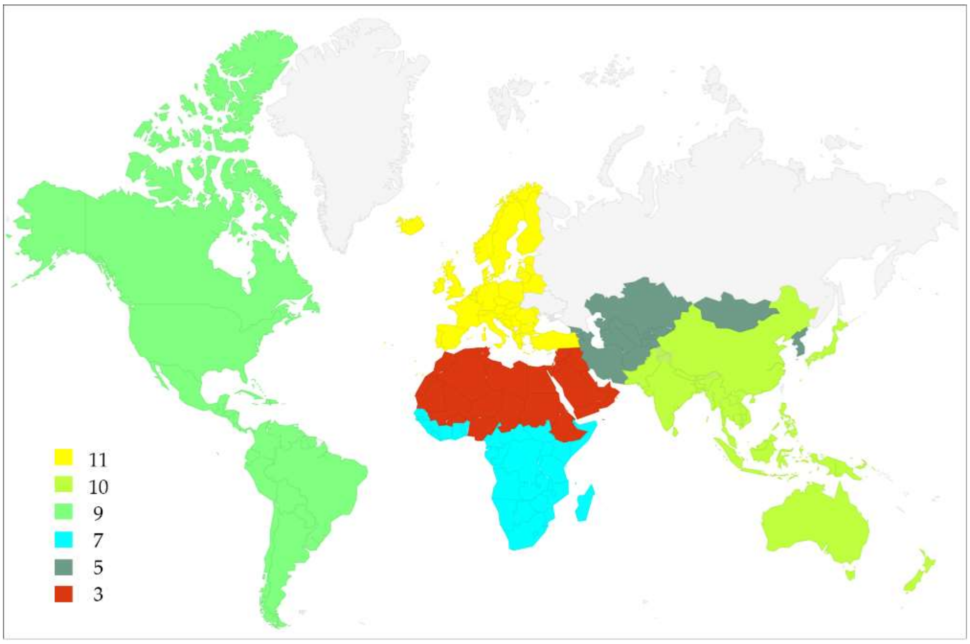

Figure 1. The map of geographic regions and continents assessed for the overall value of the state and the level of forest genetic monitoring. The color code refers to the overall values summarized for the given regions in Table 2. Areas in grey color are excluded in the assessment. The map was constructed by use of https://docs.google.com/spreadsheets (accessed 15 January 2026).

Table 2. The overall value of the state and level of forest genetic monitoring (FGM), assessed by geographic regions and continents. For the assessment, the type of biological monitoring, the mode of conservation and use of the forest genetic resources, and, furthermore, the organizational impacts related to FGM were reviewed. Referenced impacts or effects of the assessment based on the publications reviewed for geographic regions were marked by * to the given factor and the overall value of forest genetic monitoring was summarized in column "Overall value of FGM".

Geographic Region or Continent	Type of Biological Monitoring					Mode of Conservation and Use of FGRs			Organizational Impacts			Overall Value of FGM
	Forest (Health)	Provenance Trials	Genetic Studies on Tree Populations	Biodiversity	Forest Genetic	In Situ	Ex Situ	In Vitro	National Governmental	National Non-Governmental	International (FAO, Bioversity International, EUFORGEN)	
Europe & Turkey	*	*	*	*	*	*	*	*	*	*	*	11
North America (USA & Canada)	*	*	*	*		*	*	*	*	*		9
Tropical & subtropical America		*	*	*		*	*	*	*	*	*	9
Sub-Saharan Africa		*		*							*	3
Tropical & subtropical Africa		*	*	*		*		*	*	*		7
Tropical & subtropical Asia	*	*	*	*		*	*	*	*	*	*	10
Central Asia		*		*		*			*		*	5
Australia & Oceania	*	*	*	*		*	*	*	*	*	*	10

4. Discussion and Conclusions

4.1. General Conclusions of the Publications Reviewed, at the Regional and Global Level

As discussed in the Introduction, the first forest genetic monitoring projects were established in Europe, based on the genetic criteria for sustainable forest management laid down by CIFOR experts [11,43] and implemented into the management and policies of forest genetic resources at the national and pan-European levels. Historically, the driving forces of FGM projects in Europe were made up of various elements such as;

1. Forest biodiversity threats, basically by forest fragmentation, urbanization, air pollution, invasive species, and, recently, by climate change effects;
2. Policies that support general principles of the conservation of forest genetic resources have been laid down and implemented at the pan-European and national levels;
3. National institutions and international platforms have existed, and simultaneously, FGRs have been actively managed, supporting the establishment and maintenance of FGM projects;
4. Genetic background has been explored for the most important forest tree species;
5. The forests, and in general the biodiversity in Europe, have been in focus for political, economic and social aspects, and consequently, have a great impact on the public.

Forest genetic monitoring projects, both at the local and regional levels, were established, where the availability of all or most of the above-mentioned aspects and requirements produced synergistic overall effects [10,13,49]. The synergistic effects must play a crucial role, since, despite the availability of all the required background and resources, long-term FGM projects have not yet been established in many European countries.

In addition, the FGM projects exhibited a historical progression, e.g., the forest diebacks in the 1980s–1990s caused ecological damage. Therefore, the genetic structure of many forest species was later analyzed through provenance tests and molecular genetic studies. Simultaneously, conservation programmes were initiated to preserve forest genetic resources at the national or regional level, and the monitoring of forest genetic resources became more acceptable to the public, including local and regional communities and economic and political actors. Retrospectively, the first FGM projects were established in European countries where the forests have undergone similar processes in the last 50 years. The importance of forest genetic resources has long been a focus, not only for scientists but also for the public at large [10,13,49].

FGM activities show substantial variation across geographic regions. For each geographic area, the cited scientific publications were surveyed for the types of monitoring projects established and the activities reported, the current status of conservation FGRs (e.g., ex situ collections, in situ conservation stands), and the institutional background (governmental vs. non-governmental organizations, national and international actors, etc.). As a summary of the analyzed data and information from the publications referenced in this study, the FGM projects have been at varying levels of progress and have produced different outputs across continents and geographic regions, as shown in Table 2 and in Figure 1.

The color codes on the constructed map corresponded to the overall values of the regions, which were aggregated based on factors such as the progress of FGR management, the actual level of scientific activity, and, in general, the importance of FGRs. International organizations and actors, such as the FAO, Bioversity International (formerly IPGRI), and most effectively, the EUFORGEN platform, obviously play a relevant role in promoting the active management and conservation of forest genetic resources. For almost 30 years, the EUFORGEN platform in Europe has successfully promoted forest genetic conservation projects and supported numerous scientific projects focused on active FGR management. As a result, FGM projects were established at the regional level in Europe, such as the LIFEGENMON project for Central and Southern European countries (Germany, Slovenia, and Greece).

In addition, regional platforms supported by FAO and Bioversity International, such as LAFORGEN, SAFORGEN, and APFORGEN, have successfully promoted and initiated FGR-related projects across many tropical and subtropical countries. As a result of regional co-operation, significant progress in the conservation and active management of FGRs can be observed in tropical-subtropical Asian countries. Simultaneously, significant efforts were invested in research projects on economically important forest tree species (provenance trials, genetics and genomics, etc.), and the scientific outputs and findings also contributed to the active management of FGRs in the region.

4.2. Quo Vadis Forest Genetic Monitoring?

4.2.1. General Consequences of FGM Results

As a general consequence, forest genetic monitoring projects, in the strict sense of the term, have been established and managed primarily in a few European countries. In a broader sense, monitoring projects, long-term studies, and analyses focusing on biodiversity, or specifically on forest health conditions, have been established in other continents and geographic regions as well, such as North America, Tropical and subtropical Asia, and Australia & Oceania. Recently, more and more countries have recognized the importance of forest genetic resources. Forestry policies have focused on the conservation and active management of genetic resources not only in Europe but worldwide.

The first FGM projects were established decades ago, based on practical experience and the outcomes of provenance trials. This specific experience and knowledge were adapted and transmitted into the first FGM projects, mainly focusing on autochthonous species in Europe with a specific, relevant role within forest ecosystems, as model or pilot species. The first results were published after a few years of monitoring period, and those may be regarded as preliminary results of the pilot FGM projects. As a consequence, those should be re-discussed when additional monitoring data and information are published later.

Besides the preliminary results of FGM projects, notable progress was evident in the methods and science-based approaches of FGM. The LIFEGENMON project, one of the first international projects in Europe, has developed and compiled FGM manuals and guidelines for seven species, which were the focus of the project participants. The project evaluated and summarized results and field experiences, and the LIFEGENMON manuals include species-based approaches and guidelines for implementing FGM principles, as well as species-specific indicators and verifiers [13].

In general, the recently established forest genetic monitoring projects have made progress since CIFOR experts formulated the indicators and verifiers for actively managed forest genetic resources and forest genetic monitoring. The latest FAO report has also emphasized the relevance of forest genetic monitoring and recommended exploring FGM projects [56]. In this paper, we have reviewed the progress of forest genetic monitoring activities and summarized and evaluated the general trends in this field.

4.2.2. What Kind of Short-Term and Long-Term Prospects Could Be Realistic for FGM?

1. In the short term (5–10 years), there will likely be no expansion or significant progress in forest genetic monitoring. Based on the conclusions of the latest FAO report, most member states have reported no intention of establishing FGM projects [54,55]. Actually, those will typically be restricted to just a few tree species and forest ecosystems in Europe, since FGM projects (*sensu stricto*) have been initiated only in some regions. However, the continuous processing and evaluation of the results of FGM projects have been intended.
2. The social, economic, and scientific foundations and criteria discussed earlier are in place for the launch of new FGM projects in North America, Southeast Asia, and Australia. The question is whether a critical mass will be reached that shifts and accelerates the current situation and launches FGM activities similar to those reported in Europe.
3. In the longer term, it is likely that FGM projects will expand not only in Europe but also in other regions, presumably in the case of pilot species, where extensive and complex research and monitoring activities may be launched in which FGM indicators and verifiers appear in part or in whole. Those may not necessarily use the term FGM, but can utilize or adapt the elements of FGM projects.
4. Historically, the new methods and techniques in genomics were relevant driving forces in the conservation and management of forest genetic resources, which have expanded the baseline of genetic knowledge on forest tree species since the end of the 20th century. Innovation and development in genomics, especially the development of new molecular markers, such as RNA-based technologies (e.g., EPIC markers), can also support the launch of new FGM projects [59–61].
5. An interesting alternative to the monitoring projects, which are generally time-consuming and expensive, could be the utilization of simulation models optimized for various ecological factors [141–144], and provided that the simulation models

correlate or represent genetic composition and shifts. These initiatives, which are still in their early stages, may be able to replace FGM projects in many cases. FGM projects usually provide conclusions restricted to the monitored tree species and forest communities, and even their scientific outputs can be interpreted only for the given geographical region [141–144]. Additionally, the use of complementary or substitute simulation models can facilitate the adaptability of FGM project results, e.g., to other unmonitored tree species or forest communities. Nevertheless, the prospects and opportunities opened by artificial intelligence or AI-based models are also difficult to assess at this stage.

Consequences of the current ecological challenges affecting forests, such as climate change, the reduction in natural forests, and other human impacts, such as urbanization, forest fragmentation, the appearance of invasive species, etc., can be analyzed and interpreted on a scientific basis by using ecological models, based on past and present natural responses of the ecosystems. However, experience over recent years shows that the accuracy and reliability of the analytical and predictive 'big-data models' have been constantly improving, and the models will probably open a new perspective for AI-based research. Regardless of this, experimental research, provenance trials, or monitoring studies carried out in the real, existing natural environment will still be necessary for a long time to come.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/f17020165/s1, Table S1. List of keywords used for research.

Author Contributions: Conceptualization, S.B. and Á.G.-B.; methodology, S.B.; investigation, Á.G.-B., K.C. and B.P.; data curation, Á.G.-B., K.C. and B.P.; writing—original draft preparation, Á.G.-B. and S.B.; writing—review and editing, Á.G.-B., K.C., S.B. and B.P.; visualization, B.P.; supervision, S.B. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Data Availability Statement: New data not were created.

Acknowledgments: During the preparation of this manuscript/study, the authors used Perplexity AI (Sonar model, ProSearch, GPT_5.2) for the purposes of literature searches and information retrieval. The authors have reviewed and edited the output and take full responsibility for the content of this publication.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Cogbill, C.V. The effect of acid precipitation on tree growth in eastern North America. *Water Air Soil. Pollut.* **1977**, *8*, 89–93. [CrossRef]
2. McLaughlin, S.B. Effects of Air Pollution on Forests: A Critical Review. *J. Air Pollut. Control Assoc.* **1985**, *35*, 512–534. [CrossRef]
3. Schöpp, W.; Posch, M.; Mylona, S.; Johansson, M. Long-term development of acid deposition (1880–2030) in sensitive freshwater regions in Europe. *Hydrol. Earth Syst. Sci.* **2003**, *7*, 436–446. [CrossRef]
4. Michel, A.; Haggenmüller, K.; Kirchner, T.; Prescher, A.-K.; Schwärzel, K.; Wohlgemuth, L. (Eds.) Forest Condition in Europe: The 2024 Assessment. In *ICP Forests Technical Report Under the UNECE Convention on Long-Range Transboundary Air Pollution (Air Convention)*; Thünen Institute: Eberswalde, Germany, 2024; Volume 96, pp. 1–99. [CrossRef]
5. de Vries, W.; Dobbertin, M.H.; Solberg, S.; van Dobben, H.F.; Scgaub, M. Impacts of acid deposition, ozone exposure and weather conditions on forest ecosystems in Europe: An overview. *Plant Soil.* **2014**, *380*, 1–45. [CrossRef]
6. Boutin, S.; Haughland, D.L.; Schieck, J.; Herbers, J.; Bayne, E. New Approach to Forest Biodiversity Monitoring in Canada. *For. Ecol. Manag.* **2009**, *258*, S168–S175. [CrossRef]
7. Pearman, P.B.; Broennimann, O.; Aavik, T.; Albayrak, T.; Alves, P.C.; Aravanopoulos, F.A.; Bertola, L.D.; Biedrzycka, A.; Buzan, E.; Cubric-Curik, V.; et al. Monitoring of species' genetic diversity in Europe varies greatly and overlooks potential climate change impacts. *Nat. Ecol. Evol.* **2024**, *8*, 267–281. [CrossRef]

8. Feng, G.; Mi, X.; Yan, H.; Li, F.Y.; Svenning, J.-C.; Ma, K. CForBio: A Network Monitoring Chinese Forest Biodiversity. *Sci. Bull.* **2016**, *61*, 1163–1170. [CrossRef]
9. Fa, J.E.; Luiselli, L. Community Forests as Beacons of Conservation: Enabling Local Populations Monitor Their Biodiversity. *Afr. J. Ecol.* **2024**, *62*, e13179. [CrossRef]
10. Konnert, M.; Maurer, W.; Degen, B.; Kätzel, R. Genetic monitoring in forests—Early warning and controlling system for ecosystemic changes. *iForest Biogeosci. For.* **2011**, *4*, 77–81. [CrossRef]
11. Namkoong, G.; Boyle, T.; Gregorius, H.-R.; Joly, H.; Savolainen, O.; Ratnam, W.; Young, A. *Testing Criteria and Indicators for Assessing the Sustainability of Forest Management: Genetic Criteria and Indicators*; Working paper No. 10; CIFOR: Jakarta, Indonesia, 1996. [CrossRef]
12. Aravanopoulos, F.A. Conservation and Monitoring of Tree Genetic Resources in Temperate Forests. *Curr. For. Rep.* **2016**, *2*, 119–129. [CrossRef]
13. Bajc, M.; Aravanopoulos, F.A.; Westergren, M.; Fussi, B.; Kavaliauskas, D.; Alizoti, P.; Kiourtsis, F.; Kraigher, H. (Eds.) *Manual for Forest Genetic Monitoring*; Silva Slovenica Publishing Centre: Ljubjana, Slovenia, 2020. [CrossRef]
14. Mátyás, C.S.; Kramer, K. Climate change affects forest genetic resources: Consequences for adaptive management. *Forg. Policy Brief.* **2016**, *10*, 4. [CrossRef]
15. Burley, J. Review of variation in slash pine (*Pinus elliottii* Engelm.) and loblolly pine (*P. taeda* L.) in relation to provenance research. *Commonw. For. Rev.* **1966**, *45*, 322–338.
16. EI-Kassaby, Y.A.; Fashler, A.M.K.; Sziklai, O. Effect of family size and number on the accuracy and precision of the estimates of genetic parameters in the IUFRO Douglas-fir provenance-progeny trial. *For. Ecol. Manag.* **1987**, *18*, 35–48. [CrossRef]
17. Park, A.; Rodgers, J.L. Tamm Review: Provenance trials in the service of forestry assisted migration: A review of North American field trials and experiments. *For. Ecol. Manag.* **2023**, *537*, 120854. [CrossRef]
18. Ujvári Jármay, É.; Ujvári, F. Adaptation of Progenies of a Norway Spruce Provenance Test (IUFRO 1964/68) to Local Environment. *Acta Silv. Lignaria Hung.* **2006**, *2*, 47–55. [CrossRef]
19. Liepe, K.J.; Rieckmann, C.A.; Mittelberg, H.S.; Liesebach, M. Phenotypic variation in 1100 provenances of *Picea abies* measured over 50 years on 33 German trial sites. *Sci. Data* **2024**, *11*, 854. [CrossRef]
20. Kurjak, D.; Petrík, P.; Konôpková, A.R.; Gömöry, D.; Hajek, P.; Liesebach, M.; Leuschner, C.; Schuldt, B. Inter-provenance variability and phenotypic plasticity of wood and leaf traits related to hydraulic safety and efficiency in seven European beech (*Fagus sylvatica* L.) provenances differing in yield. *Ann. For. Sci.* **2024**, *81*, 11. [CrossRef]
21. Thomas, B.R.; Stoehr, M.; Schreiber, S.G.; Benowicz, A.; Schroeder, W.R.; Soolanayakanahally, R.; Stefner, C.; Elliott, K.A.; Philis, N.; Rubal, N.; et al. Tree Improvement in Canada—Past, present and future, 2023 and beyond. *For. Chron.* **2024**, *100*, 59–87. [CrossRef]
22. Bergmann, F. The allelic distribution at an acid phosphatase locus in Norway spruce (*Picea abies*) along similar climatic gradients. *Theor. Appl. Genet.* **1978**, *52*, 57–64. [CrossRef] [PubMed]
23. EI-Kassaby, Y.A.; Sziklai, O. Genetic variation of allozyme and quantitative traits in a selected Douglas-fir (*Pseudotsuga menziesii var. menziesii* (Mirb.) Franco) population. *Forest Ecol. Manag.* **1982**, *4*, 115–126. [CrossRef]
24. Tigerstedt, P.M.A. Studies on isozyme variation in marginal and central populations of *Picea abies*. *Hereditas* **1973**, *75*, 47–60. [CrossRef]
25. Schulze, E.D. Air pollution and forest decline in a spruce (*Picea abies*) forest. *Science* **1989**, *244*, 776–783. [CrossRef] [PubMed]
26. Peterson, D.L.; Arbaugh, M.J.; Robinson, L.J. Regional growth changes in ozone-stressed ponderosa pine (*Pinus ponderosa*) in the Sierra Nevada, California, USA. *Holocene* **1991**, *1*, 50–61. [CrossRef]
27. Eager, C.; Adams, M. Decline of Red Spruce in the Eastern United States. In *Ecology and Decline of Red Spruce in the Eastern United States*; Eager, C., Adams, M., Eds.; Springer: New York, NY, USA, 1992; pp. 338–382.
28. McLaughlin, S.B.; Kohut, R.J. The Effects of Atmospheric Deposition and Ozone on Carbon Allocation and Associated Physiological Processes in Red Spruce. In *Ecology and Decline of Red Spruce in the Eastern United States*; Eagar, C., Adams, M.B., Eds.; Ecological Studies; Springer: New York, NY, USA, 1992; Volume 96. [CrossRef]
29. Cape, J.N. Direct damage to vegetation caused by acid rain and polluted cloud: Definition of critical levels for forest trees. *Environ. Pollut.* **1993**, *82*, 167–180. [CrossRef] [PubMed]
30. Muzika, R.M.; Guyettea, R.P.; Zielonka, T.; Liebhold, A.M. The influence of O_3, NO_2 and SO_2 on growth of *Picea abies* and *Fagus sylvatica* in the Carpathian Mountains. *Environ. Pollut.* **2004**, *130*, 65–71. [CrossRef]
31. Savolainen, O.; Bokma, F.; Knürr, T.; Kärkkäinen, K.; Pyhäjärvi, T.; Wachowiak, W. Adaptation of forest trees to climate change. In *Climate Change and Forest Genetic Diversity: Implications for Sustainable Forest Management in Europe*; Koskela, J., Buck, A., Teissier, D.C., Eds.; Bioversity International: Rome, Italy, 2007; pp. 19–29.
32. Schaberg, P.G.; DeHayes, D.H.; Hawley, G.J.; Nijensohn, S.E. Anthropogenic alterations of genetic diversity within tree populations: Implications for forest ecosystem resilience. *For. Ecol. Manag.* **2008**, *256*, 855–862. [CrossRef]

33. Booy, G.; Hendriks, R.J.J.; Smulders, M.J.M.; Van Groenendael, J.M.; Vosman, B. Genetic Diversity and the Survival of Populations. *Plant Biol.* **2008**, *2*, 379–395. [CrossRef]
34. Müller-Starck, G. Genetic differences between "tolerant" and "sensitive" beeches (*Fagus sylvatica* L.) in an environmentally stressed adult forest stand. *Silvae Genet.* **1985**, *34*, 241–247. Available online: https://www.thuenen.de/media/institute/fg/PDF/Silvae_Genetica/1985/Vol._34_Heft_6/34_6_241.pdf (accessed on 21 January 2026).
35. Cortés, A.J.; Restrepo-Montoya, M.; Bedoya-Canas, L.E. Modern Strategies to Assess and Breed Forest Tree Adaptation to Changing Climate. *Front. Plant Sci.* **2020**, *11*, 583323. [CrossRef]
36. Gailing, O.; Budde, K.B.; Leinemann, L.; Müller, M.; Wilhelmi, S. Genetic Connectivity and Local Adaptation of Forest Trees in the Face of Climate Change. In *Ecological Connectivity of Forest Ecosystems*; Lapin, K., Oettel, J., Braun, M., Konrad, H., Eds.; Springer: Cham, Switzerland, 2025; pp. 91–114. [CrossRef]
37. Kremer, A.; Chen, J.; Lascoux, M. 'Chimes of resilience': What makes forest trees genetically resilient? *New Phytol.* **2025**, *246*, 1934–1951. [CrossRef]
38. Ekblom, R.; Galindo, J. Applications of next generation sequencing in molecular ecology of non-model organisms. *Heredity* **2011**, *107*, 1–15. [CrossRef]
39. Plomion, C.; Bartholomé, J.; Bouffier, L.; Brendel, O.; Cochard, H.; de Miguel, M.; Delzon, S.; Gonzalez-Martinez, S.C.; Guehl, J.-M.; Lagraulet, H.; et al. Understanding the genetic bases of adaptation to soil water deficit in trees through the examination of water use efficiency and cavitation resistance: Maritime pine as a case study. *J. Plant Hydraul.* **2016**, *3*, e008. [CrossRef]
40. Sáenz-Romero, C.; Kremer, A.; Nagy, L.; Újvári-Jármay, É.; Ducousso, A.; Kóczán-Horváth, A.; Hansen, J.K.; Mátyás, C. Common garden comparisons confirm inherited differences in sensitivity to climate change between forest tree species. *PeerJ* **2019**, *7*, e6213. [CrossRef] [PubMed] [PubMed Central]
41. Coşgun, S.; Gauthier, J.; Beffa, G.; Bonanomi, G.; Carraro, G.; Cherubini, P.; Gobet, E.; Leunda, M.; Manetti, M.; Mazza, G.; et al. Exploring the connection between climatic conditions and genetic properties of *Abies alba* Mill., including warm and summer-dry Mediterranean environments. *Sci. Total Environ.* **2025**, *964*, 178559. [CrossRef] [PubMed]
42. Sustainable Forest Management. Official FAO Website. Available online: https://www.fao.org/forestry/sfm/en (accessed on 8 January 2026).
43. Namkoong, G.; Boyle, T.; El-Kassaby, Y.A.; Palmberg-Lerche, C.; Eriksson, G.; Gregorius, H.R.; Joly, H.; Kremer, A.; Savolainen, O.; Wickneswari, R.; et al. *Criteria and Indicators for Sustainable Forest Management: Assessment and Monitoring of Genetic Variation*; Working paper: Forest genetic resources; FAO: Rome, Italy, 2002; 29p, Available online: https://www.cifor-icraf.org/knowledge/publication/1183/ (accessed on 21 January 2026).
44. Kätzel, R.; Maurer, W.D.; Konnert, M.; Scholz, F. Genetisches Monitoring in Wäldern. *Forst und. Holz* **2005**, *5*, 179–183.
45. Maurer, W.D. Genetisches Langzeitmonitoring im Wald unter Berücksichtigung von in-situ- und ex-situ-Erhaltungsmaßnahmen. In *Analyse und Bewertung der Genetischen Vielfalt in der Land-, Forst- und Fischereiwirtschaft zur Ableitung von Entscheidungskriterien für Erhaltungsmaßnahmen*; Begemann, F., Schröder, S., Weigend, S., Eds.; ZADI-Schriften zu genetischen Ressourcen: Bonn, Germany, 2005; Band 24, pp. 82–90. Available online: https://www.fawf.wald-rlp.de/fileadmin/website/fawfseiten/fawf/downloads/Mitteilungen/mit_59/45-56.pdf (accessed on 21 January 2026).
46. Maurer, W.D. (Ed.) *Anleitung zur Durchführung des Genetischen Monitorings für Bestandesbildende Baumarten*; Expertengruppe "Genetisches Monitoring" von BLAG: Trippstadt, Germany, 2008; pp. 1–16. Available online: https://www.genres.de/fileadmin/SITE_MASTER/content/SITE_GENRES/downloads/docs/BLAG-FGR/gm-durchfuehrung_260308_1_.pdf (accessed on 21 January 2026).
47. Degen, B.; Jolivet, C.; Liesebach, H.; Hoeltken, A.; Dounavi, A.; Fladung, F.; Naujoks, S.G.; Schneck, V.; Stauber, T.; Steiner, W.; et al. Abschlussbericht „Erfassung der Genetischen Struktur der Vogelkirsche (*Prunus avium*) als Grundlage für ein Genetisches Monitoring Wichtiger Waldbaumarten in Deutschland. 2008. Available online: https://www.yumpu.com/de/document/read/7699052/erfassung-genetischer-strukturen-wichtiger-waldbaumarten-ble (accessed on 21 January 2026).
48. EUFORGEN—Genetic Monitoring. Available online: https://www.euforgen.org/about-us/how-we-operate/discussion-platforms-and-working-groups/genetic-monitoring (accessed on 15 November 2025).
49. Aravanopoulos, F.A.; Tollefsrud, M.M.; Graudal, L.; Koskela, J.; Kätzel, R.; Soto, A.; Nagy, L.; Pilipovič, A.; Zhelev, P.; Božič, G.; et al. Development of genetic monitoring methods for genetic conservation units of forest trees in Europe. In *European Forest Genetic Resources Programme (EUFORGEN)*; Bioversity International: Rome, Italy, 2015; pp. ii–xvi+1–46, ISBN 978-92-9255-030-1.
50. European Commission. FORGER: Towards the Sustainable Management of Forest Genetic Resources in Europe (Project ID: 289119). CORDIS 2011–2015. Available online: https://cordis.europa.eu/project/id/289119 (accessed on 21 January 2026).
51. Piotti, A.; Leonardi, S.; Buiteveld, J.; Geburek, T.; Gerber, S.; Kramer, K.; Vettori, C.; Vendramin, G.G. Comparison of pollen gene flow among four European beech (*Fagus sylvatica* L.) populations characterized by different management regimes. *Heredity* **2012**, *108*, 322–331. [CrossRef]

52. Fussi, B.; Westergren, M.; Aravanopoulos, F.; Baier, R.; Kavaliauskas, D.; Finzgar, D.; Alizoti, P.; Bozic, G.; Avramidou, E.; Konnert, M.; et al. Forest genetic monitoring: An overview of concepts and definitions. *Environ. Monit. Assess.* **2016**, *188*, 493. [CrossRef]
53. Fady, B.; Cottrell, J.; Ackzell, L.; Alía, R.; Muys, B.; Prada, A.; González-Martínez, S.C. Forests and global change: What can genetics contribute to the major forest management and policy challenges of the twenty-first century? *Reg. Environ. Change* **2023**, *16*, 927–939. [CrossRef]
54. Blyth, C.; Lowe, A.; Blyth, S.T. Genetic diversity in trees and other woody plants. Chapter 5. In *The Second Report on the State of the World's Forest Genetic Resources*; FAO Commission on Genetic Resources for Food and Agriculture Assessments: Rome, Italy, 2025; pp. 47–63, ISBN 978-92-5-139699-5.
55. The State of the World's Forest Genetic Resources. In *Commission On Genetic Resources for Food and Agriculture, Food and Agriculture Organization of the United Nations*; FAO: Rome, Italy, 2014; p. 277.
56. Koskela, J.; Paradisi, D.; Trudic, B. Recommended actions for the future. Chapter 13. In *The Second Report on the State of the World's Forest Genetic Resources*; FAO Commission on Genetic Resources for Food and Agriculture assessments: Rome, Italy, 2025; pp. 171–176, ISBN 978-92-5-139699-5.
57. Schwartz, M.; Luikart, G.; Waples, R. Genetic Monitoring as a Promising Tool for Conservation and Management. *Trends Ecol. Evol.* **2007**, *22*, 25–33. [CrossRef] [PubMed]
58. Wang, L.-L.; Li, Y.; Zheng, S.-S.; Kozlowski, G.; Xu, J.; Song, Y.-G. Complete Chloroplast Genomes of Four Oaks from the Section Cyclobalanopsis Improve the Phylogenetic Analysis and Understanding of Evolutionary Processes in the Genus *Quercus*. *Genes* **2024**, *15*, 230. [CrossRef]
59. Yao, X.; Li, C.; Dick, C.W. Exon-primed intron-crossing (EPIC) markers for evolutionary studies of *Ficus* and other taxa in the fig family (Moraceae). *Appl. Plant Sci.* **2013**, *1*, 1300037. [CrossRef] [PubMed] [PubMed Central]
60. Zimmer, E.A.; Wen, J. Using nuclear gene data for plant phylogenetics: Progress and prospects. *Mol. Phylogenetics Evol.* **2012**, *65*, 774–785. [CrossRef] [PubMed]
61. Yao, X.; Liu, L.; Yan, M.; Li, D.; Zhong, C.; Huang, H. Exon primed intron-crossing (EPIC) markers reveal natural hybridization and introgression in Actinidia (Actinidiaceae) with sympatric distribution. *Biochem. Syst. Ecol.* **2015**, *59*, 246–255. [CrossRef]
62. Zanetto, A.; Kremer, G.; Müller-Starck, H.H. Hattemer, Inheritance of Isozymes in Pedunculate Oak (*Quercus robur* L.). *J. Hered.* **1996**, *87*, 364–370. [CrossRef]
63. Gömöry, D.; Yakovlev, I.; Zhelev, P.; Jedináková, J.; Paule, L. Genetic differentiation of oak populations within the *Quercus robur/Quercus petraea* complex in Central and Eastern Europe. *Heredity* **2001**, *86*, 557–563. [CrossRef] [PubMed]
64. Müller-Starck, G.; Starke, R. Inheritance of Isoenzymes in European Beech (*Fagus sylvatica* L.). *J. Hered.* **1993**, *84*, 291–296. [CrossRef]
65. Hosius, B.; Bergmann, F.; Konnert, M.; Henkel, W. A concept for seed orchards based on isoenzyme gene markers. *For. Ecol. Manag.* **2000**, *131*, 143–152. [CrossRef]
66. Shaw, K.; Stritch, L.; Rivers, M.; Roy, S.; Wilson, J.; Darbyshire, I. *Forest Genetic Resources Conservation and Management: Overview and Principles*; Food and Agriculture Organization of the United Nations: Rome, Italy, 2014.
67. Weising, K.; Gardner, R.C. A set of conserved PCR primers for the analysis of simple sequence repeat polymorphisms in chloroplast genomes of dicotyledonous angiosperms. *Genome* **1999**, *42*, 9–19. [CrossRef]
68. Provan, J.; Powell, W.; Hollingsworth, P.M. Chloroplast microsatellites: New tools for studies in plant ecology and evolution. *Trends Ecol. Evol.* **2001**, *16*, 142–147. [CrossRef] [PubMed]
69. Sebastiani, F.; Carnevale, S.; Vendramin, G.G. A new set of mono- and dinucleotide chloroplast microsatellites in *Fagaceae*. *Mol. Ecol. Notes* **2004**, *4*, 259–261. [CrossRef]
70. Steinkellner, H.; Fluch, S.; Turetschek, E.; Lexer, C.; Streiff, R.; Kremer, A.; Burg, K.; Glössl, J. Identification and characterization of (GA/CT)n- microsatellite loci from *Quercus petraea*. *Plant Mol. Biol.* **1997**, *33*, 1093–1096. [CrossRef] [PubMed]
71. Kampfer, S.; Lexer, C.; Glössl, J.; Steinkellner, H. Characterization of (GA)n Microsatellite Loci from *Quercus robur*. *Hereditas* **1998**, *129*, 183–186. [CrossRef]
72. Pastorelli, R.; Smulders, J.M.J.; Van't Westende, W.P.C.; Vosman, B.; Giannini, R.; Vettori, C.; Vendramin, G.G. Characterization of microsatellite markers in *Fagus sylvatica* L. and *Fagus orientalis* Lipsky. *Mol. Ecol. Notes* **2003**, *3*, 76–78. [CrossRef]
73. Sebastiani, F.; Pinzauti, F.; Kujala, S.T.; González-Martínez, S.C.; Vendramin, G.G. Novel polymorphic nuclear microsatellite markers for *Pinus sylvestris* L. *Conserv. Genet. Resour.* **2012**, *4*, 231–234. [CrossRef]
74. Durand, J.; Bodénès, C.; Chancerel, E.; Frigerio, J.-M.; Vendramin, G.; Sebastiani, F.; Buonamici, A.; Gailing, O.; Koelewijn, H.-P.; Villani, F.; et al. A fast and cost-effective approach to develop and map EST-SSR markers: Oak as a case study. *BMC Genom.* **2010**, *11*, 570. [CrossRef]
75. Fluch, S.; Burg, A.; Kopecky, D.; Homolka, A.; Spiess, N.; Vendramin, G.G. Characterization of variable EST SSR markers for Norway spruce (*Picea abies* L.). *BMC Res. Notes* **2011**, *4*, 401. [CrossRef] [PubMed Central]
76. Burger, K.; Müller, M.; Gailing, O. Characterization of EST-SSRs for European beech (*Fagus sylvatica* L.) and their transferability to *Fagus orientalis* Lipsky, *Castanea dentata* Bork., and *Quercus rubra* L. *Silvae Genet.* **2018**, *67*, 127–132. [CrossRef]

77. López-Aljorna, A.; Bueno, M.Á.; Aguinagalde, I.; Martín, J.P. Fingerprinting and genetic variability in cork oak (*Quercus suber* L.) elite trees using ISSR and SSR markers. *Ann. For. Sci.* **2007**, *64*, 773–779. Available online: https://hal.science/hal-00884129v1 (accessed on 15 November 2025). [CrossRef]
78. Coutinho, J.P.; Carvalho, A.; Lima-Brito, J. Genetic diversity assessment and estimation of phylogenetic relationships among 26 *Fagaceae* species using ISSRs. *Biochem. Syst. Ecol.* **2014**, *54*, 247–256. [CrossRef]
79. Sboeva, Y.; Chertov, N.; Nechaeva, Y.; Valeeva, A.; Boronnikova, S.; Kalendar, R. Genetic Diversity, Structure, and Differentiation of *Pinus sylvestris* L. Populations in the East European Plain and the Middle Urals. *Forests* **2022**, *13*, 1798. [CrossRef]
80. Gallois, A.; Audran, J.; Burrus, M. Assessment of genetic relationships and population discrimination among *Fagus sylvatica* L. by RAPD. *Theor. Appl. Genet.* **1998**, *97*, 211–219. [CrossRef]
81. Bellusci, G.; Braglia, R.; Di Marco, G.; Redi, E.L.; Canini, A.; Gismondi, A. Assessing molecular diversity among 87 species of the *Quercus* L. genus by RAPD markers. *Genet. Resour. Crop Evol.* **2023**, *70*, 2683–2694. [CrossRef]
82. Jump, A.S.; Peñuelas, J. Extensive spatial genetic structure revealed by AFLP but not SSR molecular markers in the wind-pollinated tree, *Fagus sylvatica*. *Mol. Ecol.* **2007**, *16*, 925–936. [CrossRef] [PubMed]
83. Pluess, A.R.; Weber, P. Drought-Adaptation Potential in *Fagus sylvatica*: Linking Moisture Availability with Genetic Diversity and Dendrochronology. *PLoS ONE* **2012**, *7*, e33636. [CrossRef]
84. Lepoittevin, C.; Bodénès, C.; Chancerel, E.; Villate, L.; Lang, T.; Lesur, I.; Boury, C.; Ehrenmann, F.; Zelenica, D.; Boland, A.; et al. Single-nucleotide polymorphism discovery and validation in high-density SNP array for genetic analysis in European white oaks. *Mol. Ecol. Resour.* **2015**, *15*, 1446–1459. [CrossRef]
85. Guilbaud, R.; Biselli, C.; Buiteveld, J.; Cattivelli, L.; Copini, P.; Dowkiw, A.; Esselink, D.; Fricano, A.; Guerin, V.; Jorge, V.; et al. Development of a new tool (4TREE) for adapted genome selection in European tree species. In *GenTree*; HAL: Avignon, France, 2020; (hal-02928391). Available online: https://hal.science/hal-02928391 (accessed on 15 November 2025).
86. Estravis Barcala, M.; van der Valk, T.; Chen, Z.; Funda, T.; Chaudhary, R.; Klingberg, A.; Fundova, I.; Suontama, M.; Hallingbäck, H.; Bernhardsson, C.; et al. Whole-genome resequencing facilitates the development of a 50K single nucleotide polymorphism genotyping array for Scots pine (*Pinus sylvestris* L.) and its transferability to other pine species. *Plant J.* **2024**, *117*, 944–955. [CrossRef] [PubMed]
87. Cuervo-Alarcon, L.; Arend, M.; Müller, M.; Sperisen, C.; Finkeldey, R.; Krutovsky, K.V. A candidate gene association analysis identifies SNPs potentially involved in drought tolerance in European beech (*Fagus sylvatica* L.). *Sci. Rep.* **2021**, *11*, 2386. [CrossRef]
88. Postolache, D.; Oddou-Muratorio, S.; Vajana, E.; Bagnoli, F.; Guichoux, E.; Hampe, A.; Le Provost, G.; Lesur, I.; Popescu, F.; Scotti, I.; et al. Genetic signatures of divergent selection in European beech (*Fagus sylvatica* L.) are associated with the variation in temperature and precipitation across its distribution range. *Mol. Ecol.* **2021**, *30*, 5029–5047. [CrossRef] [PubMed]
89. Cosín-Roldán, J.; de Heredia, U.L.; Soto, Á. Highly informative SNP markers for routine individual identification and certification of forest reproductive material in *Quercus ilex* and *Q. suber* and their hybrids. *For. Ecol. Manag.* **2023**, *544*, 121243. [CrossRef]
90. Parchman, T.L.; Jahner, J.P.; Uckele, K.A.; Galland, L.M.; Eckert, A.J. RADseq approaches and applications for forest tree genetics. *Tree Genet. Genomes* **2018**, *14*, 39. [CrossRef]
91. Ulaszewski, B.; Meger, J.; Burczyk, J. Comparative Analysis of SNP Discovery and Genotyping in *Fagus sylvatica* L. and *Quercus robur* L. Using RADseq, GBS, and ddRAD Methods. *Forests* **2021**, *12*, 222. [CrossRef]
92. Degen, B.; Blanc-Jolivet, C.; Bakhtina, S.; Ianbaev, R.; Yanbaev, Y.; Mader, M.; Nürnberg, S.; Schröder, H. Applying targeted genotyping by sequencing with a new set of nuclear and plastid SNP and indel loci for *Quercus robur* and *Quercus petraea*. *Conserv. Genet. Resour.* **2021**, *13*, 345–347. [CrossRef]
93. Tóth, E.G.; Cseke, K.; Benke, A.; Lados, B.B.; Tomov, V.T.; Zhelev, P.; Kámpel, J.D.; Borovics, A.; Köbölkuti, Z.A. Key triggers of adaptive genetic variability of sessile oak [*Q. petraea* (Matt.) Liebl.] from the Balkan refugia: Outlier detection and association of SNP loci from ddRAD-seq data. *Heredity* **2023**, *131*, 130–144. [CrossRef]
94. Capblancq, T.; Morin, X.; Gueguen, M.; Renaud, J.; Lobreaux, S.; Bazin, E. Climate-associated genetic variation in *Fagus sylvatica* and potential responses to climate change in the French Alps. *J. Evol. Biol.* **2020**, *33*, 783–796. [CrossRef]
95. Meger, J.; Ulaszewski, B.; Vendramin, G.G.; Burczyk, J. Using reduced representation libraries sequencing methods to identify cpDNA polymorphisms in European beech (*Fagus sylvatica* L). *Tree Genet. Genomes* **2019**, *15*, 7. [CrossRef]
96. De Kort, H.; Vandepitte, K.; Bruun, H.H.; Closset-Kopp, D.; Honnay, O.; Mergeay, J. Landscape genomics and a common garden trial reveal adaptive differentiation to temperature across Europe in the tree species *Alnus glutinosa*. *Mol. Ecol.* **2014**, *23*, 4709–4721. [CrossRef] [PubMed]
97. Islam, R.; Siwar, C.; Ismail, S.M.; Chamhuri, N.H. Criteria and Indicators for Sustainable Forest Management in Malaysia. *Am. J. Environ. Sci.* **2010**, *6*, 212–218. [CrossRef]
98. FOREST EUROPE. State of Europe’s Forests 2015. Ministerial Conference on the Protection of Forests in Europe. 2015. Available online: https://foresteurope.org/wp-content/uploads/2022/02/soef_21_12_2015.pdf (accessed on 15 November 2025).
99. Konnert, M.; Hosius, B. Contribution of forest genetics for a sustainable forest management. *Forstarchiv* **2010**, *81*, 170–174. [CrossRef]

100. Aide-Mémoire: 21st Montréal Process Working Group Meeting, Hilo, Hawaii, United States of America, 1–4 June 2010. Montréal Process. Available online: https://montreal-process.org/Resources/Meeting_Reports/Working_Group/21_e.shtml (accessed on 15 November 2025).
101. Available online: https://www.icp-forests.net/monitoring-and-research/icp-forests-manual (accessed on 15 November 2025).
102. Lefèvre, F.; Alia, R.; Bakkebø Fjellstad, K.; Graudal, L.; Oggioni, S.D.; Rusanen, M.; Vendramin, G.G.; Bozzano, M. *Dynamic Conservation and Utilization of Forest Tree Genetic Resources: Indicators for In Situ and Ex Situ Genetic Conservation and Forest Reproductive Material*; European Forest Genetic Resources Programme (EUFORGEN), European Forest Institute: Barcelona, Spain, 2020; p. 33, ISBN 978-952-5980-81-3.
103. Whittet, R.; Cavers, S.; Ennos, R.; Cottrell, J. *Genetic Considerations for Provenance Choice of Native Trees Under Climate Change in England (Forestry Commission Research Report FCRP030)*; Forestry Commission: Edinburgh, Scotland, 2019. Available online: https://cdn.forestresearch.gov.uk/2019/03/fcrp030.pdf (accessed on 15 November 2025).
104. Forest Research. *Hucking Estate Provenance Trials: Summary Report*; Forest Research: Kent, UK, 2013. Available online: https://cdn.forestresearch.gov.uk/2022/02/fr_adafor_huckingleaflet_2013.pdf?utm_source (accessed on 15 November 2025).
105. Bolte, A.; Czajkowski, T.; Cocozza, C.; Tognetti, R.; de Miguel, M.; Pšidová, E.; Ditmarová, Ĺ.; Dinca, L.; Delzon, S.; Cochard, H.; et al. Desiccation and Mortality Dynamicsin Seedlings of Different European Beech (*Fagus sylvatica* L.) Populations under Extreme Drought Conditions. *Front. Plant Sci.* **2016**, *7*, 751. [CrossRef] [PubMed]
106. Wuehlisch, G.V. Series of international provenance trials of European beech. In *Improvement and Silviculture of Beech, Proceedings from the 7th International Beech Symposium IUFRO Research Group 1.10.00, Teheran, Iran, 10–20 May 2004*; Research Institute of Forests and Rangelands (RIFR): Teheran, Iran, 2007; pp. 135–144. Available online: https://www.thuenen.de/media/publikationen/landbauforschung-sonderhefte/lbf_sh350.pdf (accessed on 15 November 2025).
107. Ürker, O.; Baykal, N.U.; Ada, E. Increasing temperatures can pose an opportunity to recover endemic and endangered oriental sweetgum tree (*Liquidambar orientalis* Mill.) from extinction. *Turk. J. Bot.* **2023**, *47*, 363–371. [CrossRef]
108. Chaplin, J. *Liquidambar orientalis*—Oriental Sweet Gum (Species Profile). 2024 European Forest Genetic Resources Programme (EUFORGEN), Hosted by the European Forest Institute (EFI). Available online: https://www.euforgen.org/species/liquidambar-orientalis (accessed on 8 December 2025).
109. Thevs, N. Forest Landscape Restoration in the Caucasus and Central Asia. (UNECE) and (FAO). Geneva Timber and Forest Discussion Paper 72, United Nations New York and Geneva, ECE/TIM/DP/72. 2019. Available online: https://unece.org/fileadmin/DAM/timber/meetings/2019/20191216/Forest_Landscape_Restoration_in_Central_Asia_and_the_Caucasus.pdf (accessed on 15 November 2025).
110. Tkacz, B.; Riitters, K.; Percy, K.E. Forest Monitoring Methods in the United States and Canada: An Overview. In *Developments in Environmental Science*; Ferretti, M., Fischer, R., Eds.; Elsevier: Amsterdam, The Netherlands, 2013; Volume 12, pp. 49–73. [CrossRef]
111. Risk, C.; McKenney, D.W.; Pedlar, J.; Lu, P. A compilation of North American tree provenance trials and relevant historical climate data for seven species. *Sci. Data* **2021**, *8*, 29. [CrossRef] [PubMed] [PubMed Central]
112. King, J.; Nienstaedt, H. Variation in eastern white pine seed sources planted in the lake states. *Silvae Genet.* **1969**, *18*, 83–86.
113. Genys, J.B. Provenance variation among different populations of *Pinus strobus* from Canada and the United States. *Can. J. For. Res.* **1987**, *17*, 228–235. [CrossRef]
114. Kriebel, H.B.; Bagley, W.T.; Deneke, F.J.; Funsch, R.W.; Roth, P.; Jokela, J.J.; Merritt, C.; Wright, J.W.; Williams, R.D. Geographic variation in *Quercus rubra* in north central United States plantations. *Silvae Genet.* **1976**, *25*, 118–122.
115. Rockwood, D.; Huber, D.; White, T. Provenance and family variability in slash pine (*Pinus elliottii var. elliottii* Engelm.) grown in southern Brazil and northeastern Argentina. *New For.* **2001**, *21*, 115–125. [CrossRef]
116. Falkenhagen, E.R. Thirty five-year results from seven *Pinus elliottii* (Engelman.) and *Pinus taeda* (L.) provenance trials in South Africa. *S. Afr. For. J.* **1978**, *107*, 22–36. [CrossRef]
117. Lu, P.; Parker, W.C.; Colombo, S.J.; Man, R. Restructuring tree provenance test data to conform to reciprocal transplant experiments for detecting local adaptation. *J. Appl. Ecol.* **2016**, *53*, 1088–1097. [CrossRef]
118. Rehfeldt, G.E.; Jaquish, B.C.; López-Upton, J.; Sáenz-Romero, C.; Clair, J.B.S.; Leites, L.P.; Joyce, D.G. Comparative genetic responses to climate for the varieties of *Pinus ponderosa* and *Pseudotsuga menziesii*: Realized climate niches. *For. Ecol. Manag.* **2014**, *324*, 126–137. [CrossRef]
119. Linser, S.; O'Hara, P. *Guidelines for the Development of a Criteria and Indicator Set for Sustainable Forest Management (ECE/TIM/DP/73)*; Clark, D., Iugov, A., Eds.; UNECE & FAO: Geneva, Switzerland; United Nations: New York, NY, USA, 2019. Available online: https://unece.org/DAM/timber/publications/DP-73-ci-guidelines-en.pdf (accessed on 15 November 2025).
120. Riina, J.; Lay Hong, T.; Leong Lee, S.; Loo, L.; Snook, L. Integrating Genetic Factors into Management of Tropical Asian Production Forests: A Review of Current Knowledge. *For. Ecol. Manag.* **2014**, *315*, 191–201. [CrossRef]

121. Dogaroglu, T.; Gunenc, E.; Manap, R.Y.; Taskin, V.; Gocmen Taskin, B.; Dogac, E. Genetic structure and phylogenetic analysis of *Liquidambar orientalis* Mill. (altingiaceae) populations based on non-coded psaA/ycf3 intergenic region in the chloroplast genome in Türkiye. *Turk. J. Biosci. Collect.* **2023**, *7*, 45–58. [CrossRef]
122. Garzon-Lopez, C.X.; Miranda, A.; Moya, D.; Andreo, V. Remote Sensing Biodiversity Monitoring in Latin America: Emerging Need for Sustained Local Research and Regional Collaboration to Achieve Global Goals. *Glob. Ecol. Biogeogr.* **2024**, *33*, e13804. [CrossRef]
123. van Zonneveld, M.; Thomas, E.; Castañeda-Álvarez, N.P.; Van Damme, V.; Alcazar, C.; Loo, J.; Scheldeman, X. Tree genetic resources at risk in South America: A spatial threat assessment to prioritize populations for conservation. *Divers. Distrib.* **2018**, *24*, 718–729. [CrossRef]
124. Pastorino, M.J.; Gallo, L.A. Preliminary operational genetic management units of a highly fragmented forest tree species of southern South America. *For. Ecol. Manag.* **2009**, *257*, 2350–2358. [CrossRef]
125. da Silva, P.H.M.; Brune, A.; Alvares, C.A.; Amaral, W.D.; de Moraes, M.L.T.; Grattapaglia, D.; de Paula, R.C. Selecting for stable and productive families of *Eucalyptus urophylla* cross a country-wide range of climates in Brazil. *Can. J. For. Res.* **2019**, *49*, 87–95. [CrossRef]
126. Jimu, L. Threats and conservation strategies for the African cherry (*Prunus africana*) in its natural range. A review. *J. Ecol. Nat. Environ.* **2011**, *3*, 118–130.
127. African Union Commission; Food and Agriculture Organization of the United Nations. *The Sustainable Forest Management Framework for Africa (2020–2030)*; Food and Agriculture Organization of the United Nations: Ababa, Ethiopia, 2020. Available online: https://faolex.fao.org/docs/pdf/au214444.pdf (accessed on 15 November 2025).
128. Vinceti, B.; Loo, J.; Gaisberger, H.; van Zonneveld, M.J.; Schueler, S.; Konrad, H.; Kadu, C.A.C.; Geburek, T. Conservation Priorities for *Prunus africana* Defined with the Aid of Spatial Analysis of Genetic Data and Climatic Variables. *PLoS ONE* **2013**, *8*, e59987. [CrossRef]
129. FAO. *Final Report on the FAO/IBPGR/UNEP Project on Genetic Resources of Arid and Semi-Arid Zone Arboreal Species for the Improvement of Rural Living*; FAO: Rome, Italy, 1988; 19p. Available online: https://www.fao.org/4/s9280e/S9280E10.htm (accessed on 21 January 2026).
130. Palmberg, C. A vital fuelwood gene pool is in danger. *Unasylva* **1981**, *33*, 22–30. Available online: https://www.fao.org/4/p3350E/p3350e04.htm?utm_source=chatgpt.com (accessed on 15 November 2025).
131. Sun, P.W.; Chang, J.T.; Luo, M.X.; Liao, P.C. Genomic insights into local adaptation and vulnerability of *Quercus longinux* to climate change. *BMC Plant Biol.* **2024**, *24*, 279. [CrossRef]
132. Zhang, J.; Huang, S.; Li, J.; Liao, L.; Jiang, X.; Xu, Y.; Yu, X.; Wu, L.; Zhao, L.; Fu, J.; et al. "Two zones and three centers" distribution and suitable areas shift of an evergreen oak in subtropical China under climate scenarios. *Ecol. Evol.* **2024**, *14*, e70300. [CrossRef]
133. Stiti, B.; Touhami, I.; Slama, S.; Ennajah, A.; Hamrouni, L.; Khouja, M.L.; Khaldi, A. Tunisia: Genetic Diversity Assessment of Cork Oak Provenance Trials in the Context of Climate Change. In *Ecological Connectivity of Forest Ecosystems*; Lapin, K., Oettel, J., Braun, M., Konrad, H., Eds.; Springer: Cham, Switzerland, 2025; pp. 635–646. [CrossRef]
134. Šeho, M.; Fussi, B.; Kavaliauskas, D. *Cedrus atlantica*—Possible alternative tree species under changing climate conditions in Central Europe. *SilvaWorld* **2025**, *4*, 23–35. [CrossRef]
135. Available online: https://www.fao.org/publications/fao-flagship-publications/the-state-of-food-and-agriculture/en (accessed on 15 November 2025).
136. Lott, R.; Read, S.M. *Status of Australia's Forest Genetic Resources 2021. Australia's Country Report for The Second Report on the State of the World's Forest Genetic Resources*; ABARES Research Report; ABARES: Canberra, Australia, 2021. [CrossRef]
137. Steane, D.A.; Potts, B.M.; McLean, E.H.; Collins, L.; Holland, B.R.; Prober, S.M.; Stock, W.D.; Vaillancourt, R.E.; Byrne, M. Genomic Scans across Three Eucalypts Suggest that Adaptation to Aridity is a Genome-Wide Phenomenon. *Genome Biol. Evol.* **2017**, *9*, 253–265. [CrossRef] [PubMed] [PubMed Central]
138. Gibson, A.; Bachelard, E.; Hubick, K. Relationship Between Climate and Provenance Variation in *Eucalyptus camaldulensis* Dehnh. *Aust. J. Plant Physiol.* **1995**, *22*, 453–460. [CrossRef]
139. Santos, W.; Aguiar, A.V.; Souza, B.M.; Araujo, D.; Machado, C.; Moraes, M.L.T.; Sebbenn, A.M.; Freitas, M.L.M. Performance and genetic variation in a provenance test of *Araucaria cunninghamii*. *Pesqui. Agropecuária Bras.* **2021**, *56*, e02170. [CrossRef]
140. Dieters, M.J.; Nikles, D.G.; Keys, M.G. Achievements in forest tree improvement in Australia and New Zealand 6: Genetic improvement and conservation of *Araucaria cunninghamii* in Queensland. *Aust. For.* **2007**, *70*, 75–85. Available online: https://era.dpi.qld.gov.au/id/eprint/903/ (accessed on 15 November 2025). [CrossRef]
141. Wesselkamp, M.; Roberts, D.R.; Dormann, C.F. Identifying potential provenances for climate-change adaptation using spatially variable coefficient models. *BMC Ecol. Evol.* **2024**, *24*, 70. [CrossRef] [PubMed]
142. Thom, D.; Rammer, W.; Albrich, K.; Braziunas, K.H.; Dobor, L.; Dollinger, C.; Hansen, W.D.; Harvey, B.J.; Hlásny, T.; Hoecker, T.J.; et al. Parameters of 150 temperate and boreal tree species and provenances for an individual-based forest landscape and disturbance model. *Data Brief* **2024**, *55*, 110662. [CrossRef]

143. Guadaño-Peyrot, C.; Vizcaíno-Palomar, N.; Mutke, S.; Alia, R.; Grivet, F.S.; Benito-Garzon, M. Disentangling key drivers for counteracting growth loss in stone pine under climate change: Results based on multisite provenance tests. *New For.* **2025**, *56*, 59. [CrossRef]
144. Oggioni, S.D.; Rossi, L.M.W.; Terzago, S.; Bohn, F.J.; Vacchiano, G. Simulating silver fir provenance responses to climate change: A forest modelling approach in the Northern Apennines. *For. Ecosyst.* **2026**, *15*, 100389. [CrossRef]