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Genetic Treasure: Conservation, Analysis, and Innovative Utilization of Tree Genetic Resources

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Abstract The conservation, analysis, and innovative utilization of tree genetic resources are critical for maintaining biodiversity, ensuring forest sustainability, and enhancing ecosystem services. This study explores various strategies and methodologies for preserving genetic diversity in tree species, emphasizing both *ex situ* and *in situ* conservation approaches. Key areas of focus include the expansion of living collections, advancements in seed storage and cryopreservation techniques, and the integration of genetic information into conservation planning. The study also highlights the importance of dynamic conservation practices that allow for evolutionary processes and the turnover of generations within forest ecosystems. Additionally, the utilization and transfer of genetic resources for reforestation, breeding, and restoration efforts are examined, with a particular emphasis on the challenges and opportunities presented by climate change, disease, and pest pressures. By leveraging molecular and quantitative genetic data, this research hopes to develop robust conservation strategies that ensure the long-term sustainability and resilience of forest genetic resources.

Keywords Genetic diversity; Conservation strategies; Tree species; *Ex situ* and *in situ* conservation; Climate adaptation

1 Introduction

Tree genetic resources are invaluable assets that contribute significantly to biodiversity and ecosystem stability. These resources encompass the genetic diversity found within and among tree species, which is crucial for their adaptation, survival, and evolution in changing environments. The conservation, analysis, and innovative utilization of tree genetic resources are essential for maintaining healthy ecosystems, supporting sustainable forestry practices, and ensuring the availability of these resources for future generations.

Tree genetic resources play a pivotal role in maintaining biodiversity and ecosystem stability. Genetic diversity within tree populations enhances their ability to adapt to environmental changes, resist pests and diseases, and maintain ecosystem functions (Zobel, 1976; Riggs, 1990; Loo et al., 2014). The genetic variation within and among tree species contributes to the resilience of forest ecosystems, enabling them to recover from disturbances and continue providing essential ecosystem services such as carbon sequestration, water regulation, and habitat for wildlife (Ledig, 1986; Aravanopoulos, 2016). Moreover, the genetic diversity of trees is a critical component of overall biodiversity, supporting the intricate web of life that depends on forest ecosystems (Rao and Hodgkin, 2004; Rodríguez-Quilón et al., 2016).

The conservation of tree genetic resources has gained increasing attention in recent years, with a focus on both *in situ* and *ex situ* strategies. *In situ* conservation involves preserving genetic diversity within natural habitats, such as protected areas and managed forests, to maintain the evolutionary processes and ecological interactions that sustain genetic diversity (Ledig, 1986; Riggs, 1990). *Ex situ* conservation, on the other hand, involves the preservation of genetic material outside natural habitats, such as in seed banks, clone banks, and botanical gardens, to safeguard genetic resources against threats like habitat loss and climate change (Šijačić-Nikolić and Milovanović, 2007; Pritchard et al., 2014). Recent advancements in biotechnology and genomic tools have also enhanced the ability to monitor and conserve genetic diversity, providing new opportunities for the effective management of tree genetic resources (Loo et al., 2014; Aravanopoulos, 2016).

The objectives of this study are to explore conservation strategies, analyze genetic diversity, and discuss innovative utilization of tree genetic resources. Specifically, this study aims to review and evaluate current *in situ* and *ex situ* conservation methods, highlighting successful case studies and identifying areas for improvement, assess the genetic diversity within and among tree species, using both traditional and modern genomic approaches, to understand the distribution and extent of genetic variation, and investigate innovative ways to utilize tree genetic resources for sustainable forestry, ecosystem restoration, and climate change mitigation, emphasizing the integration of genetic considerations into practical applications. By addressing these objectives, this study hopes to provide a comprehensive understanding of the current state of tree genetic resource conservation and utilization, offering insights and recommendations for future research and policy development.

2 Conservation of Tree Genetic Resources

2.1 Overview of conservation techniques (*in situ* and *ex situ*)

Conservation of tree genetic resources is essential for maintaining biodiversity, ecosystem stability, and the adaptive potential of tree species in the face of environmental changes. Two primary conservation techniques are employed: *in situ* and *ex situ* conservation.

In situ conservation involves protecting and managing tree species within their natural habitats. This method aims to maintain the evolutionary processes and ecological interactions that sustain genetic diversity. *In situ* conservation is often considered the most effective long-term strategy for preserving genetic diversity, as it allows species to adapt to changing environmental conditions naturally (Rajora and Mosseler, 2001; Lefèvre et al., 2013; Potter et al., 2017). Examples of *in situ* conservation include the establishment of protected areas, natural reserves, and sustainable forest management practices (Ledig, 1986; Rajora and Mosseler, 2001).

Ex situ conservation, on the other hand, involves the preservation of genetic material outside the natural habitat. This approach serves as an insurance policy against extinction and provides material for restoration, research, and public education. *Ex situ* methods include seed banks, germplasm banks, clone banks, arboreta, and cryopreservation (Ledig, 1986; Rajora and Mosseler, 2001; Pritchard et al., 2014; Potter et al., 2017). *Ex situ* conservation is particularly valuable for species with small or declining populations and those threatened by habitat loss or climate change (Pritchard et al., 2014; Potter et al., 2017).

2.2 Key challenges in conserving tree genetic resources

Several challenges hinder the effective conservation of tree genetic resources. Many tree species lack comprehensive genetic and ecological data, making it difficult to develop targeted conservation trategies (Rajora and Mosseler, 2001; Potter et al., 2017). Inadequate funding and resources often limit the scope and effectiveness of conservation efforts (Rajora and Mosseler, 2001; Aravanopoulos, 2016; Potter et al., 2017). Historically, there has been a lack of coordination within and between conservation sectors, leading to fragmented and inefficient efforts (Lefèvre et al., 2013; Potter et al., 2017). Climate change, habitat fragmentation, introduced pests, diseases, and pollution pose significant threats to tree genetic resources (Rajora and Mosseler, 2001; Rodríguez-Quilón et al., 2016; Potter et al., 2017). Economic forces often favor short-term gains over long-term conservation, leading to practices such as genetic monocultures in production plantations (Zobel, 1976; Ledig, 1986).

2.3 Success stories and best practices in tree conservation

Despite the challenges, there have been notable successes and best practices in tree conservation. The establishment of dynamic conservation units across Europe, which maintain genetic diversity within an evolutionary process, has been a significant achievement. This network includes 1967 conservation units and 2737 populations of target trees, demonstrating a coordinated effort to conserve genetic resources (Lefèvre et al., 2013). Innovative approaches that integrate *in situ* and *ex situ* conservation have shown promise. For example, the expansion of living collections and the development of cryopreservation techniques have enhanced the genetic diversity of conserved tree species (Pritchard et al., 2014). Advances in genetic monitoring have improved the ability to track changes in genetic variation and structure over time, providing valuable insights for the management of forest genetic resources (Aravanopoulos, 2016). Successful restoration projects, such as those involving Araucaria angustifolia in Brazil, have demonstrated the potential of planted forests to preserve genetic diversity and support species conservation (Stefenon et al., 2008). By addressing the key challenges and building on these successes, the conservation of tree genetic resources can be further enhanced, ensuring the resilience and sustainability of forest ecosystems for future generations.

3 Genetic Analysis of Tree Populations

3.1 Methods for assessing genetic diversity in trees

Genetic diversity in tree populations is crucial for their adaptability and long-term survival. Various molecular markers have been developed and utilized to assess this diversity. These markers include microsatellites, single nucleotide polymorphisms (SNPs), and other genomic tools. Microsatellites, for instance, have been effectively used to estimate genetic diversity at the population level in species like Prioria balsamifera and Prioria oxyphylla (Abeele et al., 2019). SNPs, on the other hand, are particularly useful for studying adaptive genetic variation and have been applied in species such as oaks to understand their adaptation to changing environments (Gailing et al., 2009). The combination of different marker types is often recommended to provide a comprehensive assessment of genetic diversity within and among tree populations (Wang and Szmidt, 2001; Porth and El-Kassaby, 2014).

3.2 Case studies: genetic analysis of endangered and keystone tree species

Several case studies highlight the application of genetic analysis in understanding and conserving endangered and keystone tree species. For example, *Prioria balsamifera*, an endangered tropical tree species, has been studied using newly developed microsatellite markers to assess its genetic diversity and inform conservation strategies (Table 1) (Abeele et al., 2019). Another study focused on *Centrolobium tomentosum*, a tropical tree species used in restoration projects, utilized a genetic simulation model to evaluate the effects of genetic diversity and population size on the viability of restored populations (Sujii et al., 2019). These studies underscore the importance of genetic analysis in developing effective conservation and management plans for tree species at risk of decline.

3.3 Role of genetic markers in understanding population structure and dynamics

Genetic markers play a pivotal role in elucidating the population structure and dynamics of tree species. They help in understanding gene flow, mating systems, and the genetic health of populations. For instance, molecular markers have been used to investigate the genetic diversity, mating system, and gene flow in Neotropical trees, providing insights into how human interventions affect these parameters (Vinson et al., 2018). Effective population size (Ne) is another critical indicator of genetic diversity, and it has been suggested that $Ne > 500$ is a suitable threshold for maintaining genetic diversity in tree populations (Hoban et al., 2020). Additionally, landscape and population genomics approaches have been proposed to assess the evolutionary potential of tree populations, focusing on adaptive genetic variation and its spatial distribution (Kort and Honnay, 2017).

In summary, the use of molecular markers and genetic analysis methods is essential for understanding the genetic diversity, population structure, and dynamics of tree species. These tools provide valuable insights that inform conservation and management strategies, ensuring the long-term survival and adaptability of tree populations in the face of environmental changes.

4 Case Studies: Innovative Utilization of Tree Genetic Resources

4.1 Application of genetic insights in breeding disease-resistant varieties

The development of disease-resistant tree varieties has become a critical focus in forestry due to the increasing threats posed by pests and pathogens, exacerbated by climate change. Traditional breeding methods have been the cornerstone of developing resistant genotypes, but recent advancements in genetic engineering have significantly accelerated this process. For instance, genome-wide association studies and genomic selection have facilitated the identification of candidate genes for resistance, enabling more precise and efficient breeding strategies (Naidoo et al., 2019). Additionally, the integration of omics information has further refined the selection process, ensuring the development of superior genotypes with enhanced resistance to biotic stress (Naidoo et al., 2019).

Table 1 Characterization of polymorphic microsatellite markers isolated from *Prioria balsamifera* (16 loci) and *Prioria oxyphylla* (15 loci) (Adopted from Abeele et al., 2019)

Locus	Primer sequences (5^0-3^0) [1]	Labelled primer	Repeat motif [2]	Allele size range (bp)	GenBank accession No.
Prioria balsamifera					
Multiplex 1					
PriB07	F: CACTGCTTAGAGCGATGCTCAGGGCAAGATGAATAATG R: AAAGGAACCACCGATGAATA	Q3-VIC	(TC)$_8$	144~147	MN648900
PriB19	F: CACTGCTTAGAGCGATGCTCTGAATTATTATCAGCCACTTC R: GGCGTTTCTTAATTTGGTTT	Q3-VIC	(TC)$_8$	198~207	MN648909
PriB23	F: CACTGCTTAGAGCGATGCTAATATGGAGTCATCGCTTCC R: GCATTCGGACAGAGGGAG	Q3-VIC	(GA)$_9$	243~254	MN648912
PriB10	F: TAGGAGTGCAGCAAGCATTTTGCATCTAAAGTTTGAGGG R: TAATGGAGCTTATGCTTTGG	Q2-NED	(AG)$_9$	146~149	MN648902
PriB22	F: TAGGAGTGCAGCAAGCATAACGGACCGGTACTTACAGA R: GCTTAGACAAATGTTAGAATCACC	Q2-NED	(TG)$_9$	203~211	MN648911
PriB04	F: CTAGTTATTGCTCAGCGGTAATATGCTTGGAATGGATGG R: ATTACTCCTTGGCGCAGTC	Q4-PET	(GA)$_8$	113~142	MN648899
PriB13	F: TGTAAAACGACGGCCAGTTGTTTACTAACTTGCAGAATCCA R: CAGTAAGGATGGCTCTCCC	Q1-6-FAM	(CT)$_{12}$	139~159	MN648905
PriB15	F: CACTGCTTAGAGCGATGCCAAGTCTACGCCAAATGGTC R: GCGTTTAAACATCAATTGGAC	Q3-VIC	(TC)$_{12}$	147~167	MN648907
PriB02	F: TAGGAGTGCAGCAAGCATTGCGTGTACATGTGTATCTCC R: AGACACCCAACTTTCAATGAT	Q2-NED	(GA)$_{10}$	95~116	MN648897
PriB14	F: TAGGAGTGCAGCAAGCATGGGAAGACAAACAAGAGTCAG R: TGACCTAAAGAATAAGACATCCC	Q2-NED	(CT)$_9$	153~157	MN648906
PriB12	F: CTAGTTATTGCTCAGCGGTAAATTTGCCCTCCCTTACAT R: TGACTACAAAGCATATGAATAGAAA	Q4-PET	(GT)$_{12}$	136~159	MN648904
PriB03	F: CACTGCTTAGAGCGATGCATCGGTGAGTACATCGAACC R: GCAGTTCAAGTTAGTTTGTGC	Q3-VIC	(AC)$_8$	106~112	MN648898
PriB11	F: CACTGCTTAGAGCGATGCCAATAGAATGATGGTCAAGAGC R: CTTCCAGAGAAACCCACCT	Q3-VIC	(CT)$_8$	144~160	MN648903
PriB18	F: TAGGAGTGCAGCAAGCATAGAGTCGTTGTGAGCTGTGA R: AGTGACACGCGTTCAAATAC	Q2-NED	(AG)$_{14}$	168~202	MN648908
PriB08	F: CTAGTTATTGCTCAGCGGTATATTGCAGCAGAGACACCA R: AGTTTCGCTCTTCTTACCGA	Q4-PET	(AG)$_8$	147~167	MN648901
PriB20	F: CTAGTTATTGCTCAGCGGTTGTGTTGCAAGAACGATAGTC R: ACAAGACTCTAAATTCCAAGACA	Q4-PET	(GA)$_{10}$	196~223	MN648910

4.2 Genetic engineering and CRISPR applications in tree improvement

CRISPR/Cas9 technology has revolutionized the field of genetic engineering, offering unprecedented precision in gene editing. This technology has been successfully applied to forest trees, enabling the development of new drought-resistant and disease-resistant cultivars (Chen and Lu, 2020). The CRISPR/Cas9 system allows for precise modifications at target genes, which is crucial for improving traits such as wood quality, stress tolerance, and growth rates (Sattar et al., 2021; Cao et al., 2022; Thapliyal et al., 2022). For example, CRISPR has been used to modify lignin biosynthesis, alter flowering onset, and enhance fruit quality in woody plants (Figure 1) (Sattar et al., 2021). Moreover, the technology's ability to produce transgene-free edited plants makes it a promising tool for sustainable forestry.

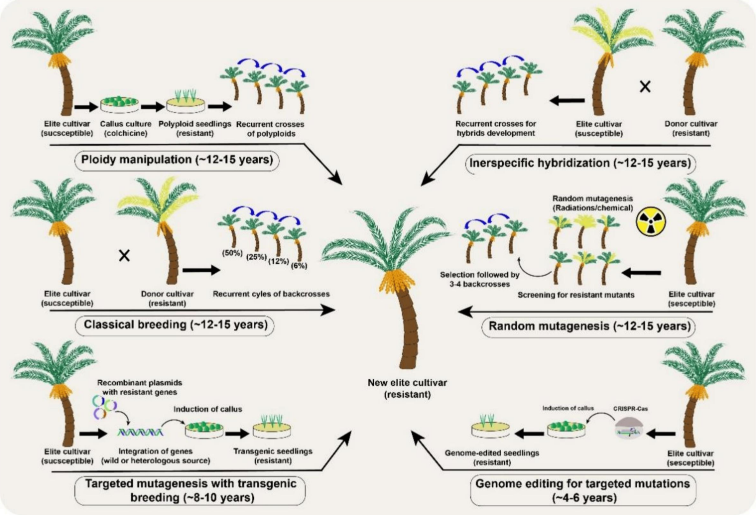

Figure 1 A comparative analysis of different conventional and the new breeding tools (NBTs) to modify desirable genetic modifications in a date palm (*Phoenix dactylifera* L.) fruit crop (Adopted from Sattar et al., 2021)

4.3 Eco-innovation: utilizing tree genetics for environmental solutions

The application of genetic insights extends beyond improving tree traits to addressing broader environmental challenges. Genetically engineered trees can play a significant role in mitigating ecological threats and enhancing forest sustainability. For instance, the establishment of genetically engineered trees in degraded woodlands can help restore these ecosystems by introducing traits that improve adaptability to changing climates (Thapliyal et al., 2022). Additionally, the use of CRISPR technology to engineer trees with enhanced photosynthetic efficiency and stress tolerance can contribute to carbon sequestration and climate resilience (Cao et al., 2022; Thapliyal et al., 2022). These eco-innovations not only support forest health but also offer solutions to global environmental issues.

In summary, the innovative utilization of tree genetic resources through advanced breeding techniques and genetic engineering holds great promise for developing disease-resistant varieties, improving tree traits, and addressing environmental challenges. The integration of CRISPR technology in these efforts has opened new avenues for sustainable forestry and ecological restoration.

5 Technological Advances in Tree Genetics

5.1 Emerging technologies for genetic sequencing and modification

Recent advancements in genetic sequencing and modification technologies have significantly enhanced our ability to study and manipulate tree genomes. High-throughput sequencing methods, such as next-generation sequencing (NGS), have revolutionized the field by providing detailed insights into the genetic makeup of various tree species. These technologies allow for the comprehensive analysis of genetic variation within and among populations, which is crucial for understanding adaptive processes and informing conservation strategies (Holliday et al., 2017). Additionally, the development of CRISPR-Cas9 and other gene-editing tools has opened new avenues for the precise modification of tree genomes, enabling the introduction of desirable traits such as disease resistance and improved growth rates (Barnes and Delborne, 2021).

5.2 Integration of omics technologies in tree genetic research

The integration of omics technologies, including genomics, transcriptomics, proteomics, and metabolomics, has provided a holistic approach to studying tree genetics. These technologies enable researchers to investigate the complex interactions between genes, proteins, and metabolites, offering a comprehensive understanding of tree biology and adaptation mechanisms. For instance, genomic data can be combined with transcriptomic and proteomic analyses to identify key regulatory networks involved in stress responses and developmental processes (Holliday et al., 2017). This multi-omics approach is particularly valuable for the conservation and breeding of forest genetic resources, as it allows for the identification of genetic markers associated with important traits and the development of more effective conservation strategies (Šijačić-Nikolić et al., 2014; Aravanopoulos, 2016).

5.3 Challenges and future directions in genetic technology application

Despite the significant progress in genetic technologies, several challenges remain in their application to tree genetics. One major challenge is the complexity of tree genomes, which are often large and highly repetitive, making sequencing and assembly difficult. Additionally, the long generation times and large population sizes of many tree species pose challenges for genetic studies and breeding programs (Holliday et al., 2017). Another challenge is the need for more efficient and cost-effective methods for genetic monitoring and conservation, particularly in the face of rapid environmental changes (Aravanopoulos, 2016).

Future directions in tree genetic research should focus on improving sequencing technologies and developing more sophisticated bioinformatics tools to handle complex genomes. There is also a need for greater collaboration between researchers, conservationists, and policymakers to ensure that genetic technologies are effectively integrated into conservation and management practices. Furthermore, addressing ethical and political considerations, such as the potential for genetic privatization and commodification, is essential for the responsible use of genetic technologies in tree conservation (Barnes and Delborne, 2021). By overcoming these challenges and leveraging emerging technologies, we can enhance our understanding of tree genetics and develop innovative strategies for the conservation and sustainable use of tree genetic resources.

6 Sustainable Management and Utilization of Genetic Resources

6.1 Strategies for sustainable forestry using genetic information

Sustainable forestry practices are increasingly reliant on the integration of genetic information to ensure the long-term viability and productivity of forest ecosystems. The use of genetic indicators to monitor threats to populations and the effectiveness of ameliorative actions is crucial for maintaining genetic diversity and adaptation potential (Loo et al., 2014). Innovative approaches, such as dynamic landscape gene-resource management, leverage natural crosses and DNA-based pedigree assembly to enhance genetic response to selection in adaptive traits, thus facilitating conservation within breeding populations (Lstibůrek et al., 2017). Additionally, marker-based pedigree reconstruction *in situ* allows for the identification of broadly adapted and productive individuals, promoting efficient management of gene resources across diverse climatic regions (Lstibůrek et al., 2020).

6.2 Impact of genetic resource management on forestry practices

The management of forest genetic resources significantly influences forestry practices by affecting population structure, mating patterns, and gene flow. Selective and clear-cut systems, followed by natural or artificial regeneration, can either compromise or enhance genetic diversity and productivity depending on the management system applied (Ratnam et al., 2014). The integration of genetic considerations into forest management and restoration projects is essential for maintaining ecosystem resilience and productivity, especially in the face of climate change (Loo et al., 2014). Furthermore, the use of genetically improved planting materials and large-scale plantations can have profound effects on natural forests, necessitating careful evaluation and sustainable management practices (Ratnam et al., 2014).

6.3 Policy frameworks supporting sustainable genetic resource utilization

Effective policy frameworks are vital for the sustainable utilization of forest genetic resources. The Global Plan of Action for the Conservation, Sustainable Use, and Development of Forest Genetic Resources emphasizes the need for increased awareness and mainstreaming of genetic considerations into forest management (Loo et al., 2014). Genetic guidelines for seedling transfer, based on DNA information, provide a foundation for reforestation and restoration efforts, ensuring that planting materials are well-adapted to local environments (Tsumura, 2022). Additionally, the integration of *ex situ* and *in situ* conservation approaches, supported by advancements in biotechnology and the establishment of seed banks, enhances the preservation of genetic diversity and supports sustainable forestry practices (Pritchard et al., 2014).

In conclusion, the sustainable management and utilization of forest genetic resources require a multifaceted approach that incorporates genetic information into forestry practices, evaluates the impacts of management systems, and is supported by robust policy frameworks. These strategies are essential for maintaining the genetic diversity and adaptive potential of forest ecosystems, ensuring their resilience and productivity for future generations.

7 Educational and Community Engagement in Genetic Conservation

7.1 Importance of community involvement in conservation efforts

Community involvement is crucial for the success of genetic conservation efforts. Engaging local communities ensures that conservation strategies are culturally relevant and sustainable. For instance, the concept of reciprocal restoration, which integrates Indigenous perspectives and cultural values, has shown promise in the restoration of the American chestnut tree in Haudenosaunee communities. This approach emphasizes the importance of kincentric relationships and spiritual responsibilities, suggesting that community-driven conservation can support broader cultural restoration efforts (Barnhill-Dilling and Delborne, 2019). Additionally, the management of genetic variation in agroforestry ecosystems highlights the need for community participation to maintain and enhance tree species diversity, which is essential for both biodiversity conservation and the livelihoods of rural communities (Dawson et al., 2009).

7.2 Educational programs to raise awareness of genetic conservation

Educational programs play a vital role in raising awareness about the importance of genetic conservation. These programs can help bridge the gap between scientific knowledge and community practices. For example, the expansion of living collections and the development of seed banks are initiatives that can be supported by educational efforts to ensure a broad genetic diversity in tree species (Pritchard et al., 2014). Moreover, the dissemination of genetic guidelines for tree species can aid non-experts in making informed decisions about seed collection and planting, thereby promoting sustainable forest management practices (Tsumura, 2022). The integration of modern molecular marker methods as genetic indicators in forest management can also be communicated through educational programs to enhance the understanding and application of genetic conservation strategies (Loo et al., 2014).

7.3 Case examples of community-driven genetic resource conservation

Several case examples illustrate the effectiveness of community-driven genetic resource conservation. The restoration of the American chestnut tree in Haudenosaunee communities is a notable example, where the integration of Indigenous knowledge and genetic engineering has the potential to support both ecological and cultural restoration (Barnhill-Dilling and Delborne, 2019). Another example is the enhancement of community seed- and seedling-exchange networks in agroforestry systems, which has been shown to improve the management and conservation of genetic diversity in tropical tree species (Dawson et al., 2009). Additionally, the establishment of common garden provenance trials to support restoration and climate change initiatives demonstrates how community involvement can contribute to the conservation of forest genetic resources (Loo et al., 2014). These examples underscore the importance of community engagement in achieving successful and sustainable genetic conservation outcomes.

8 Future Directions in Tree Genetics Research

8.1 Potential for new genetic discoveries and their applications

The future of tree genetics research holds immense potential for new genetic discoveries and their applications. Advances in genomic technologies, such as high-throughput sequencing, have significantly enhanced our understanding of the genetic architecture of tree species. These technologies enable the identification of genetic variations that contribute to traits such as pest resistance, drought tolerance, and growth rates, which are crucial for the adaptation and resilience of tree species to environmental changes (Aravanopoulos, 2016; Plomion et al., 2016; Holliday et al., 2017). The integration of genomic data with traditional genetic monitoring approaches can improve the precision of estimates of adaptive genetic potential and population genetic parameters, thereby aiding in the conservation and management of forest genetic resources (Šijačić-Nikolić et al., 2014; Aravanopoulos, 2016).

Moreover, innovative approaches in seed biology and storage preservation biotechnology, such as cryopreservation, are being developed to conserve genetic diversity in tree species, especially those under threat of extinction (Pritchard et al., 2014). These advancements not only enhance the conservation of genetic resources but also provide valuable material for restoration and breeding programs aimed at improving tree species' adaptability to future environmental conditions (Zobel, 1976; Pritchard et al., 2014).

8.2 Collaborative efforts and global initiatives in genetic conservation

Collaborative efforts and global initiatives play a pivotal role in the conservation of tree genetic resources. International conferences and workshops, such as the "Genomics and Forest Tree Genetics" conference, facilitate the exchange of information and the creation of collaborations among tree conservation stakeholders (Holliday et al., 2017; Potter et al., 2017). These platforms enable researchers, policymakers, and conservationists to discuss and develop strategies for the effective conservation and management of forest genetic resources.

Global initiatives, such as the establishment of seed banks and the integration of *ex situ* and *in situ* conservation approaches, are essential for maintaining genetic diversity and ensuring the long-term survival of tree species (Pritchard et al., 2014; Potter et al., 2017). Networks of botanic gardens, government agencies, and non-governmental organizations must continue to coordinate efforts to improve the efficiency and effectiveness of tree conservation initiatives (Potter et al., 2017). Additionally, the identification and prioritization of species and populations that require genetic conservation are critical for the success of these initiatives (Rodríguez-Quilón et al., 2016; Potter et al., 2017).

8.3 Funding and support for future tree genetics research

Securing adequate funding and support is crucial for the advancement of tree genetics research. The transition from genetic to genomic monitoring, while promising, is often limited by time-consuming procedures and funding constraints (Aravanopoulos, 2016). Therefore, increased investment in research infrastructure and the development of biostatistical tools is necessary to overcome these limitations and enhance the precision of genetic monitoring (Aravanopoulos, 2016; Plomion et al., 2016).

Furthermore, long-term planning and solid financial support are required to sustain gene conservation programs and ensure continued progress in tree breeding (Zobel, 1976). Collaborative funding mechanisms, involving both public and private sectors, can provide the necessary resources to support innovative research and conservation efforts (Potter et al., 2017). By fostering a supportive environment for tree genetics research, we can ensure the preservation and sustainable utilization of tree genetic resources for future generations.

9 Concluding Remarks

Tree genetic resources are invaluable for maintaining biodiversity, ensuring ecosystem stability, and supporting human livelihoods. The genetic diversity within tree species underpins their adaptability to changing environmental conditions, including climate change, pests, and diseases. This diversity is crucial for the long-term sustainability of forests, which provide essential ecosystem services such as carbon sequestration, water regulation, and habitat for countless species. The conservation and innovative utilization of these genetic resources are therefore paramount for both ecological and economic reasons.

This study has highlighted several key contributions to the fields of conservation biology and forestry. The study underscores the importance of integrating *ex situ* and *in situ* conservation approaches to maintain genetic diversity. This integration ensures that both living collections and natural populations are preserved, enhancing the resilience of tree species. The development of genetic monitoring techniques has been pivotal in understanding and managing genetic variation within tree populations. These techniques help in tracking changes over time and provide insights into the adaptive potential of species. The convergence of quantitative genetics and genomics has revolutionized tree breeding, enabling more precise and efficient selection of desirable traits. This has significant implications for improving tree resilience and productivity. The study emphasizes the need for global collaboration and the establishment of comprehensive databases to facilitate the sharing of genetic information and resources. This is critical for advancing research and conservation efforts worldwide.

To further advance the field of tree genetics, the following recommendations are proposed. Continued investment in genetic research is essential. This includes expanding genomic studies to cover a wider range of tree species, particularly those in tropical and under-researched regions. Strengthening policies and regulatory frameworks to support the conservation and sustainable use of tree genetic resources is crucial. This includes implementing the Nagoya Protocol to ensure fair and equitable sharing of benefits arising from the use of genetic resources. Increasing efforts in education and capacity building will help equip the next generation of scientists and forest managers with the necessary skills and knowledge to address genetic conservation challenges. Leveraging modern technologies such as high-throughput genomics, remote sensing, and bioinformatics can enhance the precision and efficiency of genetic conservation and breeding programs. Engaging local communities and stakeholders in conservation efforts is vital. Their involvement can provide valuable insights and foster a sense of ownership and responsibility towards preserving tree genetic resources. By implementing these recommendations, we can ensure the continued conservation and innovative utilization of tree genetic resources, thereby safeguarding the ecological and economic benefits they provide for future generations.

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Conflict of Interest Disclosure

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