



DOI: 10.5937/topola2413017T

UDC: 630*12

Review paper

Recent global (bio)technological advancements in the service of forest genetic resources protection under climate change

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Received: 5 April 2024; **Revised:** 25 April 2024; **Accepted:** 30 April 2024

Abstract: Climate change has been projected to negatively affect genetic resources of the forests worldwide. Thus, integrating biotechnological innovations with traditional forest conservation strategies offers as a promising pathway to enhance the resilience of forest genetic resources. Biodiversity informatics plays a crucial role in managing and analysing data, supporting informed decision-making in forest management and conservation. Advancements in genomics and sequencing technologies, such as next-generation sequencing (NGS) and whole genome sequencing (WGS), have revolutionized the understanding of complex traits in forest trees. These technologies facilitate the identification of genetic markers, aiding breeding programmes and management strategies. Clustered regularly interspaced short palindromic repeats (CRISPR, in our study referring to CRISPR-Cas9 system) technology and the development of transgenic trees offer new possibilities for improving traits like growth, stress tolerance, and wood quality in forest species, though the potential ecological impacts warrant careful evaluation. Epigenetic research in forest trees provides insights into adaptation mechanisms to environmental changes through gene expression and phenotypic variation. The synergy between biotechnological advances and conservation practices is vital for sustaining forest ecosystems amidst rapid environmental shifts. Recommendations call for fostering interdisciplinary collaborations, enhancing biodiversity informatics infrastructure, engaging stakeholders, prioritizing epigenetic research, and developing regulatory frameworks for genome editing. These steps are imperative for a holistic approach to forest conservation, ensuring the adaptive capacity of forests and safeguarding their genetic resources against the backdrop of climate change.

Keywords: biodiversity informatics, CRISPR-Cas9, epigenetics, genome, forest genetic resources.

Pregledni rad

Nedavna globalna (bio)tehnološka dostignuća u službi očuvanja šumskih genetičkih resursa u kontekstu klimatskih promena

Apstrakt: Klimatske promene negativno deluju na genetičke resurse širom sveta, stoga se integracija biotehnoloških inovacija sa tradicionalnim strategijama zaštite šumskih ekosistema pojavljuje kao obećavajući pravac za unapređenje otpornosti šumskih genetičkih resursa. Informatika biodiverziteta igra ključnu ulogu u upravljanju i analizi podataka, podržavajući informisano donošenje odluka u upravljanju i zaštiti šuma. Napredak u genomici i tehnologijama sekvenciranja, poput sekvenciranja sledeće generacije (NGS) i sekvenciranja celih genoma (WGS), unapredilo je razumevanje kompleksnih osobina šumskih vrsta drveća. Ove tehnologije olakšavaju identifikaciju genetičkih markera, što pomaže u procesima oplemenjivanja i strategijama upravljanja. Tehnologija grupisanih kratkih palindromskih ponovaka na jednakim rastojanjima (CRISPR, u našem radu se odnosi na CRISPR-Cas9 sistem) i razvoj transgenih individua nude nove mogućnosti za unapređenje osobina poput rasta, tolerantnosti na stres i kvaliteta drveta kod šumskih vrsta, dok potencijalni ekološki uticaji zahtevaju pažljivu evaluaciju. Epigenetička istraživanja kod šumskih vrsta drveća pružaju uvid u mehanizme adaptacije na promene u okruženju putem izražavanja gena i fenotipske varijacije. Sinergija biotehnološkog napretka i konzervacije je vitalna za održavanje šumskih ekosistema usred brzih promena u okruženju. Preporuke pozivaju na podsticanje interdisciplinarnih saradnji, unapređenje infrastrukture za informatiku biodiverziteta, uključivanje svih zainteresovanih aktera, davanje prioriteta epigenetičkim istraživanjima i razvoj regulatornih okvira za uređivanje genoma. Ovi koraci su ključni za holistički pristup očuvanju šuma, obezbeđujući njihov adaptivni kapacitet i zaštitu njihovih genetičkih resursa u svetlu klimatskih promena.

Ključne reči: CRISPR-Cas9, epigenetika, genom, informatika biodiverziteta, šumski genetički resursi.

1. Introduction

In response to the urgent challenge of climate change, forest genetics has embraced biotechnological innovations to protect forest genetic resources. The inception of *in vitro* cultures in the 1930s marked the beginning of a journey towards advanced genetic engineering techniques, including the potential application of CRISPR-Cas9 technology, which promises precise genome editing capabilities for enhancing forest resilience to environmental stresses (Ahuja, 2021). This technology is seen as a beacon of hope for developing trees with improved traits, such as pest resistance and drought tolerance, crucial for adapting to changing climates (Salgotra et al. 2019). Moreover, the concept of a sustainable bioeconomy has gained traction, highlighting the role of genetically diverse forests in mitigating climate change through carbon sequestration (Orlović et al. 2014). As the global community strives towards a climate-neutral future, the integration of biotechnological advancements with traditional conservation strategies offers a holistic approach to sustain forest ecosystems. This synergy between biotechnology and forest management is pivotal for ensuring the adaptive capacity of forests, securing their role in biodiversity conservation and ecosystem services in an era of rapid environmental change (Orlović et al. 2014; Andualem and Seid, 2021).

In this paper, we encapsulate the key advancements in genetic biotechnology in forestry, extending our discussion to include emerging technologies such as blockchain and satellite imaging. Drawing upon a comprehensive array of references, we provide an overview of state-of-the-art

methodologies and approaches within the realm of conservation genetics of forest trees. Despite the relatively limited information on the latter two technologies and the ongoing debate regarding their classification as biotechnologies, we have chosen to incorporate them into this review. The aim is to acquaint the technical community with the potential of these and other biotechnologies. The integration of blockchain and satellite imaging with tree genetics holds the promise of revolutionizing the preservation of vital forest gene pools globally, alongside the conservation of species and ecosystem diversities.

2. Biodiversity informatics and digital sequence information (DSI)

Bioinformatics and biodiversity informatics, while overlapping in the application of informatics to biological data, focus on distinct research areas. Nowadays, bioinformatics primarily deals with molecular and cellular biology data, such as DNA sequences and protein structures, aiding in the understanding of genetic codes and molecular functions (Lesk, 2019). On the other hand, biodiversity informatics focuses on the collection, integration, and analysis of biodiversity information like species distribution and ecological data, supporting conservation and ecological research efforts (Anderson et al. 2020). These fields differ in their core data types and objectives; bioinformatics aims at uncovering the mechanisms of life at a molecular level, while biodiversity informatics strives to understand patterns and processes at the species, ecosystem and landscape levels majorly. Biodiversity informatics is an interdisciplinary field that combines biology, computer science, and information technology to gather, manage, and analyze biodiversity data (Gadelha et al. 2021). This emerging subdiscipline of biotechnology has greatly contributed to our understanding of forest tree species and plants and covers various levels of biodiversity from genetics to species and taxa classification.

There also exists a considerable overlap between bioinformatics and biodiversity informatics in the realm of genetic diversity. Although both disciplines address genetic diversity, their approaches are markedly distinct: bioinformatics is a scientific discipline that utilizes computer technology manage and analyze biological data, particularly focusing on genetics and genomics. This field combines biology, computer science, and information technology to interpret large biological datasets, enhancing our understanding of health, disease, and biological processes in trees and other plant species. Core activities in bioinformatics involve the analysis of genetic sequences and genomic data, contributing to significant advances in forest plant health and breeding (adjusted from NCBI, 2024 definition on bioinformatics), whereas biodiversity informatics concerns itself with the organization and structural representation of genetic data, without delving into detailed analyses. Collectively, these fields offer significant complementary perspectives that enrich our understanding of biological life on Earth, including the genetic resources of plants and forests.

One example of biodiversity informatics tackling genetic diversity is the TreeGenes database (<https://treegenesdb.org/>), which provides genomic and genetic data on forest tree species including *Pinus taeda* L. and *Abies alba* Mill. (Wegrzyn et al. 2008). Another example is the Global Biodiversity Information Facility (GBIF) (<https://www.gbif.org>), a platform offering open-access biodiversity data from various sources and on many taxa, including forest tree species and plants. The International Barcode of Life project (<https://ibol.org/>) uses DNA barcoding to identify plant species, including forest tree species (Hebert et al. 2003). Finally, the Botanical Information and Ecology Network (BIEN) (<https://bien.nceas.ucsb.edu/bien/>) maintains a large database of plant traits, including those of forest tree species, for use in ecological research (Enquist, 2009).

Another successful project which is proving its usefulness in the field of genetic and biodiversity of forest tree species is Quercus Portal (<https://quercusportal.pierroton.inrae.fr/>), which provides access to a wealth of information on the various oak species and their taxonomy, distribution, morphology, and genetics. This portal allows genetic and genomic resources to be viewed in two different ways: by providing access to multiple databases from a single portal and by enabling the submission of complex queries across all databases, with different concepts to query different databases. Databases are regularly supplied and the connection to the Evoltree eLab cache system (please, see Stierschneider et

al. 2016) facilitates searching for biologically relevant responses. Quercus Portal is a vital tool for researchers, conservationists, and policymakers interested in studying and managing oak forests worldwide. The portal is regularly updated with new data and features including maps, images, and interactive tools, and it offers links to other relevant databases and resources for oak research and conservation. Quercus Portal is an example of the use of digital technologies to support the management and conservation of forest tree species (Ehrenmann et al. 2014).

There are still conflicting opinions about whether biodiversity informatics can be considered a new autonomous biotechnological subdiscipline or whether it simply supports biotechnological development. Biodiversity informatics is sometimes informally known as an entrance hall to biotechnology. Nevertheless, this new approach to big data linked to biodiversity is increasingly finding its place among researchers. It has been used in forestry for quite some time to facilitate access to exact and evidence-based data relating to the taxonomy and morphology of tree species along with the ecosystem services they supply. There are several databases with integrated user-friendly interfaces that forest practitioners can use to obtain updated and exact taxonomic names of targeted species, their worldwide distribution ranges, and life forms, and often even their usage in medicine, pharmacy, or nutrition. The way in which biodiversity informatics provides access to evidence-based data on forest tree species is accelerating decision-making in many countries and facilitating the creation of national strategies and laws regarding the utilization and conservation of forest genetic resources (FGR) – especially those identified as critically endangered by the International Union for Conservation of Nature (IUCN) (national contributions for IUCN Red Lists of threatened species, (IUCN Red Lists, 2024) and national contributions for The State of the World’s Forest Genetic Resources (FAO, 2014)). IUCN developed and FAO, Forestry Division is developing its biodiversity informatics system for storing and presenting biodiversity data, on species level). Nevertheless, consensual definitions will be laid out given time and dialogue at the global level among countries participating in the work of the Convention on Biological Diversity (CBD) and various Food and Agriculture Organization of the United Nations (FAO) bodies.

Digital Sequence Information (DSI) refers to digital representations of certain aspects of genetic resources, such as nucleotide or amino acid sequence data along with related information, that is downloadable from databases around the world. DSI is regularly used in the course of new research to avoid the need for new access to physical material. Divergent positions on whether DSI should be included in the national policies have emerged over the past few years. These issues, including how the benefits of DSI may be shared, are being discussed in the context of the CBD. To date, there is no agreement on the most appropriate way forward (Smith et al. 2020). For example, the applicability of the Nagoya Protocol to DSI is still under debate, with some arguing that it is not applicable since DSI does not involve any physical transfer of genetic resources.

As with biodiversity informatics, as a whole, there is still no final consensus on what kind of data should be included in DSI. This is especially concerning for lawyers at the national and regional level who deal with access and benefit sharing and informed consent among different parties. For now, a host of sequential data is freely available online via the National Centre for Biotechnology Information (NCBI, <https://www.ncbi.nlm.nih.gov/>) user interface. Certain types of DSI data are not publicly accessible because they originate from the private sector, where they are kept confidential to protect competitive advantages in profit-driven programs. Nevertheless, the CBD, as leader and the Commission on Genetic Resources for Food and Agriculture (CGRFA) of FAO, as a co-leader of this debate, is working hard to define what exactly can be considered digital sequence information (CBD, 2022; FAO & International Treaty on Plant Genetic Resources for Food and Agriculture, 2023). While a consensus is still lacking, many capacity-building and dialogue-based activities have been facilitated.

3. Genomics and sequencing biotechnologies – next-generation sequencing (NGS) and whole genome sequencing (WGS)

Genomics is the science of genetics based on technological methods and leading to deeper understanding of the relationship between the genetic composition of an organism and its phenotype, its genotype x environment interactions and epistasis effects (White et al. 2007). According to White et al. (2007), there are three major sub-disciplines of genomics:

- 1) structural genomics, which refers to the location of genes on chromosomes determined through DNA sequencing or genetic or physical mapping;
- 2) functional genomics, which explores the function of genes and their role in creating phenotypes;
- 3) comparative genomics, which aims to understand the structure or function of genes across taxa.

Next-generation sequencing (NGS) and whole genome sequencing (WGS) are powerful tools for analysing the genetic makeup of forest tree species. NGS enables high-throughput sequencing of millions of DNA fragments in a single run, while WGS involves sequencing the entire genome of an organism. Both methods have been used to study the genomes of numerous forest tree species, including *Pinus taeda* (Kovach et al. 2010, Caballero et al. 2021), *Picea abies* L. (Acheré et al. 2005), *Populus trichocarpa* Torr. and A. Gray (Slavov et al. 2012, Wullschleger et al. 2013), *Eucalyptus grandis* Hill. (Grattapaglia et al. 2012, Myburg et al. 2014), and *Quercus robur* L. (Scotti-Saintagne et al. 2004, Lesur et al. 2011). These technologies and the information generated and aggregated with their help in various research fields have given rise to the field of DSI, which has become a concern for both scientists and legislators alike. There are many online and open-access databases (including the ones mentioned above) offering hundreds of thousands or even millions of short, medium, and long pieces of sequential information from major biomolecules like DNA, RNA, and proteins. NGS has been used to identify genetic markers associated with wood formation and drought stress response in *P. taeda* (Wegrzyn et al. 2014) as well as candidate genes for adaptive traits in *P. abies* (Chen et al. 2019). WGS has been used to sequence the entire genomes of *P. trichocarpa* (Tuskan et al. 2006), *E. grandis* (Myburg et al. 2014), and *Q. robur* (Plomion et al. 2018), providing valuable resources for further genetic analysis and breeding programs. Overall, NGS and WGS have revolutionized the study of forest tree genomics, enabling researchers to identify important genetic variants and understand the genetic basis of complex traits. With the decreasing cost and increasing speed of sequencing technologies, these methods are becoming more and more accessible and offer great potential for improving forest tree breeding and management.

Concerning forest trees, structural genomics focused on gene discovery through genome sequencing, starting in 2004 with *P. trichocarpa* (Brunner et al. 2004) and continuing with numerous other forest tree species. One frequently used tool is expressed sequence tags (ESTs), which began with a focus on expressed genes associated with wood formation (Kirst et al. 2003) and has since been applied to numerous other traits (White et al. 2007). Additionally, genetic mapping by way of segregation and linkage analysis has significantly improved our knowledge on the gene loci of specific quantitative traits (White et al. 2007). Functional genomics studies gene function at the biochemical, cellular, developmental, and adaptive level by using comparative sequencing, gene expression analysis (DNA microarrays), quantitative trait loci (QTLs), association mapping, and other methods (White et al. 2007). Finally comparative genomics requires orthologous genetic markers to be mapped in different species to compare them within the same taxon (*P. taeda* and *P. radiata* D. Don) (Devey et al. 1999) or between genera (*P. taeda* and *Pseudotsuga menziesii* Mirb.) (Krutovsky et al. 2004).

Genome-wide association studies (GWAS) in trees are highlighted by Ashwath et al. (2023) as an effective method for identifying candidate genes associated with various plant properties by analysing the relationship between molecular markers (like SNPs) and target traits. This approach is beneficial over traditional QTL mapping, particularly in perennial plants and vegetatively propagated crops, where conventional mapping methods often fail due to limitations like a limited number of recombination events. GWAS allows for the study of more genotypes and utilizes all recombination events, enhancing the resolution of genetic associations. It supports breeders in rapidly understanding

genomes and identifying natural variations that underlie complex traits in trees, significantly speeding up the breeding process and genetic gain (Ashwath et al. 2023).

Restriction-site Associated DNA Sequencing (RAD-seq) efficiently targets and sequences DNA fragments adjacent to restriction enzyme sites, thus simplifying genotyping. This approach not only reduces the complexity of genetic data but also lowers costs, making it ideal for large-scale genetic diversity studies. Li et al. (2019), used RAD-seq for genotyping by sequencing DNA near restriction enzyme sites, which significantly enhances the discovery and typing of genetic markers across targeted species. Specifically, the study focused on the tree peony, *Paeonia suffruticosa*, using RAD-seq to generate extensive molecular markers that aid in understanding genetic diversity and facilitate linkage mapping (Li et al. 2019). There are other successful examples of application of this technology on tree species coming from genera *Acer*, *Prunus*, *Populus* and *Juglans* (Lin et al. 2022; Bao et al. 2020; Pan et al. 2022; Mu et al. 2017).

All genomics and biotechnology methods were initially discovered and further evolved to evaluate, compare, conserve, and protect forest genetic resources under the threat of climatic changes already apparent in terms of increasing temperature and drought phenomena. A comprehensive review of the current state of forest genomics is presented in Borthakur et al. (2022). Genetic variation is the fundamental source of evolutionary progress, and plant populations with low levels of genetic variation are expected to exhibit less pronounced responses to selection, which could lead to increased risk of population decline or extinction (Borthakur et al. 2022).

4. Genetic engineering – CRISPR and transgenic technologies

Implementation of Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) in the context of forest trees has provided information about biological processes associated with important traits such as wood quality or drought and pest resistance, thus facilitating the selection of suitable gene editing targets (Cao et al. 2022). CRISPR technology has opened new possibilities for genetic modification in forest tree species with the aim of enhancing desirable traits. Shanxin yang (*Populus davidiana* Dode × *P. bolleana* Lauche) is a commercially important poplar clone widely grown in northern China. An established transformation protocol for this interspecific hybrid enables researchers to simultaneously investigate the efficiency and specificity of the CRISPR/Cas9-mediated manipulation of a highly heterozygous genome. Using the phytoene desaturase gene (PDS) as an example, Wang et al. (2020) revealed that the CRISPR/Cas9 system could efficiently edit the Shanxin yang genome. Furthermore, Liu et al. (2015) successfully knocked out the endogenous PDS gene in *Populus tomentosa* Carr. via CRISPR/Cas. To study the effect of target design on the efficiency of CRISPR/Cas9-mediated gene knockout in *Populus*, they also analysed the efficiency of mutagenesis using different single-guide RNA (sgRNA) targeting the PDS DNA sequence (Liu et al. 2015). These examples highlight the potential of CRISPR technology for addressing various challenges faced by forest tree species by enhancing growth, stress tolerance, and wood quality, as well as demonstrating the broad scope of applications for the technology in the field of forestry overall. Despite the potential benefits, there are also concerns regarding unintended effects of genome editing in forest trees, such as gene flow and ecological impacts. It is therefore essential to carefully evaluate the potential risks and benefits of CRISPR applications in forest tree species.

Transgenic trees have been developed to enhance growth, productivity, and resistance to biotic and abiotic stresses. They have also been employed in a piloting function within restoration initiatives, as in the case of American chestnut tree (Barnhill-Dilling and Delborne, 2019). This case examines how such technologies intersect with Indigenous worldviews, particularly the Haudenosaunee perspectives. The paper highlights the need for a reciprocal restoration framework that not only considers the reintroduction of species like the American chestnut, but also respects and incorporates Indigenous ecological knowledge and spiritual practices. This approach advocates for engagement with Indigenous communities in setting restoration priorities and making decisions about the use of genetic engineering in conservation of particular species. The most comprehensive overview of

genetically modified transformants (GMT) was provided by Chang et al. (2018), who presented more than 30 forest tree species from the genera *Betula*, *Juglans*, *Castanea*, *Populus*, *Quercus*, *Eucalyptus*, and *Robinia*. The majority of the mentioned transgenic research targets adaptively important traits such as pest and abiotic stress resistance.

Significant strides have been made in combating Japanese cedar pollinosis, a severe pollen allergy syndrome, through innovative CRISPR/Cas9 genome editing techniques. By specifically targeting the *cjasos5* gene in Sugi trees (*Cryptomeria japonica* D. Don), researchers succeeded in producing pollen-free variants of this economically and environmentally significant tree species. This groundbreaking work not only offers a promising approach to reducing the prevalence of pollen-induced allergies, but also underscores the potential of genome editing technology in forestry and environmental management, marking a pivotal step towards sustainable allergy mitigation and biodiversity conservation (Nishiguchi et al. 2023).

Genetic modifications in poplar trees have emerged as a promising strategy to improve their utility in biofuel production. Efforts focusing on altering the expression of key genes responsible for the synthesis of lignin, cellulose, and hemicellulose have led to notable decreases in wood's natural resistance to enzymatic breakdown, crucial for efficient biofuel conversion (Bryant et al. 2020). These modifications are not only pivotal for enhancing the bioconversion process but also offer a deeper understanding of the cellular mechanisms governing plant growth and cell wall composition, setting a foundation for future advancements in renewable energy sources (Bryant et al. 2020).

5. Epigenetics in forest trees and their genetic resources

Epigenetic effects are alterations induced by environmental changes that do not directly alter the DNA sequence but can lead to changes in gene expression and thus influence how species respond to environmental changes (Loo, 2016). Epigenetic phenomena have been recorded in some tree species, mostly conifers. For example, the temperature during embryogenesis of Norway spruce (*P. abies*) was found to influence the expression of genes responsible for the timing of bud burst (Carneros et al. 2017; Yakovlev et al. 2014). Epigenetics is also defined as the mechanisms that affect gene expression or the activity of transposable elements (TEs) without alterations in the DNA sequence (Amaral et al. 2020). DNA methylation is the most studied epigenetic mark in mammals and plants (Kakoulidou et al. 2021), and numerous studies have shown its relation to drought (Gourcilleau et al. 2010; Raj et al. 2011; Correia et al. 2016; Le Gac et al. 2019), temperature extremes (Carón et al. 2014; Dewan et al. 2018; Yakovlev et al. 2011), salt stress (Liu et al. 2019; Murata et al. 2012), and phenotypic plasticity (Skinner, 2015). Studies have shown that epigenetic marks can be transmitted to subsequent generations (Johnsen et al. 2005). Epigenetics also includes many other processes besides methylation, however; a detailed review of the current state of research and future challenges is presented by Amaral et al. (2020).

Epigenetic modifications play an important role in the regulation of gene expression and phenotypic variation in forest tree species, helping them to produce seeds that are better suited to new climatic conditions, and therefore to adapt within a single generation. Zhang et al. (2020) presented cross-cutting biotechnological power to tackle epigenetic phenomena in *P. trichocarpa*. They analysed single-base resolution methylomes of primary stems (PS), transitional stems (TS), and secondary stems (SS) of *P. trichocarpa* using a high-throughput bisulfite sequencing technique, as well as investigating the effects of 5mC methylation on the expression of genes involved in wood formation. Chen et al. (2021) performed a comprehensive analysis of morphological observations, transcriptome profiles, the DNA methylome, and miRNAs of the cambium in *P. tomentosa* during the transition from dormancy to activation. Their findings improve our systems-level understanding of the existing epigenomic diversity within the annual growth cycle of trees. These studies demonstrate the potential of research on epigenetics in forest trees to provide insights into the molecular mechanisms underlying important traits and inform breeding and management strategies.

García-García et al. (2022) discuss the challenges in studying epigenetic modifications in forest tree species, emphasizing the role of epigenetic changes in adapting to climate change when genetic

shifts cannot occur rapidly enough. Heer et al. (2018) utilized targeted bisulfite sequencing to investigate methylation patterns in Norway spruce, revealing that epigenetic variations could be a pathway for plants to respond to environmental changes, highlighting the potential of epigenetics in understanding tree adaptation.

There is also other significant information on epigenetics in forest trees and their related genetic resources. Batalova and Krutovsky (2023) summarize genetic and epigenetic mechanisms of longevity in forest trees, highlighting the role of epigenetic regulators in maintaining genome integrity and defence responses, crucial for tree longevity. Klupczyńska and Ratajczak (2021) discuss the effects of DNA methylation on gene expression and adaptation to environmental change, underlining the significance of epigenetic modifications for tree conservation in forest ecosystems facing global warming. These studies collectively highlight the critical role of epigenetic research in enhancing our understanding of forest trees' adaptive capacity to rapidly changing environments.

6. FGR and other artificial technologies – blockchain and satellite imaging

Climate-Smart Forestry (CSF) is an approach within sustainable forest management aimed at responding to climate change. This includes strategies to develop suitable management responses that enhance the provision of ecosystem services. The definition emphasizes the integration of adaptation, mitigation, and social dimensions to ensure that these aspects are not developed in isolation (Bowditch et al. 2020). In CSF, deep tech, and artificial technologies such as blockchain and satellite imaging can play significant roles. Blockchain can enhance transparency and traceability in sustainable forest management by securely tracking and verifying forestry products from origin to market, fostering compliance with environmental standards. Meanwhile, satellite imaging can be utilized to monitor forest health and changes over time, enabling precise assessment of carbon storage, forest cover, and the impact of climate change on forest ecosystems, thus informing, and improving conservation and restoration efforts.

The integration of blockchain technology¹ and satellite imaging is revolutionizing the conservation of forest genetic resources by enhancing the accuracy and transparency of monitoring and reporting mechanisms. Blockchain technology significantly benefits the forestry sector by promoting sustainability, reducing costs, creating jobs, and attracting investment (He and Turner, 2022). It enhances sustainable forestry practices through smart monitoring of deforestation and biodiversity conservation (Howson et al. 2019). The technology also offers economic advantages by lowering transaction and production costs, despite its high initial implementation expense. Furthermore, it opens new employment opportunities for professionals specialized in cryptography and smart contracts. Blockchain also attracts investments by ensuring transparency in forestry transactions, thereby increasing investor confidence, and encouraging diverse investments (Howson et al. 2019). These advantages collectively highlight blockchain's role in transforming forestry into a more sustainable, efficient, and competitive sector (He and Turner, 2022).

Malipatil et al. (2023) developed a machine-learning algorithm, RF-Ranger, utilizing high-resolution satellite images for monitoring reforestation efforts, achieving a categorization accuracy of 97.5% and a Macro-F1 score of 97.4%, demonstrating the potential for large-scale application in forest regeneration areas. Employment of Landsat satellite imagery in Vietnam by V. Phuong and B. Thien (2023) to detect significant changes in forest cover over three decades, highlighted this technology in identifying deforestation and the effectiveness of conservation policies. Vinod et al. (2022) assessed

¹ Blockchain technology is a decentralized digital ledger that records transactions across multiple computers in a way that ensures the integrity and security of the data. These records, or blocks, are linked using cryptography, creating an immutable chain. This structure prevents any single point of failure and does not require a trusted third party, making blockchain a robust and transparent way to record and share data across a network.

For further reading on blockchain technology: Nakamoto, S. (2008). *Bitcoin: A peer-to-peer electronic cash system*. Retrieved from <https://bitcoin.org/bitcoin.pdf>

Trees Outside Forest (TOF) in urban landscapes using high-resolution satellite images and deep learning techniques, showcasing advanced methods for urban forestry conservation. .

Zhang et al. (2023) propose a forest resource management system that leverages blockchain technology, coupled with drone on-site verification, to ensure data security, improve management credibility and efficiency, and cost-effectiveness. This system highlights blockchain's potential for enhancing data credibility, cooperation mechanisms, intelligent decision-making, and sustainable development in forest resource management (Zhang et al. 2023). Although the direct application of blockchain in the conservation of forest genetic resources is still emerging, the principles of data security and traceability inherent in blockchain technology are applicable to the management and conservation of these resources.

The FAO has developed the System for Earth Observation Data Access, Processing, and Analysis for Land Monitoring (SEPAL, <https://www.fao.org/in-action/sepal/en>). This system assists countries in monitoring forests and land use effectively. SEPAL features a user-friendly interface that runs on cloud-based supercomputers, providing users with exceptional access to satellite data. This access is crucial for enhancing climate change mitigation strategies and creating policies for land use that are based on solid data. The system also plays a crucial role in enhancing countries' abilities to meet reporting requirements under international environmental agreements, such as the United Nations Framework Convention on Climate Change (UNFCCC). Furthermore, SEPAL aids in the assessment of carbon stocks and changes within forested areas, contributing significantly to efforts in climate change mitigation and adaptation.

Integrating blockchain and satellite imaging into the genetic assessment of forest ecosystems offers a cutting-edge approach that marries precision with security. Through the lens of satellite imaging, researchers gain unparalleled insights into the spatial distribution and genetic diversity of forests, enabling targeted conservation efforts (Petrou et al. 2015). Concurrently, blockchain technology offers a robust framework for managing the resulting genetic data, safeguarding its authenticity and facilitating seamless collaboration across scientific communities (Alghazwi et al. 2022). This synergistic application not only enhances our understanding of forest ecosystems, but also paves the way for innovative conservation strategies.

7. Conclusions

The integration of biotechnological innovations, such as CRISPR-Cas9, with traditional forest conservation strategies offers a promising path to enhancing forest resilience to environmental stresses. This synthesis of modern and conventional methods is critical for sustaining forest ecosystems and their biodiversity. Biodiversity informatics, a field that combines biology, computer science, and information technology, has significantly contributed to understanding and conserving forest genetic resources. It enables the effective management and analysis of biodiversity data, facilitating informed decision-making in forest management and conservation. Advances in genomics and sequencing technologies, including NGS and WGS, have revolutionized the study of forest tree genomics. These technologies have enabled the identification of genetic markers and the understanding of the genetic basis of complex traits in forest trees, which are vital for breeding programs and management strategies. CRISPR technology and the development of transgenic trees have opened new avenues for enhancing desirable traits in forest species, such as growth, stress tolerance, and wood quality. However, it is essential to evaluate the potential risks and benefits carefully, considering the ecological impacts of genome editing. The study of epigenetics in forest trees has unveiled how epigenetic modifications can influence gene expression and phenotypic variation, providing insights into their adaptation to environmental changes. This research underscores the importance of epigenetic mechanisms in the context of climate change and forest conservation.

Based on these conclusions, the following recommendations are proposed:

- **Foster interdisciplinary collaboration:** encourage collaborations between geneticists, biotechnologists, conservationists, and policymakers to integrate biotechnological

advancements with traditional conservation practices, ensuring a holistic approach to forest management and conservation.

- **Invest in biodiversity informatics infrastructure:** expand investments in biodiversity informatics infrastructure to improve data collection, management, and analysis capabilities. This will enhance understanding and conservation efforts for forest genetic resources.
- **Enhance public and stakeholder engagement:** increase awareness and engagement among stakeholders and the public about the potential and challenges of genomic and biotechnological applications in forestry. Transparent communication and ethical considerations should be prioritized to address concerns and expectations.
- **Prioritize epigenetic research:** support and prioritize research on epigenetic mechanisms in forest trees, emphasizing their role in adaptation to environmental changes. This research could lead to novel approaches in breeding and conservation strategies that account for rapid climate change.
- **Develop and implement regulatory frameworks:** develop comprehensive regulatory frameworks to guide the application of genome editing technologies in forestry. These frameworks should ensure ecological safety, prevent unintended consequences, and support the sustainable use of genetic modifications for forest conservation.

Acknowledgement

The study was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Contract No. 451-03-66/2024-03/200197). This research was also done under the project of Uni Belgrade: Climate attribution SRB 23/24 (Mentoring programme for young researchers to adopt advance knowledge in climate research and to effectively communicate their results), grant Number: G-2311-67522, funded by European Climate Foundation.

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