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# Precision Editing: Revolutionary Applications of Genome Editing Technology in Tree Breeding

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**Abstract** Precision genome editing technologies, particularly CRISPR/Cas systems, have revolutionized tree breeding by enabling targeted modifications with unprecedented accuracy. This study explores the transformative applications of genome editing in tree breeding, focusing on the advancements in CRISPR/Cas9 and its variants, such as base editing and prime editing. These technologies facilitate precise genetic alterations, enhancing traits like disease resistance, yield, and environmental stress tolerance. This study also discusses the development of efficient delivery systems and the challenges associated with off-target effects and editing efficiency. By summarizing recent progress and future prospects, this study highlights the potential of precision genome editing to drive sustainable and innovative tree breeding practices.
**Keywords** CRISPR/Cas9; Tree breeding; Genome editing; Base editing; Prime editing

## 1 Introduction

Tree breeding has long been a critical component of forestry and agriculture, aimed at improving traits such as growth rate, wood quality, disease resistance, and environmental adaptability. The economic and ecological importance of forest trees necessitates continuous advancements in breeding techniques to ensure sustainable forest management and productivity (Cao et al., 2022). Traditional tree breeding methods, which rely on selecting and crossing superior trees, have significantly contributed to the development of improved tree varieties. However, these methods are often time-consuming and labor-intensive, requiring multiple generations to achieve desired traits (Bewg et al., 2018).

Despite their successes, traditional tree breeding methods face several limitations. The high degree of genome heterozygosity in outcrossing trees poses a significant challenge, as sequence polymorphisms at target sites can render conventional breeding techniques less effective. Additionally, the lengthy process of multigenerational crosses to obtain homozygous knockouts (KO) further delays the development of improved tree varieties (Bewg et al., 2018). Moreover, the reliance on natural or artificially induced genetic variations often results in unpredictable outcomes, making it difficult to achieve precise modifications (Hua et al., 2019). These limitations underscore the need for more efficient and precise breeding techniques.

The advent of genome editing technologies, particularly CRISPR/Cas systems, has revolutionized plant genetics and breeding by enabling precise, targeted modifications of the genome (Chen et al., 2019). These technologies offer a powerful and versatile tool for analyzing gene function and achieving precise genetic modifications in virtually any species, including forest trees (Cao et al., 2022). Genome editing allows for the rapid introduction of improvements directly into elite varieties, bypassing the need for laborious characterization of multiple generations (Hua et al., 2019). Recent developments in base editing and prime editing technologies have further enhanced the precision and efficiency of genome editing, enabling single-base resolution changes without the need for double-stranded breaks or donor DNA templates (Molla et al., 2021). These advancements hold great promise for accelerating the development of high-yielding, climate-resilient, and disease-resistant tree varieties, thereby addressing the limitations of traditional breeding methods and contributing to sustainable forestry and agriculture (Yin and Qiu, 2019; Xia et al., 2021; Nerkar et al., 2022).

This study aims to explore the revolutionary applications of precision genome editing technologies in tree breeding. By reviewing the latest advancements and their implications for tree genetics, this study provides a comprehensive understanding of how these technologies can overcome the limitations of traditional breeding methods and address the pressing challenges faced by modern forestry, and examine the current state of genome editing in trees, including successful applications and ongoing research, and discuss the potential for these technologies to transform tree breeding practices. Ultimately, this study aims to highlight the potential of precision genome editing to contribute to sustainable forestry and the development of climate-resilient tree species.

## 2 Genome Editing Technologies

### 2.1 Overview of genome editing tools

#### 2.1.1 Zinc finger nucleases (ZFNs)

Zinc Finger Nucleases (ZFNs) are engineered DNA-binding proteins that facilitate targeted editing of the genome by creating double-strand breaks (DSBs) at specific locations. These breaks are then repaired by the cell's natural repair mechanisms, such as non-homologous end joining (NHEJ) or homology-directed repair (HDR). ZFNs are composed of a DNA-binding domain, which can be customized to target specific DNA sequences, and a DNA-cleavage domain derived from the FokI restriction enzyme. This technology has been successfully applied in various plant species, including hexaploid bread wheat, where ZFN-mediated editing introduced specific amino acid changes to confer herbicide resistance (Ran et al., 2018).

#### 2.1.2 Transcription activator-like effector nucleases (TALENs)

Transcription Activator-Like Effector Nucleases (TALENs) are another class of engineered nucleases used for precise genome editing. Similar to ZFNs, TALENs consist of a customizable DNA-binding domain and a FokI nuclease domain. The DNA-binding domain of TALENs is derived from transcription activator-like effectors (TALEs) of plant pathogenic bacteria, which can be engineered to recognize specific DNA sequences. TALENs have been widely used in plant genome editing due to their high specificity and efficiency. They offer a versatile tool for introducing targeted modifications in plant genomes, facilitating the development of crops with desirable traits.

#### 2.1.3 Clustered regularly interspaced short palindromic repeats (CRISPR/Cas)

The CRISPR/Cas system, particularly the CRISPR/Cas9 and CRISPR/Cas12a variants, has revolutionized genome editing due to its simplicity, efficiency, and versatility. This system uses a guide RNA (gRNA) to direct the Cas nuclease to a specific DNA sequence, where it creates a DSB. The DSBs can be repaired by NHEJ, leading to insertions or deletions (indels), or by HDR if a donor template is provided. The CRISPR/Cas system has become the most popular method for plant genome editing, enabling precise modifications and the development of crops with improved traits (Kim and Kim, 2019).

### 2.2 Comparison of different genome editing technologies

Each genome editing technology has its own advantages and limitations. ZFNs and TALENs offer high specificity due to their customizable DNA-binding domains, but their design and construction can be complex and time-consuming. In contrast, the CRISPR/Cas system is easier to design and implement, making it more accessible to researchers. CRISPR/Cas also allows for multiplexing, where multiple genes can be edited simultaneously, which is more challenging with ZFNs and TALENs (Ran et al., 2018; Kim and Kim, 2019).

While ZFNs and TALENs have been successfully used in various plant species, the CRISPR/Cas system has rapidly become the preferred tool due to its efficiency and ease of use. The expanding CRISPR/Cas toolbox, including various Cas enzymes and engineered components, continues to enhance its capabilities and applications in plant genome editing (Kim and Kim, 2019).

In summary, while ZFNs and TALENs have paved the way for precise genome editing, the CRISPR/Cas system has emerged as the most versatile and widely adopted technology, driving significant advancements in plant breeding and the development of crops with desirable traits.

# 3 Applications in Tree Breeding

## 3.1 Improving disease resistance

### 3.1.1 Case studies of disease resistance improvement

Genome editing technologies, particularly CRISPR/Cas9, have been successfully applied to enhance disease resistance in various plant species. For instance, the development of disease-resistant crops through precise genome modifications has been demonstrated in several studies. These modifications include the introduction of resistance genes or the alteration of susceptibility genes to confer resistance against bacterial, fungal, and viral pathogens (Nerkar et al., 2022). Specific case studies have shown that editing genes related to disease resistance can significantly reduce the impact of diseases on crop yield and quality, thereby contributing to sustainable agriculture (Yin and Qiu, 2019).

### 3.1.2 Mechanisms of resistance gene editing

The mechanisms underlying resistance gene editing involve the precise modification of target genes to enhance their resistance properties. CRISPR/Cas9 and its variants, such as base editors and prime editors, enable targeted nucleotide substitutions and precise gene corrections without the need for double-stranded breaks or donor DNA templates (Figure 1) (Hua et al., 2021; Molla et al., 2021). These tools can be used to knock out susceptibility genes or introduce beneficial mutations that enhance the plant's innate immune response, thereby improving disease resistance (Chen et al., 2019; Abdelrahman et al., 2021).

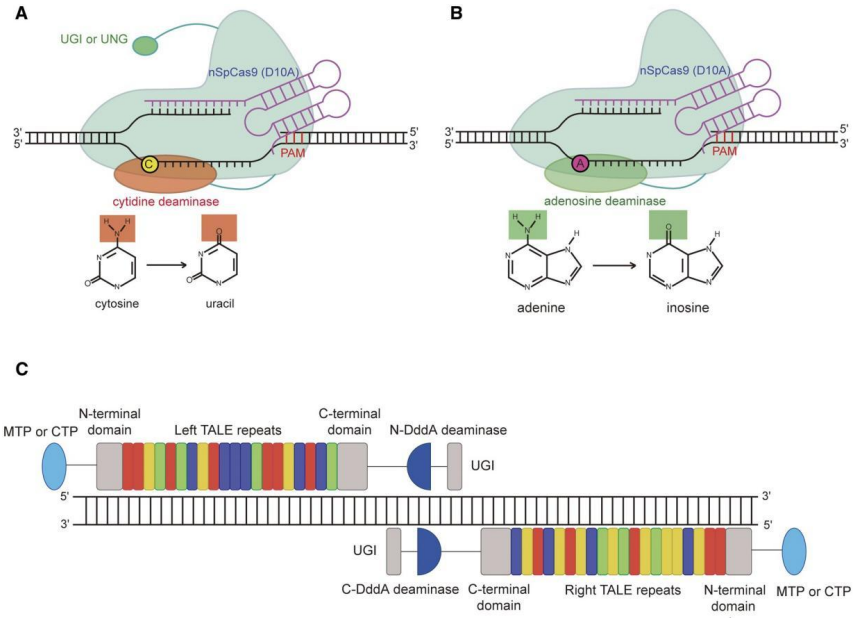


Figure 1 The architecture of base editors (Adopted from Hua et al., 2021)

Image caption: Panel A depicts the cytosine base editor (CBE), which uses an SpCas9 (D10A) nickase fused with a cytidine deaminase and a uracil glycosylase inhibitor (UGI) to convert cytosine (C) to uracil (U), leading to a C to T transition upon DNA replication; Panel B shows the adenine base editor (ABE), which employs an evolved adenosine deaminase to convert adenine (A) to inosine (I), resulting in an A to G transition; Panel C presents the DddAtox-derived cytosine base editor, which is designed for targeting plant organelles like mitochondria and chloroplasts, highlighting the versatility and specificity of these gene-editing tools in various cellular contexts (Adapted from Hua et al., 2021)

## 3.2 Enhancing growth and yield

### 3.2.1 Genetic modifications for faster growth

Genome editing technologies have been employed to enhance the growth rate of trees by targeting genes involved in growth regulation. For example, modifications in genes that control hormone pathways or cell division can lead to faster growth and increased biomass production (Chen et al., 2019; Nerkar et al., 2022). These genetic modifications are achieved through precise edits that optimize the expression of growth-related genes, resulting in trees that grow more rapidly and efficiently (Hahne et al., 2019).

3.2.2 Yield improvement through gene editing

Improving yield through gene editing involves the precise modification of genes that influence traits such as fruit size, number, and quality. CRISPR/Cas9 and other genome editing tools have been used to enhance yield by targeting genes associated with these traits, leading to significant improvements in crop productivity (Nerkar et al., 2022). For instance, multiplex genome-editing technologies allow for the simultaneous modification of multiple genes, resulting in cumulative effects that boost overall yield (Abdelrahman et al., 2021).

### 3.3 Modifying wood properties

3.3.1 Lignin content and composition modification

Modifying lignin content and composition is crucial for improving the industrial usability of wood. Genome editing technologies enable precise alterations in lignin biosynthesis pathways, resulting in wood with desirable properties such as reduced lignin content or altered lignin composition (Chen et al., 2019). These modifications can enhance the efficiency of wood processing and the quality of wood products, making them more suitable for various industrial applications (Hahne et al., 2019).

3.3.2 Enhancing wood quality for industrial use

Enhancing wood quality through gene editing involves targeting genes that influence wood density, strength, and other physical properties. By precisely editing these genes, researchers can develop tree varieties with superior wood quality that meets specific industrial requirements (Chen et al., 2019). This includes modifications that improve the mechanical properties of wood, making it more durable and suitable for construction and other uses (Hahne et al., 2019).

### 3.4 Environmental stress tolerance

3.4.1 Editing for drought and salinity tolerance

Genome editing technologies have been applied to enhance the tolerance of trees to environmental stresses such as drought and salinity. By targeting genes involved in stress response pathways, researchers can develop tree varieties that are more resilient to adverse environmental conditions (Nerkar et al., 2022). These modifications can improve water use efficiency and salt tolerance, enabling trees to thrive in challenging environments (Chen et al., 2019).

3.4.2 Enhancing tolerance to temperature extremes

Enhancing tolerance to temperature extremes involves the precise modification of genes that regulate heat and cold stress responses. Genome editing tools such as CRISPR/Cas9 have been used to introduce beneficial mutations that enhance the ability of trees to withstand extreme temperatures (Nerkar et al., 2022). These modifications can help mitigate the impact of climate change on tree growth and productivity, ensuring the sustainability of tree breeding programs (Chen et al., 2019).

By leveraging the power of precision genome editing technologies, researchers are making significant strides in improving various aspects of tree breeding, from disease resistance and growth enhancement to wood quality and environmental stress tolerance. These advancements hold great promise for the future of sustainable forestry and agriculture.

## 4 Case Studies

### 4.1 Fruit trees

4.1.1 Apple genome editing for disease resistance

Genome editing has been successfully applied to enhance disease resistance in apple trees by targeting specific genes associated with susceptibility to pathogens. For instance, the CRISPR/Cas9 system has been utilized to knock out susceptibility genes, thereby conferring resistance to diseases such as fire blight and apple scab. These diseases are caused by the bacteria *Erwinia amylovora* and the fungus Venturia inaequalis, respectively, and are major threats to apple production (Yin and Qiu, 2019; Zhou et al., 2020; Keul et al., 2022).

One notable example is the editing of the *MdDIPM* gene in apple, which is known to be involved in the susceptibility to fire blight (Figure 2). By knocking out this gene, researchers have successfully developed apple lines that exhibit enhanced resistance to this devastating disease (Yin and Qiu, 2019). Similarly, targeting the *MdMLO* gene, which is associated with powdery mildew susceptibility, has resulted in apple varieties with improved resistance to this fungal pathogen (Zhou et al., 2020; Keul et al., 2022).

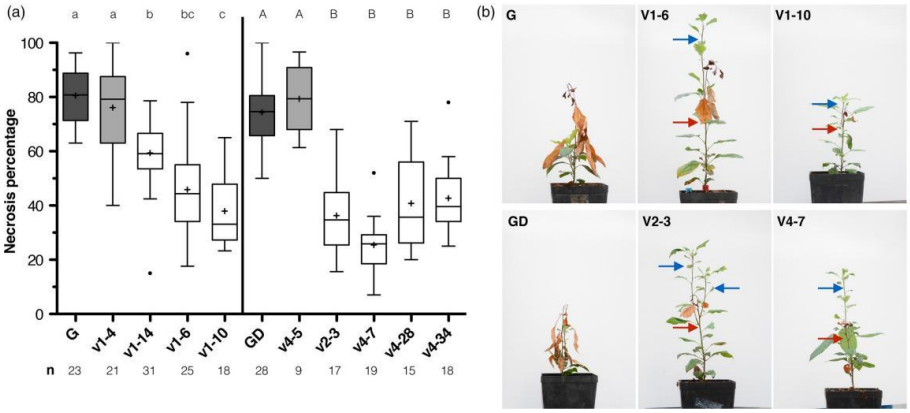


Figure 2 Fire blight severity in MdDIPM4-edited plants of 'Gala' and 'Golden Delicious' cultivars (Adopted from Pompili et al., 2019)

Image caption: (a) Boxplot summarizing the percentage of necrosis (calculated as length of the necrosis/total length of the shoot × 100) of candidate MdDIPM4 CRISPR/Cas9-edited plants inoculated by the method of scissor with *Erwinia amylovora* strain Ea273. The number of inoculated biological replicates for each line is indicated (n). Boxes comprise values between 25% and 75% of the group. Horizontal central lines represent medians. Mean is shown as+. Whiskers (Tukey) determine values within ±1.5 interquartile ranges from the median. Circles indicate outliers. Lettering indicates statistically significant differences between plant lines (for 'Gala' lower case, for 'Golden Delicious' upper case) according to Kruskal–Wallis test followed by multiple comparison of mean rank ($\alpha = 0.05$). (b) Pictures, taken 1 month after inoculation, showing the fire blight-induced necrotic phenotype in wild-type and some transgenic lines. Red and blue arrows indicate the interruption of necrosis and new regenerated shoots, respectively. Gala (G); Golden Delicious (GD) (Adopted from Pompili et al., 2019)

Pompili et al. (2019) demonstrates that CRISPR/Cas9-mediated editing of the *MdDIPM4* gene in apple cultivars 'Gala' and 'Golden Delicious' significantly reduces susceptibility to fire blight, caused by *Erwinia amylovora*. The graph shows a substantial decrease in necrosis percentages in edited lines compared to non-edited controls, indicating successful gene editing. Edited lines exhibit a reduced rate of disease progression and show new, healthy shoot growth post-infection, unlike the continuous disease progression observed in control plants. This highlights the potential of CRISPR/Cas9 technology in enhancing disease resistance in apple cultivars, paving the way for improved crop resilience and productivity. The visual comparison of plants also underscores the practical benefits of genetic editing in real-world agricultural applications.

The precision and efficiency of CRISPR/Cas9 have also enabled the development of apple varieties with multiple disease resistances. For example, simultaneous editing of multiple susceptibility genes has been demonstrated, leading to apple trees that are resistant to both fire blight and apple scab (Yin and Qiu, 2019; Zhou et al., 2020; Keul et al., 2022). This multi-target approach not only enhances disease resistance but also reduces the need for chemical treatments, promoting more sustainable apple production.

#### 4.1.2 Citrus gene editing for HLB resistance

Huanglongbing (HLB), also known as citrus greening disease, is one of the most devastating diseases affecting citrus crops worldwide. The disease is caused by the bacterium *Candidatus liberibacter* asiaticus and leads to significant yield losses and tree mortality. Traditional breeding methods have struggled to develop HLB-resistant citrus varieties due to the complex genetics and long generation times of citrus trees. However, recent advancements in genome editing technologies have opened new avenues for developing HLB-resistant citrus.

One promising approach involves the use of base editors, such as adenine base editors (ABE) and cytosine base editors (CBE), which enable precise genome modifications without introducing double-strand breaks (DSBs). This method reduces the risk of genome instability and unpredictable outcomes associated with DNA repair mechanisms. For instance, researchers have successfully adapted ABE to edit the TATA box in the promoter region of the canker susceptibility gene *LOB1* from TATA to CACA in grapefruit (*Citrus paradise*) and sweet orange (*Citrus sinensis*). The TATA-edited plants exhibited resistance to the canker pathogen *Xanthomonas citri* subsp. *Citri* (Xcc) (Huang et al., 2021).

Additionally, CBE has been employed to edit the acetolactate synthase (*ALS*) gene in citrus, resulting in herbicide-resistant plants. Notably, the ALS-edited plants were transgene-free, as the *Cas9* gene was undetectable in the herbicide-resistant citrus plants. This represents a significant milestone, as it demonstrates the potential for developing transgene-free, gene-edited citrus varieties using CRISPR technology (Huang et al., 2021).

### 4.2 Forest trees

#### 4.2.1 Poplar genome editing for bioenergy production

Poplar trees have emerged as a significant focus for genome editing due to their potential in bioenergy production. The application of CRISPR technology in poplar has demonstrated promising results in enhancing wood properties, which are crucial for efficient bioenergy production (Figure 3).

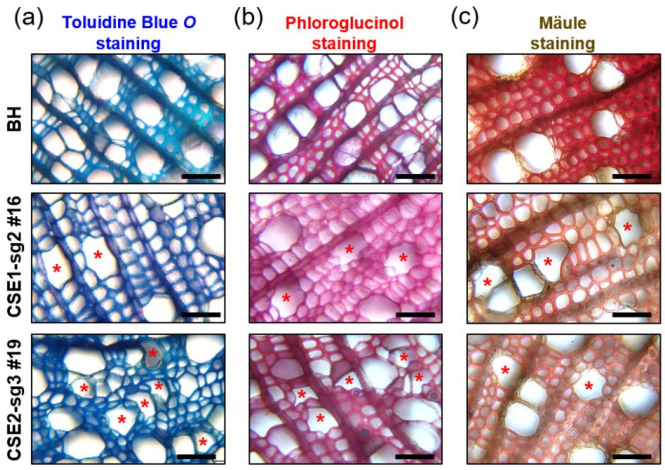


Figure 3 Transgenic CSE-CRISPR hybrid poplars have irregularly shaped xylem vessel cells (Adopted from Jang et al., 2021)

Image caption: Stem anatomy of hybrid poplars (8-month-old LMO field grown) was assessed by (a) toluidine blue, (b) phloroglucinol-HCl, and (c) Mäule staining. Collapsed irregular vessels are marked with asterisks. Scale bars represent 50 μm (Adopted from Jang et al., 2021)

Jang et al. (2021) illustrates the structural and compositional changes in xylem vessels of CRISPR/Cas9-edited hybrid poplars with *CSE* gene knockouts. Both CSE1-sg2 and CSE2-sg3 transgenic lines show significant abnormalities in xylem vessel formation, characterized by collapsed and irregularly shaped cells. This is a clear indication of compromised secondary cell wall development. Additionally, the reduced red staining intensity in both phloroglucinol and Mäule staining assays suggests a substantial decrease in overall lignin content and S-lignin content, respectively. This study highlights the effectiveness of CRISPR/Cas9 in elucidating gene functions and modifying plant traits, offering potential applications in improving wood quality and biofuel production through targeted genetic modifications.

One notable study utilized multiplex CRISPR editing to target lignin biosynthesis genes in poplar. Lignin, a complex biopolymer in wood, poses a challenge for bioenergy production due to its resistance to chemical and enzymatic degradation. By editing multiple genes involved in lignin biosynthesis, researchers were able to significantly alter the lignin composition and improve the wood's carbohydrate-to-lignin ratio. This modification led to a 228% increase in the wood carbohydrate-to-lignin ratio compared to wild-type poplar, resulting in more efficient fiber pulping and reduced carbon emissions (Sulis et al., 2023).

The success of this approach highlights the potential of CRISPR technology to overcome the genetic complexity and plasticity of lignin in poplar. The study produced 174 edited poplar variants, demonstrating the feasibility of large-scale genome editing for bioenergy applications. The edited poplar trees not only showed improved wood properties but also maintained growth rates comparable to wild-type trees, ensuring that the modifications did not adversely affect overall tree health and productivity (Sulis et al., 2023).

4.2.2 Pine gene editing for improved timber quality

The application of genome editing technologies, particularly CRISPR/Cas9, has revolutionized the field of plant breeding, including the improvement of timber quality in pine trees. The economic and ecological significance of forest trees has driven the need for advanced breeding techniques to enhance desirable traits such as wood quality, pest resistance, and climate resilience (Zhu and Ge, 2017).

Recent advancements in genome sequencing and the accumulation of genetic resources have identified numerous genes associated with wood quality in pine trees. These genetic insights have facilitated the selection of precise gene editing targets, enabling the modification of specific traits to improve timber quality. For instance, CRISPR/Cas9 technology has been employed to target genes involved in lignin biosynthesis, a key component affecting wood density and strength. By precisely editing these genes, researchers have been able to produce pine trees with enhanced wood properties, which are crucial for the timber industry (Zhu and Ge, 2017).

## 5 Ethical, Legal, and Social Considerations

### 5.1 Ethical concerns in genome editing of trees

The application of genome editing technologies in tree breeding raises several ethical concerns. One primary issue is the potential for unintended ecological consequences. Trees play a crucial role in ecosystems, and altering their genetic makeup could have unforeseen effects on biodiversity and ecosystem stability (Yin and Qiu, 2019; Nerkar et al., 2022). Additionally, there is a moral debate surrounding the manipulation of natural organisms for human benefit, which some argue could lead to a slippery slope of further genetic modifications in other species (WareJoncas et al., 2018). The long lifespan of trees also means that any genetic changes could have long-term impacts that are difficult to predict and manage (Hua et al., 2021).

### 5.2 Regulatory frameworks and approval processes

The regulatory landscape for genome editing in trees is complex and varies significantly across different regions. In many countries, genome-edited plants, including trees, are subject to stringent regulatory frameworks that assess their safety and environmental impact before approval (Yin and Qiu, 2019; Nerkar et al., 2022). For instance, the European Union has a rigorous approval process that includes risk assessments and public consultations. In contrast, some countries have more lenient regulations, which can lead to discrepancies in the global market and trade of genome-edited products (Abdelrahman et al., 2021). The development of international guidelines and harmonization of regulatory frameworks is essential to ensure the safe and ethical use of genome editing technologies in tree breeding (Mueller et al., 2018).

### 5.3 Public perception and acceptance

Public perception and acceptance of genome editing in trees are critical factors that influence the adoption and success of these technologies. There is often a significant gap between scientific advancements and public understanding, leading to skepticism and resistance (Yin and Qiu, 2019; Nerkar et al., 2022). Effective communication and education strategies are necessary to bridge this gap and address public concerns about the safety, ethics, and environmental impact of genome-edited trees (Molla et al., 2021). Engaging with stakeholders, including environmental groups, policymakers, and the general public, is crucial to build trust and acceptance (Suh et al., 2022). Transparency in the research and development process, as well as clear labeling of genome-edited products, can also help in gaining public support (Hua et al., 2021).

## 6 Future Prospects and Challenges

### 6.1 Advancements in genome editing technologies

Recent advancements in genome editing technologies, particularly the development of CRISPR/Cas systems, have

revolutionized plant genetics and breeding. These technologies enable precise modifications at specific sites within the genome, which is a significant improvement over traditional genetic engineering methods that often result in random insertions of foreign DNA (Molla et al., 2021; Nerkar et al., 2022). The introduction of base editors and prime editors has further enhanced the precision of genome editing, allowing for single-base resolution changes without the need for double-stranded breaks or donor DNA templates (Hua et al., 2021). These advancements have been successfully demonstrated in various plant species, showing promising results in improving crop traits such as disease resistance, abiotic stress tolerance, and yield (Chen et al., 2019; Hua et al., 2021).

### 6.2 Integration of genome editing with traditional breeding methods

Integrating genome editing technologies with traditional breeding methods offers a synergistic approach to crop improvement. Traditional breeding has been instrumental in developing hybrid varieties with improved productivity, but it is often limited by the existing gene pools (Nerkar et al., 2022). Genome editing can overcome these limitations by introducing new genetic variations directly into elite varieties, thus accelerating the breeding process (Hua et al., 2019). This integration can enhance the efficiency of breeding programs by enabling precise modifications that are difficult to achieve through conventional methods alone (Chen et al., 2019). For instance, multiplex genome-editing technologies allow for simultaneous modifications at multiple loci, providing a powerful tool for complex trait improvement (Abdelrahman et al., 2021).

### 6.3 Overcoming technical and biological challenges

Despite the significant progress, several technical and biological challenges remain in the application of genome editing technologies. One major challenge is the efficiency of homology-directed repair (HDR) in plants, which is often low and limits the precision of genome editing (Hua et al., 2021; Molla et al., 2021). Additionally, the delivery of genome editing components into plant cells, especially in species with complex genomes, poses another hurdle (Mueller et al., 2018; Suh et al., 2022). Advances in delivery systems, such as DNA-free methods and improved vector designs, are being developed to address these issues. Furthermore, off-target effects and the potential for unintended genetic changes necessitate the development of more specific and efficient editing tools. Overcoming these challenges will be crucial for the broader application of genome editing in plant breeding.

### 6.4 Potential for global impact on forestry and agriculture

The potential global impact of genome editing technologies on forestry and agriculture is immense. By enabling the development of high-yielding, climate-resilient crops, genome editing can significantly contribute to food security and sustainable agriculture (Nerkar et al., 2022). The ability to precisely modify genes associated with disease resistance, stress tolerance, and other agronomic traits can lead to the creation of crops that are better suited to withstand the challenges posed by global climate change (Yin and Qiu, 2019). Additionally, the application of these technologies in forestry can enhance the growth and resilience of tree species, contributing to sustainable forest management and conservation efforts (Chen et al., 2019). As these technologies continue to evolve, their integration into breeding programs worldwide holds the promise of transforming agricultural and forestry practices, leading to more productive and resilient ecosystems.

## 7 Concluding Remarks

The advent of precision genome editing technologies, particularly CRISPR/Cas systems, base editors, and prime editors, has revolutionized the field of tree breeding. These tools enable precise modifications at specific genomic loci, which is a significant advancement over traditional breeding methods that rely on random mutagenesis and selection. Base editing and prime editing, in particular, have shown promise in introducing single-base changes without the need for double-stranded breaks, thereby increasing the efficiency and accuracy of genome editing in plants. These technologies have been successfully applied to improve various agronomic traits, including disease resistance, stress tolerance, and yield enhancement.

Genome editing holds transformative potential for tree breeding by enabling the rapid and precise introduction of desirable traits. This can significantly shorten the breeding cycle, which is particularly beneficial for trees that have long generation times. The ability to introduce specific genetic changes without incorporating foreign DNA

also addresses regulatory and public acceptance issues associated with genetically modified organisms (GMOs). Furthermore, multiplex genome-editing technologies allow for the simultaneous modification of multiple genes, thereby facilitating the development of trees with complex trait improvements. These advancements are expected to lead to the creation of tree varieties that are more resilient to climate change, pests, and diseases, thereby contributing to sustainable forestry and agriculture.

Despite the significant advancements, there are still challenges that need to be addressed to fully realize the potential of genome editing in tree breeding. These include improving the efficiency and specificity of editing tools, developing better delivery systems, and understanding the long-term effects of genome edits. Continued research is essential to overcome these challenges and to refine the technologies for broader applications. Additionally, collaboration among researchers, breeders, policymakers, and industry stakeholders is crucial to ensure the responsible development and deployment of genome-edited trees. Such collaborative efforts will help in addressing regulatory hurdles, public concerns, and ethical considerations, thereby paving the way for the widespread adoption of precision genome editing in tree breeding.

By harnessing the power of precision genome editing, we can usher in a new era of tree breeding that is more efficient, precise, and sustainable. Continued innovation and collaboration will be key to unlocking the full potential of these revolutionary technologies.

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## Conflict of Interest Disclosure

The author affirms that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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