



The Development of Forest Genetic Breeding and the Application of Genome Selection and CRISPR/Cas9 in Forest Breeding

Ye Zhao ^(D), Yanting Tian, Yuhan Sun *^(D) and Yun Li *^(D)

Engineering Technology Research Center of Black Locust of National Forestry and Grassland Administration, National Engineering Research Center of Tree Breeding and Ecological Restoration, Key Laboratory of Genetics and Breeding in Forest Trees and Ornamental Plants of Ministry of Education, College of Biological Sciences and Technology, Beijing Forestry University, Beijing 100083, China

* Correspondence: sunyuhan@bjfu.edu.cn (Y.S.); yunli@bjfu.edu.cn (Y.L.)

Abstract: With the birth of classical genetics, forest genetic breeding has laid a foundation in the formation of the basic theories of population genetics, quantitative genetics, cytogenetics, and molecular genetics. Driven by the rapid growth of social demand for wood and other forest products, modern genetics, biotechnology, biostatistics, crop and animal husbandry breeding theories, and technical achievements have been continuously introduced for innovation, thus forming a close combination of genetic basic research and breeding practice. Forest tree breeding research in the world has a history of more than 200 years. By the middle of the 20th century, the forest tree genetic breeding system was gradually formed. After entering the 21st century, the in-depth development stage of molecular design breeding was opened. With the continuous improvement of traditional genetic breeding methods, emerging modern bioengineering technology has also continuously promoted the development of forest genetic breeding. This study mainly summarizes the research history of forest tree genetics and breeding, as well as discusses the application of modern bioengineering technology represented by genome selection and gene editing in forest tree breeding, so as to provide better reference for forest tree breeding research.

Keywords: forest genetic breeding; gene selection; CRISPR/Cas9

1. Introduction

Based on genetics, forest genetic breeding is to study the breeding and cultivation of new forest varieties, and to explore the theory and method of forest reproduction. Forest genetic research in the world has a history of more than 200 years [1-3]. It has experienced three stages: birth and foundation stage, formation stage, and further development stage (Figure 1). At present, it has gradually formed a mature system based on traditional breeding methods and supplemented by modern molecular biology techniques. Since the birth of forest genetic breeding, many excellent varieties have been cultivated through traditional breeding methods, which has become an important part of forest breeding history. However, traditional breeding methods have the disadvantages of long cycle, poor predictability, and low efficiency. The contradiction between the demand for rapid directional breeding of new varieties and the bottleneck effect of traditional breeding was increasingly apparent. With the development of biological technology, new breeding theories and methods are constantly emerging. Modern forest breeding technology represented by molecular breeding has greatly promoted the process of directional breeding of new forest varieties. Through modern forest tree breeding technology systems such as genome selection and gene editing, the process of forest tree genetic improvement can be accelerated, efficient forest tree breeding can be realized, and the innovation ability of forest tree seed industry can be improved.



Citation: Zhao, Y.; Tian, Y.; Sun, Y.; Li, Y. The Development of Forest Genetic Breeding and the Application of Genome Selection and CRISPR/Cas9 in Forest Breeding. *Forests* **2022**, *13*, 2116. https://doi.org/10.3390/ f13122116

Academic Editor: Jorge Manuel P.L. Canhoto

Received: 19 November 2022 Accepted: 8 December 2022 Published: 10 December 2022

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/).



Figure 1. Development stages of forest genetic breeding: birth and foundation stage (1821–1950), formation stage (1950–2000), and further development stage (2000–present).

2. Birth and Foundation of Forest Genetic Breeding

Although the practice of forest genetic breeding has a long history, modern forest genetic breeding research began to appear in the 19th century. In 1821, De Vilmorin studied the differences in growth, stem form, needles, buds and cones of different provenances of *Pinus sylvestris* in Paris, which became the beginning of modern forest genetic breeding [1]. In 1892, the International Union of Forest Research Organizations (IUFRO), established in Germany, assigned forest genetic breeding to the Department of Physiology and Genetics, and formulated the international provenance test plan for major tree species at the first meeting, leading the development of forest genetic breeding.

After entering the 20th century, with the sharp increase in demand for wood, forest resources cultivation and utilization of some European industrialized countries began to pay attention to provenance test. In 1907, IUFRO organized the first international provenance trial of *Pinus sylvestris* in Germany, Sweden, Austria, Switzerland, and other countries, and demonstrated that there were geographical provenance variations in tree growth, morphology, and adaptability, and that trait variations were continuous and heritable; the concepts of continuous gradient variation and gradient group were further proposed [2–5]. Since then, IUFRO organized the second international provenance trial project including *Pinus sylvestris* and *Picea abies* in 1938, and further incorporated *Larix decidua* into the provenance trial plan in 1944 [5]. Several provenance experiments have prompted the combination of genetic theory research and forest tree breeding practice. After decades of efforts, the main afforestation tree species in foreign countries, including those with small natural distribution areas, have been subjected to provenance tests.

The construction of seed orchard also gradually began. In 1787, German scientist F.A.L. von Burgsdorf proposed to construct seed orchards through asexual reproduction.

To increase the quinine content of cinchona trees, the Dutch first established the *Cinchona calisaya* seed orchard in Java in 1880 [6]. Since then, Sweden, Finland, Denmark, Norway, and other Nordic countries have also built a number of *Scots pine, Norway spruce, Larix decidua*, and other seed orchards to promote the development of local plantations [7,8].

Hybridization was an active field of plant breeding in the 19th century. German scientist Klotzch first tested the hybridization between *Pinus sylvestris* and *Pinus nigra* Arn. in 1845. In 1912, Henry carried out interspecific hybridization of poplar (*Populus* spp.), oak (*Quercus* spp.), and other tree species, and selected fast-growing and adaptable poplar (*P.generosa*), representing the rise of hybrid breeding. Since then, the United States, the Soviet Union, Italy, Germany, Japan, and other countries have carried out large-scale hybrid experiments of *Populus*, *Quercus*, *Salix*, *Betula*, *Larix*, *Robinia pseudoacacia*, and *Cryptomeria japonica* [9–12]. Taking poplar hybridization as an example, in 1929, Jacometti used *P. canadensis* and *P. deltoides* angulata 'Carolin' to breed 'I-214' poplar ($P. \times$ canadensis 'I-214'), which has been widely introduced around the world for its fast growth and strong adaptability [13]. In 1945, the hybridization experiment between *P. hopeiensis* and *P. tomentosa* started the journey of forest tree hybridization in China [14]. The discovery of triploid black poplar is the starting point of forest tree polyploid breeding in 1935 [15].

3. Forming Stage of Forest Genetic Breeding

In the 1950s, due to the sharp increase in wood consumption, forest land area was shrinking, and problems such as increasing the unit area of wood production became urgent, which greatly promoted the development of forest genetic breeding. In addition, the gradual development of biological technology, molecular markers, genetic engineering, and other biological techniques began to be widely used in forest genetic breeding. In order to meet the demand for wood, Australia, New Zealand, and other countries began to introduce pine trees. Since then, many countries have performed large-scale introduction, *Eucalyptus* spp., *Populus nigra, Populus deltoides, Pinus radiata, Pinus elliottii*, and other tree species, which have gradually become international afforestation tree species [16–19].

Seed orchards have been developed since the 1950s and became popular around the world in the 1960s. Nearly 90 seed orchards have been established in about 50 countries on five continents, involving *Pinus radiata*, *Picea abies*, *Rhus typhina* L., *Cunninghamia lanceolata*, and other tree species, but most of them were coniferous species; thus, countries around the world began to change from the main way of afforestation from relying on seed reproduction to seed orchards [20,21]. For example, in the United States, through the use of preferred genetic testing seed orchard technology, by 1991, a total of about 4000 hm² seed orchards had been built, gradually developing from primary seed orchards, thinning seed orchards, 1.5th- and second-generation seed orchards to third-generation seed orchards [22]. A large number of theoretical and technical achievements of seed orchards were reported in terms of breeding strategy, clone arrangement, pollen dispersal law, grafting technique, tree management, flowering and fruiting promotion, indirect selection, and pest control [23–25]. Forest breeding and seed orchard construction also began to shift to an enterprise-led approach [18]. China began to build Chinese fir clone seed orchards in 1964, and then began to receive the attention of the forestry production department; accordingly, seed orchard construction has rapidly developed. By the end of 1997, the area of seed orchards in mainland China reached 15,420 hm², with the construction of more than 40 kinds of tree species, but most of the primary seed orchards were established using 1.5th-generation seed orchard, a few species were built using second-generation seed orchard, and individual tree species were build using third-generation seed orchard [6].

Hybrid breeding was still popular at this stage, and a variety of heterosis tree species were successfully cultivated, among which *Populus, Eucalyptus, Pinus,* and *Larix* achieved remarkable results. *E. grandis* \times *E.urophylla*, derived from Aracruz, Brazil, grows faster, germinates more vigorously, and is more resistant to canker disease [6]. *E. grandis* \times *E. camal-dulensis*, bred in South Africa, shows a significantly higher growth rate, drought resistance, and papermaking ability than the hybrid's parents [26]. Since the 1950s, Germany, Bel-

gium, Greece, Asia, Japan, and South Korea have implemented a large number of pine intergeneric hybridization studies, leading to the cultivation of *P. rigida* Mill × *P. taeda* L., *P. taeda* L. × *P. banksiana* Lamb., *P. sylvestris* L. × *P. nigra* Arn., and *P. thunbergii* Parl. × *P. massoniana* Lamb. The hybrid of *L. decidua* Mill. × *L. kaempferi* Carr. cultivated in Germany, has higher growth than its parents [6]. During this period, China performed extensive hybridization studies and cultivated a number of hybrid tree species. By the 1970s, China had cultivated a number of fast-growing, high-quality, disease-resistant poplar hybrid varieties, with the clones of *P. euramericana* CL. 'Zhonglin46' and *P. euramericana* CL. 'Zhonglin Sanbei 1' being widely used throughout the country [27]. The hybridization of *Eucalyptus* began in the 1960s. Although it developed slowly in the early stage, cross-breeding was gradually carried out on the basis of introduction and provenance experiments, with *E. grandis* and *E. urophylla* showing the best results [28–30]. The cross-breeding of *Pinus* also began in the 1960s, and the hybrid varieties obtained had higher economic benefits [6].

In the 1950s–1970s, forest ploidy breeding was widely investigated, and a series of haploid, triploid, and tetraploid varieties were obtained in Populus, Betula, Robinia pseudoacacia, Morus, and Hevea brasiliensis [31–35]. However, due to the limitations of theory and technical methods, there has been no significant breakthrough in ploidy breeding, with only polyploid varieties such as Morus and Robinia pseudoacacia and hybrid triploid varieties such as *P. tremula* L. \times *P. tremuloides* being applied in production. In the 1990s, quite a few triploid *P. tomentosa* varieties with fast growth, long fibers, and low lignin content were successfully selected by backcrossing the natural 2n pollen of *P. tomentosa* with *P. tomentosa* \times *P. bolleana*, which caused an upsurge in polyploid breeding [36–38]. Haploidy by anther culture was first achieved in *Datura stramonium* in 1964 [39]. Owing to the long reproductive cycle of forest trees, the physiological status of donor plants was greatly affected by the temperature and precipitation of the year, which in turn affected anther culture, resulting in poor repeatability of the experiment, seriously limiting the application and development of anther culture in forest trees. The study of forest haploid breeding has decreased rapidly since the 1990s, remaining in a semi-stagnant state for a long time.

Since the 1960s, the demands of wood pulp papermaking and other forest industries have surged; thus, countries began to focus on clone breeding. With the progress of modern biology, plant growth regulators and all-optical spray seedling technology have been widely used, such that the rooting rate of cutting seedlings has been significantly improved, with even coniferous tree species such as *P. abies* and *P. radiata* D. Don also achieving large-scale cutting propagation [40]. Tissue culture technology has been applied to forest tree asexual reproduction, and more than 200 kinds of trees from more than 30 families have obtained complete plants through tissue or organ culture. Among them, excellent varieties of *Populus* and *Eucalyptus* have achieved large-scale asexual reproduction by tissue culture [41]. Somatic embryo induction technology has also made a breakthrough in conifers, becoming an effective approach for the genetic improvement of tree species which can only reproduce via seeds [42]. *P. radiata* D. Don, *P. abies* (L.) Karst., *P. taeda* L., *Pseudotsuga menziesii* (Mirb.) Franco, and other tree species were introduced to large-scale afforestation applications through somatic embryo reproduction [43].

4. In-Depth Development of Forest Genetic Breeding

With the development of genome sequencing technology, forest genetic breeding research has entered the post-genome era. Since the first publication of the *P. trichocarpa* genome in 2006 [44], nearly 50 forest genomes have been published, namely, *Norway spruce* [45], *Phyllostachys heterocycla* [46], *E. grandis* [47], *B. pendula* [48], *Eucommia ul-moides* [49], *Liriodendron* [50], Chinese pine [51], and others [52–67]. Organelle genome sequencing represented by the mitochondrial genome and chloroplast genome has also developed rapidly and is widely used in forest trees [68–82]. With the development of single-cell sequencing technology, this technology has been successfully applied to reveal the intracellular dynamics of single cells in forest trees [83–88]. With the reduction in cost

and the continuous improvement of technology, single-cell sequencing still has broad application prospects in forest trees. On this basis, combined with the results of transcriptomics, metabolomics, proteomics, and degradation, massive function genes regulating important traits have been mapped and cloned, and the genetic regulation mechanisms of some important traits such as growth, development, and stress resistance have been analyzed from different levels of transcriptional regulation and post-transcriptional regulation [89–97]. In addition, quantitative trait locus (QTL) mapping [98–104], genome-wide association study (GWAS) [105–112], marker-assisted selection (MAS) [113–118], genomic selection or genome-wide selection (GS), and other techniques have been widely used to analyze the difference of forest traits [119,120].

Transgenic studies became a research trend at this stage; however, limited by the establishment of the transgenic system, only a few species such as *Populus*, *Pinus*, and *Eucalyptus* were successfully implemented to obtain a transgenic forest [121–127]. Genetic engineering is controversial because of its potential harm to the environment, and the longterm stability of transgenic trees remains to be studied. However, no effect of exogenous genes on the biodiversity of arthropods or soil bacteria has been found in field safety tests on transgenic trees [128–133]. China is the only country that has commercialized genetically modified poplar species (*Populus nigra* lines with Bt and *Populus* \times *aldatomentosa* Cl.741 with BtCry1Ac and API), causing widespread concern in the world [134]. Strict transgenic plant safety regulatory policies and measures temporarily limit the application of transgenic varieties. Transgenic forests are still in the growth and development stage, with further research on pest resistance and stress resistance mechanisms required before actual production. The development of gene editing technology has solved people's concerns about the safety of transgenic plants, and the CRISPR/Cas9 system has shown strong fixed-point editing capabilities in the field of gene editing [135,136]. In 2015, researchers from the University of Georgia used Cas9 to successfully knock out lignin synthesis-related enzyme genes in *P. tomentosa*, the first successful application of the CRISPR/Cas system to edit offspring in woody plants [137].

At present, ploidy breeding is also valued, with triploid breeding results being particularly prominent. *P. abies, Thuja plicata, Cryptomeria japonica, Encephalartos hildebrandtii, Ginkgo biloba, Morus alba* L., *Toxicodendron vernicifluum* (Stokes) F. A. Barkl., *Acacia dealbata, Salix, P. deltoides, P. alba, P. balsamifera, P. tomentosa,* and other natural polyploids have been detected [37,138–145]. Triploids of *Populus, Salix, Betula, Acacia auriculiformis, Morus,* and others have also been obtained by hybridization, from which new varieties were selected for production [37,146–148]. In addition, triploids obtained by chromosome doubling of male and female gametes were successfully reported in *P. tremula* L., *P. tremuloides, P. deltoides* Marshall., *P. balsamifera, P. alba* L., *P. tomentosa* × *P. bolleana, P. alba* × *P. glandulosa, P. tomentosa, P. adenopoda, P. canescens, Morus alba, Eucommia ulmoides,* and *Eucalyptus* [33,149–158]. Triploid angiosperms tend to have fast-growing characteristics, but most of the triploid gymnosperms grow slowly and have poor fertility. In addition, forest triploids also have the genetic characteristics of huge cells and organs, significantly increased secondary metabolites, and enhanced resistance [141].

5. Application of Genome Selection in Forest Genetic Breeding

Genome-wide selection (GS) is a new method for breeding selection using high-density molecular markers, which was first proposed by Meuwissen et al. [159,160]. By measuring a large number of molecular markers across the whole genome, GS can estimate the effect values of different chromosome fragments or single markers, and then accumulate the chromosome fragments or all marker effect values in the whole genome to obtain the genomic estimated breeding value (GEBV). The individual breeding value can be estimated by combining phenotypic and marker information, and early individual prediction and selection can be made according to the breeding value to shorten the generation interval, accelerate the breeding process, improve the selection accuracy, and save costs [161]. After constructing two populations, i.e., the training population (TP) and candidate popula-

tion/testing population, the effect value of each marker can be estimated on the basis of the phenotype and genotype data of the TP, and a prediction model of genotype and phenotype can be established. Then, the GEBV can be estimated using the known genotype data and the SNP effect estimates of individuals in the candidate population. Finally, the reserved individuals can be selected from the candidate groups according to the GEBV ranking. The theoretical hypothesis is that, in the high-density SNP markers distributed throughout the genome, at least one SNP can be in linkage disequilibrium (LD) with the quantitative trait locus (QTL) affecting the target trait, such that the effect of each QTL can be reflected by an SNP [162]. At present, the commonly used GS models include rrBLUP [163], synbreed [164], GBLUP [165], BGLR [166], GVCBLUP [167], GAPIT [168], sommer [169], BLUPGA [170], and Bayes Alphabet [171]. It is necessary to design breeding programs according to the actual needs and construct corresponding GS models for specific groups and target traits.

The research on forest tree genome selection has mainly been based on perennial cross-pollinated tree species with a long growth cycle and high heterozygosity. At present, genome selection research has been carried out in *Picea*, *Pinus*, *Populus*, *Hevea*, and *Eucalyptus* (Table 1). The application of genome selection in forest trees is helpful to shorten the breeding cycle, improve the selection efficiency, and accelerate the genetic improvement process. Wong and Bernardo [172] systematically compared phenotypic selection, MAS, and GS through *Elaeis guineensis* simulation data and found that GS had better selectivity and could still obtain certain genetic gain in breeding populations with a long generation interval and small sample size. In addition, genome selection has the advantages of low cost, high accuracy, high selection efficiency, and more genetic variation information in forest tree breeding [173,174].

Genus	Species	Reference
Elaeis	E. guineensis E. oleifera	[175,176] [177]
Eucalyptus	E. grandis × E. urophylla E. pellita F. Muell. E. robusta Sm. E. benthamii Maiden & Cambage. E. nitens (H.Deane & Maiden) Maiden. E. urophylla × E. grandis E. grandis E. globulus Labill. E. dunni Maiden E. cladocalyx F. Muell. E. camaldulensis E. grandis E. grandis E. polybractea	$\begin{bmatrix} 178-181 \\ [182,183] \\ [184] \\ [182] \\ [185,186] \\ [178] \\ [187,188] \\ [187,188] \\ [189,190] \\ [191] \\ [192] \\ [193] \\ [47] \\ [170] \end{bmatrix}$
Hevea	H. brasiliensis	[55,194–197]
Picea	P. abies P. glauca P. sitchensis P. mariana (Mill.) Britton.	[198] [199–202] [203] [198,204,205]
Pinus	<i>P. pinaster</i> <i>P. taeda</i> <i>P. contorta</i> Douglas ex Loudon <i>P. radiata</i> D. Don <i>P. sylvestris</i> Thunb.	[206] [207–209] [210] [186,211] [212]
Populus	P. deltoides W. Bartram ex Marshall P. trichocarpa P. euphratica P. nigra L	[213] [44] [214] [215]
Castanea	C. dentata	[216]
Pseudotsuga	P. menziesii (Mirb.) Franco	[217]

Table 1. Application of GS in woody plants.

Although forest genome selection has achieved certain results, compared with crops, development has been slow with low accuracy, limited by many factors. Reference genome quality is a prerequisite for GS to be applied to the genetic improvement of target species. However, the genome quality of forest tree species is generally lower than that of crops, which limits the application of GS in forest tree genetic improvement. Moreover, forest trees, especially coniferous trees, have larger genomes, leading to a significant increase in GS costs [218]. The prediction model can affect the accuracy of genome prediction; however, currently developed statistical models and analytical tools struggle to meet the application requirements of forest tree genome selection. Forest tree species generally have the characteristics of a long generation time, long juvenile phase, and giant plant size, which makes it difficult to apply forest tree genome selection in multigeneration families for breeding [219]. The genetic relationship between the reference population and the candidate population used to construct the genomic selection model also affects the accuracy of the genomic breeding estimates to some extent. A closer genetic relationship between two populations results in more accurate genomic breeding estimates [220-224]. Trees have complex target traits and heritability, and the heritability of growth traits and wood traits changes with the increase of tree age, resulting in low prediction accuracy [225–227]. In addition, factors such as marker density, population structure, trait heritability, population size and relationship, and the number and distribution of target trait loci also affect the accuracy of tree genome selection [228]. These limitations of GS also affect its application in forest tree breeding. GS mainly considers additive effects, whereas dominant effects and interaction effects are not included in the breeding value estimation model. GS is currently mainly carried out in forest varieties, while, for forest hybrid varieties, GS prediction accuracy is reduced. The prediction effect of individual breeding value with a distant genetic relationship among forest tree varieties is not ideal. The cost of obtaining GS genome information is high, but the results of multi-omics research have not been fully utilized. Compared with the sparse matrix of traditional BLUP, GS needs to use the dense matrix calculated using genomic information to estimate the parameters of the mixed model and calculate the model, which is more complicated.

At present, GS technology has been widely used in the genetic improvement of crops and other plants. Although some achievements have been made in forest breeding, it still has great potential. With the continuous development of genome sequencing technology and the improvement of analysis platforms, the background data of genomics, phenomics, and genetics of forest trees are steadily improving, thereby providing strong technical support and data support for GS research of forest tree species. The gradually improved GS technology can also greatly promote the development of forest breeding. However, selective breeding of forest tree genomes still faces some challenges. Firstly, genome quality is the basis for GS research. However, the quality of genome assembly of forest tree species is generally low; thus, improving the accuracy and quality of the reference genome remains an important condition for high-quality forest GS research. Secondly, choosing a reasonable statistical model is necessary for GS research. The selection of statistical models should fully consider the characteristics of target tree species and target traits. The computational efficiency and accuracy of statistical models ensure the accuracy of GS research. The perennial attribute makes the target trait data of forest tree species longitudinal, and GS statistical models and analysis software with the ability to process longitudinal trait data are still needed. Thirdly, multi-trait composite selection is needed forest GS research. At present, the study of forest GS focuses on the estimation of the genomic breeding value of a single trait, but the cultivation of new varieties with multiple dominant traits is a necessity for forest genetic improvement. Fourthly, the emergence of new technologies has been the driving force of forest GS research. CRISPR/Cas9 technology can be used not only for genome editing, but also for identifying precise locations in the genome to induce mitotic recombination. The combination of GS and genome editing (GE) can accelerate forest tree breeding. With the continuous development of pan-genome genotyping and interpolation

techniques, the development of structural variations or special markers of subpopulations can promote the wide application of GS in forest tree breeding.

6. Application of CRISPR/Cas9 Technology in Forest Tree Breeding

The CRISPR/Cas9 system is currently recognized as the most promising gene editing technology. The Cas9 protein binds to the artificially designed sgRNA to form an sgRNA-Cas9 protein complex and binds to a specific nucleotide sequence under its guidance. After sgRNA binds to Cas9 protein and targets a specific genomic site, Cas9 is cleaved to produce double-strand breaks (DSBs), which are repaired by cell-autonomous nonhomologous end joining (NHEJ) or homology-directed repair (HR), resulting in base insertion or deletion at the target site, thus inactivating gene function [136]. Compared with zinc finger nucleases (ZFNs) and transcription activator-like effector nucleases (TALENs), the CRISPR/Cas9 system has a simple design process, convenient operation, and high gene editing efficiency, and it has played an important role in the precision breeding of major food and economic crops. The CRISPR/Cas9 system has been applied in a variety of plants following success in gene targeting experiments in Arabidopsis thaliana, rice (Oryza sativa L.) and other plants. CRISPR/Cas9 system has good application prospects in improving crop yield, improving crop quality, and cultivating new varieties with disease resistance and stress resistance [229–232]. Forest trees have the biological characteristics of a long growth cycle, high genetic heterozygosity, and complex genome ploidy. Immature genetic transformation systems also lead to a limitation of CRISPR/Cas9 in forest tree genetic improvement. At present, CRISPR/Cas9 has been successfully applied to only a few forest species (Table 2), such as Populus, Parasponia andersonii, Jatropha curcas, Hevea brasiliensis, and Citrus. Citrus sinensis (L.) Osbeck was the first woody plant to undergo gene editing using CRISPR/Cas9. Jia and Wang used Xanthomonas citri subsp.-promoted Agroinfiltration for the CsPDS in Citrus sinensis (L.) Osbeck and confirmed the feasibility of the system in *Citrus sinensis* (L.) Osbeck for the first time in detached leaves, but they did not obtain complete gene-edited plants [233]. Subsequently, several research teams have been committed to improving transformation methods and gene editing efficiency, and gene editing lines capable of stable inheritance have been obtained in C. sinensis Osbeck [234], Pon*cirus trifoliate* L. Raf. × *C. sinensis* L. Osb. [235] and *C. paradisi* [236]. Poplar is not only an important timber species and model tree species for genetic research of woody plants, but also the most successful tree species for CRISPR/Cas9 application. In 2015, Tsai's team from the University of Georgia in the United States successfully edited the lignin synthesisrelated enzyme gene 4-coumarate coenzyme A ligase genes 4CL1 and 4CL2 in the hybrid *P. tremula* \times *P. alba*, opening the door for poplar gene editing [237]. In the same year, a team led by Keming Luo from Southwest University of China successfully knocked out the phytoene desaturase gene (PDS) in *P. tomentosa* Carr. to obtain albino poplar material [238]. Since then, CRISPR/Cas9 has been widely used in the genetic improvement of poplar and has been widely used in the analysis of poplar growth and development, abiotic stress response, and biotic stress response (Table 2). Cassava (Manihot esculenta) is one of the important edible plants in the tropics and one of the main raw materials for industrial flour. Odipio et al. [239] first established the CRISPR/Cas9 gene editing system in cassava for the *MePDS* gene and obtained independent transgenic plants. Since then, CRISPR/Cas9 has also been used to breed cassava varieties resistant to Cassava brown streak virus (CBSV) and African cassava mosaic virus (ACMV) [240]. Jatropha (Jatropha curcas) seeds can be refined into biodiesel, which is a new source of biomass energy. JcCYP735, a rate-limiting enzyme gene for cytokinin synthesis in Jatropha, was edited by CRISPR/Cas, and the mutant showed plant dwarfing [241]. Hevea brasiliensis, Parasponia andersonii, and Dendrocalamus have also been used to establish perfect CRISPR/Cas9 systems [242-246].

Genus	Species	Genes	Phenotype	Reference
Populus	P. canescens P. tremula	SOC1, FUL, NFP-like genes, TOZ19		[245]
	P. alba × P. glandulosa P. alba × P. glandulosa P. alba var. pyramidalis	PdNF-YB21 PagDA1 Hyg	Drought resistance Promoting xylem formation	[246] [247] [248]
	P. tomentosa	PtSGT1, PtSGT4	Regulating cellulose synthesis in cell wall	[249]
	P. tomentosa Carr. clone 741	PtoDET2	wall thickness	[250]
	P. tomentosa Carr. clone 741	MYB115	Reduced proanthocyanidin accumulation	[251]
	P. tomentosa Carr. clone 741	PtoMYB156	wall formation	[252]
	P. tomentosa Carr. clone 741	PtoMYB170 PtrMYB57	Regulates lignin deposition	[253]
	P. tomentosa Carr. clone 741 P. tomentosa Carr. clone 741	JMJ25	Increased anthocyanin accumulation	[255]
	P. tomentosa Carr. clone 741	MYB189	Regulating secondary cell-wall	[256]
	P. tomentosa Carr. clone 741 P. tomentosa Carr. clone 741 P. tremula × P. alba clone INRA 717-IB4	PtoDWF4 PtrWRKY18, PtrWRKY35 GNC	Reduced xylem development Melampsora resistance Drought stress tolerance	[257] [258] [259]
	<i>P. tremula</i> \times <i>P. alba</i> clone INRA 717-IB4	4CL1, 4CL2	Decreased lignin content, discoloration	[237]
	<i>P. tremula</i> \times <i>P. alba</i> clone INRA 717-IB4	LEAFY	of stems	[260]
	<i>P. tremula</i> \times <i>P. alba</i> clone INRA 717-IB4 <i>P. tremula</i> \times <i>P. alba</i> clone INRA 717-IB4	BRANCHED1, BRANCHED2 LHY2	Bud outgrowth control Photoperiodic growth	[261] [262]
	<i>P. tremula</i> \times <i>P. alba</i> clone INRA 717-IB4	PeuBELL15	and lignin	[263]
	<i>P. tremula</i> \times <i>P. alba</i> clone INRA 717-IB4	SHR MVP186 MVP138 MVP38	Affecting endoderm single-cell layer	[264]
	<i>P. tremula</i> \times <i>P. tremuloides</i> clone T89	BRC1	Photoperiodic control of seasonal growth	[266]
	<i>P. alba</i> <i>P. alba</i> yar, pyramidalis	PalCESA4 PalWRKY77	Affecting cellulose content	[267]
	P. alba x P. glandulosa	CSE	Increased lignocellulose biomass	[269]
	P. alba x P. glandulosa P tomentosa	PagPDS1 GATA19	Chlorophyll biosynthesis Photosynthesis and growth	[270]
	P. tomentosa	PtoLAC14	Integrated enhancement on biomass	[272]
	P. tomentosa Carr. clone 741	PtoPDS	enzymatic saccharification Chlorophyll biosynthesis	[238]
	P. tremula	ARR17	Regulating gender	[273]
	P. tremula \times P. alba P. tremula L. \times P. tremuloides Michx.	CSE1, CSE2 VNS	Reduced lignin and increased cellulose Secondary cell-wall thinning	[274]
	P. tremula \times P. alba	PovSAP	Impaired growth, complete sterility with	[276]
	P. tremula \times P. alba	PtaSUT4	no initiation of inflorescences Orchestration of ROS, antioxidant, starch utilization and RWC dynamics	[277]
	<i>P.tremula</i> \times <i>P. tremuloides</i>	FT1, FT2	Yearly growth cycle	[278]
	P.tremula × P. tremuloides P. trichocarna	PGM PtrHSFB3-1. PtrMYB092	Starch biosynthesis Reduced lignin and increased cellulose	[279]
	P. trichocarpa	PtrADA2b-3	Drought resistance	[281]
	P. trichocarpa P. trichocarpa	PtrMYB074, PtrWRKY19	Strong drought-tolerant	[282]
	P. trichocarpa	<i>PtrCesA4, PtrCes7A/B</i> or 8 <i>A/B</i>	Cellulose biosynthesis	[284]
	P. trichocarpa L.	PHBMT1	p-hydroxybenzoylated lignin structures	[285]
Citrus	C. sinensis cv. Valencia	CsPDS	Chlorophyll biosynthesis	[233]
	C. paradisi	CsLOB1	Canker resistance	[236,286]
Poncirus	P. trifoliate L. × C. sinensis L. Osb P. trifoliate L. × C. sinensis L. Osb	PDS Cs7g03360	Chlorophyll biosynthesis Leaf development	[235] [287]
Manihot	M. esculenta	MePDS	Chlorophyll biosynthesis	[239]
	M. esculenta cv. 60444 M. esculenta	nCBP-1, nCBP-2 AC2, AC3	Biotic stress response Biotic stress response	[288] [289]
Hevea	H. brasiliensis	FT, TFL1	Early flowering	[243]
Jatropha	J. curcas	JcCYP735A	Growth and flowering regulation	[241]
Parasponia	P. andersonii	PanHK4, PanEIN2, PanNSP1, PanNSP2	Nodule formation, layer activity, plant sex	[290]
Bambusa	B. oldhamii	PDS	Chlorophyll biosynthesis	[242]
Dendrocalamus	D. latiflorus Munro	DlmPSY1-A, DlmPSY1-B, DlmPSY1-C, GRG1	Whitening, increased plant height	[244]
Juglans	J. regia L.	JrPDS	Chlorophyll biosynthesis	[291]
Picea	P. glauca	DXS1	Albino somatic embryo (SE) plants	[292]
<i>Cryptomeria</i> Castanea	<i>C. japonica</i> <i>C. sativa</i> Mill	CjChlI PDS	Whitening Chlorophyll biosynthesis	[293] [294]
Eucalyptus	Eucalyptus	FT	No statistical difference in seedling vegetative growth rate or leaf morphology	[295]

 Table 2. Application of CRISPR/Cas system in woody plants.

Although CRISPR/Cas9 has achieved certain results in forest tree breeding, compared with crops, the application of CRISPR/Cas9 system in gene function research and variety

improvement of woody plants was is lagging behind, and most of these plants are still in the initial stage of gene editing system establishment. The preparation, efficient transformation. and regeneration of protoplasts for most forest species remains a technical problem. Therefore, the development of efficient protoplast transformation and regeneration systems plays an important role in the development of gene editing in trees. The selection of efficient editing targets relies on the existing plant sgRNA online database, which currently contains only a few woody plant genome information. The establishment of a public network platform for sgRNA design and detection of off-target effects for woody plants, and the collection of more varieties of genome data, especially the genome information of commonly used forest varieties, will be beneficial to increasing the application range of the CRISPR/Cas9 system. At present, research on the CRISPR/Cas9 system in forestry has mostly focused on economic forests and model plants, with relatively few studies on gymnosperms. Therefore, genome sequencing, CRISPR/Cas9 system optimization, and transformation system improvement in gymnosperms are essential. With the help of the CRISPR/Cas9 system, the literature has mainly focused on the role of target genes in growth and development, whereas research on environmental stress is still scarce. The CRISPR/Cas9 system requires Agrobacterium-mediated genetic transformation to obtain stable transgenic lines, but it is also accompanied by the insertion of exogenous DNA; hence, it is difficult to obtain noncontaminated gene editing plants via hybridization in the short term. Forest trees have a long growth cycle and juvenile period, with slow growth. The transgenic trees obtained using CRISPR/Cas9 systems have a large number of chimeras, and it is difficult to obtain homozygous tree varieties via hybridization technology in a short time. The off-target effects of CRISPR/Cas9 are common in forest trees; therefore, it is important to reduce their rate of occurrence. In addition, many new technologies derived from CRISPR/Cas9 system, such as CRISPR/Cpf1 system, targeted gene activation and inhibition, gene directional knock-in, and base editing technology (cytosine base editor and adenine base editor), are still very limited in woody plants; thus, broadening the application scope of these new technologies in trees will also become a future development direction.

7. Conclusions

After more than 200 years of development, modern forest genetic breeding has formed a complete system based on traditional breeding methods, supplemented by current biological techniques. The traditional breeding system based on hybrid breeding and seed orchard selection still occupies the dominant position in the breeding and production of forest varieties. The development of emerging biotechnology has greatly promoted the process of forest genetic breeding. It is still the development trend and emphasis of forestry genetics and breeding to select forestry varieties with high yield, high quality, strong resistance, and extensive influence before applying them to production. There are still many problems to be solved related to modern forest tree breeding basic theories or technical methods in guiding the rapid development of forest breeding. At present, popular varieties often have a single excellent trait, which cannot satisfy the needs of society. It is particularly important to cultivate excellent varieties that take into account yield and resistance. With global warming and the deterioration of the ecological environment, it is becoming more necessary to breed and cultivate new forest varieties with wide planting range, strong adaptability, and good tolerance through genetic breeding technology in harsh environments such as salinity and drought. With the development and continuous change of social needs, some forest varieties have aged and can no longer meet the needs of modern society. Therefore, it is crucial to continue to upgrade and cultivate tree species with high economic benefits, in line with the needs of social development. In addition, we should pay attention to the collection, protection, evaluation, and utilization of gene resources, strengthen the evaluation and management of collected and preserved gene resources, deepen the analysis of genetic information of main forest germplasm resources, and construct a database of important traits of main forest germplasm resources. Additional goals include strengthening the exploration of forest tree natural polyploid germplasm

resources, developing new polyploid induction technology, especially for fast-growing and precious tree species, further improving the polyploid induction rate, comprehensively utilizing heterosis and ploidy advantage, and achieving rapid improvement of forest tree multi-objective traits. More genetic transformation systems of forest varieties should be established, and biotechnologies such as transgenic and gene editing should be used to rapidly integrate superior traits and shorten the breeding cycle. Breeding methods should be continuously innovated, new breeding methods in animal and crop breeding should be actively absorbed, and forest tree breeding methods should be enriched in order to increase the diversity of forest tree breeding.

Author Contributions: Design, Y.S. and Y.L.; writing—original draft preparation, Y.Z. and Y.T.; writing—review and editing, Y.S. and Y.L. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the National Natural Science Foundation of China (31971675) and the Major National Science and Technology Projects (2018ZX08020002-003-002).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Informed consent was obtained from all subjects involved in the study.

Data Availability Statement: Not applicable.

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

References

- 1. Langlet, O. Two hundred years genecology. Taxon 1971, 20, 653–721. [CrossRef]
- 2. Adams, W.T. Forest Genetics; John Wiley & Sons: New York, NY, USA, 1984.
- 3. Langlet, O. A cline or not a cline? A question of scots pine. *Silvae Genet.* **1959**, *8*, 13–22.
- 4. Huxley, J. Clines: An auxiliary taxonomic principle. Nature 1938, 142, 219-220. [CrossRef]
- 5. Veen, B. General remarks on provenance research in forestry. *Euphytica* **1954**, *3*, 89–96. [CrossRef]
- 6. Chen, X.Y.; Shen, X.H. Forest Breeding; Chinese Forestry Publishing House: Beijing, China, 2005.
- Lindgren, D.; Karlsson, B.; Andersson, B.; Prescher, F. The Swedish Seed Orchard Program for Scots pine and Norway spruce. In Proceedings of the Seed Orchard Conference, Umeå, Sweden, 26–28 September 2007; pp. 142–154.
- 8. Toda, R. A brief review and conclusions of the discussion on seed orchards. Silvae Genet. 1963, 13, 1–4.
- 9. Johnson, L.P.V. A descriptive list of natural and artificial interspecific hybrids in North American forest-tree genera. *Can. Med. Assoc. J.* **1929**, *21*, 441. [CrossRef]
- 10. Zobel, B.; Talbert, J. Applied Forest Tree Improvement; John Wiley & Sons: Hoboken, NJ, USA, 1984.
- 11. Du, C.; Teissier, E. Breeding strategies with poplars in Europe. For. Ecol. Manag. 1984, 8, 23–39. [CrossRef]
- 12. White, T.L.; Adams, W.T.; Neale, D.B. Forest Genetics; Cabi: Wallingford, UK, 2007.
- 13. Nilsson-Ehle, H.; Tidn, S.P. Production of forest trees with increased chromosome number and increased timber yield. *Sven. Papp Tidn* **1938**, *2*, 299–330.
- 14. Ye, P.Z.; Gao, Z.D.; Chen, Y.M.; Chen, J.; Wang, Z.R.; Chen, Y.W.; Wu, H.J.; Wu, S.P. Summary report on distant hybrid breeding experiment among poplar species. *J. Nanjing For. Univ. (Nat. Sci. Ed.)* **1959**, *2*, 25–42. [CrossRef]
- 15. Bergstr, M.I. On the progeny of diploid × triploid *Populus tremula*: With special reference to the occurrence of tetraploidy. *Hereditas* **1940**, *26*, 191–201. [CrossRef]
- 16. Wasshausen, L.D. Eucalypt Domestication and Breeding; Oxford University Press: Oxford, UK, 1996.
- 17. Peter, F. Growing exotic forests. For. Sci. 1988, 1, 252–253. [CrossRef]
- 18. Ruotsalainen, S. Increased forest production through forest tree breeding. Scand. J. For. Res. 2014, 29, 333–344. [CrossRef]
- 19. Balocchi, C.E. Realised versus operational gain: The role of propagation strategies. FRI Bull. 1997, 253–255.
- 20. Kleinschmit, J. A programme for large-scale cutting propagation of Norway spruce. N. Z. J. For. Sci. 1974, 4, 359–366.
- 21. Shen, X.H. Seed Orchard Technique; Beijing Science and Technology Press: Beijing, China, 1992.
- 22. Li, B.; Mckeand, S.; Weir, R. Tree improvement and sustainable forestry—Impact of two cycles of loblolly pine breeding in the USA. Int. J. For. Genet. 1999, 64, 229–234.
- 23. Williams, C.G. Accelerated short-term genetic testing for loblolly-pine families. Can. J. For. Res. 1988, 18, 1085–1089. [CrossRef]
- 24. Hasan, O.; Reid, J.B. Reid reduction of generation time in *Eucalyptus globulus*. *Plant Growth Regul.* **1995**, *17*, 53–60. [CrossRef]
- 25. Greenwood, M.S.; Adams, G.W.; Gillespie, M. Stimulation of flowering by grafted black spruce and white spruce: A comparative study of the effects of gibberellin A4/7, cultural treatments, and environment. *Can. J. For. Res.* **1991**, *21*, 395–400. [CrossRef]
- Gardner, R.A.W.; Little, K.M.; Arbuthnot, A. Wood and fibre productivity potential of promising new eucalypt species for coastal Zululand, South Africa. *Aust. For.* 2007, 70, 37–47. [CrossRef]
- 27. Xu, W.Y.; Huang, D.S.; Ma, C.G.; Tu, H.F.; Liu, Q.Z. Sexual hybridization of poplar. For. Sci. 1956, 2, 215–225.

- Potts, B.M.; Dungey, H.S. Interspecific hybridization of *Eucalyptus*: Key issues for breeders and geneticists. *New For.* 2004, 27, 115–138. [CrossRef]
- 29. Brisola, S.H. Demarco stem anatomical analysis of *Eucalyptus grandis*, *E. urophylla* and *E. grandis x urophylla*: Wood development and its industrial importance. *Sci. For.* **2011**, *39*, 317–330.
- 30. Denison, N.P.; Quaile, D.R. The applied clonal eucalypt programme in mondi forests. J. S. Afr. For. Assoc. 1987, 142, 60–67. [CrossRef]
- 31. Weisgerber, H. 25 years of forest tree breeding in Hesse. *Allg. Forstz.* **1980**, *66*, 665.
- 32. Suryanarayana, N. Cytomorphological studies in triploid mulberry evolved by diploidization of female gamete cells. *Cytologia* **1989**, *54*, 13–19. [CrossRef]
- 33. Mashkina, O.S. Method of obtaining diploid pollen of woody species. *Lesoved* 1989, 1, 19–25.
- 34. Einspahr, D.W. Production and utilization of triploid hybrid aspen. *Iowa State J. Res.* **1984**, *58*, 401–409.
- 35. Kang, X. Research progress and prospect of triploid breeding of forest trees. Sci. Sin. Vitae 2003, 25, 5. (In Chinese) [CrossRef]
- 36. Zhang, Z.Y.; Li, F.L. Studies on chromosome doubling and triploid breeding of white poplar (I)—The techniques of the pollen chromosome doubling. *J. Beijing For. Univ.* **1992**, *14*, 52–58.
- 37. Kang, X.Y. Research progress and prospect of triploid breeding of forest trees. Sci. Sin. Vitae 2020, 50, 136–143. (In Chinese) [CrossRef]
- 38. Zhu, Z.T.; Lin, H.B.; Kang, X.Y. Studies on allotriploid breeding of Populus tomentosa B301 clones. Sci. Silvae Sin. 1995, 31, 499–505.
- 39. Guha, S.; Maheshwari, S.C. In vitro production of embryos from anthers of Datura. Nature 1964, 204, 497. [CrossRef]
- 40. Talbert, C.B.; Ritchie, G.A.; Gupta, P. Conifer Vegetative Propagation: An Overview from a Commercialization Perspective; Springer: Berlin/Heidelberg, Germany, 1993.
- Jishen, S. The challenges to forestry biotechnology and tree breeding in the 21th century. *Rev. China Agric. Sci. Technol.* 2000, 24, 36–41. [CrossRef]
- Hakman, I.; Arnold, S.V. Plantlet regeneration through somatic embryogenesis in *Picea abies* (Norway Spruce). *J. Plant Physiol.* 1985, 121, 149–158. [CrossRef]
- Grossnickle, S.C.; Cyr, D.; Polonenko, D.R. Somatic embryogenesis tissue culture for the propagation of conifer seedlings: A technology comes of age. *Tree Plant. Notes* 1996, 47, 48–57.
- Tuskan, G.A.; Difazio, S.; Jansson, S.; Bohlmann, J.; Grigoriev, I.; Hellsten, U.; Putnam, N.; Ralph, S.; Rombauts, S.; Salamov, A. The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science* 2006, 313, 1596–1604. [CrossRef]
- 45. Nystedt, B.; Street, N.R.; Wetterbom, A.; Zuccolo, A.; Lin, Y.; Scofield, D.G.; Vezzi, F.; Delhomme, N.; Giacomello, S.; Alexeyenko, A. The Norway spruce genome sequence and conifer genome evolution. *Nature* **2013**, *497*, 579–584. [CrossRef]
- 46. Peng, Z.; Lu, Y.; Li, L.; Zhao, Q.; Feng, Q.; Gao, Z.; Lu, H.; Hu, T.; Yao, N.; Liu, K.; et al. The draft genome of the fast-growing non-timber forest species moso bamboo (*Phyllostachys heterocycla*). *Nat. Genet.* **2013**, 45, 456–461. [CrossRef]
- 47. Myburg, A.A.; Grattapaglia, D.; Tuskan, G.A.; Hellsten, U.; Hayes, R.D.; Grimwood, J.; Jenkins, J.; Lindquist, E.; Tice, H.; Bauer, D.; et al. The genome of *Eucalyptus grandis*. *Nature* **2014**, *510*, 356–362. [CrossRef]
- Salojärvi, J.; Smolander, O.; Nieminen, K.; Rajaraman, S.; Safronov, O.; Safdari, P.; Lamminmäki, A.; Immanen, J.; Lan, T.; Tanskanen, J. Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. *Nat. Genet.* 2017, 49, 904–912. [CrossRef] [PubMed]
- 49. Wuyun, T.N.; Wang, L.; Liu, H.; Wang, X.; Zhang, L.; Bennetzen, J.L.; Li, T.; Yang, L.; Liu, P.; Du, L. The hardy rubber tree genome provides insights into the evolution of polyisoprene biosynthesis. *Mol. Plant* **2018**, *3*, 429–442. [CrossRef]
- 50. Chen, J.; Hao, Z.; Guang, X.; Zhao, C.; Wang, P.; Xue, L.; Zhu, Q.; Yang, L.; Sheng, Y.; Zhou, Y. Liriodendron genome sheds light on angiosperm phylogeny and species–pair differentiation. *Nat. Plants* **2019**, *5*, 18–25. [CrossRef] [PubMed]
- 51. Niu, S.; Li, J.; Bo, W.; Yang, W.; Zuccolo, A.; Giacomello, S.; Chen, X.; Han, F.; Yang, J.; Song, Y. The Chinese pine genome and methylome unveil key features of conifer evolution. *Cell* **2022**, *185*, 204–217. [CrossRef] [PubMed]
- 52. Yang, Y.; Huang, L.; Xu, C.; Qi, L.; Wu, Z.; Li, J.; Chen, H.; Wu, Y.; Fu, T.; Zhu, H.; et al. Chromosome-scale genome assembly of areca palm (*Areca catechu*). *Mol. Ecol. Resour.* 2021, *21*, 2504–2519. [CrossRef] [PubMed]
- Song, E.; Park, S.; Kim, S. Primers for complete chloroplast genome sequencing in Magnolia. *Appl. Plant Sci.* 2019, 7, e11286. [CrossRef] [PubMed]
- 54. Xing, Y.; Liu, Y.; Zhang, Q.; Nie, X.; Sun, Y.; Zhang, Z.; Li, H.; Fang, K.; Wang, G.; Huang, H.; et al. Hybrid de novo genome assembly of Chinese chestnut (*Castanea mollissima*). *GigaScience* **2019**, *8*, giz112. [CrossRef]
- 55. Rahman, A.Y.; Usharraj, A.O.; Misra, B.B.; Thottathil, G.P.; Jayasekaran, K.; Feng, Y.; Hou, S.; Ong, S.Y.; Ng, F.L.; Lee, L.S.; et al. Draft genome sequence of the rubber tree *Hevea brasiliensis*. *BMC Genom.* **2013**, *14*, 75. [CrossRef]
- 56. Kui, L.; Majeed, A.; Dong, Y. Reference-grade Taxus genome unleashes its pharmacological potential. *Trends Plant Sci.* 2022, *1*, 10–12. [CrossRef]
- 57. Liu, W.; Guo, W.; Chen, S.; Xu, H.; Zhao, Y.; Chen, S.; You, X. A high-quality reference genome sequence and genetic transformation system of *Aralia elata*. *Front. Plant Sci.* 2022, *13*, 538. [CrossRef]
- 58. Ithnin, M.; Vu, W.T.; Shin, M.; Suryawanshi, V.; Sherbina, K.; Zolkafli, S.H.; Serdari, N.M.; Amiruddin, M.D.; Abdullah, N.; Mustaffa, S.; et al. Genomic diversity and genome-wide association analysis related to yield and fatty acid composition of wild American oil palm. *Plant Sci.* 2021, 304, 110731. [CrossRef]
- 59. Mishra, B.; Ulaszewski, B.; Meger, J.; Aury, J.; Bodénès, C.; Lesur-Kupin, I.; Pfenninger, M.; Da Silva, C.; Gupta, D.K.; Guichoux, E.; et al. A chromosome-level genome assembly of the European beech (*Fagus sylvatica*) reveals anomalies for organelle DNA integration, repeat content and distribution of SNPs. *Front. Genet.* 2022, *12*, 691058. [CrossRef] [PubMed]

- Mosca, E.; Cruz, F.; Gómez-Garrido, J.; Bianco, L.; Rellstab, C.; Brodbeck, S.; Csilléry, K.; Fady, B.; Fladung, M.; Fussi, B.; et al. A reference genome sequence for the European silver fir (*Abies alba* Mill.): A community-generated genomic resource. *G3 Genes Genomes Genet.* 2019, 9, 2039–2049. [CrossRef] [PubMed]
- 61. Ning, D.; Wu, T.; Xiao, L.; Ma, T.; Fang, W.; Dong, R.; Cao, F. Chromosomal-level assembly of Juglans sigillata genome using Nanopore, BioNano, and Hi-C analysis. *GigaScience* **2020**, *9*, giaa006. [CrossRef] [PubMed]
- Sowjanya, P.R.; Shilpa, P.; Patil, G.P.; Babu, D.K.; Sharma, J.; Sangnure, V.R.; Mundewadikar, D.M.; Natarajan, P.; Marathe, A.R.; Reddy, U.K.; et al. Reference quality genome sequence of Indian pomegranate cv. 'Bhagawa' (*Punica granatum* L.). *Front. Plant Sci.* 2022, 13, 2678. [CrossRef] [PubMed]
- 63. Zhang, J.; Yuan, H.; Li, Y.; Chen, Y.; Liu, G.; Ye, M.; Yu, C.; Lian, B.; Zhong, F.; Jiang, Y.; et al. Genome sequencing and phylogenetic analysis of allotetraploid *Salix matsudana* Koidz. *Hortic. Res.* **2020**, *7*, 201. [CrossRef]
- Babu, B.K.; Rani, K.L.M.; Sahu, S.; Mathur, R.K.; Kumar, P.N.; Ravichandran, G.; Anitha, P.; Bhagya, H.P. Development and validation of whole genome-wide and genic microsatellite markers in oil palm (*Elaeis guineensis* Jacq.): First microsatellite database (OpSatdb). Sci. Rep. 2019, 9, 1899. [CrossRef]
- Wang, L.; Lee, M.; Wan, Z.Y.; Ye, B.; Alfiko, Y.; Rahmadsyah, R.; Purwantomo, S.; Song, Z.; Suwanto, A.; Yue, G.H. Chromosomelevel reference genome provides insights into divergence and stress adaptation of the African oil palm. *Genom. Proteom. Bioinform.* 2022, *in press.* [CrossRef]
- Gagalova, K.K.; Warren, R.L.; Coombe, L.; Wong, J.; Nip, K.M.; Yuen, M.M.S.; Whitehill, J.G.A.; Celedon, J.M.; Ritland, C.; Taylor, G.A.; et al. Spruce giga-genomes: Structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. *Plant J.* 2022, 111, 1469–1485. [CrossRef]
- 67. Shen, T.; Qi, H.; Luan, X.; Xu, W.; Yu, F.; Zhong, Y.; Xu, M. The chromosome-level genome sequence of the camphor tree provides insights into *Lauraceae* evolution and terpene biosynthesis. *Plant Biotechnol. J.* **2022**, *20*, 244–246. [CrossRef]
- Park, J.; Kim, Y.; Xi, H.; Kwon, W.; Kwon, M. The complete chloroplast and mitochondrial genomes of Hyunsasi tree, *Populus alba* × *Populus glandulosa* (Salicaceae). *Mitochondr. DNA Part B Resour.* 2019, 4, 2521–2522. [CrossRef] [PubMed]
- 69. Liu, H.; Li, W.; Xie, X.; Zhang, X.; Sun, C.; Xu, J.; Lu, Y. The complete chloroplast genome of *Hemiptelea davidii* (Ulmaceae), the only species of the genus *Hemiptelea*. *Mitochondr*. *DNA Part B Resour*. **2019**, *4*, 229–230. [CrossRef]
- 70. Zhu, Z.; Li, X. The complete chloroplast genome sequence of *Podocarpus macrophyllus* (*Podocarpaceae*) and phylogenetic analysis. *Mitochondr. DNA Part B Resour.* 2022, 7, 1263–1264. [CrossRef] [PubMed]
- Ding, S.; Dong, X.; Yang, J.; Guo, C.; Cao, B.; Guo, Y.; Hu, G. Complete chloroplast genome of *Clethra fargesii* Franch., an original sympetalous plant from central China: Comparative analysis, adaptive evolution, and phylogenetic relationships. *Forests* 2021, 12, 441. [CrossRef]
- 72. Shao, Y.; Shi, Z.; Wang, Z.; Wang, W.; Chen, Y.; Wen, Q. The complete chloroplast genome of *Abies ernestii* Rehder (*Pinaceae*) and its phylogenetic implications. *Mitochondr. DNA Part B Resour.* **2022**, *7*, 1497–1503. [CrossRef]
- 73. Ren, R.; Li, X. Characterization of the complete chloroplast genome of *Salix linearistipularis* (Franch.) Hao 1936. *Mitochondr. DNA Part B Resour.* 2021, *6*, 2764–2766. [CrossRef]
- Kim, K.; Lee, S.C.; Yang, T.J. The complete chloroplast genome sequence of *Dendropanax morbifera* (Leveille). *Mitochondr. DNA* Part A 2016, 27, 2923–2924. [CrossRef]
- 75. Deng, X.; Jiang, Z.; Huang, J.; Zhang, X. Characterization of the complete chloroplast genome of sugar maple (*Acer saccharum*). *Mitochondr. DNA Part B Resour.* **2019**, *5*, 21–22. [CrossRef]
- 76. Zhuang, W.; Shu, X.; Zhang, M.; Wang, T.; Zhang, F.; Wang, N.; Wang, Z. Characterization of the complete chloroplast genome of *Populus deltoides* Zhonglin 2025. *Mitochondr. DNA Part B Resour.* **2020**, *5*, 3723–3724. [CrossRef]
- 77. Zhou, J.; Zhang, S.; Wang, J.; Shen, H.; Ai, B.; Gao, W.; Zhang, C.; Fei, Q.; Yuan, D.; Wu, Z.; et al. Chloroplast genomes in *Populus* (Salicaceae): Comparisons from an intensively sampled genus reveal dynamic patterns of evolution. *Sci. Rep.* 2021, *11*, 9471. [CrossRef]
- Liu, M.; Lu, J.; Li, Y.; Zhang, L. Complete chloroplast genome of *Engelhardtia fenzlii* (Juglandaceae). Mitochondr. DNA Part B Resour. 2021, 6, 288–289. [CrossRef] [PubMed]
- 79. Ma, Q.G.; Zhang, J.G.; Zhang, J.P. The complete chloroplast genome of Catalpa. *Mitochondr. DNA Part B* 2020, *5*, 1800–1801. [CrossRef]
- Zhang, G.; Wang, Z.; Yan, T. The complete chloroplast genome sequence of *Elaeocarpus decipiens* (*Elaeocarpaceae*). *Mitochondr. DNA* Part B Resour. 2021, 6, 3130–3131. [CrossRef] [PubMed]
- Jackman, S.D.; Warren, R.L.; Gibb, E.A.; Vandervalk, B.P.; Mohamadi, H.; Chu, J.; Raymond, A.; Pleasance, S.; Coope, R.; Wildung, M.R.; et al. Organellar genomes of white spruce (*Picea glauca*): Assembly and annotation. *Genome Biol. Evol.* 2016, *8*, 29–41. [CrossRef]
- 82. Zhang, R.; Yang, J.; Hu, H.; Xia, R.; Li, Y.; Su, J.; Li, Q.; Liu, Y.; Qin, L. A high level of chloroplast genome sequence variability in the *Sawtooth Oak* Quercus acutissima. *Int. J. Biol. Macromol.* **2020**, *152*, 340–348. [CrossRef]
- Conde, D.; Triozzi, P.M.; Pereira, W.J.; Schmidt, H.W.; Balmant, K.M.; Knaack, S.A.; Redondo-López, A.; Roy, S.; Dervinis, C.; Kirst, M. Single-nuclei transcriptome analysis of the shoot apex vascular system differentiation in *Populus*. *Development* 2022, 149, dev200632. [CrossRef]
- Turner, G.W.; Parrish, A.N.; Zager, J.J.; Fischedick, J.T.; Lange, B.M. Assessment of flux through oleoresin biosynthesis in epithelial cells of loblolly pine resin ducts. J. Exp. Bot. 2019, 70, 217–230. [CrossRef]

- 85. Li, H.; Dai, X.; Huang, X.; Xu, M.; Wang, Q.; Yan, X.; Sederoff, R.R.; Li, Q. Single-cell RNA sequencing reveals a high-resolution cell atlas of xylem in *Populus. J. Integr. Plant Biol.* **2021**, *63*, 1906–1921. [CrossRef]
- Xie, J.; Li, M.; Zeng, J.; Li, X.; Zhang, D. Single-cell RNA sequencing profiles of stem-differentiating xylem in poplar. *Plant Biotechnol. J.* 2022, 20, 417–419. [CrossRef]
- Wang, Q.; Wu, Y.; Peng, A.; Cui, J.; Zhao, M.; Pan, Y.; Zhang, M.; Tian, K.; Schwab, W.; Song, C. Single-cell transcriptome atlas reveals developmental trajectories and a novel metabolic pathway of catechin esters in tea leaves. *Plant Biotechnol. J.* 2022, 20, 2089–2106. [CrossRef]
- Tang, W.; Tang, A.Y. Biological significance of RNA-seq and single-cell genomic research in woody plants. J. For. Res. 2019, 30, 1555–1568. [CrossRef]
- Kim, M.; Bae, E.; Lee, H.; Ko, J. Current understanding of the genetics and molecular mechanisms regulating wood formation in plants. *Genes* 2022, 13, 1181. [CrossRef] [PubMed]
- 90. Sulis, D.B.; Wang, J.P. Regulation of lignin biosynthesis by post-translational protein modifications. *Front. Plant Sci.* **2020**, *11*, 914. [CrossRef]
- Mohamed, I.A.A.; Shalby, N.; El-Badri, A.M.; Batool, M.; Wang, C.; Wang, Z.; Salah, A.; Rady, M.M.; Jie, K.; Wang, B.; et al. RNA-seq analysis revealed key genes associated with salt tolerance in rapeseed germination through carbohydrate metabolism, hormone, and MAPK signaling pathways. *Ind. Crop. Prod.* 2022, 176, 114262. [CrossRef]
- Zhao, Y.; Xin, D.; Lu, W.; Zong, X.; Niu, Y.; Guo, X.; Ma, Y.; Qiang, W.; Su, H.; Zhang, S.; et al. PeMPK7 is induced in an ROS-dependent manner and confers poplar para-hydroxybenzoic acid stress resistance through the removal of ROS. *Ind. Crop. Prod.* 2022, *182*, 114861. [CrossRef]
- Rodrigues, A.M.; Miguel, C.; Chaves, I.; António, C. Mass spectrometry-based forest tree metabolomics. *Mass Spectrom. Rev.* 2021, 40, 126–157. [CrossRef]
- Hill, R.A.; Wong Bajracharya, J.; Anwar, S.; Coles, D.; Wang, M.; Lipzen, A.; Ng, V.; Grigoriev, I.V.; Martin, F.; Anderson, I.C.; et al. Abscisic acid supports colonization of *Eucalyptus grandis* roots by the mutualistic ectomycorrhizal fungus *Pisolithus microcarpus*. *New Phytol.* 2022, 233, 966–982. [CrossRef]
- 95. Vergara, A.; Haas, J.C.; Aro, T.; Stachula, P.; Street, N.R.; Hurry, V. Norway spruce deploys tissue-specific responses during acclimation to cold. *Plant Cell Environ.* **2022**, *45*, 427–445. [CrossRef]
- 96. Modesto, I.; Inácio, V.; Van de Peer, Y.; Miguel, C.M. MicroRNA-mediated post-transcriptional regulation of *Pinus pinaster* response and resistance to pinewood nematode. *Sci. Rep.* **2022**, *12*, 5160. [CrossRef]
- 97. Haas, J.C.; Vergara, A.; Serrano, A.R.; Mishra, S.; Hurry, V.; Street, N.R. Candidate regulators and target genes of drought stress in needles and roots of *Norway spruce*. *Tree Physiol*. **2021**, *41*, 1230–1246. [CrossRef]
- Liu, G.; Yang, Q.; Gao, J.; Wu, Y.; Feng, Z.; Huang, J.; Zou, H.; Zhu, X.; Chen, Y.; Yu, C.; et al. Identify of fast-growing related genes especially in height growth by combining QTL analysis and transcriptome in *Salix matsudana* (Koidz). *Front. Genet.* 2021, 12, 596749. [CrossRef] [PubMed]
- Laoué, J.; Depardieu, C.; Gérardi, S.; Lamothe, M.; Bomal, C.; Azaiez, A.; Gros-Louis, M.; Laroche, J.; Boyle, B.; Hammerbacher, A.; et al. Combining QTL mapping and transcriptomics to decipher the genetic architecture of phenolic compounds metabolism in the conifer White Spruce. *Front. Plant Sci.* 2021, *12*, 675108. [CrossRef] [PubMed]
- 100. Hernández, M.A.; Butler, J.B.; Ammitzboll, H.; Weller, J.L.; Vaillancourt, R.E.; Potts, B.M. Genetic control of the operculum and capsule morphology of *Eucalyptus globulus*. Ann. Bot. 2022, 130, 97–108. [CrossRef] [PubMed]
- Bentley, N.; Grauke, L.J.; Ruhlman, E.; Klein, R.R.; Kubenka, K.; Wang, X.; Klein, P. Linkage mapping and QTL analysis of pecan (*Carya illinoinensis*) full-siblings using genotyping-by-sequencing. *Tree Genet. Genomes* 2020, 16, 83. [CrossRef]
- 102. Hernández, M.A.; Butler, J.B.; Ammitzboll, H.; Freeman, J.S.; Reilly-Wapstra, J.O.; Vaillancourt, R.E.; Potts, B.M. Genetic variation in fire recovery and other fire-related traits in a global eucalypt species. *Tree Genet. Genomes* **2022**, *18*, 42. [CrossRef]
- Freeman, J.S.; Slavov, G.T.; Butler, J.B.; Frickey, T.; Graham, N.J.; Klápště, J.; Lee, J.; Telfer, E.J.; Wilcox, P.; Dungey, H.S. High density linkage maps, genetic architecture, and genomic prediction of growth and wood properties in *Pinus radiata*. *BMC Genom*. 2022, 23, 731. [CrossRef]
- 104. Du, C.; Sun, P.; Cheng, X.; Zhang, L.; Wang, L.; Hu, J. QTL mapping of drought-related traits in the hybrids of *Populus deltoides* 'Danhong'×Populus simonii 'Tongliao1'. *BMC Plant Biol.* **2022**, 22, 238. [CrossRef]
- 105. Guo, M.; Zhang, Z.; Cheng, Y.; Li, S.; Shao, P.; Yu, Q.; Wang, J.; Xu, G.; Zhang, X.; Liu, J.; et al. Comparative population genomics dissects the genetic basis of seven domestication traits in jujube. *Hortic. Res.* **2020**, *7*, 89. [CrossRef]
- 106. Santini, F.; Kefauver, S.C.; Araus, J.L.; Resco, D.D.V.; Martin, G.S.; Grivet, D.; Voltas, J. Bridging the genotype-phenotype gap for a Mediterranean pine by semi-automatic crown identification and multispectral imagery. *New Phytol.* 2021, 229, 245–258. [CrossRef]
- 107. Mähler, N.; Schiffthaler, B.; Robinson, K.M.; Terebieniec, B.K.; Vučak, M.; Mannapperuma, C.; Bailey, M.E.S.; Jansson, S.; Hvidsten, T.R.; Street, N.R. Leaf shape in *Populus tremula* is a complex, omnigenic trait. *Ecol. Evol.* **2020**, *10*, 11922–11940. [CrossRef]
- 108. Sawitri; Tani, N.; Na'iem, M.; Widiyatno; Indrioko, S.; Uchiyama, K.; Suwa, R.; Ng, K.K.S.; Lee, S.L.; Tsumura, Y. Potential of genome-wide association studies and genomic selection to improve productivity and quality of commercial timber species in tropical rainforest, a case study of *Shorea platyclados. Forests* 2020, *11*, 239. [CrossRef]

- 109. Francisco, F.R.; Aono, A.H.; Da Silva, C.C.; Gonçalves, P.S.; Scaloppi, E.J., Jr.; Le Guen, V.; Fritsche-Neto, R.; Souza, L.M.; Souza, A.P.D. Unravelling rubber tree growth by integrating GWAS and biological network-based approaches. *Front. Plant Sci.* 2021, 12, 2719. [CrossRef] [PubMed]
- Chen, Z.; Zan, Y.; Zhou, L.; Karlsson, B.; Tuominen, H.; García-Gil, M.R.; Wu, H.X. Genetic architecture behind developmental and seasonal control of tree growth and wood properties in Norway spruce. *Front. Plant Sci.* 2022, 13, 128. [CrossRef] [PubMed]
- 111. Chen, Z.; Zan, Y.; Milesi, P.; Zhou, L.; Chen, J.; Li, L.; Cui, B.; Niu, S.; Westin, J.; Karlsson, B.; et al. Leveraging breeding programs and genomic data in Norway spruce (*Picea abies* L. Karst) for GWAS analysis. *Genome Biol.* **2021**, 22, 179. [CrossRef] [PubMed]
- 112. Tan, B.; Ingvarsson, P.K. Integrating genome-wide association mapping of additive and dominance genetic effects to improve genomic prediction accuracy in *Eucalyptus*. *Plant Genome* **2022**, *15*, e20208. [CrossRef] [PubMed]
- 113. Feng, J.; Jiang, Y.; Yang, Z.; Chen, S.; El-Kassaby, Y.A.; Chen, H. Marker-assisted selection in *C. oleifera* hybrid population. *Silvae Genet.* **2020**, *69*, 63–72. [CrossRef]
- 114. Moriguchi, Y.; Ueno, S.; Hasegawa, Y.; Tadama, T.; Watanabe, M.; Saito, R.; Hirayama, S.; Iwai, J.; Konno, Y. Marker-assisted selection of trees with male sterility 1 in *Cryptomeria japonica* D. Don. *Forests* **2020**, *11*, 734. [CrossRef]
- 115. Liu, J.; Sniezko, R.A.; Sissons, R.; Krakowski, J.; Alger, G.; Schoettle, A.W.; Williams, H.; Zamany, A.; Zitomer, R.A.; Kegley, A. Association mapping and development of marker-assisted selection tools for the resistance to White Pine blister rust in the Alberta limber Pine populations. *Front. Plant Sci.* 2020, 11, 557672. [CrossRef]
- 116. Maruyama, T.E.; Tsuruta, M.; Ueno, S.; Kawakami, K.; Bamba, Y.; Moriguchi, Y. An improved and simplified propagation system for Pollen-Free Sugi (*Cryptomeria japonica*) via somatic embryogenesis. *Front. Plant Sci.* **2022**, *13*, 825340. [CrossRef]
- 117. Cao, S.; Duan, H.; Sun, Y.; Hu, R.; Wu, B.; Lin, J.; Deng, W.; Li, Y.; Zheng, H. Genome-wide association study with growth-related traits and secondary metabolite contents in red- and white-heart Chinese fir. *Front. Plant Sci.* **2022**, *13*, 922007. [CrossRef]
- Maruyama, T.E.; Ueno, S.; Hirayama, S.; Kaneeda, T.; Moriguchi, Y. Somatic embryogenesis and plant regeneration from Sugi (Japanese Cedar, *Cryptomeria japonica* D. Don, *Cupressaceae*) seed families by marker assisted selection for the male sterility allele ms1. *Plants* 2020, *9*, 1029. [CrossRef] [PubMed]
- Lebedev, V.G.; Lebedeva, T.N.; Chernodubov, A.I.; Shestibratov, K.A. Genomic selection for forest tree improvement: Methods, achievements and perspectives. *Forests* 2020, *11*, 1190. [CrossRef]
- 120. Grattapaglia, D.; Silva-Junior, O.B.; Resende, R.T.; Cappa, E.P.; Müller, B.S.; Tan, B.; Isik, F.; Ratcliffe, B.; El-Kassaby, Y.A. Quantitative genetics and genomics converge to accelerate forest tree breeding. *Front. Plant Sci.* **2018**, *9*, 1693. [CrossRef]
- 121. Yin, Y.; Wang, C.; Xiao, D.; Liang, Y.; Wang, Y. Advances and perspectives of transgenic technology and biotechnological application in forest trees. *Front. Plant Sci.* **2021**, *12*, 786328. [CrossRef] [PubMed]
- 122. Tang, W.; Tang, A.Y. Transgenic woody plants for biofuel. J. For. Res. 2014, 25, 225–236. [CrossRef]
- 123. Tran, N.H.T.; Oguchi, T.; Akatsuka, N.; Matsunaga, E.; Kawaoka, A.; Yamada, A.; Ozeki, Y.; Watanabe, K.N.; Kikuchi, A. Development and evaluation of novel salt-tolerant *Eucalyptus* trees by molecular breeding using an RNA-Binding-Protein gene derived from common ice plant (*Mesembryanthemum crystallinum* L.). *Plant Biotechnol. J.* 2019, 17, 801–811. [CrossRef]
- 124. An, P.; Qin, R.; Zhao, Q.; Li, X.; Wang, C.; Cao, Q.; Zhang, H.; Zhang, L. Genetic transformation of *LoHDZ2* and analysis of its function to enhance stress resistance in *Larix olgensis*. *Sci. Rep.* **2022**, *12*, 12831. [CrossRef]
- 125. Jia, H.; Chen, J.; Zhang, L.; Zhang, L. The first report on transgenic hairy root induction from the stem of tung tree (*Vernicia fordii*). *Plants* **2022**, *11*, 1315. [CrossRef]
- 126. Wang, C.; Wang, Y.; Zou, J.; Peng, R.; Yu, Q.; Liu, G.; Jiang, J. Selection of elite lines of *BpGH3.5*-transgenic *Betula platyphylla* using growth adaptability analysis. *J. For. Res.* **2022**, *33*, 1891–1901. [CrossRef]
- 127. Ma, M.; Chen, X.; Yin, Y.; Fan, R.; Li, B.; Zhan, Y.; Zeng, F. DNA methylation silences exogenous gene expression in transgenic birch progeny. *Front. Plant Sci.* 2020, *11*, 523748. [CrossRef]
- Wang, S.; Liu, J.; Dong, Y.; Li, Y.; Huang, Y.; Ren, M.; Yang, M.; Wang, J. Dynamic monitoring of the impact of insect-resistant transgenic poplar field stands on arthropod communities. *For. Ecol. Manag.* 2022, 505, 119921. [CrossRef]
- 129. Huang, Y.; Dong, Y.; Ren, Y.; Wang, S.; Li, Y.; Du, K.; Lin, X.; Yang, M. Niches and seasonal changes, rather than transgenic events, affect the microbial community of *Populus* × *euramericana* 'Neva'. *Front. Microbiol.* **2022**, *12*, 805261. [CrossRef] [PubMed]
- Fan, J.; Dong, Y.; Yu, X.; Yao, L.; Li, D.; Wang, J.; Yang, M. Assessment of environmental microbial effects of insect-resistant transgenic *Populus × euramericana* cv. '74/76' based on high-throughput sequencing. *Acta Physiol. Plant.* 2020, 42, 167. [CrossRef]
- 131. Zuo, L.; Yang, R.; Zhen, Z.; Liu, J.; Huang, L.; Yang, M. A 5-year field study showed no apparent effect of the Bt transgenic 741 poplar on the arthropod community and soil bacterial diversity. *Sci. Rep.* **2018**, *8*, 1956. [CrossRef]
- 132. Ren, Y.; Zhou, X.; Dong, Y.; Zhang, J.; Wang, J.; Yang, M. Exogenous gene expression and insect resistance in dual Bt toxin *Populus × euramericana* 'Neva' transgenic plants. *Front. Plant Sci.* **2021**, *12*, 660226. [CrossRef]
- Tran, N.T.; Oguchi, T.; Matsunaga, E.; Kawaoka, A.; Watanabe, K.N.; Kikuchi, A. Evaluation of potential impacts on biodiversity of the salt-tolerant transgenic *Eucalyptus* camaldulensis harboring an RNA chaperonic RNA-Binding-Protein gene derived from common ice plant. *Transgen. Res.* 2021, 30, 23–34. [CrossRef]
- 134. Lu, M.Z.; Hu, J.J. Research and application of transgenic poplars in China. China For. Sci. Technol. 2006, 20, 1–4. [CrossRef]
- 135. Liu, H.; Chen, W.; Li, Y.; Sun, L.; Chai, Y.; Chen, H.; Nie, H.; Huang, C. CRISPR/Cas9 technology and its utility for crop improvement. *Int. J. Mol. Sci.* 2022, 23, 10442. [CrossRef]
- 136. Qiao, H.; Wu, J.; Zhang, X.; Luo, J.; Wang, H.; Ming, D. The advance of CRISPR-Cas9-based and NIR/CRISPR-Cas9-based imaging system. *Front. Chem.* **2021**, *9*, 1–17. [CrossRef]

- 137. Pourcel, C.; Salvignol, G.; Vergnaud, G. CRISPR elements in Yersinia pestis acquire new repeats by preferential uptake of bacteriophage DNA, and provide additional tools for evolutionary studies. *Microbiology* **2005**, *151*, 653–663. [CrossRef]
- 138. Šmarda, P.; Horová, L.; Knápek, O.; Dieck, H.; Dieck, M.; Ražná, K.; Hrubík, P.; Orlóci, L.; Papp, L.; Veselá, K. Multiple haploids, triploids, and tetraploids found in modern-day "living fossil" *Ginkgo biloba*. *Hortic. Res.* 2018, *5*, 55. [CrossRef] [PubMed]
- Nghiem, Q.C.; Griffin, A.R.; Harwood, C.E.; Harbard, J.L.; Le, S.; Price, A.; Koutoulis, A. Occurrence of polyploidy in populations of Acacia dealbata in south-eastern Tasmania and cytotypic variation in reproductive traits. *Aust. J. Bot.* 2018, 66, 152–160. [CrossRef]
- 140. Mason, A.S. Polyploidy and Hybridization for Crop Improvement; CRC Press: Boca Raton, FL, USA, 2017.
- 141. Ahuja, M.R. Polyploidy in gymnosperms: Revisited. Silvae Genet. 2005, 54, 59–69. [CrossRef]
- 142. Anamthawat-Jónsson, K.; Karlsdóttir, L.; Thórsson, A.T.; Jóhannsson, M.H. Naturally occurring triploid birch hybrids from woodlands in Iceland are partially fertile. *New For.* **2021**, *52*, 659–678. [CrossRef]
- 143. Farhat, P.; Takvorian, N.; Avramidou, M.; Garraud, L.; Adams, R.P.; Siljak-Yakovlev, S.; Kharrat, M.B.D.; Robert, T. First evidence for allotriploid hybrids between *Juniperus thurifera* and *J. sabina* in a sympatric area in the French Alps. *Ann. For. Sci.* 2020, 77, 93. [CrossRef]
- Śmíd, J.; Douda, J.; Krak, K.; Mandák, B. Analyses of hybrid viability across a hybrid zone between two alnus species using microsatellites and cpDNA markers. *Genes* 2020, 11, 770. [CrossRef]
- 145. Vašková, D.; Kolarčik, V. Breeding systems in diploid and polyploid Hawthorns (*Crataegus*): Evidence from experimental pollinations of *C. monogyna*, *C. subsphaerica*, and natural hybrids. *Forests* **2019**, *10*, 1059. [CrossRef]
- 146. Serapiglia, M.J.; Gouker, F.E.; Hart, J.F.; Unda, F.; Mansfield, S.D.; Stipanovic, A.J.; Smart, L.B. Ploidy level affects important biomass traits of novel shrub willow (*Salix*) hybrids. *BioEnergy Res.* **2015**, *8*, 259–269. [CrossRef]
- 147. Nghiem, Q.C.; Griffin, A.R.; Harwood, C.E.; Harbard, J.L.; Huy, T.H.; Koutoulis, A. Seed development following reciprocal crossing among autotetraploid and diploid *Acacia mangium* and diploid *A. auriculiformis. Aust. J. Bot.* 2016, 64, 20–31. [CrossRef]
- 148. Wang, L.; Tu, M.; Li, J.; Sun, S.; Song, H.; Xu, Z.; Chen, D.; Liang, G. Photosynthetic efficiency and glyco-metabolism changes in artificial triploid loquats contribute to heterosis manifestation. *Int. J. Mol. Sci.* **2022**, *23*, 11337. [CrossRef]
- 149. Wang, J.; Kang, X.Y.; Li, D.L.; Chen, H.W.; Zhang, P.D. Induction of diploid eggs with colchicine during embryo sac development in *Populus. Silvae Genet.* **2010**, *59*, 40–48. [CrossRef]
- 150. Li, Y.; Wang, Y.; Wang, P.; Yang, J.; Kang, X. Induction of unreduced megaspores in *Eucommia ulmoides* by high temperature treatment during megasporogenesis. *Euphytica* **2016**, *212*, 515–524. [CrossRef]
- 151. Yang, J.; Wang, J.; Liu, Z.; Xiong, T.; Lan, J.; Han, Q.; Li, Y.; Kang, X. Megaspore chromosome doubling in *Eucalyptus urophylla* ST Blake induced by colchicine treatment to produce triploids. *Forests* **2018**, *9*, 728. [CrossRef]
- Yao, P.; Li, G.; Long, Q.; He, L.; Kang, X. Microsporogenesis and induction of unreduced pollen with high temperatures in rubber tree clone RRIM 600. *Forests* 2017, *8*, 152. [CrossRef]
- 153. Li, Y.H.; Kang, X.Y.; Wang, S.D.; Zhang, Z.H.; Chen, H.W. Triploid induction in *Populus alba x P. glandulosa* by chromosome doubling of female gametes. *Silvae Genet.* **2008**, *57*, 37. [CrossRef]
- 154. Carlson, C.H.; Choi, Y.; Chan, A.P.; Town, C.D.; Smart, L.B. Nonadditive gene expression is correlated with nonadditive phenotypic expression in interspecific triploid hybrids of willow (*Salix* spp.). *G3 Genes Genomes Genet.* 2022, 12, jkab436. [CrossRef]
- 155. Thorsson, A.T.; Palsson, S.; Sigurgeirsson, A.; Anamthawat-Jonsson, K. Morphological variation among *Betula nana* (diploid), *B. pubescens* (tetraploid) and their triploid hybrids in Iceland. *Ann. Bot.* **2007**, *99*, 1183–1193. [CrossRef]
- 156. Li, Y.; Yang, J.; Song, L.; Qi, Q.; Du, K.; Han, Q.; Kang, X. Study of variation in the growth, photosynthesis, and content of secondary metabolites in *Eucommia triploids*. *Trees* **2019**, *33*, 817–826. [CrossRef]
- 157. Liu, S.; Zhang, C.; Yang, W.; Li, X.; Hou, L.; Li, M.; Pang, X.; Li, Y. Hybrid triploid induced by megaspore chromosome doubling in Jujube (*Ziziphus jujuba* Mill.) 'Maya' and its characteristics. *Forests* **2021**, *12*, 112. [CrossRef]
- 158. Li, H.; Gan, J.; Xiong, H.; Mao, X.; Li, S.; Zhang, H.; Hu, G.; Liu, C.; Fu, J. Production of triploid germplasm by inducing 2n pollen in Longan. *Horticulturae* 2022, *8*, 437. [CrossRef]
- 159. Meuwissen, T.H.; Solberg, T.R.; Shepherd, R.; Woolliams, J.A. A fast algorithm for BayesB type of prediction of genome-wide estimates of genetic value. *Genet. Sel. Evol.* **2009**, *41*, 2. [CrossRef] [PubMed]
- Meuwissen, T.H.; Hayes, B.J.; Goddard, M.E. Prediction of total genetic value using genome-wide dense marker maps. *Genetics* 2001, 157, 1819–1829. [CrossRef] [PubMed]
- 161. Jonas, E.; de Koning, D. Does genomic selection have a future in plant breeding? *Trends Biotechnol.* **2013**, *31*, 497–504. [CrossRef] [PubMed]
- 162. Crossa, J.; Pérez-Rodríguez, P.; Cuevas, J.; Montesinos-López, O.; Jarquín, D.; De Los Campos, G.; Burgueño, J.; González-Camacho, J.M.; Pérez-Elizalde, S.; Beyene, Y. Genomic selection in plant breeding: Methods, models, and perspectives. *Trends Plant Sci.* 2017, 22, 961–975. [CrossRef]
- 163. Endelman, J.B. Ridge regression and other kernels for genomic selection with R package rrBLUP. *Plant Genome* **2011**, *4*, 255–258. [CrossRef]
- 164. Wimmer, V.; Albrecht, T.; Auinger, H.; Schön, C. Synbreed: A framework for the analysis of genomic prediction data using R. *Bioinformatics* **2012**, *28*, 2086–2087. [CrossRef]

- 165. Desta, Z.A.; Ortiz, R. Genomic selection: Genome-wide prediction in plant improvement. *Trends Plant Sci.* **2014**, *19*, 592–601. [CrossRef]
- 166. Pérez, P.; de Los Campos, G. Genome-wide regression and prediction with the BGLR statistical package. *Genetics* **2014**, *198*, 483–495. [CrossRef]
- 167. Wang, C.; Prakapenka, D.; Wang, S.; Pulugurta, S.; Runesha, H.B.; Da, Y. GVCBLUP: A computer package for genomic prediction and variance component estimation of additive and dominance effects. *BMC Bioinform.* **2014**, *15*, 1–9. [CrossRef]
- 168. Lipka, A.E.; Tian, F.; Wang, Q.; Peiffer, J.; Li, M.; Bradbury, P.J.; Gore, M.A.; Buckler, E.S.; Zhang, Z. GAPIT: Genome association and prediction integrated tool. *Bioinformatics* **2012**, *28*, 2397–2399. [CrossRef]
- 169. Covarrubias-Pazaran, G. Genome-assisted prediction of quantitative traits using the R package sommer. *PLoS ONE* **2016**, *11*, e156744. [CrossRef] [PubMed]
- 170. Kainer, D.; Stone, E.A.; Padovan, A.; Foley, W.J.; Külheim, C. Accuracy of genomic prediction for foliar terpene traits in *Eucalyptus* polybractea. G3 Genes Genomes Genet. 2018, 8, 2573–2583. [CrossRef] [PubMed]
- 171. Zhao, T.; Fernando, R.; Cheng, H. Interpretable artificial neural networks incorporating Bayesian alphabet models for genomewide prediction and association studies. *G3* **2021**, *11*, b228. [CrossRef] [PubMed]
- 172. Wong, C.K.; Bernardo, R. Genome wide selection in oil palm: Increasing selection gain per unit time and cost with small populations. *Theor. Appl. Genet.* **2008**, *116*, 815–824. [CrossRef] [PubMed]
- 173. Grattapaglia, D.; Resende, M.D. Genomic selection in forest tree breeding. Tree Genet. Genomes 2011, 7, 241–255. [CrossRef]
- 174. Isik, F. Genomic selection in forest tree breeding: The concept and an outlook to the future. New For. 2014, 45, 379–401. [CrossRef]
- 175. Kwong, Q.B.; Ong, A.L.; Teh, C.K.; Chew, F.T.; Tammi, M.; Mayes, S.; Kulaveerasingam, H.; Yeoh, S.H.; Harikrishna, J.A.; Appleton, D.R. Genomic selection in commercial perennial crops: Applicability and improvement in oil palm (*Elaeis guineensis* Jacq.). Sci. Rep. 2017, 7, 2872. [CrossRef]
- 176. Cros, D.; Tchounke, B.; Nkague-Nkamba, L. Training genomic selection models across several breeding cycles increases genetic gain in oil palm in silico study. *Mol. Breed.* **2018**, *38*, 89. [CrossRef]
- 177. Singh, R.; Ong-Abdullah, M.; Low, E.L.; Manaf, M.A.A.; Rosli, R.; Nookiah, R.; Ooi, L.C.; Ooi, S.E.; Chan, K.; Halim, M.A. Oil palm genome sequence reveals divergence of interfertile species in old and new worlds. *Nature* 2013, *500*, 335–339. [CrossRef]
- 178. Tan, B.; Grattapaglia, D.; Martins, G.S.; Ferreira, K.Z.; Sundberg, B.; Ingvarsson, P.K. Evaluating the accuracy of genomic prediction of growth and wood traits in two Eucalyptus species and their F1 hybrids. *BMC Plant Biol.* **2017**, *17*, 110. [CrossRef]
- 179. Resende, M.D.; Resende, M.F., Jr.; Sansaloni, C.P.; Petroli, C.D.; Missiaggia, A.A.; Aguiar, A.M.; Abad, J.M.; Takahashi, E.K.; Rosado, A.M.; Faria, D.A. Genomic selection for growth and wood quality in *Eucalyptus*: Capturing the missing heritability and accelerating breeding for complex traits in forest trees. *New Phytol.* **2012**, *194*, 116–128. [CrossRef] [PubMed]
- Cappa, E.P.; de Lima, B.M.; Da Silva, O.B., Jr.; Garcia, C.C.; Mansfield, S.D.; Grattapaglia, D. Improving genomic prediction of growth and wood traits in Eucalyptus using phenotypes from non-genotyped trees by single-step GBLUP. *Plant Sci.* 2019, 284, 9–15. [CrossRef] [PubMed]
- Tan, B.; Grattapaglia, D.; Wu, H.X.; Ingvarsson, P.K. Genomic relationships reveal significant dominance effects for growth in hybrid *Eucalyptus*. *Plant Sci.* 2018, 267, 84–93. [CrossRef] [PubMed]
- Müller, B.S.; Neves, L.G.; de Almeida Filho, J.E.; Resende, M.F.; Muñoz, P.R.; Dos Santos, P.E.; Kirst, M.; Grattapaglia, D. Genomic prediction in contrast to a genome-wide association study in explaining heritable variation of complex growth traits in breeding populations of *Eucalyptus*. *BMC Genom.* 2017, *18*, 524. [CrossRef] [PubMed]
- 183. Thavamanikumar, S.; Arnold, R.J.; Luo, J.; Thumma, B.R. Genomic studies reveal substantial dominant effects and improved genomic predictions in an open-pollinated breeding population of *Eucalyptus pellita*. G3 Genes Genomes Genet. 2020, 10, 3751–3763. [CrossRef]
- 184. Rambolarimanana, T.; Ramamonjisoa, L.; Verhaegen, D.; Leong Pock Tsy, J.; Jacquin, L.; Cao-Hamadou, T.; Makouanzi, G.; Bouvet, J. Performance of multi-trait genomic selection for *Eucalyptus robusta* breeding program. *Tree Genet. Genomes* 2018, 14, 71. [CrossRef]
- Suontama, M.; Klápště, J.; Telfer, E.; Graham, N.; Stovold, T.; Low, C.; McKinley, R.; Dungey, H. Efficiency of genomic prediction across two *Eucalyptus nitens* seed orchards with different selection histories. *Heredity* 2019, 122, 370–379. [CrossRef]
- Klápště, J.; Dungey, H.S.; Telfer, E.J.; Suontama, M.; Graham, N.J.; Li, Y.; McKinley, R. Marker selection in multivariate genomic prediction improves accuracy of low heritability traits. *Front. Genet.* 2020, *11*, 499094. [CrossRef]
- 187. Cappa, E.P.; El-Kassaby, Y.A.; Muñoz, F.; Garcia, M.N.; Villalba, P.V.; Klápště, J.; Poltri, S.N.M. Genomic-based multiple-trait evaluation in *Eucalyptus grandis* using dominant DArT markers. *Plant Sci.* **2018**, 271, 27–33. [CrossRef]
- 188. Mphahlele, M.M.; Isik, F.; Mostert-O'Neill, M.M.; Reynolds, S.M.; Hodge, G.R.; Myburg, A.A. Expected benefits of genomic selection for growth and wood quality traits in *Eucalyptus grandis*. *Tree Genet. Genomes* **2020**, *16*, 49. [CrossRef]
- Ballesta, P.; Maldonado, C.; Pérez-Rodríguez, P.; Mora, F. SNP and haplotype-based genomic selection of quantitative traits in Eucalyptus globulus. Plants 2019, 8, 331. [CrossRef] [PubMed]
- 190. Durán, R.; Isik, F.; Zapata-Valenzuela, J.; Balocchi, C.; Valenzuela, S. Genomic predictions of breeding values in a cloned *Eucalyptus* globulus population in Chile. *Tree Genet. Genomes* **2017**, *13*, 74. [CrossRef]
- Jurcic, E.J.; Villalba, P.V.; Pathauer, P.S.; Palazzini, D.A.; Oberschelp, G.P.; Harrand, L.; Garcia, M.N.; Aguirre, N.C.; Acuña, C.V.; Martínez, M.C. Single-step genomic prediction of *Eucalyptus dunnii* using different identity-by-descent and identity-by-state relationship matrices. *Heredity* 2021, 127, 176–189. [CrossRef]

- 192. Ballesta, P.; Bush, D.; Silva, F.F.; Mora, F. Genomic predictions using low-density SNP markers, pedigree and GWAS information: A case study with the non-model species *Eucalyptus cladocalyx*. *Plants* **2020**, *9*, 99. [CrossRef] [PubMed]
- 193. Hirakawa, H.; Nakamura, Y.; Kaneko, T.; Isobe, S.; Sakai, H.; Kato, T.; Hibino, T.; Sasamoto, S.; Watanabe, A.; Yamada, M. Survey of the genetic information carried in the genome of *Eucalyptus camaldulensis*. *Plant Biotechnol.* **2011**, *28*, 471–480. [CrossRef]
- 194. Cros, D.; Mbo-Nkoulou, L.; Bell, J.M.; Oum, J.; Masson, A.; Soumahoro, M.; Tran, D.M.; Achour, Z.; Le Guen, V.; Clement-Demange, A. Within-family genomic selection in rubber tree (*Hevea brasiliensis*) increases genetic gain for rubber production. *Ind. Crop. Prod.* 2019, 138, 111464. [CrossRef]
- 195. Souza, L.M.; Francisco, F.R.; Gonçalves, P.S.; Scaloppi, E.J., Jr.; Le Guen, V.; Fritsche-Neto, R.; Souza, A.P. Genomic selection in rubber tree breeding: A comparison of models and methods for managing G× E interactions. *Front. Plant Sci.* 2019, 10, 1353. [CrossRef]
- 196. Tang, C.; Yang, M.; Fang, Y.; Luo, Y.; Gao, S.; Xiao, X.; An, Z.; Zhou, B.; Zhang, B.; Tan, X. The rubber tree genome reveals new insights into rubber production and species adaptation. *Nat. Plants* **2016**, *2*, 16073. [CrossRef]
- 197. Lau, N.; Makita, Y.; Kawashima, M.; Taylor, T.D.; Kondo, S.; Othman, A.S.; Shu-Chien, A.C.; Matsui, M. The rubber tree genome shows expansion of gene family associated with rubber biosynthesis. *Sci. Rep.* **2016**, *6*, 28594. [CrossRef]
- Chen, Z.; Baison, J.; Pan, J.; Karlsson, B.; Andersson, B.; Westin, J.; García-Gil, M.R.; Wu, H.X. Accuracy of genomic selection for growth and wood quality traits in two control-pollinated progeny trials using exome capture as the genotyping platform in Norway spruce. *BMC Genom.* 2018, 19, 946. [CrossRef]
- 199. Beaulieu, J.; Doerksen, T.; Clément, S.; MacKay, J.; Bousquet, J. Accuracy of genomic selection models in a large population of open-pollinated families in white spruce. *Heredity* **2014**, *113*, 343–352. [CrossRef] [PubMed]
- Beaulieu, J.; Doerksen, T.K.; MacKay, J.; Rainville, A.; Bousquet, J. Genomic selection accuracies within and between environments and small breeding groups in white spruce. *BMC Genom.* 2014, 15, 1048. [CrossRef] [PubMed]
- Lenz, P.; Nadeau, S.; Azaiez, A.; Gérardi, S.; Deslauriers, M.; Perron, M.; Isabel, N.; Beaulieu, J.; Bousquet, J. Genomic prediction for hastening and improving efficiency of forward selection in conifer polycross mating designs: An example from white spruce. *Heredity* 2020, 124, 562–578. [CrossRef] [PubMed]
- 202. Beaulieu, J.; Nadeau, S.; Ding, C.; Celedon, J.M.; Azaiez, A.; Ritland, C.; Laverdière, J.P.; Deslauriers, M.; Adams, G.; Fullarton, M. Genomic selection for resistance to spruce budworm in white spruce and relationships with growth and wood quality traits. *Evol. Appl.* 2020, 13, 2704–2722. [CrossRef]
- 203. Fuentes-Utrilla, P.; Goswami, C.; Cottrell, J.E.; Pong-Wong, R.; Law, A.; Hara, S.W.A.; Lee, S.J.; Woolliams, J.A. QTL analysis and genomic selection using RADseq derived markers in Sitka spruce: The potential utility of within family data. *Tree Genet. Genomes* 2017, 13, 33. [CrossRef]
- 204. Lenz, P.R.; Nadeau, S.; Mottet, M.J.; Perron, M.; Isabel, N.; Beaulieu, J.; Bousquet, J. Multi-trait genomic selection for weevil resistance, growth, and wood quality in Norway spruce. *Evol. Appl.* **2020**, *13*, 76–94. [CrossRef]
- Ratcliffe, B.; El-Dien, O.G.; Cappa, E.P.; Porth, I.; Klápště, J.; Chen, C.; El-Kassaby, Y.A. Single-step BLUP with varying genotyping effort in open-pollinated *Picea glauca*. G3 Genes Genomes Genet. 2017, 7, 935–942. [CrossRef]
- Isik, F.; Bartholomé, J.; Farjat, A.; Chancerel, E.; Raffin, A.; Sanchez, L.; Plomion, C.; Bouffier, L. Genomic selection in maritime pine. *Plant Sci.* 2016, 242, 108–119. [CrossRef]
- 207. Resende, M., Jr.; Muñoz, P.; Acosta, J.J.; Peter, G.F.; Davis, J.M.; Grattapaglia, D.; Resende, M.; Kirst, M. Accelerating the domestication of trees using genomic selection: Accuracy of prediction models across ages and environments. *New Phytol.* 2012, 193, 617–624. [CrossRef]
- 208. Resende, M., Jr.; Munoz, P.; Resende, M.D.; Garrick, D.J.; Fernando, R.L.; Davis, J.M.; Jokela, E.J.; Martin, T.A.; Peter, G.F.; Kirst, M. Accuracy of genomic selection methods in a standard data set of loblolly pine (*Pinus taeda* L.). *Genetics* 2012, 190, 1503–1510. [CrossRef]
- 209. Zapata-Valenzuela, J.; Whetten, R.W.; Neale, D.; McKeand, S.; Isik, F. Genomic estimated breeding values using genomic relationship matrices in a cloned population of loblolly pine. *G3 Genes Genomes Genet.* **2013**, *3*, 909–916. [CrossRef] [PubMed]
- 210. Ukrainetz, N.K.; Mansfield, S.D. Assessing the sensitivities of genomic selection for growth and wood quality traits in lodgepole pine using Bayesian models. *Tree Genet. Genomes* **2020**, *16*, 14. [CrossRef]
- 211. Li, Y.; Klápště, J.; Telfer, E.; Wilcox, P.; Graham, N.; Macdonald, L.; Dungey, H.S. Genomic selection for non-key traits in radiata pine when the documented pedigree is corrected using DNA marker information. *BMC Genom.* 2019, 20, 1026. [CrossRef] [PubMed]
- 212. Calleja-Rodriguez, A.; Pan, J.; Funda, T.; Chen, Z.; Baison, J.; Isik, F.; Abrahamsson, S.; Wu, H.X. Evaluation of the efficiency of genomic versus pedigree predictions for growth and wood quality traits in Scots pine. *BMC Genom.* 2020, 21, 796. [CrossRef] [PubMed]
- Alves, F.C.; Balmant, K.M.; Resende, M.F., Jr.; Kirst, M.; de Los Campos, G. Accelerating forest tree breeding by integrating genomic selection and greenhouse phenotyping. *Plant Genome* 2020, 13, e20048. [CrossRef] [PubMed]
- Ma, T.; Wang, J.; Zhou, G.; Yue, Z.; Hu, Q.; Chen, Y.; Liu, B.; Qiu, Q.; Wang, Z.; Zhang, J. Genomic insights into salt adaptation in a desert poplar. *Nat. Commun.* 2013, 4, 2797. [CrossRef]
- Rincent, R.; Charpentier, J.; Faivre-Rampant, P.; Paux, E.; Le Gouis, J.; Bastien, C.; Segura, V. Phenomic selection is a low-cost and high-throughput method based on indirect predictions: Proof of concept on wheat and poplar. *G3 Genes Genomes Genet.* 2018, *8*, 3961–3972. [CrossRef]

- Sandercock, A.M.; Westbrook, J.W.; Zhang, Q.; Johnson, H.A.; Saielli, T.M.; Scrivani, J.A.; Fitzsimmons, S.F.; Collins, K.; Perkins, M.T.; Craddock, J.H. Frozen in time: Rangewide genomic diversity, structure, and demographic history of relict American chestnut populations. *Mol. Ecol.* 2022, *31*, 4640–4655. [CrossRef]
- Thistlethwaite, F.R.; Ratcliffe, B.; Klápště, J.; Porth, I.; Chen, C.; Stoehr, M.U.; El-Kassaby, Y.A. Genomic prediction accuracies in space and time for height and wood density of Douglas-fir using exome capture as the genotyping platform. *BMC Genom.* 2017, 18, 930. [CrossRef]
- 218. Street, N.R. Genomics of forest trees—ScienceDirect. Adv. Bot. Res. 2019, 89, 1–37. [CrossRef]
- Iwata, H.; Minamikawa, M.F.; Kajiya-Kanegae, H.; Ishimori, M.; Hayashi, T. Genomics-assisted breeding in fruit trees. *Breed. Sci.* 2016, 66, 100–115. [CrossRef] [PubMed]
- Hayes, B.J.; Pryce, J.; Chamberlain, A.J.; Bowman, P.J.; Goddard, M.E. Genetic architecture of complex traits and accuracy of genomic prediction: Coat colour, milk-fat percentage, and type in Holstein cattle as contrasting model traits. *PLoS Genet.* 2010, *6*, e1001139. [CrossRef] [PubMed]
- Hayes, B.J.; Bowman, P.J.; Chamberlain, A.J.; Goddard, M.E. Invited review: Genomic selection in dairy cattle: Progress and challenges. J. Dairy Sci. 2009, 92, 433–443. [CrossRef] [PubMed]
- Liu, H.; Zhou, H.; Wu, Y.; Li, X.; Zhao, J.; Zuo, T.; Zhang, X.; Zhang, Y.; Liu, S.; Shen, Y. The impact of genetic relationship and linkage disequilibrium on genomic selection. *PLoS ONE* 2015, *10*, e132379. [CrossRef]
- 223. Habier, D.; Tetens, J.; Seefried, F.; Lichtner, P.; Thaller, G. The impact of genetic relationship information on genomic breeding values in German Holstein cattle. *Genet. Sel. Evol.* **2010**, *42*, 5. [CrossRef]
- Ma, P.; Huang, J.; Gong, W.; Li, X.; Gao, H.; Zhang, Q.; Ding, X.; Wang, C. The impact of genomic relatedness between populations on the genomic estimated breeding values. J. Anim. Sci. Biotechnol. 2018, 9, 1–6. [CrossRef]
- Pliura, A.; Zhang, S.Y.; Bousquet, J.; MacKay, J. Age trends in genotypic variation of wood density and its intra-ring components in young poplar hybrid crosses. *Ann. For. Sci.* 2006, 63, 673–685. [CrossRef]
- 226. Osorio, L.F.; White, T.L.; Huber, D.A. Age trends of heritabilities and genotype-by-environment interactions for growth traits and wood density from clonal trials of Eucalyptus grandis Hill ex Maiden. *Silvae Genet.* 2001, 50, 108–116.
- Dhillon, G.P.S.; Singh, A.; Sidhu, D.S. Variation, inheritance and correlation of growth characteristics of *Populus deltoides* Bartr. at various ages in the central-plain region of Punjab, India. *For. Stud. China* 2010, 12, 126–130. [CrossRef]
- Ahmar, S.; Ballesta, P.; Ali, M.; Mora-Poblete, F. Achievements and challenges of genomics-assisted breeding in forest trees: From marker-assisted selection to genome editing. *Int. J. Mol. Sci.* 2021, 22, 10583. [CrossRef]
- 229. Khan, S.H. Genome-editing technologies: Concept, pros, and cons of various genome-editing techniques and bioethical concerns for clinical application. *Mol. Ther.-Nucl. Acids* **2019**, *16*, 326–334. [CrossRef] [PubMed]
- Li, J.; Norville, J.E.; Aach, J.; McCormack, M.; Zhang, D.; Bush, J.; Church, G.M.; Sheen, J. Multiplex and homologous recombination–mediated genome editing in *Arabidopsis* and *Nicotiana benthamiana* using guide RNA and Cas9. *Nat. Biotechnol.* 2013, 31, 688–691. [CrossRef] [PubMed]
- Shan, Q.; Wang, Y.; Li, J.; Zhang, Y.; Chen, K.; Liang, Z.; Zhang, K.; Liu, J.; Xi, J.J.; Qiu, J. Targeted genome modification of crop plants using a CRISPR-Cas system. *Nat. Biotechnol.* 2013, *31*, 686–688. [CrossRef] [PubMed]
- Nekrasov, V.; Staskawicz, B.; Weigel, D.; Jones, J.D.; Kamoun, S. Targeted mutagenesis in the model plant *Nicotiana benthamiana* using Cas9 RNA-guided endonuclease. *Nat. Biotechnol.* 2013, *31*, 691–693. [CrossRef] [PubMed]
- 233. Jia, H.; Wang, N. Targeted genome editing of sweet orange using Cas9/sgRNA. PLoS ONE 2014, 9, e93806. [CrossRef] [PubMed]
- 234. Peng, A.; Chen, S.; Lei, T.; Xu, L.; He, Y.; Wu, L.; Yao, L.; Zou, X. Engineering canker-resistant plants through CRISPR/Cas9-targeted editing of the susceptibility gene *CsLOB1* promoter in citrus. *Plant Biotechnol. J.* 2017, 15, 1509–1519. [CrossRef] [PubMed]
- Zhang, F.; LeBlanc, C.; Irish, V.F.; Jacob, Y. Rapid and efficient CRISPR/Cas9 gene editing in Citrus using the YAO promoter. *Plant Cell Rep.* 2017, *36*, 1883–1887. [CrossRef] [PubMed]
- 236. Jia, H.; Orbovic, V.; Jones, J.B.; Wang, N. Modification of the PthA4 effector binding elements in Type I CsLOB1 promoter using Cas9/sg RNA to produce transgenic Duncan grapefruit alleviating Xcc∆pthA4: DCsLOB1.3 infection. *Plant Biotechnol. J.* 2016, 14, 1291–1301. [CrossRef]
- Zhou, X.; Jacobs, T.B.; Xue, L.; Harding, S.A.; Tsai, C. Exploiting SNPs for biallelic CRISPR mutations in the outcrossing woody perennial *Populus* reveals 4-coumarate: CoA ligase specificity and redundancy. *New Phytol.* 2015, 208, 298–301. [CrossRef]
- Fan, D.; Liu, T.; Li, C.; Jiao, B.; Li, S.; Hou, Y.; Luo, K. Efficient CRISPR/Cas9-mediated targeted mutagenesis in *Populus* in the first generation. *Sci. Rep.* 2015, 5, 12217. [CrossRef]
- Odipio, J.; Alicai, T.; Ingelbrecht, I.; Nusinow, D.A.; Bart, R.; Taylor, N.J. Efficient CRISPR/Cas9 genome editing of phytoene desaturase in cassava. *Front. Plant Sci.* 2017, *8*, 1780. [CrossRef] [PubMed]
- 240. Rybicki, E.P. CRISPR-Cas9 strikes out in cassava. Nat. Biotechnol. 2019, 37, 727-728. [CrossRef] [PubMed]
- Cai, L.; Zhang, L.; Fu, Q.; Xu, Z. Identification and expression analysis of cytokinin metabolic genes *IPTs*, *CYP735A* and *CKXs* in the biofuel plant *Jatropha curcas*. *PeerJ* 2018, 6, e4812. [CrossRef] [PubMed]
- Lin, C.S.; Hsu, C.T.; Yang, L.H.; Lee, L.Y.; Fu, J.Y.; Cheng, Q.W.; Wu, F.H.; Hsiao, H.C.W.; Zhang, Y.; Zhang, R. Application of protoplast technology to CRISPR/Cas9 mutagenesis: From single-cell mutation detection to mutant plant regeneration. *Plant Biotechnol. J.* 2018, 16, 1295–1310. [CrossRef] [PubMed]
- Fan, Y.; Xin, S.; Dai, X.; Yang, X.; Huang, H.; Hua, Y. Efficient genome editing of rubber tree (*Hevea brasiliensis*) protoplasts using CRISPR/Cas9 ribonucleoproteins. *Ind. Crop. Prod.* 2020, 146, 112146. [CrossRef]

- 244. Ye, S.; Chen, G.; Kohnen, M.V.; Wang, W.; Cai, C.; Ding, W.; Wu, C.; Gu, L.; Zheng, Y.; Ma, X. Robust CRISPR/Cas9 mediated genome editing and its application in manipulating plant height in the first generation of hexaploid Ma bamboo (*Dendrocalamus latiflorus* Munro). *Plant Biotechnol. J.* **2020**, *18*, 1501. [CrossRef]
- Bruegmann, T.; Deecke, K.; Fladung, M. Evaluating the Efficiency of gRNAs in CRISPR/Cas9 mediated genome editing in Poplars. Int. J. Mol. Sci. 2019, 20, 3623. [CrossRef]
- Zhou, Y.; Zhang, Y.; Wang, X.; Han, X.; An, Y.; Lin, S.; Shen, C.; Wen, J.; Liu, C.; Yin, W. Root-specific NF-Y family transcription factor, PdNF-YB21, positively regulates root growth and drought resistance by abscisic acid-mediated indoylacetic acid transport in *Populus. New Phytol.* 2020, 227, 407–426. [CrossRef]
- 247. Tang, X.; Wang, C.; Chai, G.; Wang, D.; Xu, H.; Liu, Y.; He, G.; Liu, S.; Zhang, Y.; Kong, Y. Ubiquitinated DA1 negatively regulates vascular cambium activity through modulating the stability of WOX4 in *Populus*. *Plant Cell* **2022**, *34*, 3364–3382. [CrossRef]
- 248. Ma, J.; Wan, D.; Duan, B.; Bai, X.; Bai, Q.; Chen, N.; Ma, T. Genome sequence and genetic transformation of a widely distributed and cultivated poplar. *Plant Biotechnol. J.* **2019**, *17*, 451–460. [CrossRef]
- Xue, Y.; Li, S.; Miao, D.; Huang, S.; Guo, B.; Li, S.; An, X. Investigation of PtSGT1 and PtSGT4 function in cellulose biosynthesis in Populus tomentosa using CRISPR/Cas9 technology. Int. J. Mol. Sci. 2021, 22, 13200. [CrossRef] [PubMed]
- Fan, C.; Yu, H.; Qin, S.; Li, Y.; Alam, A.; Xu, C.; Fan, D.; Zhang, Q.; Wang, Y.; Zhu, W. Brassinosteroid overproduction improves lignocellulose quantity and quality to maximize bioethanol yield under green-like biomass process in transgenic poplar. *Biotechnol. Biofuels* 2020, 13, 9. [CrossRef] [PubMed]
- Wang, L.; Ran, L.; Hou, Y.; Tian, Q.; Li, C.; Liu, R.; Fan, D.; Luo, K. The transcription factor *MYB115* contributes to the regulation of proanthocyanidin biosynthesis and enhances fungal resistance in poplar. *New Phytol.* 2017, 215, 351–367. [CrossRef] [PubMed]
- Yang, L.; Zhao, X.; Ran, L.; Li, C.; Fan, D.; Luo, K. *PtoMYB156* is involved in negative regulation of phenylpropanoid metabolism and secondary cell wall biosynthesis during wood formation in poplar. *Sci. Rep.* 2017, 7, srep41209. [CrossRef]
- Xu, C.; Fu, X.; Liu, R.; Guo, L.; Ran, L.; Li, C.; Tian, Q.; Jiao, B.; Wang, B.; Luo, K. *PtoMYB170* positively regulates lignin deposition during wood formation in poplar and confers drought tolerance in transgenic Arabidopsis. *Tree Physiol.* 2017, 37, 1713–1726. [CrossRef]
- Wan, S.; Li, C.; Ma, X.; Luo, K. *PtrMYB57* contributes to the negative regulation of anthocyanin and proanthocyanidin biosynthesis in poplar. *Plant Cell Rep.* 2017, *36*, 1263–1276. [CrossRef]
- 255. Fan, D.; Wang, X.; Tang, X.; Ye, X.; Ren, S.; Wang, D.; Luo, K. Histone H3K9 demethylase JMJ25 epigenetically modulates anthocyanin biosynthesis in poplar. *Plant J.* 2018, 96, 1121–1136. [CrossRef]
- Jiao, B.; Zhao, X.; Lu, W.; Guo, L.; Luo, K. The R2R3 MYB transcription factor *MYB189* negatively regulates secondary cell wall biosynthesis in *Populus. Tree Physiol.* 2019, 39, 1187–1200. [CrossRef]
- 257. Shen, Y.; Li, Y.; Xu, D.; Yang, C.; Li, C.; Luo, K. Molecular cloning and characterization of a brassinosteriod biosynthesis-related gene *PtoDWF4* from *Populus tomentosa*. *Tree Physiol.* **2018**, *38*, 1424–1436. [CrossRef]
- Jiang, Y.; Guo, L.; Ma, X.; Zhao, X.; Jiao, B.; Li, C.; Luo, K. The WRKY transcription factors *PtrWRKY18* and *PtrWRKY35* promote Melampsora resistance in *Populus. Tree Physiol.* 2017, 37, 665–675. [CrossRef]
- Shen, C.; Zhang, Y.; Li, Q.; Liu, S.; He, F.; An, Y.; Zhou, Y.; Liu, C.; Yin, W.; Xia, X. PdGNC confers drought tolerance by mediating stomatal closure resulting from NO and H₂O₂ production via the direct regulation of *PdHXK1* expression in *Populus*. *New Phytol.* 2021, 230, 1868–1882. [CrossRef] [PubMed]
- Elorriaga, E.; Klocko, A.L.; Ma, C.; Strauss, S.H. Variation in mutation spectra among CRISPR/Cas9 mutagenized poplars. *Front. Plant Sci.* 2018, 9, 594. [CrossRef] [PubMed]
- Muhr, M.; Paulat, M.; Awwanah, M.; Brinkkötter, M.; Teichmann, T. CRISPR/Cas9-mediated knockout of Populus BRANCHED1 and BRANCHED2 orthologs reveals a major function in bud outgrowth control. *Tree Physiol.* 2018, 38, 1588–1597. [CrossRef] [PubMed]
- 262. Ramos-Sanchez, J.M.; Triozzi, P.M.; Alique, D.; Geng, F.; Gao, M.; Jaeger, K.E.; Wigge, P.A.; Allona, I.; Perales, M. LHY2 integrates night-length information to determine timing of poplar photoperiodic growth. *Curr. Biol.* 2019, 29, 2402–2406. [CrossRef] [PubMed]
- Han, X.; An, Y.; Zhou, Y.; Liu, C.; Yin, W.; Xia, X. Comparative transcriptome analyses define genes and gene modules differing between two Populus genotypes with contrasting stem growth rates. *Biotechnol. Biofuels* 2020, 13, 139. [CrossRef] [PubMed]
- Triozzi, P.M.; Schmidt, H.W.; Dervinis, C.; Kirst, M.; Conde, D. Simple, efficient and open-source CRISPR/Cas9 strategy for multi-site genome editing in *Populus tremula* × *alba*. *Tree Physiol.* 2021, *41*, 2216–2227. [CrossRef]
- 265. Bewg, W.P.; Harding, S.A.; Engle, N.L.; Vaidya, B.N.; Zhou, R.; Reeves, J.; Horn, T.W.; Joshee, N.; Jenkins, J.W.; Shu, S. Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA. *Plant Physiol.* 2022, 189, 516–526. [CrossRef]
- Maurya, J.P.; Singh, R.K.; Miskolczi, P.C.; Prasad, A.N.; Jonsson, K.; Wu, F.; Bhalerao, R.P. Branching regulator BRC1 mediates photoperiodic control of seasonal growth in hybrid aspen. *Curr. Biol.* 2020, 30, 122–126. [CrossRef]
- Nayeri, S.; Baghban Kohnehrouz, B.; Ahmadikhah, A.; Mahna, N. CRISPR/Cas9-mediated P-CR domain-specific engineering of CESA4 heterodimerization capacity alters cell wall architecture and improves saccharification efficiency in poplar. *Plant Biotechnol.* J. 2022, 20, 1197–1212. [CrossRef]
- Jiang, Y.; Tong, S.; Chen, N.; Liu, B.; Bai, Q.; Chen, Y.; Bi, H.; Zhang, Z.; Lou, S.; Tang, H. The *PalWRKY77* transcription factor negatively regulates salt tolerance and abscisic acid signaling in *Populus*. *Plant J.* 2021, 105, 1258–1273. [CrossRef]

- 269. Jang, H.; Bae, E.; Kim, M.; Park, S.; Choi, N.; Pyo, S.; Lee, C.; Jeong, H.; Lee, H.; Choi, Y. CRISPR-Knockout of CSE gene improves saccharification efficiency by reducing lignin content in hybrid poplar. *Int. J. Mol. Sci.* 2021, 22, 9750. [CrossRef] [PubMed]
- 270. Bae, E.; Choi, H.; Choi, J.W.; Lee, H.; Kim, S.; Ko, J.; Choi, Y. Efficient knockout of the phytoene desaturase gene in a hybrid poplar (*Populus alba* × *Populus glandulosa*) using the CRISPR/Cas9 system with a single gRNA. *Transgenic Res.* 2021, 30, 837–849. [CrossRef] [PubMed]
- 271. An, Y.; Zhou, Y.; Han, X.; Shen, C.; Wang, S.; Liu, C.; Yin, W.; Xia, X. The GATA transcription factor GNC plays an important role in photosynthesis and growth in poplar. *J. Exp. Bot.* 2020, *71*, 1969–1984. [CrossRef] [PubMed]
- 272. Qin, S.; Fan, C.; Li, X.; Li, Y.; Hu, J.; Li, C.; Luo, K. LACCASE14 is required for the deposition of guaiacyl lignin and affects cell wall digestibility in poplar. *Biotechnol. Biofuels* 2020, 13, 197. [CrossRef] [PubMed]
- 273. Leite Montalvão, A.P.; Kersten, B.; Kim, G.; Fladung, M.; Müller, N.A. ARR17 controls dioecy in Populus by repressing B-class MADS-box gene expression. *Philos. Trans. R. Soc. B* 2022, 377, 20210217. [CrossRef]
- 274. de Vries, L.; Brouckaert, M.; Chanoca, A.; Kim, H.; Regner, M.R.; Timokhin, V.I.; Sun, Y.; De Meester, B.; Van Doorsselaere, J.; Goeminne, G. CRISPR-Cas9 editing of CAFFEOYL SHIKIMATE ESTERASE 1 and 2 shows their importance and partial redundancy in lignification in Populus tremula× P. alba. *Plant Biotechnol. J.* 2021, 19, 2221–2234. [CrossRef]
- 275. Takata, N.; Awano, T.; Nakata, M.T.; Sano, Y.; Sakamoto, S.; Mitsuda, N.; Taniguchi, T. Populus NST/SND orthologs are key regulators of secondary cell wall formation in wood fibers, phloem fibers and xylem ray parenchyma cells. *Tree Physiol.* 2019, 39, 514–525. [CrossRef]
- Azeez, A.; Busov, V. CRISPR/Cas9-mediated single and biallelic knockout of poplar STERILE APETALA (PopSAP) leads to complete reproductive sterility. *Plant Biotechnol. J.* 2021, 19, 23. [CrossRef]
- 277. Harding, S.A.; Tuma, T.T.; Aulakh, K.; Ortega, M.A.; Ci, D.; Ou, Y.; Tsai, C. Tonoplast sucrose trafficking modulates starch utilization and water deficit behavior in poplar leaves. *Plant Cell Physiol.* **2022**, *63*, 1117–1129. [CrossRef]
- André, D.; Marcon, A.; Lee, K.C.; Goretti, D.; Zhang, B.; Delhomme, N.; Schmid, M.; Nilsson, O. FLOWERING LOCUS T paralogs control the annual growth cycle in *Populus* trees. *Curr. Biol.* 2022, 13, 2988–2996. [CrossRef]
- 279. Wang, W.; Talide, L.; Viljamaa, S.; Niittylä, T. Aspen growth is not limited by starch reserves. *Curr. Biol.* **2022**, *32*, 3619–3627. [CrossRef] [PubMed]
- Liu, B.; Liu, J.; Yu, J.; Wang, Z.; Sun, Y.; Li, S.; Lin, Y.J.; Chiang, V.L.; Li, W.; Wang, J.P. Transcriptional reprogramming of xylem cell wall biosynthesis in tension wood. *Plant Physiol.* 2021, 186, 250–269. [CrossRef] [PubMed]
- Li, S.; Lin, Y.J.; Wang, P.; Zhang, B.; Li, M.; Chen, S.; Shi, R.; Tunlaya-Anukit, S.; Liu, X.; Wang, Z. The AREB1 transcription factor influences histone acetylation to regulate drought responses and tolerance in *Populus trichocarpa*. *Plant Cell* 2019, 31, 663–686. [CrossRef] [PubMed]
- Wang, Z.; Mao, Y.; Guo, Y.; Gao, J.; Liu, X.; Li, S.; Lin, Y.J.; Chen, H.; Wang, J.P.; Chiang, V.L. MYB transcription factor161 mediates feedback regulation of secondary wall-associated NAC-Domain1 family genes for wood formation. *Plant Physiol.* 2020, 184, 1389–1406. [CrossRef]
- 283. Liu, H.; Gao, J.; Sun, J.; Li, S.; Zhang, B.; Wang, Z.; Zhou, C.; Sulis, D.B.; Wang, J.P.; Chiang, V.L. Dimerization of *PtrMYB074* and *PtrWRKY19* mediates transcriptional activation of PtrbHLH186 for secondary xylem development in Populus trichocarpa. *New Phytol.* 2022, 234, 918. [CrossRef]
- 284. Xu, W.; Cheng, H.; Zhu, S.; Cheng, J.; Ji, H.; Zhang, B.; Cao, S.; Wang, C.; Tong, G.; Zhen, C. Functional understanding of secondary cell wall cellulose synthases in *Populus trichocarpa* via the Cas9/gRNA-induced gene knockouts. *New Phytol.* 2021, 231, 1478–1495. [CrossRef]
- Zhao, Y.; Yu, X.; Lam, P.; Zhang, K.; Tobimatsu, Y.; Liu, C. Monolignol acyltransferase for lignin p-hydroxybenzoylation in *Populus*. *Nat. Plants* 2021, 7, 1288–1300. [CrossRef]
- 286. Jia, H.; Zhang, Y.; Orbović, V.; Xu, J.; White, F.F.; Jones, J.B.; Wang, N. Genome editing of the disease susceptibility gene CsLOB 1 in citrus confers resistance to citrus canker. *Plant Biotechnol. J.* 2017, 15, 817–823. [CrossRef]
- Jia, H.; Xu, J.; Orbović, V.; Zhang, Y.; Wang, N. Editing citrus genome via SaCas9/sgRNA system. Front. Plant Sci. 2017, 8, 2135. [CrossRef]
- 288. Gomez, M.A.; Lin, Z.D.; Moll, T.; Chauhan, R.D.; Hayden, L.; Renninger, K.; Beyene, G.; Taylor, N.J.; Carrington, J.C.; Staskawicz, B.J. Simultaneous CRISPR/Cas9-mediated editing of cassava eIF 4E isoforms nCBP-1 and nCBP-2 reduces cassava brown streak disease symptom severity and incidence. *Plant Biotechnol. J.* 2019, 17, 421–434. [CrossRef]
- Mehta, D.; Stürchler, A.; Anjanappa, R.B.; Zaidi, S.S.; Hirsch-Hoffmann, M.; Gruissem, W.; Vanderschuren, H. Linking CRISPR-Cas9 interference in cassava to the evolution of editing-resistant geminiviruses. *Genome Biol.* 2019, 20, 80. [CrossRef] [PubMed]
- 290. Van Zeijl, A.; Wardhani, T.A.; Seifi Kalhor, M.; Rutten, L.; Bu, F.; Hartog, M.; Linders, S.; Fedorova, E.E.; Bisseling, T.; Kohlen, W. CRISPR/Cas9-mediated mutagenesis of four putative symbiosis genes of the tropical tree *Parasponia andersonii* reveals novel phenotypes. *Front. Plant Sci.* 2018, 9, 284. [CrossRef]
- 291. Walawage, S.L.; Zaini, P.A.; Mubarik, M.S.; Martinelli, F.; Balan, B.; Caruso, T.; Leslie, C.A.; Dandekar, A.M. Deploying genome editing tools for dissecting the biology of nut trees. *Front. Sustain. Food Syst.* **2019**, *3*, 100. [CrossRef]
- Cui, Y.; Zhao, J.; Gao, Y.; Zhao, R.; Zhang, J.; Kong, L. Efficient multi-sites genome editing and plant regeneration via somatic embryogenesis in *Picea glauca*. Front. Plant Sci. 2021, 12, 2198. [CrossRef]

- 293. Nanasato, Y.; Mikami, M.; Futamura, N.; Endo, M.; Nishiguchi, M.; Ohmiya, Y.; Konagaya, K.; Taniguchi, T. CRISPR/Cas9mediated targeted mutagenesis in Japanese cedar (*Cryptomeria japonica* D. Don). *Sci. Rep.* **2021**, *11*, 16186. [CrossRef] [PubMed]
- 294. Pavese, V.; Moglia, A.; Corredoira, E.; Martínez, M.T.; Torello Marinoni, D.; Botta, R. First report of CRISPR/Cas9 gene editing in *Castanea sativa* Mill. *Front. Plant Sci.* **2021**, *12*, 728516. [CrossRef]
- 295. Elorriaga, E.; Klocko, A.L.; Ma, C.; Du Plessis, M.; An, X.; Myburg, A.A.; Strauss, S.H. Genetic containment in vegetatively propagated forest trees: CRISPR disruption of LEAFY function in Eucalyptus gives sterile indeterminate inflorescences and normal juvenile development. *Plant Biotechnol. J.* 2021, 19, 1743–1755. [CrossRef] [PubMed]