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Review

Will "Tall Oaks from Little Acorns Grow"? White Oak (*Quercus alba*) Biology in the Anthropocene

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Abstract: *Quercus alba* L., also known as white oak, eastern white oak, or American white oak, is a quintessential North American species within the white oak section (*Quercus*) of the genus *Quercus*, subgenus *Quercus*. This species plays a vital role as a keystone species in eastern North American forests and plays a significant role in local and regional economies. As a long-lived woody perennial covering an extensive natural range, *Q. alba*'s biology is shaped by a myriad of adaptations accumulated throughout its natural history. Populations of *Q. alba* are crucial repositories of genetic, genomic, and evolutionary insights, capturing the essence of successful historical adaptations and ongoing responses to contemporary environmental challenges in the Anthropocene. This intersection offers an exceptional opportunity to integrate genomic knowledge with the discovery of climate-relevant traits, advancing tree improvement, forest ecology, and forest management strategies. This review provides a comprehensive examination of the current understanding of *Q. alba*'s biology, considering past, present, and future research perspectives. It encompasses aspects such as distribution, phylogeny, population structure, key adaptive traits to cyclical environmental conditions (including water use, reproduction, propagation, and growth), as well as the species' resilience to biotic and abiotic stressors. Additionally, this review highlights the state-of-the-art research resources available for the *Quercus* genus, including *Q. alba*, showcasing developments in genetics, genomics, biotechnology, and phenomics tools. This overview lays the groundwork for exploring and elucidating the principles of longevity in plants, positioning *Q. alba* as an emerging model tree species, ideally suited for investigating the biology of climate-relevant traits.

Keywords: *Quercus alba*; adaptations; environmental stress; Anthropocene; woody perennial; climate-relevant traits; research resources

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1. Introduction

Oaks (*Quercus* spp.), as long-lived deciduous trees, are central to the biology of our planet, both as individual species and as members of complex ecosystems. Oaks underpin many regional and local economies worldwide and have been of great cultural significance for eons. Collectively, oak species contribute, either directly or indirectly, to human nutrition, medicines, energy, paper, construction materials, and ornamental landscape applications, and are socially and culturally significant, even in our advanced technology era [1]. Oaks are often dominant species within natural ecosystems, store significant amounts of sequestered carbon, provide ecosystem services such as water purification and oxygen production, and serve as keystone species that anchor complex multi-trophic communities [2]. These attributes derive in large part from the life history strategy of trees as long-living woody perennial plants, with the ability to adapt acutely and chronically to ever-changing environmental conditions [3,4]. Critically, the genomic evidence reveals that oaks have so far exhibited rapid adaptation to the changing climate of the Anthropocene [5], a chapter in history that is only just beginning.

1.1. Quercus alba L.

Quercus alba is the archetypic representative of the *Quercus* ('white oak') section of the oak genus *Quercus* (for phenotypic identifiers see Figure 1A), one of eight genera in the Fagaceae (beech) family. In eastern North America, one of the most important tree species to communities, regional economies, and industries, as well as being a keystone species of natural forest ecosystems [2]. The species accounts for the largest volume of oak lumber harvested from US forests, for use in flooring, furniture, construction, and the production of millions of barrels every year for the wine and spirits industry [6,7]. *Quercus alba* acorns serve as an important dietary component for many wild animal species, of prime importance after extirpation of the American chestnut (*Castanea dentata*).

Quercus alba has historically been a dominant canopy species in the central and eastern hardwood forests of North America from pre-European settlement times, providing important ecosystem services including habitat for a wide diversity of organisms, sequestering carbon, and filtering air and water [8–13] (Figure 1B). With the changing land-use patterns, *Q. alba* recruitment (growth into the forest canopy) declined during the 20th century with a concomitant decrease in white oak presence in North American forests (Figure 1C). Contrastingly, other oaks prospered during this period, leading to several important questions whose answers are critical to forecasting the future of the species, especially in rapidly changing climate scenarios. As posed by Abrams (2003 [8]), "Why did white oak, among all the upland oaks, dominate in the presettlement forest? What restricted the development of red oak in the presettlement forest on sites that it currently dominates? What role did anthropogenic factors play in the expansion of red oak and chestnut oak versus white oak? What ecophysiological limitations make white oak more susceptible than other oaks to the dramatic changes in land use over the past few hundred years?" Key to answering these questions is understanding the oak trait biology associated with competitive success in environmental niche adaptations. Thus, in *Q. alba* and other sympatric forest tree species, a more systematic, integrative understanding is needed; this would ideally encompass root/mycorrhizal biology, root/stem/leaf water transport, and vascular dynamics, as well as the physiological and genetic control of these traits and phenology, masting, and seedling regeneration in normal and abiotic/biotic stress conditions. Predicting the future competitive success of *Q. alba* in a rapidly changing climate (Figure 1D) will rely on understanding the degree of the plasticity of these traits and the reproductive, recruitment, and evolutionary constraints on long-lived perennial species.

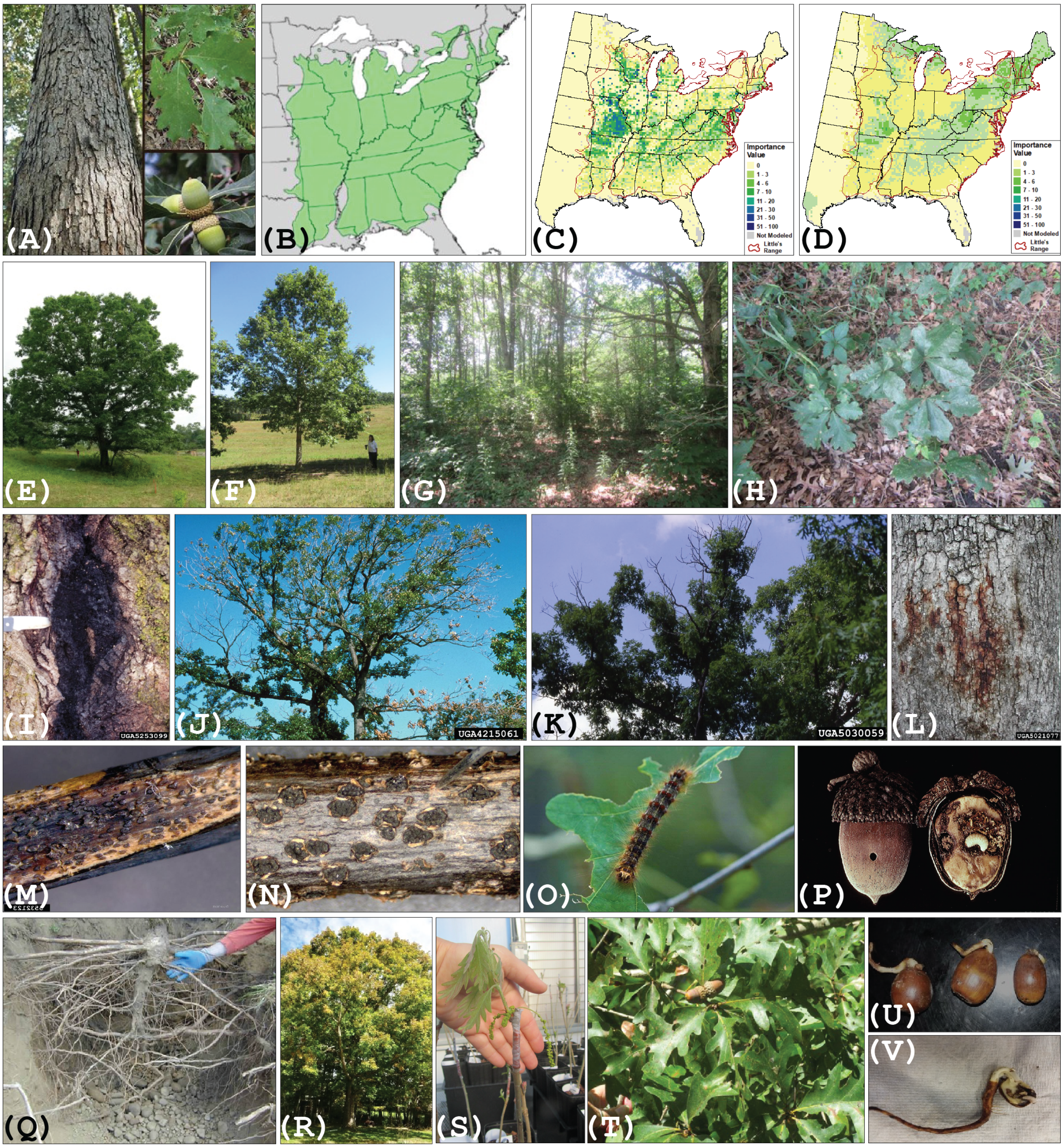

Figure 1. *Q. alba*, its range, and examples of healthy and disease/pest conditions. (**A**) *Q. alba* identifiers—bark, leaves, acorns; (**B**) Historical natural range of *Q. alba*; (**C**) Current Forest Inventory and Analysis; (**D**) Projected future habitat under harsh climate scenario; (**E**) Very old, healthy pasture tree; (**F**) Healthy seed orchard tree, Murphy NC; (**G**) White oak forest stand; (**H**) Natural regeneration; (**I**) *Phytophthora* root and crown rot; (**J**) Tree with oak wilt from *Bretziella fagacearum*; (**K**) Tree with oak decline; (**L**) Hypoxylon cankers; (**M**) Anthracnose (*Discula quercina*); (**N**) *Botryosphaeria* cankers; (**O**) *Lymantia dispar* (gypsy moth); (**P**) Acorn and nut weevils (Genus Curculio); (**Q**) Roots of 25-year-old oak tree showing taproot; (**R**) Masting *Q. alba* tree, Garrett County, MD, 2022; (**S**) Catkin on flowering *Q. alba* graft in the greenhouse; (**T**) Close-up of healthy branch with mature acorns; (**U**) Weevil exiting germinating acorn (long, healthy taproot, but the shoot is damaged and will not emerge); (**V**) Germinating acorns. Credits: (**A**) Laura DeWald; (**B**) The United States Geological Survey;

(**C**,**D**) USDA Forest Service https://www.fs.usda.gov/nrs/atlas/tree/802 (accessed on 30 November 2023); (**E**) John Carlson; (**F**–**H**) Laura DeWald; (**I**,**K**) Joseph OBrien, USDA Forest Service, https://www.bugwood.org/; (**J**) Fred Baker, Utah State University, https://www.bugwood.org/; (**L**) Pennsylvania Department of Conservation and Natural Resources—Forestry, https://www.bugwood.org/; (**M**,**N**) Bruce Watt, University of Maine, https://www.bugwood.org/; (**O**) John Ghent_Bugwood.org; (**P**) Louisiana State University, https://www.bugwood.org/; (**Q**) USDA Forest Service https://www.fs.usda.gov/; (**R**) William Buckel; (**S**–**V**) Laura DeWald.

1.2. Challenges for Oaks in the Anthropocene

Due to the continued rapid warming of the Earth during the Anthropocene, climate change is and will continue to impact the sustainability of global forest tree resources, both directly and indirectly [5]. Given sufficient time as regional climate conditions change, species may adapt to changing environments. However, rapid environmental changes pose major challenges to perennial species with very long generation times. This is particularly true for trees which can have long juvenility periods and cycles of flowering, seed production, and seed germination that are dependent on specific environmental conditions. Since adaptation relies on reproduction, the continued survival of long-lived species in their current locations is particularly uncertain. Indeed, direct impacts of recent global warming on tree reproduction are being reported in both fruit orchard and forest trees [14–19], and research is needed to understand the impact on perennials as climate change advances.

Considering the importance of oaks to ecosystems and the human endeavor, it is surprising how fragmented our climate-relevant knowledge of the biology of oak species is in comparison to that of economically important herbaceous species [20]. This is, in part, the result of long-lived perennial trees having been considered difficult models for the study of basic cellular, physiological, or genetic processes. Multiple reasons for this are apparent, but, particularly, the long sexual generation times and difficult asexual propagation methods are considered most inhibitory for basic research. This contrasts with annual crops and model plants where generation cycles can be months, not decades, providing well-controlled genetic materials for study. However, the realities of climate change, an ever-increasing population needing shelter and energy, and our emerging understanding of the crucial role that oak trees play in our environment have become compelling forces for important oak biology research across all levels, from cellular and whole-plant physiology, genetics, and genomics to forest ecology and species conservation. Rapidly advancing molecular technologies and large-scale, big data-driven approaches have generated powerful model systems for trees [21–24]. The study of oak biology provides new opportunities to delve deeper into the key features that define woody perennial plants and are shared among oaks and other hardwood forest trees [25].

The intent of this communication is to present an emerging picture of the current knowledge on *Q. alba* biology drawn from previous, ongoing, and future research perspectives as an example of a North American oak species that is critically important to regional/global economies and natural ecosystems. It is particularly timely as the sustainability of forests, including oak forests, are impacted by a rapidly changing environment. This overview aims to provide a foundation for defining and studying the emerging principles of long-lived perennial trees with a special emphasis on challenges posed to *Q. alba* in the Anthropocene, especially those related to the need for mitigation of climate change impacts and improvement of natural regeneration. For more detailed reviews of related phylogeny, diversity, ecology, and evolutionary studies on other *Quercus* species from the growing global community of oak researchers, readers are directed to other recent works such as [26,27].

2. Phylogeny and Distribution

Oaks (*Quercus* L., Fagaceae) are a large global genus of woody plants that dominate northern temperate deciduous forests [28]. Recent phylogenic divisions of the genus based on morphology and molecular genetics data divide the genus *Quercus* into two subgenera: subgenus *Cerris*, comprised of the three sections *Cyclobalanopsis*, *Cerris*, and *Ilex*; and subgenus *Quercus*, comprised of the five sections: *Lobatae* (red oaks), *Protobalanus* (intermediate oaks), *Ponticae* (California oaks), *Virentes* (live oaks), and *Quercus* (white oaks) [29,30] (Figure 2A). *Quercus* sect. *Quercus* includes 146 species distributed throughout North America, Central America, Western Eurasia, East Asia, and North Africa [31], of which 112 are found in North America (45 in the US and 67 in Mexico) [32,33]. Recent studies using genome sequencing technologies revealed that American oaks arose in North America and spread to the south, similar to pines [32–34] (Figure 2B). This dispersal pattern resulted in four major lineages. Species in the red and white oak sections radiated sympatrically and broadly across the north. Live oak and golden cup oak section species showed a much higher rate of parallel diversification, potentially driven by the more recent adaptation to milder niches in Mexico, based on climate and regional moisture gradients, relative to long-term diversifications [32,33] (Figure 2A).

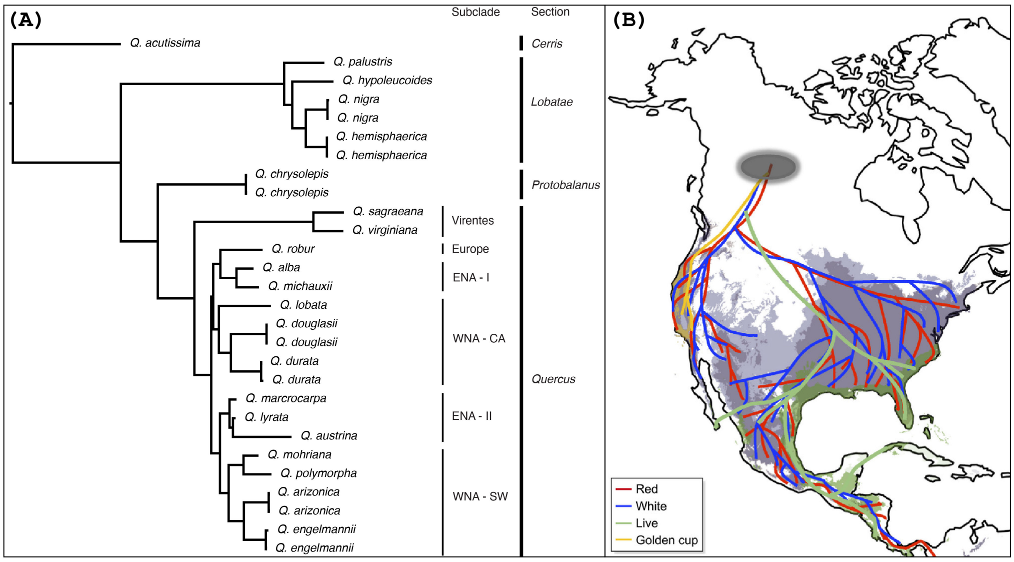

Figure 2. Phylogeny and speciation of clades in North American Oaks. (**A**) Phylogenetic tree of *Quercus*, focusing on species within the North American clade, from maximum likelihood analysis of RADseq data [31]; (**B**) Suggested migration routes from a common refugia pattern that can account for the sympatric parallel adaptive radiation of the four oak clades in North America [32,33].

North America has the greatest number of oak species (~240), encompassing the red, white, and intermediate sections of species and ranging from the east to west coast, from southern Canada through Mexico, and beyond to the Andes of Columbia [35]. Oaks populate a moisture gradient of environments, from the dry mesic conditions of the southwestern United States and Mexico, to the wet conditions in the southern limits of the northern boreal forest in northeastern US and southeastern Canada [35–38].

Quercus alba is one of the most widely distributed tree species in North America and grows throughout much of the eastern United States. Its historical distribution ranged from Maine to northern Florida, north through southern Ontario and Quebec, and west to Iowa, Kansas, Oklahoma, and Minnesota (Figure 1B) [37,39]. It is a relatively common as well as wide-spread species, but its abundance and ecological importance vary greatly with habitat factors across its range [2,32,40]. In addition to historical trends, recent declines in *Q. alba* oak populations within eastern forests from overharvesting, high grading, inconsistent regeneration, and poor regeneration are raising concerns [8,41] (Figure 1C). In addition, the range, abundance, and ecological importance of *Q. alba* is expected to shift as the climate changes [42] (Figure 1C,D).

3. White Oak Regeneration and Recruitment

A prominent factor affecting the eastern oak resources has been the ecological legacy of change in human disturbance patterns on the landscape. Prior to European settlement, the region's oak forests were maintained through periodic disturbances which included the use of fire by Native Americans [43,44]. The nature and intensity of post-European settlement disturbance combined with factors such as the demise of the America chestnut increased the prominence of oak on the landscape [44–46]. Since the mid-20th century, fire has been largely removed as a landscape-level disturbance [43], with the intensity and spatial magnitude of other human disturbance on the region's forests greatly increasing.

The demographic and distribution patterns of the eastern oak resources reflect the historical timeline of human use and successional responses of forest communities (Figure 1C,D). The contemporary age structure of the region's oak forests is skewed toward older age classes, with 60 to 70% of forests today between the ages of 40 and 100 years old and only 5 to 10% of oak forests being less than 10 years old [47,48] (Figure 1E,F). Near-term oak supplies are stable due to the large standing volumes in largely even-aged forests whose origin was facilitated by late 19th and early 20th century land-use and disturbance patterns. However, widespread recruitment failures throughout its geographic range have been reported by forest managers for many years [49]. Oaks in the canopy are being replaced by non-oak species [50,51] from forest successional dynamics that are influenced by the high levels of deer herbivory and a reduced frequency of low intensity fire which results in increased competition for light, water, and nutrients [44,50,52–56]. As overstory oaks are eliminated through natural mortality and harvesting, the inadequate recruitment of competitive *Q. alba* seedlings results in stand compositional shifts toward more shade-tolerant species such as red maple (*Acer rubrum* L.) and American beech (*Fagus grandifolia* Ehrh.) [37,57,58]. In these shaded conditions, the relatively poor competitiveness of *Q. alba* is due to slow above-ground juvenile growth and a preferential allocation of resources to the root system, combined with intermediate shade tolerance [34,57,59]. In recognition of the lack of *Q. alba* recruitment and large-scale species compositional shifts, efforts to conserve and restore oak ecosystems have been increasing (e.g., [51,60,61]). In addition to a variety of management approaches that are being tested and implemented (e.g., [52,62–65]), organizations such as the White Oak Initiative (www.whiteoakinitiative.org) have been created in order to support the sustainable growth of the *Q. alba* resources [66].

4. Climate Change and *Quercus alba* Biology: Direct Impacts

As sessile organisms, temperate trees have developmental and reproductive systems that are optimized for the annual cycle of changing environmental conditions. From studies of different plant species, these systems are sensitive to light/dark cycling, day/night temperatures, water availability, or a combination of the three. For a tree species in a particular climate zone, there are several key physiological systems adapted to the cyclic changing environmental conditions. These include but are not limited to: (1) tree water maintenance and transport systems; (2) juvenility and reproductive systems; (3) meristematic growth and development systems; and (4) abiotic and biotic cellular stress response systems. All these systems are composed of phenotypic traits that are critical for maintaining the species in its current environment. For *Q. alba*, as discussed above, of great interest are traits that maintain regeneration (flowering, pollination, seed development, and seedling survival and growth), enhance recruitment (drought and shade tolerance and sapling survival and growth) (Figure 1H), and tolerate or resist biotic (pathogens and pests) (Figure 1I–P) and abiotic stress.

Adaptation can be a long-term process depending on the phenotypic plasticity and genetic basis for any trait, especially for species with long generation times. Therefore, rapid climate change poses a significant threat to the continued presence of such species in their current environment. To predict the future success and distribution of oaks in the changing temperate forest zones with the objective of potentially assisting its future success, we must know: (1) Which adaptive traits were key to the oaks' success in their extant locations? (2) What is the degree and mechanism of phenotypic plasticity and/or genetic variation for these traits required by individuals or populations for adaptation? (3) What genes or molecular networks control the climate critical traits? (4) Which of these traits should be prioritized as targets for oak management, reforestation, and genetic improvement efforts in the future? The following are examples of oak traits likely to be important in their adaptive responses to rapid climate change.

4.1. Water Relations: Control of Root Growth in Oaks

Predicting the future success and distribution of *Q. alba* in North America relies heavily on our understanding of the physiology and genetics underlying this species' ability to adapt to the direct impacts of increased environmental warming. Although we have very limited knowledge of this in *Q. alba*, significant studies of drought tolerance and related traits, such as water-use efficiency in other models for annual and woody plant species [67–69], have provided research targets and foundational studies for deployment in the research on *Q. alba*. From the genetic perspective, several studies have revealed the sources of variation and candidate genes underlying drought tolerance and adaptation in European white oaks [70–74]. Unlike four other northeastern oaks studied by Reed and Kaye [75], *Q. alba* is responsive to rich soil composition and higher moisture levels, associated shale vs. sand bedrock. However, data and publications on the performance of *Q. alba* on different types of soil are scarce (for more information on site recommendations for *Q. alba*, refer to [76]). As *Q. alba* have a taproot architecture (Figure 1Q), presumably to enable deep soil water acquisition under drought conditions, studies focusing on the control of the development of this root form in woody plant species are particularly relevant.

Oaks exhibit both shallow and deep rooting systems, allowing them to access water at multiple depths in the soil profile during the annual cycles of rain and drought. They successfully compete with species possessing rooting systems more specialized for deep soil (e.g., maples and pines) [36]. The rooting architecture of oaks in concert with stem vascular organization (ring porous) and leaf structural features (thickness, stomatal size) enable oaks to exploit niches across regional and climatic zones greatly differing in hydrologic conditions [36,37], from mesic to xeric. Equally important, oaks survive and prosper in a broad range of different edaphic conditions and drought stress, due to the structural features of oak vascular tissues such as tyloses (vascular structures arising post-differentiation that limit the diffusion of liquids through the wood sample [77], deep rooting, and the ability to form and sustain mycorrhizal associations with a high diversity of fungi; for review, see [78]). *Quercus* species distributions provide excellent examples of how these anatomical traits and their associated physiological systems have enabled the species to become dominant in North American forests across a large range of environments (for a review of physiological characteristics, see [32,36,37,40,79]).

A recent review by Kościelniak et al. [80] lays out the current status of our understanding of taproot development and its control while highlighting several questions that need future study: "(1) how does organization and cellular signaling enable a taproot to grow and penetrate deep soil layers, (2) what internal factors enable taproots to grow rapidly and penetrate deep soil layers (Figure 1Q), and (3) how does soil water limitation induce the vertical growth of taproots (Figure 1Q). Aside from the unanswered questions above, how much does the genetic control of cell division explain the continued maintenance of root growth and apical dominance of taproot meristems?" As outlined by Kościelniak et al. [80], emerging concepts in the control of root growth come from studies of models such as *Arabidopsis* and other model tree species (e.g., *Populus* species). The control of root growth and architecture is related to phytohormone balance and pathway regulation, plant growth and development transcription factors, microRNAs, and signal transduction pathways. Additionally, emerging studies indicate that epigenetic factors likely also play a key role in the adaptive responses of trees to environmental change (for review, see [81,82]). In the case of epigenetics, work in *Populus* species on drought stress transcriptomic responses of clonally propagated material planted in differing geographic regions demonstrates specific DNA methylation patterning correlated with provenance and drought stress transcriptomic responses [82]. These types of studies linking local adaptation to epigenetic marks in reference to oak adaptation could unlock potential plasticity targets for the improvement of the species.

4.2. Reproduction

In European white oaks, Caignard et al. [83] presented evidence that increasing temperatures associated with climate change are responsible for an observed increased seed production in environments that are historically cooler and currently not impacted by water deficit. This contrasts to studies of other oak species in regions experiencing both temperature increase and water deficit, whereby tree growth and survival were negatively impacted by a warming climate [84]. Effects on other aspects of oak reproduction (e.g., masting) and the effects of other environmental changes (e.g., drought) need to be established before any meaningful modelling about the future habitat of deciduous oaks in the temperate forests. Current predictions suggest that oaks will expand northward with changing climate zones and retreat in warmer drought-prone areas. A recent limited provenance study of *Q. alba* performance suggests that white oaks from northern temperate locations, when challenged with more southerly climate conditions, do not perform as well as trees from more southern provenances, suggesting that there may be a fitness cost for *Q. alba* as the climate zones shift further northward [85]. Research into the fundamental genetics and physiology of oak species regeneration in response to environmental conditions are needed to predict outcomes and produce strategies in order to promote the continued presence and establishment of white oaks.

4.3. Pollination

Long-distance pollination is a well-established feature of the maintenance of genetic diversity within oak stands [86] (for review, see [7]). Multiple studies of isolated stands have revealed that long-distance pollen dispersal is evident and leads to the conclusion that the fragmentation of oak populations due to repurposed land use may not necessarily lead to local losses in genetic diversity [87–98]. However, other barriers may lead to loss of diversity or inbreeding, such as genetically determined fertilization incompatibilities and/or timing of flowering, which may play a significant role in determining the genetic architecture of oak forest stands, despite pollen dispersal [86]. Thus, climate change could lead to local maladaptation, due to incompatible phenology, making it difficult to predict future oak sustainability for species such as *Q. alba*, for which we know little regarding these traits and at what spatial scales these traits have adapted.

4.4. Flowering

Oaks are monoecious, with staminate and pistillate flowers on the same tree. Little is known of the physiology or genetics of the regulation of flowering in oaks. Contrastingly, there is a substantial body of growing knowledge about the molecular basis of flowering control in some model forest and fruit tree species (for recent review, see [99]). Both floral and leaf bud dormancy are initiated and controlled by key environmental factors such as light (day length), cold (chilling requirement), and stress (abiotic: heat, cold, osmotic; biotic: pathogens and pests). All of these will likely be significantly impacted by climate change. The establishment, maintenance, and release of dormancy are regulated by gene networks that respond to these different environmental cues, depending on the individual adaptation of a particular species or population. For example, *Prunus* fruit trees, such as peach (*P. persica*), establish, maintain, and release bud dormancy via pathways that are sensitive to temperature [100], while in *Populus* species, these steps are regulated more by day length [101] (reviewed by [102,103]). In general, these networks involve light response networks, temperature response networks, hormone pathways, cell cycle control, epigenetics, and others [99,100]. Genomics-based research on dormancy in the European pedunculate oak (*Q. robur*) has highlighted some of the gene networks evident in these previous fruit and forest tree studies, suggesting that oaks may utilize similar genetic control mechanisms as other tree species [104]. However, it is difficult to predict and improve the performance of *Q. alba* in terms of flowering traits (Figure 1S) without first obtaining substantial knowledge of the physiological, ecological, and genetic systems that underpin these traits in this species.

4.5. Masting

Masting is a population scale synchronous flowering event observed in certain tree species. However, as pointed out in a detailed review of the genetic control of masting [105], the manifestation of this event is dependent on the diversity in the flowering control mechanism among individual members of the species (diversity) and the coordinated response of these individuals within a population and year (synchrony). A resource-driven pollen limitation hypothesis was directly supported for two European oaks species, *Q. petrea* and *Q. robur* [106]. From studies of other perennial and annual plant species, the physiological and genetic control of masting could likely involve molecular networks controlling flowering and dormancy release [99,105,107]; abiotic and biotic stress response [108]; seed maturation, meristem growth, and developmental control [80,109]; root/shoot communication and sink-source physiology [110,111]; the epigenetic regulation of gene activity [112], and potentially others. Although not possible in the past, access to gene information in oaks is rapidly increasing (see Emerging tools and resources for oak biology and improvement, below) and the stage is ideally set to make significant progress in understanding the physiological and genetic underpinnings of this important climate critical trait in *Q. alba* (Figure 1R,T,U).

4.6. Seed Germination

In oaks, there are contrasting climate-related seedling germination strategies. In general, white oaks do not exhibit a stratification requirement and germinate in the fall, concomitant with acorn drop (Figure 1U), while red oak acorns overwinter and germinate the following spring during more favorable growing temperatures [113,114]. In some red oaks, this stratification requirement is not absolute as acorns will germinate without prior cold treatment (e.g., *Quercus pagoda* Raf. [115]); however, the germination efficiency increases substantially with cold treatment [113,115], leading to the conclusion that red oaks exhibit a physiological dormancy, rather than true dormancy (endodormancy) which is associated with cell cycle arrest and chill requirement for dormancy release. Unfortunately, we know very little about the genetics and physiology of this climate critical trait in oaks in contrast to what is known regarding annual crop and model species plants. In recent years, through studies of annual crop models, *Arabidopsis*, and a few woody perennial species (e.g., peach, poplar, and grape), major advances have been made in our understanding of the genetic and physiological underpinnings of seed and bud dormancy in plants. For reviews on seed germination, see [116], and for bud dormancy, [99]. However, much of our knowledge of seed dormancy and germination control comes from studies of plants with orthodox (annual) or typical seeds, such as *Arabidopsis*, whereby seeds mature concomitant with desiccation. This is not the case for recalcitrant or intermediate seed species, including oaks or other nut-producing species like chestnut, for which the desiccation of seeds after maturity significantly negatively impacts seed viability and germination [113,117].

The relationship between the chemistry, germination timing, and dispersal of acorns has been an area of interest for quite some time. An early study on germination in oaks [113] suggested that the fat content of acorns may be related to the germination control in red oak acorns and not the tannin content of the seed. Subsequent reports on northern red oak (*Quercus rubra*) and *Q. alba* germination and dispersal over the following decades were synthesized into a Differential Dispersal Hypothesis (DDH) [118], based on the characteristics of acorns reported to affect germination, feeding, and dispersal by animals.

The DDH summarized the primary features of *Q. alba* acorns affecting dispersal, such as low tannin and low-fat content, and early germination, predisposing *Q. alba* acorns to immediate and/or selective consumption (relative to northern red oak) in autumn, or embryo excision by squirrels prior to cashing. In northern red oak, acorns traits affecting dispersal included high tannin and high fat content, with delayed germination, associated with the selective caching of northern red oak acorns (relative to *Q. alba*) for later consumption during winter. Overall, the DDH predicted that northern red oak acorns would be selectively scatter-hoarded by animals across greater dispersal distances than *Q. alba*, especially smaller-seeded acorns, which jays could disperse over very long distances, primarily into open areas suitable for oak regeneration. More recently, studies in sawtooth white oak (*Q. aliena* var. *accuserata*) suggested that the acorn pericarp and cotyledons contain substances that inhibit germination, and that the removal of the pericarp and a portion of the cotyledon can increase germination efficiency [119]. The germination morphology of *Q. alba* seeds (the plumule separated from the cotyledons) (Figure 1U,V) promotes seedling establishment in case of pruning by rodents [120]. The comparison of red and white oak species acorns by maturity and germination demonstrates that transitions from maturation to germination show changes in cellular location and the metabolism of lipids, insoluble and soluble carbohydrates, and proteins (reviewed by [121]). Many features of the interaction of the genotype, phylogeny, ecotype, and physiology of seed germination remain to be clarified. For a more comprehensive history and detailed overview of ecology and biology research findings for oak seed dispersal, see [122]. Recent phylogenomic analyses have also highlighted the importance of seed structure and germination in the radiation of species, as well as introgression, within the Fagaceae family [123].

4.7. Seedling Growth Control

In oaks, some studies examine the effect of seed size on seed germination and seedling survival (for review see [124]). Among species, the question of seed size versus seed abundance for optimal species survival seems not to be an issue of a simple tradeoff but may also incorporate the longevity of the large-seeded species and the consequences of continued reproduction over extended time periods. Among and within species studies suggest that the larger seeds may have a significant advantage in germination and subsequent seedling recruitment [113,125–128]. Llanderal-Mendoza et al. [126] suggest that decreases in acorn size along latitudinal climatic differences in *Q. rugosa* in Mexico effect successful recruitment whereby the northward expansion of the species range has led to smaller-sized acorns with a reduction in germination and recruitment. Conclusions from this work were supported and further extended to other *Quercus* species in Mexico [127], whereby they demonstrated that, in a common garden experiment for seven red oak species and three white oak species, acorn fresh weight was positively correlated with germination efficiency, and acorn dry matter was driving this correlation. Furthermore, they demonstrated that nutritional storage compounds and not water content were responsible for this result. This size effect was consistent when compared between red and white oak species, as well as within red and white oak species. Finally, a recent study [128] demonstrated that large seed size was positively correlated with seed viability in *Q. robur* acorns collected from multiple sites in Croatia over a ten-year period.

Larger seedlings can improve the competitive status of oak regeneration relative to average-sized seedlings [34,52,129]. Extra-large seedlings [130–132] can be planted to enrich advanced natural regeneration and may be especially critical when harvesting occurs in years of poor mast production, which is a regular occurrence with *Q. alba* [133]. While these seedling size considerations are important, the genetic potential of the seedlings is also important for successful regeneration. Thus, the development of high-quality, well-performing *Q. alba* seedlings for artificial regeneration should be achievable through a combination of tree genetic improvement and good nursery and planting practices [132].

Unfortunately, it is difficult to predict how results from orthodox annual seed plants will translate to oaks and other nut-producing trees. However, we now have the genomic resources and materials in key oak species to bridge this knowledge gap. As stated in [134], "hardwood seed production, seed harvest, and seedling production must be approached as a coordinated system where all aspects from flower initiation to seed development, harvest, and storage to seedling production, transplanting and establishment are integrated. The best approach to insure predictable amounts of high-quality seeds and seedlings is to establish and manage seed orchards and use container production". However, sustained regenerative success in the forest in the long term will rely on an understanding of the genetic and environmental interplay on climate-relevant traits that underpin seed production, germination, and seedling establishment (Figure 1H,R–V). The contrasting strategies of flowering, seed maturation, seed germination, and seedling growth control between sympatric white and red oaks species is ideal for delimiting the genetic architecture of these climate-relevant traits and predicting the impact of climate change on their manifestation. This can lead to optimized management and tree improvement strategies incorporating genetic and physiological knowledge-based inputs.

5. Climate Change and *Quercus alba* Biology: Indirect Impacts

While the rapidly changing climate can directly impact tree growth and reproduction, it also indirectly impacts tree survival by altering the distributions of pests and pathogens, potentially leading to increased pest and pathogen pressure on native tree populations (for a review, see [135–137]). Oaks are susceptible to native and non-native pathogens (Table 1 and Figure 1I–P). Alone, many of these pests and pathogens are not necessarily lethal to the host; however, in concert with the plant stress imposed by a rapidly changing climate, these pathogens can significantly contribute to oak decline [138]. Therefore, the introduction of novel non-native pathogens or the climate-driven expansion of native pathogen ranges can be extremely detrimental to previously unexposed forest trees (for examples, see [139]). A case in point from a related Fagaceae species is the spread and subsequent impact on the American Chestnut of *Phytophthora cinnamomi* post its introduction to the eastern US [140,141]. This oomycete pathogen is hosted by over 5000 different plant species (for a review, see [142]) (see Figure 1I for *Phytophthora* root and crown rots in *Q. alba*) and is a major destructive pathogen of members of the Fagaceae. Its introduction into the southeastern US has created a major complication to the planned introduction of chestnut blight-resistant American chestnut from chestnut restoration programs. In oaks, its northward expansion with global warming is already impacting oaks and other forest trees as part of the oak decline syndrome in North America and Europe [143–145]. Another *Phytophthora* species, *P. ramorum*, is responsible for sudden oak death on California oaks (primarily *Quercus agrifolia*, coast live oak, in the red oak subgenus *Erythrobalanus*) and the related tanoak species *Notholithocarpus densiflorus* in the Fagaceae family, as well as other plant species in the western US. Its impact is predicted to mount with increased microclimate variability that is associated with climate change [146–148].

Many different diseases affect white oaks, including canker rots [149,150], oak anthracnose [151,152], leaf blisters [153], stem canker [154], oak wilt [155], oak decline [156], and stem decay [150] (Figure 1I–P for *Q. alba* images). Of all these diseases, oak decline and oak wilt are the two most devastating, with major impacts on oak survival and acorn production, resulting in altered forest structure and composition over time. Several additional diseases and insects that are rarely fatal can also impact acorn production and are expected to increase as climate change advances [157]. These relevant pathogens and pests are tabulated below (Table 1). For a more comprehensive discussion of each, see the Supplementary Materials (File S1) on diseases and pests of *Q. alba*.

Table 1. Pests and pathogens of *Quercus alba*.

Disease	Pathogen/Pest	Relevant Classification	Key Features	*Q. alba* Resistance?	References
Oak wilt	*Bretziella fagacearum* (Bretz) (Microascales: Certocystidaceae) (formerly *Ceratocystis fagacearum*)	Ascomycete fungus Necrotrophic	Vascular wilt, vectored through root grafts and sap-feeding beetles Scolytidae and Nitidulidae.	Somewhat resistant, exhibiting slower fungal growth.	[158–174]
Oak decline	*Agrilus bilineatus* Weber and *Armillaria mellea* [Vahl. Ex Fr.] and *Phytophthora cinnamomi*	Coleptylebran beetle and oomycete hemibiotroph interaction.	Caused by the interaction between severely stressed trees, secondary pests, such as the two-lined chestnut borer, and root diseases like armillaria root rot and ink disease.	Less susceptible than other North American oak species and less severe in young (less than 70 years) and heterogenous stands.	[175–181]
Hypoxylon cankers	*Hypoxylon atropunctatum* (Schw. ex Fr.) Cke	Ascomycete fungus Necrotrophic	Less pathogenic fungal species that frequently accompanies dieback.	Live healthy unstressed trees less susceptible.	[179]
Root and crown rot	*Phytophthora cinnamomi*	Oomycete hemibiotrophic	Extirpated American chestnut and a component of oak decline.	White oaks less effected by this pathogen?	[140–148,157]
Anthracnose	*Dendrostoma leiphaemia* Senan. and K.D. Hyde *(formerly Discula quercina* (Westend.) Arx Anamorph of Ascomycete *Apiognomonia quercina.*	Ascomycete fungus hemibiotrophic	One of the most damaging leaf and twig diseases, impacting reproduction and masting; widespread across North America.	Leaves are less susceptible as they age due to thicker protective cuticle; large range of the pathogen across a variety of climates suggests adaptation to distinct climates	[151,155,182]
Twig, branch and rots cankers	*Botryosphaeria spp. (including B. rhodina* [Berk. and Curt.] von Arx, *B. dothidea* [Moug. ex Fr.] Ces. and de Not., *B. obtusa* [Schw.] Shoemaker, and *B. quercum* [Sch.: Fr.] Saccardo) and *Botryodiplodia gallae* (Schw.) Petrak and Sydow	Ascomycete fungus necrotrophic/hemi biotrophic?	Can play role in oak decline syndrome.	Most susceptible under drought or cold stress.	[183]
Spongy moth (formally gypsy moth)	*Lymantia dispar*	Lepidopteran insect	A significant insect pest of *Q. alba* forests, usually in low numbers but occasionally surges surging to severe outbreaks.	*Q. alba* is preferred over the hundreds of tree species spongy moth caterpillars feed on.	[184–192]
Acorn weevil	*Curculio* and *Conotrachelus* spp.	Coleopteran insect	The major oak seed predator and a factor in the reduced regeneration in the eastern United States.	Unknown.	[193–196]

6. Emerging Tools and Resources for White Oak Biology Research and Genetic Improvement

6.1. Genomics/Genetics

The high diversity in adaptive traits and genes and the rapidly growing genomic resources for oaks make them a model clade for the integration of population, evolutionary, and ecological research, such as association mapping (Genome-wide Association Analyses, GWAS), landscape genetics, population epigenomics, paleogenomics, and phylogenomics studies. High density genetic linkage maps and Quantitative Trait Locus (QTL) studies are important tools for the detection of chromosomal regions associated with adaptive trait variation for the validation of causal associations in GWAS and of outlier loci between ecologically contrasting populations.

Due to the great ecological importance of oaks as keystone tree species across many northern hemisphere forest ecosystems, genomic resources and their applications in research have been increasing rapidly (as recently reviewed by [197,198]). This is particularly true for the white oak section, *Quercus* (sometimes referred to as subgenus *Leucobalanus*), for which sequence-based genetic markers, high density genetic linkage maps, QTLs, transcriptome resources, and whole genome assemblies are available for multiple species. Recently, the development of genomic, transcriptomic, and experimental resources for the genus *Quercus* and their applications of these resources to population genomic analyses were reviewed [199]. Here, we describe the genomics and genetics tools and resources available for white oaks. Table S1 (Supplementary Materials) summarizes the state-of-the-art genomic/genetic resources for white oak species.

Oak Genetic Maps and Genomes

Before whole genome sequencing efforts became commonplace, studies of oak genomes focused on determining the total nuclear content, the number of chromosomes, and the ploidy. The Plant DNA C-value database [200] contains details for DNA content studies across 29 oak species, which found a relatively small genome size of 0.5 to 1.22 C(pg), equivalent to a haploid genome content of 489 Mb to 1193 Mb [201–207]. Chromosome characterization in 22 of those species found 12 haploid chromosomes in a diploid state, unusually consistent for a species-rich genus [202–207].

Despite the laborious and expensive process of oak breeding, which must contend with long generation times, huge space requirements and irregular masting, pedigreed populations have been developed and leveraged in order to generate several genetic maps using a variety of marker types. The two largest and most dense are the composite genetic map for *Q. robur* and *Q. petraea* with 4261 SNP (Single Nucleotide Polymorphism) markers across 742 cM [208] and the framework genetic map for *Q. rubra* with 849 SNP markers across 652 cM [209]. The composite genetic map for *Q. robur* and *Q. petraea* was assembled from five full-sib mapping families from controlled intra- and interspecific crosses. The families were previously validated using multi-allelic microsatellite markers [210,211]. A high-density composite map could be assembled due to the high collinearity between the maps for the two species [208]. By contrast, the *Q. rubra* mapping population and genetic linkage map were developed using the paternity exclusion approach, in which full-sibs are identified with DNA markers from open-pollinated progeny families from a pair of neighboring trees.

The *Q. robur* and *Q. petraea* high-density composite map has been used to identify genomic regions associated with the adaptive traits and signatures of selection across species [212]. The evaluation of markers showing segregation distortion suggested that male gametophytic selection may be serving as a pre-zygotic reproductive barrier, at least partially, between the species [199]. The high collinearity between *Q. petraea* and *Q. robur* crosses [208] and *Q. rubra* (Northern red oak) genetic maps [209] enables the comparative mapping of adaptive traits and the identification of conserved genomic regions important in the environmental adaptation between oak sub-sections. Lower density genetic maps and full-sib families have also been generated for QTL analyses in European white oaks for a variety of traits including late flushing [213,214], bud burst timing [213,215], height growth [213], leaf morphology [213,216], water use efficiency [217], stomatal density [212], response to waterlogging [218], seed production and seed mass [219], and branching traits [220]. Applications for genetic maps in oak species have been more extensively reviewed [199]. The colocation of QTL for the timing of vegetative bud burst [221] between oak and chestnut (*Castanea sativa* Mill.) indicates that the genetic architecture of important adaptive traits may be conserved, even at the family level in the Fagaceae.

The high-density *Q. robur* and *Q. petraea* composite gene-based linkage map was also used to anchor and order scaffolds in the *Q. robur* genome assembly [222]. Subsequently, the high-density linkage map [208] was used to determine the number and location of quantitative trait loci (QTLs) underlying variation in resistance to *Erysiphe alphitoides* and *P. cinnamomi* infections along with QTLs for phenology and height growth, followed by the identification of candidate genes by reference to the genome assembly [223]. Likewise, the *Q. rubra* genetic linkage map was used to validate Hi-C chromosome-level scaffolding and to choose the orientation of the chromosomes in the recently reported reference genome assembly for *Q. rubra* [224].

Recent technological advances have simultaneously accelerated the production and the quality of sequenced reference genomes. The earliest oak genomes emerged as short read assemblies at the scaffold level for *Q. robur* [225], *Q. lobata* [226], and *Q. suber* [227]. Improvements to the *Q. robur* genome resulted in the first chromosome scale genome for oaks [222]. Currently, eleven *Quercus* species have high-quality, chromosome scale genomes, most of which are from the past year (Table 2). Two of these, *Q. robur* [228] and *Q. glauca* [229], provide haplotype resolved assemblies, i.e., a complete genomic sequence for both chromosomes, assembled independently from a diploid individual. Neither has a peer-reviewed citation but both are in public repositories. The early estimates of genome size, chromosome number, and ploidy have been borne out by the sequenced genomes to date, which range in size from 733 Mb to 926 Mb. Furthermore, no whole genome duplication events have been found since the ancient γ hexaploidization event shared by core eudicots [222,226,230–232].

The comparative analysis of the *Quercus* genomes has revealed some strongly conserved genome patterns. Oak species analyzed thus far have high genome heterozygosity, ranging from 0.5% in *Q. lobata* to 2.15% in *Q. variabilis* [222,230–233]. Despite this nucleotide level heterozygosity within species, the overall chromosome scale structure is highly conserved between species with one-to-one correspondence of the 12 chromosomes and no large rearrangements that would block hybridization. In contrast, large gene family expansions and contractions are still occurring through prevalent genome-wide tandem duplication blocks [222,230–233]. Plomion et al. [222] and Sork et al. [233] provided an in-depth analysis of this phenomenon and found that these blocks may have anywhere from a few to dozens of genes, and preferentially contain gene families that are characteristic of disease resistance, especially the NBS-type and RLK-type. Plomion et al. [222] estimated that *Q. robur* had twice the proportion of R genes to total genes in comparison to other plant species with sequenced genomes. This led to the hypothesis that R gene expansion contributes to the long lifespan and broad niche occupation of oaks in general [222,233]. Complicating this hypothesis, the R gene complement was found to be greatly reduced in *Q. mongolica*, with one third to one half as many genes in the major R gene families (NBS-type, RLP-type, and RLK-type) as in *Q. lobata* and *Q. robur*. Further clade-wide research in the R gene family expansion and contraction would be intriguing, particularly if assessed in terms of oak radiation, speciation, and adaptation.

Table 2. Currently available genomes for *Quercus* species.

Species	Subgenus	Section	Year	Genome Size (Mb)	Contig N50 (Mb)	Protein Coding Genes	Public Availability	References
Q. rubra	Quercus	Lobatae	2022	733	1.9	33,333	Phytozome v2.1	[224]
Q. lobata	Quercus	Quercus	2022	844	1	41,714	NCBI v3.2, accession GCA_001633185.5	[226,233]
Q. robur	Quercus	Quercus	2022	789 (H1); 762 (H2)	16 (H1); 1.6 (H2)	41,871	NCBI dhQueRobu3.1, accessions GCF_932294415.1 for main assembly (H1) and GCA_932294425.1 for alternate assembly (H2)	[228]
Q. glauca	Cerris	Cyclobalanopsis	2022	903 (NCBI); 865 (Hap1 FS); 896 (Hap2 FS)	7.6 (NCBI); 7.9 (Hap 1 FS); 7.3 (Hap 2 FS)	37,460 (H1); 38,312 (H2)	Genome haplotype 1 (Hap1) assembly only available at NCBI Accession GCA_023736055.1. Assembly and annotation available at figshare (FS; https://figshare.com/articles/dataset/High-quality_haplotype-resolved_genome_assemblies_of_ring-cup_oak/20448339/1 (accessed on 28 November 2023)). There is discrepancy between the Hap1 in NCBI and FigShare; NCBI appears to have more unplaced scaffolds available.	[229]
Q. gilva	Cerris	Cyclobalanopsis	2022	890	28.3	36,442	Genome from NCBI GCA_023621385.1; gene annotation from FigShare (https://doi.org/10.6084/m9.figshare.20411082.v3 (accessed on 28 November 2023))	[230]
Q. mongolica	Quercus	Quercus	2022	810	2.4	36,553	Genome from NCBI accession GCA_011696235.1; annotation from figshare (https://figshare.com/articles/dataset/A_chromosome-scale_genome_assembly_of_the_Mongolian_oak_Quercus_mongolica_/11888118/2 (accessed on 28 November 2023))	[231]
Q. variabilis	Cerris	Cerris	2022	796	26	32,466	China National GeneBank DataBase accession CNP0003390. No gene sequences available, annotation provided as gff3.	[232]
Q. dentata	Quercus	Quercus	2023	894	4.2	31,584	Genome from NCBI GCA_028216015.1, gene annotation from FigShare https://doi.org/10.6084/m9.figshare.21624159.v1 (accessed on 28 November 2023). Genome and annotation available from China National GeneBank Database accession GWHBRAD00000000	[234]

Table 2. *Cont.*

Species	Subgenus	Section	Year	Genome Size (Mb)	Contig N50 (Mb)	Protein Coding Genes	Public Availability	References
Q. acutissima	Cerris	Cerris	2022	756	1.4	31,490	Genome Warehouse in National Genomics Data Center accession GWHBGBO00000000	[235]
Q. ilex subsp. ballota	Cerris	Ilex	2023	842.2	3.3	39,443	Genome from NCBI GCA_032727855.1; no annotation publicly available.	[236]
Q. aquifolioides	Cerris	Ilex	2022	957	1.2	26,441	Genome from NCBI GCA_019022515.1, no annotation available. Sequence data deposited in the CNGB Sequence Archive (CNSA, https://db.cngb.org/cnsa/) of China National GeneBank DataBase (CNGBdb) repository, accession number CNP0003530, CNP0002992	[237]

As many of these papers emerged during 2022, almost all compare their genome to the few earlier chromosome-scale assemblies, *Q. robur* and *Q. lobata*. The plethora of oak genomes, with more to come, opens new avenues for broad comparative genomics and evolution research across the entire clade. One potential difficulty for researchers is finding and downloading genomes. The genomes we found are not available in any central location; indeed, we had to visit five different online resources to find and download the genome assemblies and annotations: NCBI Assembly (mirrored by ENA and DDBJ [238], figshare [239], Phytozome [240], CNCB-NGDC Genome Warehouse (National Genomics Data Center, China National Center for Bioinformation [241], and CNGBdb (China National GeneBank DataBase [242]. Annotations were not available for three of the genomes, and one had no gene sequences, only a gene structure file (gff3 format). This presents a major challenge to researchers. There is no central repository to identify and download genomes, and, further, there is no enforcement of shared file structure or file completeness. This problem is not restricted to oaks or to plants in general; it is an international, clade agnostic problem that must be addressed through community demand, unified and enforced submission requirements by funders and journals, data sharing between databases, and stable funding for biocuration at community databases, such as TreeGenes [243], that host and curate genomic resources.

Genomics research in oak is providing unprecedented new resolutions to studies of evolution, adaptation, and speciation. Oaks are famously a “worst case scenario for the biological species concept” [244], with many sympatric species maintaining species identity while also continuing to hybridize, forming a syngameon [245]. Lazic et al. [197] offer a comprehensive review of adaptive divergence research, highlighting the ongoing efforts to characterize the genomic signatures of this seeming contradiction. Previous studies on red oaks in North America and white oaks in both Europe and North America have reported that, while sympatric oak species each have a unique, detectable genetic identity, gene-flow occurs at relatively high rates (9–20%) between sympatric species pairs. In fact, it appears that related oaks hybridize wherever species ranges overlap (e.g., [246–249]), resulting in strong regional signals of introgression [250,251]. Hybrids are generally restricted to contact zones between species where local distributions overlap, which permits species to remain genetically and ecologically distinct [252,253]. Alleles may nevertheless introgress beyond the margins of contemporary species overlaps [212,254], leading to interspecific gene flow between species with different local adaptations. Furthermore, hybridization can be detected even beyond closely related sympatric oak species, i.e., between oak phylogenetic sections. Zhou et al. [230] detected significant gene flow among 41% of 12 species pairs tested between sections *Quercus* (white oaks) and *Ponticae* (California oaks). Kremer and Hipp [26] also found evidence of past introgression between *Quercus* and *Ponticae* sections, and more broadly across the Fagaceae family. This evidence of gene flow and subsequent genomic introgression suggests that it has contributed to adaptation in the past and may be a key resource for future adaptation in the face of climate change. Gaining further understanding of the adaptive divergence through hybridization and introgression could be invaluable to addressing climate change. As species range shifts, new opportunities for genome shuffling may be necessary for adaptation and long-term survival in new ecological niches [199].

Mechanisms underlying the maintenance of the identity of species amid gene flow within syngameons are also under investigation. In addition to pre-zygotic isolation mechanisms [242,254–256], postzygotic isolation also plays a role in the maintenance of species identity under most environmental conditions (e.g., [257,258]). Genome-wide genetic patterns differentiating oak species with different local adaptations have been detected as signatures of selection in the face of gene flow. Genome regions of high interspecific differentiation, surrounded by regions with low differentiation, distributed across nine of the twelve chromosomes, have been observed when *Q. robur* and *Q. petraea* were compared via genome scanning [199,259–263]. Gailing et al. [199] pointed out that such patterns have been predicted by models of early stages of ecological speciation amid gene flow and strong divergent selection [262–264], as is the case for the interfertile species *Q. robur* and *Q. petraea*. Furthermore, Gailing et al. [199] noted that levels of adaptive trait and gene introgression may be related to the differences in adaptations to environmental conditions, such as drought adaptation between the red oak species *Q. rubra* and *Q. ellipsoidalis* [248,265].

Considering the extensive work in genomics of white oak species presented in Table S1, and the sequencing efforts shown in Table 1, surprisingly little has been reported for *Q. alba*, arguably the most important white oak species of eastern North American forests. To address the paucity of genomics research in *Q. alba*, recent private/public partnerships (White Oak Genomics Working group, UKY; White Oak Genetics Improvement Initiative, UKY) are focusing on building *Q. alba* genetics/genomics research infrastructure, integrated with a *Q. alba* breeding and improvement program. This group has recently completed a high-quality, haplotype resolved genome sequence for *Q. alba* that will underpin much of the future white oak genetics/genomics and tree improvement research (Staton personal communication).

6.2. Genetics and Tree Improvement

Traditionally, tree improvement programs are preceded by one or more provenance trials established at common locations (i.e., common gardens), using seeds from multiple known origins (i.e., provenances or seed sources). Forest tree populations (e.g., provenances) adapt through natural selection, migration, and phenotypic plasticity in response to environmental conditions [266–272], and these mechanisms can be assessed in provenance trials planted at common locations. When such provenance tests include seed sources and planting locations representing different geographic or ecological zones, information can also be inferred regarding the performance and expected resilience of trees to future climates [273–277]. For example, the measurement of the timing of bud flushing in common garden experiments that includes sampling across latitudinal and elevational gradients provides an ideal opportunity to investigate the potential impact of climate change on the tested species [278]. Furthermore, such trials can also be designed in a nested provenance/progeny test configuration which facilitates the evaluation and selection of parent trees (backward selection) or high-performing offspring (forward selection) in order to advance tree improvement.

Tree genetic improvement for long-rotation hardwoods, including the oaks, remains less developed than that for shorter-rotation tree species [279], such as pines (*Pinus*) and poplars (*Populus*). Savill and Kanowski [280] described tree improvement strategies for European white oaks, and numerous studies have examined genetic variation patterns for some of these species (e.g., [281,282]). Most *Q. alba* genetic research has also focused on population structure [268,283,284], speciation and taxonomy delineation, or the quantification of variation for a variety of traits (e.g., [34,194,285–289]).

Quercus alba Tree Improvement

An assessment of early *Q. alba* tree improvement goals and activities in the US was summarized by Steiner [9], along with the prediction that few would ultimately be impactful without the deliberate steps to transfer genetic gains from seed orchards to operational plantations. This prediction was later substantiated in a review of forest genetics and tree improvement research in the US [289]. Provenance trials for *Q. alba* have been limited in scope and number, however, they have included only partial coverage of the natural range due to research objectives and practical limitations associated with the rarity of masting (wide-spread seed production) and lack of seed dormancy. Two examples are known—both sampling several provenances from multiple states [271,290,291], although representing relatively local (sub-regional) areas. The studies showed minor variation at the provenance level in the common garden plantings while demonstrating the potential for early selection (<10 years) on height growth.

The University of Tennessee Tree Improvement Program (http://treeimprovement.utk.edu/), established in 1959, includes the development of *Q. alba* seed orchards based on results from multiple progeny trials conducted at locations across Tennessee, US, some of which have progressed through 2–3 generations [290,292,293]. Most recently, the White Oak Genetics and Tree Improvement Program (WOGTIP) was initiated in 2019 in the Department of Forestry and Natural Resources at the University of Kentucky, in partnership with the USDA Forest Service, Southern Research Sation, in order to provide a sustainable supply of high-quality *Q. alba* seeds and seedlings to support the conservation, restoration, and management of *Q. alba* throughout the species range [294].

The WOGTIP is a collaborative project being conducted in three phases: (1) the collection of acorns and scions on a range-wide basis; (2) progeny testing at multiple sites across the range to identify parent trees that produce high-quality offspring; and (3) the development of seed orchards for acorn production and seedling deployment. The WOGTIP represents the only known effort to establish a range-wide provenance study of *Q. alba* [294]. The seed and scion collection effort has been highly successful due to the participation of volunteers from federal and state agencies, academic institutions, NGOs, woodland owners, and citizen volunteers. To date (2023), seeds have been collected from over 500 mother trees and a network of over 25 regional progeny tests have been planted. The scions collected from the mother trees are being grafted to create a clone bank; this will conserve genetic material for the establishment of seed orchards following parental selection, based on progeny performance in the nursery and field tests (Figure 1S).

In addition to the tree improvement specific objectives, the WOGTIP range-wide provenance test and regional progeny trials will provide research materials for the genetic assessment of important climate relevant traits, including stem growth rate, stem dieback, apical dominance, epicormic branching, crown architecture, spring and fall phenology, early flowering, and viable seed yield. The design of the studies will allow for quantitative genetic estimates of heritability, genetic correlations, and genotype–environment interaction, as well as genotype–phenotype–environment association analyses that can be used to develop seed source transfer tools for mitigating climate change. The provenance test and progeny trials will also provide a rich source of materials for studies of hybridization and introgression between *Q. alba* and other co-occurring white oaks across the range, including chinkapin, swamp white, chestnut, and/or post oak species for which the trial seedling leaf morphologies suggest are occurring in areas of the *Q. alba* range where other species overlaps occur.

6.3. Biotechnologies (Propagation, Tissue Culture, Transgenics)

6.3.1. Oak Propagation

The ability to vegetatively propagate individual genotypes is critical for establishing clonal seed orchards for tree improvement (Figure 1E) and for simplifying the interpretation of results from genetics, genomics, physiological, and other oak biology studies. In addition to the propagation of oaks from somatic embryos, there are several reports on the successful vegetative propagation of oak species using stem propagation from coppiced trees (reviews: [295–297]), in which hedge orchards could be used for clonal propagation, in addition to seed orchards (Figure 1E,S). Further development of rapid, inexpensive, genotype-neutral stem propagation techniques for *Q. alba* and other oak species are essential to the basic study of climate critical trait biology and for oak improvement programs and should be a priority for future research efforts with white oak.

6.3.2. Transgenic Oaks

Transgene technologies applied to forest trees have a dual purpose: (1) they enable the testing of candidate genes for traits critical as breeding targets, and (2) they provide a direct means to engineer traits in order to meet difficult-to-reach tree improvement goals, such as resistance to an introduced, invasive pathogen or pest. In the case of oaks, there have been several reports of success in the application of these technologies.

Successful *Agrobacterium tumefacians*-mediated transformation has been demonstrated in cork oak, *Q. suber*, by Alvarez et al. [298] and Sanchez et al. [299] with embryogenic cultures, and also by Alvarez et al. [300] with embryogenic masses containing the bar gene from *Streptomyces hygroscopicus*; similar results have been shown with *Q. robur* embryogenic tissues by Vidal et al. [301]. Subsequently, Mallon et al. [302] demonstrated the successful *A. tumefacians*-mediated transformation of *Q. robur* embryogenic tissue with a chestnut thaumatin-like protein gene, CsTL1, that had been shown to confer resistance to fungal pathogens in chestnuts [303]. In this report, they also demonstrated the subsequent regeneration of transgenic plants expressing the transgene. Similarly, Cano et al. [304] demonstrated the successful transformation and regeneration of Holm oak (*Q. ilex*) with the same CsTL1 gene from chestnuts. More recently, Serrazina et al. [305] demonstrated the successful *A. tumefacians*-mediated transformation of *Q. ilex* with the Ginkbilobin-2 homologous domain gene (Cast_Gnk2-like), which had previously been shown to exhibit antifungal activity [306]. The in vitro analysis of the transgenic plants demonstrated some resistance to the *P. cinnamomi* as judged by increased time post-inoculation to plant death of transgenic plants when compared to controls.

6.3.3. Transgenic *Quercus alba*

Progress has been made in the application of in vitro techniques for the propagation of *Q. alba* and other North American oaks which are notoriously difficult to propagate vegetatively. This prompted investigations into in vitro propagation. Sources and developmental stages of explant tissues were determined to be of primary importance in the successful initiation of somatic embryogenesis (SE) cultures for trees, including *Q. alba* [307–309], Merkle, pers. comm.). Highly productive *Q. alba* embryogenic cultures were obtained from immature seed explants. Somatic embryos were produced from the cultures and somatic seedlings were regenerated from them following a pre-germination cold treatment and culturing on basal WPM with activated charcoal in a lighted incubator. The somatic seedings continued growth following the transfer to ex vitro conditions (Figure 3; Merkle, unpublished). The establishment of prolific shoot cultures from forced shoots of six-to-seven-year-old trees was reported as an efficient means of micropropagation for *Q. alba*, *Q. bicolor*, and *Q. rubra*, albeit genotype-dependent [309]. This led to success, as reported by Corredoira et al. [310], in obtaining somatic embryogenesis and plant regeneration from shoot apices and leaf explants of shoot cultures derived from *Q. alba* trees. SE rates varied from 0 to 50%, depending on the explant source and genotype. These approaches using shoot explants represented a break-through in providing true clonal propagation of the donor genotype, thus avoiding genetic recombination at the seed embryo stage. It is expected that *Agrobacterium*-mediated transformation systems based on binary plant expression vectors and inducible gene constructs should be adaptable to *Q. alba* transformation, as successfully tested in chestnut [311], poplar [312], *Arabidopsis* [313], and other systems. The AlcR/alcA system exhibits little or no basal expression in plants and permits the rapid, reversible induction of transgene expression [312,314].

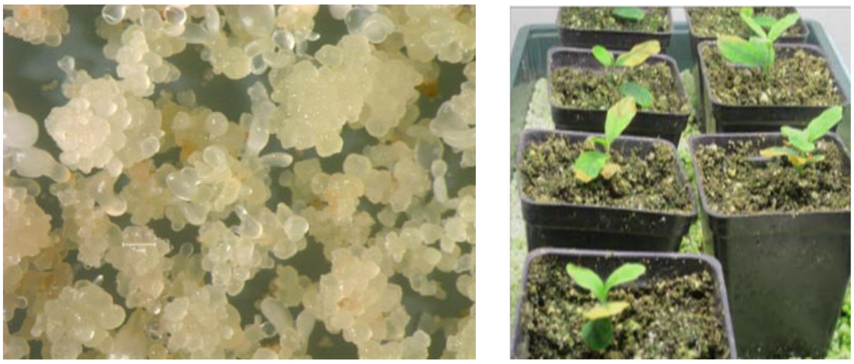

Figure 3. Embryogenic *Q. alba* culture (**left**) and *Q. alba* somatic seedlings (**right**). (courtesy S. Merkel).

6.4. Phenomics Field Scale Technologies for Oak Research

A critical need exists for determining the genomic/genetic underpinnings controlling phenotypic traits that affect key life-cycle processes of the oak forest, including regeneration, recruitment, and growth dynamics. Relying entirely on traditional common garden testing for phenotyping will extend tree improvement timelines by several decades. A field and forest-scale tree phenotyping platform would facilitate identifying and measuring key traits of white oaks in natural regeneration landscapes as well as planted field trials. This phenotypic information can then be integrated with existing and emerging genomics resources for white oak in order to track critical traits in white oak improvement programs, white oak forest management, and future reforestation initiatives.

Quadcopter drones offer an exceptional platform for conducting remote sensing over large plantations and forested areas with limited personnel. Drone-based sensors are already in widespread use for forest health monitoring and tree phenotyping [315,316]. The capabilities of these sensors and accompanying analyses characterize many aspects of tree physiology and above-ground anatomy. Individual tree segmentation and species identification are possible from both drone-based imagery and drone-based Light Detection and Ranging (LiDAR) [317–319]. Near-infrared (NIR), wide-infrared, and RGB sensors can be used to effectively measure tree water stress via various indices, such as the Normalized Difference Vegetation Index (NDVI) [320,321]. With the aid of machine-learning algorithms, both hyperspectral imagery and LiDAR accurately estimate tree height and Diameter at Breast Height (DBH) [321–323].

Several examples of studies focused specifically on the remote sensing of North American oak species have been published in the last few years. Mazis et al. [324] used hyperspectral imagery in a high-throughput plant phenotyping (HTPP) setting to assess biophysical traits and drought response in two white oak section species: swamp white oak, *Quercus bicolor*, and dwarf chestnut oak, *Quercus prinoides*. Using hyperspectral images, the study calculated 12 vegetation indices (VIs) and found that Vogelmann and Maccioni indices had the greatest potential for assessing oak seedling performance and health in drought conditions. These findings provide a ground-truthed method for rapid phenotyping that could be tested in white oak using drone-based hyperspectral sensors.

An additional study focused on oak wilt disease, which significantly threatens oak-dominated forests in the Eastern US. Sapes et al. [325] assessed the use of visible near-infrared (VNIR) and short-wave infrared (SWIR) in the detection of oak wilt and developed a stepwise approach to distinguish red oaks, *Q. rubra*, from other species in the canopy, and to also distinguish infected from uninfected red oaks. This study provides a framework for the future studies of oak wilt disease identification in white oaks. The combination of drone-based remote sensing, proximal hyperspectral sensing, and machine learning offers transformative potential in oak phenomics. These technologies enable efficient, large-scale phenotypic data collection, critical for elucidating genotype–phenotype relationships in a field progeny test or forest setting.

7. Conclusions and Perspectives

This review has taken a broad look into the research that has provided our current understanding of the biology of oaks, with a focus on *Q. alba*, from its natural history, phylogenetic placement, and ecological role as a keystone species, to the biotic and abiotic challenges facing the species. In addition, we have identified genomic, genetic, and biotechnology resources and tools that are providing new insights into the physiology of adaptive traits of *Q. alba* and a renewed potential for tree improvement to contribute to the performance metrics in forest management. Although species in the North American and Eurasian white oak clade have been the subject of research by silviculturists, forest ecologists and geneticists, and tree physiologists and pathologists for decades, an integration of the knowledge gained and tools developed across these disciplines is needed to develop the silvicultural practices required to assure the sustainability of *Q. alba*–through improved regeneration and recruitment, increased resistance and tolerance to invasive pathogens and pests, and enhanced resilience to abiotic stress as induced by climate change.

If we are to answer yes to the title of our review, many small steps will be needed, adding to the knowledge base distilled here and leveraging the available technologies and resources discussed. To start, reliable regeneration and recruitment, no small thing, are necessary to provide the acorns that will develop into tall oaks. In the near-term, given shortages in the smaller age classes of *Q. alba* and climate change mandates to mitigate and adapt, large numbers of seedlings will need to be planted across and within various sites and silvicultural prescriptions. Ensuring high-quality planting stock, both physiologically through nursery production and outplanting and genetically though appropriate and improved seed sources, will be the first steps. The traits discussed here will need to be studied, managed, and improved in the *Q. alba* populations selected for future environments. In addition, the following challenges will need to be met in order to facilitate the study, management, and improvement of the traits required for the successful regeneration and recruitment and adaptation to climate change: (1) the development of forest-/field-scale phenomics platforms to link genes to traits; (2) the development of robust gene testing platforms and transformation technologies, (e.g., Crisper/CAS); (3) the development of efficient plant propagation protocols for germplasm conservation and experimental analyses; (4) the establishment of provenance/progeny trials for forest/field-scale analyses; (5) the development of methods to reduce the juvenility period, enabling rapid breeding and early seed production; (6) the development and production of genetically improved seed and high-quality seedlings for tree planting efforts; and (7) the development and broad-scale implementation of genetically informed, ecologically sound, and climate forward silvicultural practices for tree planting and early stand development.

Beyond *Q. alba* per se, we are in a period of climate crisis that is driving several mitigation approaches such as numerous broadscale, worldwide, tree planting initiatives [326–331]; however laudable these activities are, there is a danger of putting large numbers of trees on the landscape without any consideration of the longer-term consequences, including initial survival, competition control and early stand development, fire, and other environment risks. This potential "Band-Aid approach" can lead to even greater problems. The need for the large-scale reforestation of *Q. alba* and other forest tree species is a problem that requires solutions supported by experimental knowledge (e.g., as generated from the WOGTIP and working to overcome the challenges described above) integrated from multiple disciplines, including silviculture, soils, ecology, physiology, genetics, and climatology in order to ensure that these new forests continue to survive and produce tall trees, including oaks, in a future planetary environment that will be potentially quite different from the one today.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/f15020269/s1, Table S1: An annotated listing of genetic and genomic resources for white oak species (genus *Quercus* subgenus *Quercus* section *Quercus*) is provided, with references [332–347], as supplemental Excel file "Table S1: White oak genomic/genetic resources". The supplemental file contains separate worksheets for Microsatellite (simple sequence repeat) DNA markers ('SSRs'), Single Nucleotide Polymorphism DNA markers ('SNPs'), Quantitative Trait Loci ('QTLs'), Expressed Sequence Tags ('ESTs'), nuclear genome assemblies ('nGenomes'), and chloroplast genome assemblies ('cpGenomes'). The spreadsheets are organized by species and by publication date, from earliest to latest. Additional information includes numbers of markers and sources of sequence data; Supplementary File S1: Pests and Diseases background information (References [122,152,158–175,177–196,348,349] are cited in File S1).

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References

1. Hacket-Pain, A.; Bogdziewicz, M. Climate Change and Plant Reproduction: Trends and Drivers of Mast Seeding Change. *Philos. Trans. R. Soc. B Biol. Sci.* **2021**, *376*, 20200379. [CrossRef]
2. Fralish, J.S. *The Keystone Role of Oak and Hickory in the Central Hardwood Forest*; Gen. Tech. Rep. SRS-73; U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 2004; pp. 78–87.
3. Binder, S.; Haight, R.G.; Polasky, S.; Warziniack, T.; Mockrin, M.H.; Deal, R.L.; Arthaud, G. *Assessment and Valuation of Forest Ecosystem Services: State of the Science Review*; Gen. Tech. Rep. NRS-170; U.S. Department of Agriculture, Forest Service, Northern Research Station: Newtown Square, PA, USA, 2017; pp. 1–47.
4. Grattapaglia, D.; Plomion, C.; Kirst, M.; Sederoff, R.R. Genomics of Growth Traits in Forest Trees. *Curr. Opin. Plant Biol.* **2009**, *12*, 148–156. [CrossRef]
5. Saleh, D.; Chen, J.; Leplé, J.-C.; Leroy, T.; Truffaut, L.; Dencausse, B.; Lalanne, C.; Labadie, K.; Lesur, I.; Bert, D.; et al. Genome-Wide Evolutionary Response of European Oaks during the Anthropocene. *Evol. Lett.* **2022**, *6*, 4–20. [CrossRef] [PubMed]
6. Gollihue, J.; Pook, V.G.; DeBolt, S. Sources of Variation in Bourbon Whiskey Barrels: A Review. *J. Inst. Brew.* **2021**, *127*, 210–223. [CrossRef]
7. Mosedale, J.R.; Feuillat, F.; Baumes, R.; Dupouey, J.-L.; Puech, J.-L. Variability of Wood Extractives among *Quercus robur* and *Quercus petraea* Trees from Mixed Stands and Their Relation to Wood Anatomy and Leaf Morphology. *Can. J. For. Res.* **1998**, *28*, 994–1006. [CrossRef]
8. Abrams, M.D. Where Has All the White Oak Gone? *BioScience* **2003**, *53*, 927. [CrossRef]
9. Steiner, K. Genetic Improvement of Oaks in North America. *Ann. Des Sci. For.* **1993**, *50* (Suppl. S1), 359s–367s. [CrossRef]
10. Stringer, J.; Morris, D. *Landowners Guide to: Understanding the Importance of White Oak*; FOR-147; Cooperative Extension Service, University of Kentucky, Department of Forestry and Natural Resources: Lexington, KY, USA, 2022; p. 3.
11. Abrams, M.D. History of eastern oak forests. In *Managing Oak Forests in the Eastern United States*; Keyser, P.D., Fearer, T., Harper, C.A., Eds.; CRC Press: Boca Raton, FL, USA, 2016; pp. 7–17.
12. Abrams, M.D.; Nowacki, G.J.; Hanberry, B.B. Oak forests and woodlands as Indigenous landscapes in the Eastern United States. *J. Torrey Bot. Soc.* **2021**, *149*, 101–121. [CrossRef]
13. Whitney, G.G. *From Coastal Wilderness to Fruited Plain: A History of Environmental Change in Temperate North America from 1500 to the Present*; Cambridge University Press: Cambridge, UK, 1996.
14. Bogdziewicz, M.; Hacket-Pain, A.; Kelly, D.; Thomas, P.A.; Lageard, J.; Tanentzap, A.J. Climate warming causes mast seeding to break down by reducing sensitivity to weather cues. *Glob. Change Biol.* **2021**, *27*, 1952–1961. [CrossRef] [PubMed]
15. Pesendorfer, M.B.; Ascoli, D.; Bogdziewicz, M.; Hacket-Pain, A.; Pearse, I.S.; Vacchiano, G. The ecology and evolution of synchronized reproduction in long-lived plants. *Philos. Trans. R. Soc. B* **2021**, *376*, 20200369. [CrossRef]
16. Bogdziewicz, M.; Kelly, D.; Thomas, P.A.; Lageard, J.G.A.; Hacket-Pain, A. Climate Warming Disrupts Mast Seeding and Its Fitness Benefits in European Beech. *Nat. Plants* **2020**, *6*, 88–94. [CrossRef]

17. Nussbaumer, A.; Waldner, P.; Apuhtin, V.; Aytar, F.; Benham, S.; Bussotti, F.; Eichhorn, J.; Eickenscheidt, N.; Fabianek, P.; Falkenried, L.; et al. Impact of Weather Cues and Resource Dynamics on Mast Occurrence in the Main Forest Tree Species in Europe. *For. Ecol. Manag.* **2018**, *429*, 336–350. [CrossRef]
18. Fraga, H.; Moriondo, M.; Leolini, L.; Santos, J.A. Mediterranean Olive Orchards under Climate Change: A Review of Future Impacts and Adaptation Strategies. *Agronomy* **2021**, *11*, 56. [CrossRef]
19. Leisner, C.P. Review: Climate Change Impacts on Food Security-Focus on Perennial Cropping Systems and Nutritional Value. *Plant Sci.* **2020**, *293*, 110412. [CrossRef]
20. Tuskan, G.A.; Groover, A.T.; Schmutz, J.; DiFazio, S.P.; Myburg, A.; Grattapaglia, D.; Smart, L.B.; Yin, T.; Aury, J.M.; Kremer, A.; et al. Hardwood Tree Genomics: Unlocking Woody Plant Biology. *Front. Plant Sci.* **2018**, *9*, 1799. [CrossRef] [PubMed]
21. Abbott, A.G.; Georgi, L.L.; Yvergniaux, D.; Wang, Y.; Blenda, A.V.; Reighard, G.L.; Martinez Inigo, M.J.; Sosinski, B. Peach: The Model Genome for Rosaceae. *Acta Hortic.* **2002**, *575*, 145–155. [CrossRef]
22. Jansson, S.; Douglas, C.J. Populus: A Model System for Plant Biology. *Annu. Rev. Plant Biol.* **2007**, *58*, 435–458. [CrossRef]
23. Jansson, S.; Bhalerao, R.; Groover, A. Springerlink, Online Service. In *Genetics and Genomics of Populus*; Springer: New York, NY, USA, 2010; Volume 8.
24. Arús, P.; Verde, I.; Sosinski, B.; Zhebentyayeva, T.; Abbott, A.G. The Peach Genome. *Tree Genet. Genomes* **2012**, *8*, 531–547. [CrossRef]
25. Friedman, J.; Rubin, M.J. All in good time: Understanding annual and perennial strategies in plants. *Am. J. Bot.* **2015**, *102*, 497–499. [CrossRef]
26. Kremer, A.; Hipp, A.L. Oaks: An Evolutionary Success Story. *New Phytol.* **2019**, *226*, 987–1011. [CrossRef]
27. Hipp, A.L.; Manos, P.S.; Hahn, M.; Avishai, M.; Bodénès, C.; Cavender-Bares, J.; Crowl, A.A.; Deng, M.; Denk, T.; Fitz-Gibbon, S.; et al. Genomic Landscape of the Global Oak Phylogeny. *New Phytol.* **2019**, *226*, 1198–1212. [CrossRef]
28. Nixon, K.C. Global and neotropical distribution and diversity of oak (genus Quercus) and oak forests. In *Ecology and Conservation of Neotropical Montane Oak Forests*; Kappelle, M.D., Ed.; Springer: Berlin/Heidelberg, Germany, 2006; pp. 3–13.
29. Denk, T.; Grimm, G.W.; Manos, P.S.; Deng, M.; Hipp, A.L. An Updated Infrageneric Classification of the Oaks: Review of Previous Taxonomic Schemes and Synthesis of Evolutionary Patterns. In *Oaks Physiological Ecology. Exploring the Functional Diversity of Genus Quercus L.*; Gil-Pelegrín, E., Peguero-Pina, J.J., Sancho-Knapik, D., Eds.; Springer International Publishing: Cham, Switzerland, 2017.
30. McVay, J.D.; Hauser, D.; Hipp, A.L.; Manos, P.S. Phylogenomics reveals a complex evolutionary history of lobed-leaf white oaks in western North America. *Genome* **2017**, *60*, 733–742. [CrossRef]
31. Hipp, A.L.; Eaton, D.A.R.; Cavender-Bares, J.; Fitzek, E.; Nipper, R.; Manos, P.S. A Framework Phylogeny of the American Oak Clade Based on Sequenced RAD Data. *PLoS ONE* **2014**, *9*, e93975. [CrossRef]
32. Cavender-Bares, J. Diversification, adaptation, and community assembly of the American oaks (Quercus), a model clade for integrating ecology and evolution. *New Phytol.* **2019**, *221*, 669–692. [CrossRef]
33. Hipp, A.L.; Manos, P.S.; González-Rodríguez, A.; Hahn, M.; Kaproth, M.; McVay, J.D.; Avalos, S.V.; Cavender-Bares, J. Sympatric Parallel Diversification of Major Oak Clades in the Americas and the Origins of Mexican Species Diversity. *New Phytol.* **2017**, *217*, 439–452. [CrossRef] [PubMed]
34. Johnson, P.S.; Shifley, S.R.; Rogers, R.; Dey, D.C.; Kabrick, J.M. *The Ecology and Silviculture of Oaks*; CABI: Wallingford, UK, 2019.
35. Bölöni, J.; Aszalós, R.; Frank, T.; Ódor, P. Forest Type Matters: Global Review about the Structure of Oak Dominated Old-Growth Temperate Forests. *For. Ecol. Manag.* **2021**, *500*, 119629. [CrossRef]
36. Abrams, M.D. Adaptations and Responses to Drought in Quercus Species of North America. *Tree Physiol.* **1990**, *7*, 227–238. [CrossRef] [PubMed]
37. Abrams, M. Distribution, Historical Development and Ecophysiological Attributes of Oak Species in the Eastern United States. *Ann. Sci. For.* **1996**, *53*, 487–512. [CrossRef]
38. Cavender-Bares, J.M.; Nelson, E.; Meireles, J.E.; Lasky, J.R.; Miteva, D.A.; Nowak, D.J.; Pearse, W.D.; Helmus, M.R.; Zanne, A.E.; Fagan, W.F.; et al. The Hidden Value of Trees: Quantifying the Ecosystem Services of Tree Lineages and Their Major Threats across the Contiguous US. *PLOS Sustain. Transform.* **2022**, *1*, e0000010. [CrossRef]
39. Little, E.L., Jr. *Atlas of United States Trees: Conifers and Important Hardwoods*, 1st ed.; U.S. Department of Agriculture, Forest Service: Washington, DC, USA, 1971; Volume 1, pp. 328–329.
40. Rogers, R. Quercus alba L. White oak. In *Silvics of North America: Hardwoods*; Burns, R.M., Ed.; USDA Forest Service: Washington, DC, USA, 1990; pp. 605–613.
41. Dey, D.C. Sustaining Oak Forests in Eastern North America: Regeneration and Recruitment, the Pillars of Sustainability. *For. Sci.* **2014**, *60*, 926–942. [CrossRef]
42. Zhu, K.; Woodall, C.W.; Clark, J.S. Failure to Migrate: Lack of Tree Range Expansion in Response to Climate Change. *Glob. Change Biol.* **2012**, *18*, 1042–1052. [CrossRef]
43. Brose, P.H.; Schuler, T.M.; Van Lear, D.; Berst, J. Bringing Fire Back: The Changing Regimes of the Appalachian Mixed-Oak Forests. *J. For.* **2001**, *99*, 30–35.
44. Nowacki, G.J.; Abrams, M.D. The Demise of Fire and "Mesophication" of Forests in the Eastern United States. *BioScience* **2008**, *58*, 123–138. [CrossRef]

45. Nowacki, G.J.; Abrams, M.D.; Lorimer, C.G. Composition, Structure, and Historical Development of Northern Red Oak Stands along an Edaphic Gradient in North-Central Wisconsin. *For. Sci.* **1990**, *36*, 276–292. [CrossRef]
46. Nowacki, G.J.; Abrams, M.D. Community, Edaphic, and Historical Analysis of Mixed Oak Forests of the Ridge and Valley Province in Central Pennsylvania. *Can. J. For. Res.* **1992**, *22*, 790–800. [CrossRef]
47. Shifley, S.R.; Thompson, F.R., III. Spatial and Temporal Patterns in the Amount of Young Forests and Implications for Biodiversity. In *Sustaining Young Forest Communities: Ecology and Management of Early Successional Habitats in the Central Hardwood Region, USA*; Greenberg, C.H., Collins, B.S., Thompson, F.R., Eds.; Springer: Dordrecht, The Netherlands; New York, NY, USA, 2011.
48. Shifley, S.R.; Aguilar, F.X.; Song, N.; Stewart, S.I.; Nowak, D.J.; Gormanson, D.D.; Moser, W.K.; Wormstead, S.; Greenfield, E.J. *Forests of the Northern United States*; Gen. Tech. Rep. NRS-90; Northern Research Station: Newtown Square, PA, USA, 2012; p. 202.
49. Merritt, C. An overview of oak regeneration problems. In *Regenerating Oaks in Upland Hardwood Forests*; Holt, H.A., Fischer, B.C., Eds.; Purdue University: West Lafayette, IN, USA, 1979; pp. 1–10.
50. Lorimer, C.G. Causes of the oak regeneration problem. In *Oak Regeneration: Serious Problems, Practical Recommendations*; Loftis, D., Ed.; USDA Forest Service Gen. Tech. Rep. SE-84; U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 1993; pp. 14–39.
51. Hutchinson, T.F.; Yaussy, D.A.; Long, R.P.; Rebbeck, J.; Sutherland, E.K. Long-Term (13-Year) Effects of Repeated Prescribed Fires on Stand Structure and Tree Regeneration in Mixed-Oak Forests. *For. Ecol. Manag.* **2012**, *286*, 87–100. [CrossRef]
52. Loftis, D.L. Upland oak regeneration and management. In *Upland Oak Ecology Symposium: History, Current Conditions, and Sustainability*; Spetich, M.A., Ed.; USDA Forest Service Gen. Tech. Rep. SRS-73; U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 2004; pp. 163–167.
53. McEwan, R.W.; Dyer, J.M.; Pederson, N. Multiple Interacting Ecosystem Drivers: Toward an Encompassing Hypothesis of Oak Forest Dynamics across Eastern North America. *Ecography* **2010**, *34*, 244–256. [CrossRef]
54. Brose, P.H.; Dey, D.C.; Phillips, R.J.; Waldrop, T.A. A Meta-Analysis of the Fire-Oak Hypothesis: Does Prescribed Burning Promote Oak Reproduction in Eastern North America? *For. Sci.* **2013**, *59*, 322–334. [CrossRef]
55. Frelich, L.E.; Reich, P.B.; Peterson, D.W. The Changing Role of Fire in Mediating the Relationships among Oaks, Grasslands, Mesic Temperate Forests, and Boreal Forests in the Lake States. *J. Sustain. For.* **2017**, *36*, 421–432. [CrossRef]
56. Brose, P.H.; Van Lear, D.H. Responses of hardwood advance regeneration to seasonal prescribed fires in oak-dominated shelterwood stands. *Can. J. For. Res.* **1998**, *28*, 331–339. [CrossRef]
57. Loftis, D.L. Predicting Post-Harvest Performance of Advance Red Oak Reproduction in the Southern Appalachians. *For. Sci.* **1990**, *36*, 908–916.
58. Dey, D.C.; Fan, Z. A review of fire and oak regeneration and overstory recruitment. In Proceedings of the 3rd Fire in Eastern Oak Forests Conference, Carbondale, IL, USA, 20–22 May 2008; Hutchinson, T.F., Ed.; USDA Forest Service Gen. Tech. Rep. NRS-P-46. U.S. Department of Agriculture, Forest Service, Northern Research Station: Newtown Square, PA, USA, 2009; pp. 2–20.
59. Rebbeck, J.; Gottschalk, K.; Scherzer, A. Do Chestnut, Northern Red, and White Oak Germinant Seedlings Respond Similarly to Light Treatments? Growth and Biomass. *Can. J. For. Res.* **2011**, *41*, 2219–2230. [CrossRef]
60. Packard, S. Restoring Oak Ecosystems. *Ecol. Restor.* **1993**, *11*, 5–16. [CrossRef]
61. Abella, S.R.; Jaeger, J.F.; Gehring, D.H.; Jacksy, R.G.; Menard, K.S.; High, K.A. Restoring Historic Plant Communities in the Oak Openings Region of Northwest Ohio. *Ecol. Restor.* **2001**, *19*, 155–160. [CrossRef]
62. Stringer, J.W. *Oak Regeneration Using the Two-Age System*; Gen. Tech. Rep. SRS-48; USDA Forest Service, Southern Research Station: Asheville, NC, USA, 2002; pp. 379–382.
63. Brose, P.H.; Gottschalk, K.W.; Horsley, S.B.; Knopp, P.D.; Kochenderfer, J.N.; McGuinness, B.J.; Miller, G.W.; Ristau, T.E.; Stoleson, S.H.; Stout, S.L. *Prescribing Regeneration Treatments for Mixed-Oak Forests in the Mid-Atlantic Region*; Gen. Tech. Rep. NRS-33; U.S. Department of Agriculture, Forest Service, Northern Research Station: Newtown Square, PA, USA, 2008.
64. Parrott, D.L.; Lhotka, J.M.; Stringer, J.W. Effects of midstory removal on underplanted black oak and white oak in the western Cumberland plateau. In Proceedings of the 17th Central Hardwood Forest Conference. USDA Forest Service General Technical Report NRSP-Northern Research Station, Newtown Square, PA, USA, 5–7 April 2010; pp. 270–276.
65. Spetich, M.A. Survival of *Quercus alba* (White Oak) Advance Reproduction in Small Group and Single Tree Openings. *Forests* **2020**, *11*, 889. [CrossRef]
66. Fortuna, N. In it for the long haul: White Oak Initiative formulates 50-year strategy to conserve cornerstone species. *Woodland* **2021**, *9*, 34–40.
67. Hatfield, J.L.; Dold, C. Water-Use Efficiency: Advances and Challenges in a Changing Climate. *Front. Plant Sci.* **2019**, *10*, 103. [CrossRef] [PubMed]
68. Soh, W.K.; Yiotis, C.; Murray, M.; Parnell, A.; Wright, I.J.; Spicer, R.A.; Lawson, T.; Caballero, R.; McElwain, J.C. Rising CO_2 drives divergence in water use efficiency of evergreen and deciduous plants. *Sci. Adv.* **2019**, *5*, 7906. [CrossRef]
69. Durand, M.; Brendel, O.; Buré, C.; Le Thiec, D. Altered Stomatal Dynamics Induced by Changes in Irradiance and Vapour-Pressure Deficit under Drought: Impacts on the Whole-Plant Transpiration Efficiency of Poplar Genotypes. *New Phytol.* **2019**, *222*, 1789–1802. [CrossRef]
70. Torres-Ruiz, J.M.; Kremer, A.; Carins Murphy, M.R.; Brodribb, T.; Lamarque, L.J.; Truffaut, L.; Bonne, F.; Ducousso, A.; Delzon, S. Genetic Differentiation in Functional Traits among European Sessile Oak Populations. *Tree Physiol.* **2019**, *39*, 1736–1749. [CrossRef]

71. Homolka, A.; Schueler, S.; Burg, K.; Fluch, S.; Kremer, A. Insights into Drought Adaptation of Two European Oak Species Revealed by Nucleotide Diversity of Candidate Genes. *Tree Genet. Genomes* **2013**, *9*, 1179–1192. [CrossRef]
72. Arend, M.; Kuster, T.; Gunthardt-Goerg, M.S.; Dobbertin, M. Provenance-Specific Growth Responses to Drought and Air Warming in Three European Oak Species (*Quercus robur, Q. petraea* and *Q. pubescens*). *Tree Physiol.* **2011**, *31*, 287–297. [CrossRef]
73. Spieß, N.; Oufir, M.; Matušíková, I.; Stierschneider, M.; Kopecky, D.; Homolka, A.; Burg, K.; Fluch, S.; Hausman, J.-F.; Wilhelm, E. Ecophysiological and Transcriptomic Responses of Oak (Quercus Robur) to Long-Term Drought Exposure and Rewatering. *Environ. Exp. Bot.* **2012**, *77*, 117–126. [CrossRef]
74. Magalhães, A.P.; Verde, N.; Reis, F.; Martins, I.; Costa, D.; Lino-Neto, T.; Castro, P.H.; Tavares, R.M.; Azevedo, H. RNA-Seq and Gene Network Analysis Uncover Activation of an ABA-Dependent Signalosome during the Cork Oak Root Response to Drought. *Front. Plant Sci.* **2016**, *6*, 1195. [CrossRef]
75. Reed, W.P.; Kaye, M.W. Bedrock Type Drives Forest Carbon Storage and Uptake across the Mid-Atlantic Appalachian Ridge and Valley, U.S.A. *For. Ecol. Manag.* **2020**, *460*, 117881. [CrossRef]
76. Tirmenstein, D.A. Quercus alba. In *Fire Effects Information System, [Online]*; U.S. Department of Agriculture, Forest Service, Rocky Mountain Research Station, Fire Sciences Laboratory (Producer): Fort Collins, CO, USA, 1991. Available online: https://www.fs.usda.gov/database/feis/plants/tree/quealb/all.html (accessed on 30 November 2023).
77. De Micco, V.; Balzano, A.; Wheeler, E.A.; Baas, P. Tyloses and gums: A review of structure, function and occurrence of vessel occlusions. *IAWA J.* **2016**, *37*, 186–205. [CrossRef]
78. Allen, M. Managing Oak Woodlands in a Dynamic World. In Proceedings of the 7th California Oak Symposium, Visalia, CA, USA, 3–6 November 2014; General Technical Report PSW-GTR-251 FS. U.S. Department of Agriculture, Forest Service, Pacific Southwest Research Station: Berkeley, CA, USA, 2015.
79. Kaproth, M.A.; Hahn, M.; Manos, P.S.; Hipp, L.; González-Rodríguez, A.; Cavender-Bares, J. Functional Leaf and Stem Traits of the Oaks of the Americas. Retrieved from the Data Repository for the University of Minnesota. 2020. Available online: https://hdl.handle.net/11299/214055 (accessed on 29 November 2023).
80. Kościelniak, P.; Glazińska, P.; Kęsy, J.; Zadworny, M. Formation and Development of Taproots in Deciduous Tree Species. *Front. Plant Sci.* **2021**, *12*, 772567. [CrossRef]
81. Bräutigam, K.; Vining, K.J.; Lafon-Placette, C.; Fossdal, C.G.; Mirouze, M.; Marcos, J.G.; Fluch, S.; Fraga, M.F.; Guevara, M.Á.; Abarca, D.; et al. Epigenetic Regulation of Adaptive Responses of Forest Tree Species to the Environment. *Ecol. Evol.* **2013**, *3*, 399–415. [CrossRef]
82. Raj, S.; Bräutigam, K.; Hamanishi, E.T.; Wilkins, O.; Thomas, B.R.; Schroeder, W.W.; Mansfield, S.D.; Plant, A.L.; Campbell, M.M. Clone History Shapes *Populus* Drought Responses. *Proc. Natl. Acad. Sci. USA* **2011**, *108*, 12521–12526. [CrossRef] [PubMed]
83. Caignard, T.; Kremer, A.; Firmat, C.; Nicolas, M.; Venner, S.; Delzon, S. Increasing Spring Temperatures Favor Oak Seed Production in Temperate Areas. *Sci. Rep.* **2017**, *7*, 8555. [CrossRef]
84. Petritan, A.M.; Petritan, I.C.; Hevia, A.; Walentowski, H.; Bouriaud, O.; Sánchez-Salguero, R. Climate Warming Predispose Sessile Oak Forests to Drought-Induced Tree Mortality regardless of Management Legacies. *For. Ecol. Manag.* **2021**, *491*, 119097. [CrossRef]
85. Thomas, A.M.; Coggeshall, M.V.; O'Connor, P.A.; Nelson, D.C. Climate Adaptation in White Oak (*Quercus alba*, L.): A Forty-Year Study of Growth and Phenology. *Forests* **2024**. *submitted*.
86. Ashley, M.V. Answers Blowing in the Wind: A Quarter Century of Genetic Studies of Pollination in Oaks. *Forests* **2021**, *12*, 575. [CrossRef]
87. Dow, B.D.; Ashley, M.V. Microsatellite Analysis of Seed Dispersal and Parentage of Saplings in Bur Oak, Quercus Macrocarpa. *Mol. Ecol.* **1996**, *5*, 615–627. [CrossRef]
88. Dow, B.D. High Levels of Gene Flow in Bur Oak Revealed by Paternity Analysis Using Microsatellites. *J. Hered.* **1998**, *89*, 62–70. [CrossRef]
89. Dow, B.D.; Ashley, M.V. Factors influencing male mating success in bur oak, Quercus macrocarpa. *New For.* **1998**, *15*, 161–180. [CrossRef]
90. Streiff, R.; Ducousso, A.; Lexer, C.; Steinkellner, H.; Gloessl, J.; Kremer, A. Pollen dispersal inferred from paternity analysis in a mixed oak stand of *Quercus robur* L. and *Q. petraea* (Matt.) Liebl. *Mol. Ecol.* **1999**, *8*, 831–841. [CrossRef]
91. Valbuena-Carabãa, M.; González-Martínez, S.C.; Sork, V.L.; Collada, C.; Soto, A.; Goicoechea, P.G.; Gil, L. Gene flow and hybridisation in a mixed oak forest (*Quercus pyrenaica* Willd. and *Quercus petraea* (Matts.) Liebl.) in central Spain. *Heredity* **2005**, *95*, 457–465. [CrossRef]
92. Craft, K.J.; Ashley, M.V. Landscape genetic structure of bur oak (*Quercus macrocarpa*) savannas in Illinois. *For. Ecol. Manag.* **2007**, *239*, 13–20. [CrossRef]
93. Craft, K.J.; Ashley, M.V. Pollen-mediated gene flow in isolated and continuous stands of bur oak, *Quercus macrocarpa* (Fagaceae). *Am. J. Bot.* **2010**, *97*, 1999–2006. [CrossRef]
94. Nakanishi, A.; Tomaru, N.; Yoshimaru, H.; Kawahara, T.; Manabe, T.; Yamamoto, S. Patterns of pollen flow and genetic differentiation among pollen pools in *Quercus salicina* in a warm temperate old-growth evergreen broad-leaved forest. *Silvae Genet.* **2004**, *53*, 258–264. [CrossRef]
95. Nakanishi, A.; Tomaru, N.; Yoshimaru, H.; Manabe, T.; Yamamoto, S. Effects of seed- and pollen-mediated gene dispersal on genetic structure among *Quercus salicina* saplings. *Heredity* **2009**, *102*, 182–189. [CrossRef] [PubMed]

96. Abraham, S.T.; Zaya, D.N.; Koenig, W.D.; Ashley, M.V. Interspecific and intraspecific pollination patterns of valley oak, *Quercus lobata*, in a mixed stand in Coastal Central California. *Int. J. Plant Sci.* **2011**, *172*, 691–699. [CrossRef]
97. Hampe, A.; Pemonge, M.-H.; Petit, R.J. Efficient mitigation of founder effects during the establishment of a leading-edge oak population. *Proc. R. Soc. B Biol. Sci.* **2013**, *280*, 20131070. [CrossRef] [PubMed]
98. Gerber, S.; Chadoeuf, J.; Gugerli, F.; Lascoux, M.; Buiteveld, J.; Cottrell, J.; Dounavi, A.; Fineschi, S.; Forrest, L.L.; Fogelqvist, J.; et al. High rates of gene flow by pollen and seed in oak populations across Europe. *PLoS ONE* **2014**, *9*, e85130. [CrossRef]
99. Yang, Q.; Gao, Y.; Wu, X.; Moriguchi, T.; Bai, S.; Teng, Y. Bud endodormancy in deciduous fruit trees: Advances and prospects. *Hortic. Res.* **2021**, *8*, 139. [CrossRef] [PubMed]
100. Abbott, A.G.; Zhebentyayeva, T.; Barakat, A.; Liu, Z. The genetic control of bud-break in trees. In *Advances in Botanical Research*; Plomion, C., Blondon, A.-F., Eds.; Academic Press: New York, NY, USA, 2015; pp. 201–228.
101. Böhlenius, H.; Huang, T.; Charbonnel-Campaa, L.; Brunner, A.M.; Jansson, S.; Strauss, S.H.; Nilsson, O. *CO/FT* Regulatory Module Controls Timing of Flowering and Seasonal Growth Cessation in Trees. *Science* **2006**, *312*, 1040–1043. [CrossRef] [PubMed]
102. Singh, R.K.; Maurya, J.P.; Azeez, A.; Miskolczi, P.; Tylewicz, S.; Stojkovič, K.; Delhomme, N.; Busov, V.; Bhalerao, R.P. A genetic network mediating the control of bud break in hybrid aspen. *Nat. Commun.* **2018**, *9*, 4173. [CrossRef]
103. Azeez, A.; Zhao, Y.C.; Singh, R.K.; Yordanov, Y.S.; Dash, M.; Miskolczi, P.; Stojkovič, K.; Strauss, S.H.; Bhalerao, R.P.; Busov, V.B. EARLY BUD-BREAK 1 and EARLY BUD-BREAK 3 control resumption of poplar growth after winter dormancy. *Nat. Commun.* **2021**, *12*, 1123. [CrossRef]
104. Lesur, I.; Le Provost, G.; Bento, P.; Da Silva, C.; Leplé, J.-C.; Murat, F.; Ueno, S.; Bartholomé, J.; Lalanne, C.; Ehrenmann, F.; et al. The oak gene expression atlas: Insights into Fagaceae genome evolution and the discovery of genes regulated during bud dormancy release. *BMC Genom.* **2015**, *16*, 112. [CrossRef]
105. Satake, A.; Kelly, D. Supplementary material from "Studying the genetic basis of masting". *R. Soc. Collect.* **2021**, *376*, 20210116. [CrossRef]
106. Schermer, É.; Bel-Venner, M.C.; Fouchet, D.; Siberchicot, A.; Boulanger, V.; Caignard, T.; Thibaudon, M.; Oliver, G.; Nicolas, M.; Gaillard, J.M.; et al. Pollen limitation as a main driver of fruiting dynamics in oak populations. *Ecol. Lett.* **2019**, *22*, 98–107. [CrossRef]
107. Yu, J.; Conrad, A.O.; Decroocq, V.; Zhebentyayeva, T.; Williams, D.E.; Bennett, D.; Roch, G.; Audergon, J.-M.; Dardick, C.; Liu, Z.; et al. Distinctive Gene Expression Patterns Define Endodormancy to Ecodormancy Transition in Apricot and Peach. *Front. Plant Sci.* **2020**, *11*, 180. [CrossRef] [PubMed]
108. Kobayashi, M.J.; Takeuchi, Y.; Kenta, T.; Kume, T.; Diway, B.; Shimizu, K.K. Mass flowering of the tropical tree *Shorea beccariana* was preceded by expression changes in flowering and drought responsive genes. *Mol. Ecol.* **2013**, *22*, 4767–4782. [CrossRef]
109. Hacket-Pain, A.J.; Friend, A.D.; Lageard, J.G.A.; Thomas, P.A. The influence of masting phenomenon on growth–climate relationships in trees: Explaining the influence of previous summers' climate on ring width. *Tree Physiol.* **2015**, *35*, 319–330. [CrossRef]
110. Baslam, M.; Mitsui, T.; Sueyoshi, K.; Ohyama, T. Recent Advances in Carbon and Nitrogen Metabolism in C3 Plants. *Int. J. Mol. Sci.* **2021**, *22*, 318. [CrossRef]
111. Tegeder, M.; Masclaux-Daubresse, C. Source and sink mechanisms of nitrogen transport and use. *New Phytol.* **2018**, *217*, 35–53. [CrossRef]
112. Kurpisz, B.; Pawłowski, T.A. Epigenetic Mechanisms of Tree Responses to Climatic Changes. *Int. J. Mol. Sci.* **2022**, *23*, 13412. [CrossRef]
113. Korstian, C.F. *Factors Controlling Germination and Early Survival in Oaks*; Yale University School of Forestry Bulletin No. 19; Yale University Press: New Haven, CT, USA, 1927; 115p.
114. Olsen, D.F.; Boyce, S.G. Factors Affecting Acorn Production and Germination and Early Growth of Seedlings and Seedling Sprouts. In Proceedings of the Oak Symposium Proceedings, Morgantown, WV, USA, 16–20 August 1971; U.S. Department of Agriculture, Forest Service, Northeastern Forest Experiment Station: Upper Darby, PA, USA, 1971; pp. 44–48.
115. Hawkins, T.S. The Influence of Dormancy Break Requirements on Germination and Viability Responses to Winter Submergence in Acorns of Three Bottomland Red Oak (*Sect. Lobatae*) Species. *For. Sci.* **2019**, *65*, 556–561. [CrossRef]
116. Carrera-Castaño, G.; Calleja-Cabrera, J.; Pernas, M.; Gómez, L.; Oñate-Sánchez, L. An Updated Overview on the Regulation of Seed Germination. *Plants* **2020**, *9*, 703. [CrossRef]
117. Sung, S.-J.S.; Kormanik, P.P.; Cook, C.D.; Zarnoch, S.J.; Kormanik, T.L. Effect of Acorn Moisture Content at Sowing on Germination and Seedling Growth of White Oak and Northern Red Oak. In Proceedings of the 13th Biennial Southern Silvicultural Research Conference, Memphis, TN, USA, 28 February–4 March 2005; Kristina, F.C., Ed.; Gen. Tech. Rep. SRS-92. U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 2006; pp. 241–246.
118. Steele, M.A.; Smallwood, P.; Terzaghi, W.B.; Carlson, J.E.; Contreras, T.; McEuen, A. Oak dispersal syndromes: Do red and white oaks exhibit different dispersal strategies? In *Upland Oak Ecology Symposium*; Gen. Tech. Rep. SRS–73; U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 2002; pp. 72–77.
119. Liu, Y.; Liu, G.; Li, Q.; Liu, Y.; Hou, L.; Li, G.L. Influence of pericarp, cotyledon and inhibitory substances on sharp tooth oak (*Quercus aliena var. acuteserrata*) germination. *PLoS ONE* **2012**, *7*, 47682. [CrossRef]
120. Yi, X.; Yang, Y.; Curtis, R.; Bartlow, A.W.; Agosta, S.J.; Steele, M.A. Alternative strategies of seed predator escape by early-germinating oaks in Asia and North America. *Ecol. Evol.* **2012**, *2*, 487–492. [CrossRef]

121. Bonner, F.T.; Vozzo, J.A. *Seed Biology and Technology of Quercus*; Gen. Tech. Rep. SO-66; U.S. Department of Agriculture, Forest Service, Southern Forest Experiment Station: New Orleans, LA, USA, 1987.
122. Steele, M.A. *Oak Seed Dispersal: A Study in Plant-Animal Interactions*; The Johns Hopkins University Press: Baltimore, MD, USA, 2021.
123. Zhou, B.F.; Yuan, S.; Crowl, A.A.; Liang, Y.Y.; Shi, Y.; Chen, X.Y.; An, Q.Q.; Kang, M.; Manos, P.S.; Wang, B. Phylogenomic analyses highlight innovation and introgression in the continental radiations of Fagaceae across the Northern Hemisphere. *Nat. Commun.* **2022**, *13*, 1320. [CrossRef]
124. Moles, A.T.; Westoby, M. Seedling survival and seed size: A synthesis of the literature. *J. Ecol.* **2004**, *92*, 372–383. [CrossRef]
125. Long, T.; Jones, R. Seedling growth strategies and seed size effects in fourteen oak species native to different soil moisture habitats. *Trees* **1996**, *11*, 1–8. [CrossRef]
126. Llanderal-Mendoza, J.; Gugger, P.F.; Oyama, K.; Uribe-Salas, D.; Gonzales-Rodriguez, A. Climatic determinants of acorn size and germination percentage of *Quercus rugosa* (Fagaceae) along a latitudinal gradient in Mexico. *Bot. Sci.* **2017**, *95*, 37–45. [CrossRef]
127. Sánchez-Montes de Oca, E.J.; Badano, E.I.; Silva-Alvarado, L.-E.; Flores, J.; Barragán-Torres, F.; Flores-Cano, J.A. Acorn weight as determinant of germination in red and white oaks: Evidences from a common-garden greenhouse experiment. *Ann. For. Sci.* **2018**, *75*, 12. [CrossRef]
128. Gavranović Markić, A.; Bogdan, S.; Gradečki Poštenjak, M.; Lanšćak, M.; Vujnović, Z.; Bogunović, S.; Ivanković, M. Acorn Yields and Seed Viability of Pedunculate Oak in a 10-year Period in Forest Seed Objects across Croatia. *South-East Eur. For.* **2022**, *13*, 27–36. [CrossRef]
129. Brose, P.H.; Van Lear, D.H. Survival of hardwood regeneration during prescribed fires: The importance of root development and root collar location. In *Upland Oak Ecology Symposium: History, Current Conditions, and Sustainability*; Spetich, M.A., Ed.; SRS-73, Gen. Tech. Rep; U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 2004; pp. 123–127.
130. Kormanik, P.P.; Sung, S.-J.; Zarnoch, S.J.; Tibbs, G.T. Artificial regeneration of northern red oak and white oak on high-quality sites: Effect of root morphology and relevant biological characteristics. In Proceedings of the 2001 National Silviculture Workshop; Parker, S., Hummel, S.S., Eds.; Gen. Tech. Rep. PNW-GTR-546. USDA Forest Service Pacific Northwest Research Station: Portland, OR, USA, 2002; pp. 83–91.
131. Kormanik, P.P.; Sung, S.-J.; Kormanik, T.L. Growing, selecting, and establishing 1-0 *Quercus rubra* and *Q. alba* seedlings for rapid growth and early acorn production on forested lands in the southeastern United States. *J. Int. Oak Soc.* **2004**, *15*, 119–125.
132. Sung, S.-J.; Kormanik, P.P.; Zarnoch, S.J. Growth and development of first-year nursery-grown white oak seedlings of individual mother trees. In Proceedings of the Eleventh Biennial Southern Silvicultural Research Conference, Knoxville, TN, USA, 20–22 March 2022; Outcalt, K.W., Ed.; Gen. Tech. Rep., SRS-48. USDA Forest Service, Southern Research Station: Asheville, NC, USA, 2002; Volume 622, pp. 346–351.
133. Greenberg, C.H.; Parresol, B.R. Dynamics of acorn production by five species of southern Appalachian oaks. In *Oak Forest Ecosystems: Ecology and Management for Wildlife*; McShea, W.J., Healy, W.M., Eds.; Johns Hopkins University Press: Baltimore, MD, USA, 2002; pp. 149–172.
134. Struve, D.K. Seed Conditioning of Red Oak: A Recalcitrant North American Seed. *Sci. Agric. Piracicaba* **1998**, *55*, 67–73. [CrossRef]
135. Sturrock, R. Climate Change and Forest Diseases: Using Today's Knowledge to Address Future Challenges. *For. Syst.* **2012**, *21*, 329–336. [CrossRef]
136. Tiberi, R.; Branco, M.; Bracalini, M.; Croci, F.; Panzavolta, T. Cork Oak Pests: A Review of Insect Damage and Management. *Ann. For. Sci.* **2016**, *73*, 219–232. [CrossRef]
137. Jactel, H.; Koricheva, J.; Castagneyrol, B. Responses of Forest Insect Pests to Climate Change: Not so Simple. *Curr. Opin. Insect Sci.* **2019**, *35*, 103–108. [CrossRef]
138. Haavik, L.J.; Billings, S.A.; Guldin, J.M.; Stephen, F.M. Emergent Insects, Pathogens and Drought Shape Changing Patterns in Oak Decline in North America and Europe. *For. Ecol. Manag.* **2015**, *354*, 190–205. [CrossRef]
139. Loo, J.A. Ecological Impacts of Non-Indigenous Invasive Fungi as Forest Pathogens. *Biol. Invasions* **2008**, *11*, 81–96. [CrossRef]
140. Anagnostakis, S.L. The Effect of Multiple Importations of Pests and Pathogens on a Native Tree. *Biol. Invasions* **2001**, *3*, 245–254. [CrossRef]
141. Sena, K.; Crocker, E.; Vincelli, P.; Barton, C. *Phytophthora cinnamomi* as a Driver of Forest Change: Implications for Conservation and Management. *For. Ecol. Manag.* **2018**, *409*, 799–807. [CrossRef]
142. Hardham, A.R.; Blackman, L.M. *Phytophthora cinnamomi* . *Mol. Plant Pathol.* **2018**, *19*, 260–285. [CrossRef]
143. Garbelotto, M.; Hüberli, D.; Shaw, D. First Report on an Infestation of *Phytophthora cinnamomi* in Natural Oak Woodlands of California and Its Differential Impact on Two Native Oak Species. *Plant Dis.* **2006**, *90*, 685. [CrossRef] [PubMed]
144. McConnell, M.E.; Balci, Y. *Phytophthora cinnamomias* a Contributor to White Oak Decline in Mid-Atlantic United States Forests. *Plant Dis.* **2014**, *98*, 319–327. [CrossRef]
145. Moricca, S.; Linaldeddu, B.T.; Ginetti, B.; Scanu, B.; Franceschini, A.; Ragazzi, A. Endemic and Emerging Pathogens Threatening Cork Oak Trees: Management Options for Conserving a Unique Forest Ecosystem. *Plant Dis.* **2016**, *100*, 2184–2193. [CrossRef]
146. Garbelotto, M.; Hayden, K.J. Sudden Oak Death: Interactions of the Exotic Oomycete *Phytophthora ramorum* with Naïve North American Hosts. *Eukaryot. Cell* **2012**, *11*, 1313–1323. [CrossRef]

147. DiLeo, M.V.; Bostock, R.M.; Rizzo, D.M. Microclimate Impacts Survival and Prevalence of *Phytophthora ramorum* in Umbellularia Californica, a Key Reservoir Host of Sudden Oak Death in Northern California Forests. *PLoS ONE* **2014**, *9*, e98195. [CrossRef]
148. Kozanitas, M.; Metz, M.R.; Osmundson, T.W.; Serrano, M.S.; Garbelotto, M. The Epidemiology of Sudden Oak Death Disease Caused by *Phytophthora ramorum* in a Mixed Bay Laurel-Oak Woodland Provides Important Clues for Disease Management. *Pathogens* **2022**, *11*, 250. [CrossRef]
149. Banerjee, S. An Oak (*Quercus Robur* L.) Canker Caused by Stereum Rugosum (Pers.) Fr. *Trans. Br. Mycol. Soc.* **1956**, *39*, 267-IN5. [CrossRef]
150. Davidson, R.W.; Campbell, W.A.; Vaughn, D.B. *Fungi Causing Decay of Living Oaks in the Eastern United States and Their CuItural Identification*; Technical Bulletin No. 785; US Department of Agriculture: Washington, DC, USA, 1942.
151. Fergus, C.L. Relation of weather to the severity of white oak anthracnose. *Phytopathology* **1953**, *43*, 103–105.
152. Neely, D.; Himelick, E.B. Characteristics and Nomenclature of the Oak Anthracnose Fungus. *Phytopathology* **1967**, *57*, 1230–1236.
153. Goode, M.J. Control of oak leaf-blister in Mississippi. *Phytopathology* **1953**, *43*, 472.
154. Reed, S.E.; EngLish, J.T.; Muzika, R.M. Investigation of Rapid White Oak (*Quercus alba*) Mortality within the Ozark Plateau and Adjacent Forest-Prairie Transition Ecoregion. In *Forest Health Monitoring: National Status, Trends, and Analysis*; Gen. Tech. Rep.; U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 2015; p. 127.
155. Gibbs, J.N. Oak Wilt. *Arboric. J.* **1978**, *3*, 351–356. [CrossRef]
156. Oak, S.W.; Spetich, M.A.; Morin, R.S. Oak decline in central hardwood forests: Frequency, spatial extent, and scale. In *Natural Disturbances and Historic Range of Variation: Type, Frequency, Severity, and Post-Disturbance Structure in Central Hardwood Forests USA*; Greenberg, C., Collins, B., Eds.; Springer: Cham, Switzerland, 2015; Volume 32, pp. 49–71.
157. Serrano, M.S.; Romero, M.Á.; Homet, P.; Gómez-Aparicio, L. Climate Change Impact on the Population Dynamics of Exotic Pathogens: The Case of the Worldwide Pathogen Phytophthora Cinnamomi. *Agric. For. Meteorol.* **2022**, *322*, 109002. [CrossRef]
158. De Beer, Z.W.; Marincowitz, S.; Duong, T.A.; Wingfield, M.J. Bretziella, a New Genus to Accommodate the Oak Wilt Fungus, *Ceratocystis Fagacearum* (Microascales, Ascomycota). *MycoKeys* **2017**, *27*, 1–19. [CrossRef]
159. Henry, B.W. Oak Wilt: Its Significance, Symptoms and Cause. *Phytopathology* **1944**, *34*, 636–647.
160. Gibbs, J.N. *The Transmission of Oak Wilt*; North Central Forest Experiment Station, Forest Service, U.S. Department of Agriculture: St. Paul, MN, USA, 1980.
161. True, R.P. Oak Wilt in West Virginia. Oak Wilt West Virginia, 448t. 1960. Available online: https://researchrepository.wvu.edu/wv_agricultural_and_forestry_experiment_station_bulletins/649 (accessed on 28 November 2023).
162. Bretz, T.W. *Plant Diseases: The Yearbook of Agriculture: Oak Wilt, a New Threat*; USDA: Washington, DC, USA, 1953.
163. Juzwik, J.; Harrington, T.C.; MacDonald, W.L.; Appel, D.N. The Origin of *Ceratocystis Fagacearum*, the Oak Wilt Fungus. *Annu. Rev. Phytopathol.* **2008**, *46*, 13–26. [CrossRef] [PubMed]
164. Cervenka, V.J.; Skalbeck, T.C.; Kyhl, J.F.; Blackford, D.C.; Juzwik, J.; Seybold, S.J. *How to Identify Common Nitidulid Beetles Associated with Oak Wilt Mats in Minnesota*; USDA Forest Service, North Central Research Station: St. Paul, MN, USA, 2001; Volume 71.
165. Epstein, A.H. Root graft transmission of tree pathogens. *Annu. Rev. Phytopathol.* **1978**, *16*, 181–192. [CrossRef]
166. Oak, S.W. Native Diseases and Insects That Impact Oaks. In *Oak Forest Ecosystems: Ecology and Management for Wildlife*; Johns Hopkins University Press: Baltimore, MD, USA, 2002; pp. 80–99.
167. Pokorny, J. How to collect field samples and identify the oak wilt fungus in the laboratory. In Proceedings of the Shade Tree Wilt Diseases: A National Conference, St. Paul, MN, USA, 25–28 August 1999; American Phytopathological Society (APS Press): St. Paul, MN, USA, 2001; p. 139.
168. O'Brien, J.G.; Mielke, M.E.; Starkey, D.; Juzwik, J. *How to Prevent and Control Oak Wilt*; USDA Forest Service, State and Private Forestry: St. Paul, MN, USA, 2000.
169. Young, R.A. Studies in oak wilt caused by *Chalara quercina*. *Phytopathology* **1949**, *38*, 425–441.
170. Anderson, R.L.; Skilling, D.D. *Oak Wilt Damage: A Survey in Central Wisconsin*; Station Paper; U.S. Department of Agriculture, Forest Service, North Central Forest Experiment Station: St. Paul, MN, USA, 1955; p. 11.
171. Liese, W.; Ruetze, M. Development of a Fumigation Treatment of Oak Logs against Ceratocystis Fagacearum. *EPPO Bull.* **1985**, *15*, 29–36. [CrossRef]
172. MacDonald, W.L.; Schmidt, E.L.; Harner, E.J. Methyl Bromide Eradication of the Oak Wilt Fungus from Red and White Oak Logs. *For. Prod. J.* **1985**, *35*, 11–16.
173. Schmidt, E.L.; Ruetze, M.M.; French, D.W. Methyl bromide treatment of oak wilt infected logs: Laboratory and preliminary field fumigations [*Ceratocystis fagacearum*]. *For. Prod. J.* **1982**, *32*, 46–49.
174. Yang, A.; Seabright, K.; Juzwik, J.; Myers, S.W.; Taylor, A. Survival of the Oak Wilt Fungus in Logs Fumigated with Sulfuryl Fluoride and Methyl Bromide. *For. Prod. J.* **2019**, *69*, 87–95. [CrossRef]
175. Manion, P.D. *Tree Disease Concepts*; Prentice-Hall, Inc.: Hoboken, NJ, USA, 1981; p. 399.
176. Lawrence, R.; Moltzan, B.; Moser, W.K. Oak decline and the future of Missouri's forests. *Mo. Conserv.* **2002**, *63*, 11–18.
177. Wargo, P.M.; Houston, D.R. Infection of defoliated sugar maple trees by Armillaria mellea. *Phytopathology* **1974**, *64*, 817–822. [CrossRef]
178. Wargo, P.M.; Houston, D.R.; LaMadeleine, L.S. *Oak Decline*; Forest Insect and Disease Leaflet 165; U.S. Department of Agriculture Forest Service: Washington, DC, USA, 1983; 8p.

179. Starkey, D.A.; Oliveria, F.; Mangini, A.; Mielke, M. *Oak Decline and Red Oak Borer in the Interior Highlands of Arkansas and Missouri: Natural Phenomena, Severe Occurrences*; Gen. Tech. Rep. SRS-73; U.S. Department of Agriculture, Forest Service, Southern Research Station: Asheville, NC, USA, 2004; pp. 217–222.
180. Wargo, P.M. *Armillariella mellea* and *Agrilus bilineatus* and Mortality of Defoliated Oak Trees. *For. Sci.* **1977**, *23*, 485–492.
181. Starkey, D.A.; Oak, S.W.; Ryan, G.W.; Tainter, F.H.; Redmond, C.; Brown, H.C. *Evaluation of Oak Decline Areas in the South*; Protection Report R8-PR (USA); U.S. Department of Agriculture, Forest Service: Atlanta, GA, USA, 1989.
182. Senanayake, I.C.; Jeewon, R.; Chomnunti, P.; Wanasinghe, D.N.; Norphanphoun, C.; Karunarathna, A.; Pem, D.; Perera, R.H.; Camporesi, E.; McKenzie, E.H.C.; et al. Taxonomic Circumscription of Diaporthales Based on Multigene Phylogeny and Morphology. *Fungal Divers.* **2018**, *93*, 241–443. [CrossRef]
183. Sinclair, W.A.; Lyon, H.H.; Johnson, W.T. *Diseases of Trees and Shrubs*; Cornell University Press: Ithaca, NY, USA, 1987.
184. Elkinton, J.S.; Healy, W.M.; Liebhold, A.M.; Buonaccorsi, J.P. Gypsy moths and forest dynamics. In *Oak Forest Ecosystems: Ecology and Management for Wildlife*; Johns Hopkins University Press: Baltimore, MD, USA, 2002; pp. 100–112.
185. EDDMapS. Early Detection & Distribution Mapping System. The University of Georgia—Center for Invasive Species and Ecosystem Health. Available online: http://www.eddmaps.org/ (accessed on 27 November 2023).
186. Elkinton, J.S.; Liebhold, A.M. Population Dynamics of Gypsy Moth in North America. *Annu. Rev. Entomol.* **1990**, *35*, 571–596. [CrossRef]
187. Williams, D.W.; Fuester, R.W.; Metterhouse, W.W.; Balaam, R.J.; Bullock, R.H.; Chianese, R.J.; Reardo, R.C. Incidence and Ecological Relationships of Parasitism in Larval Populations of Lymantria Dispar (*Lepidoptera: Lymantriidae*). *Biol. Control* **1992**, *2*, 35–43. [CrossRef]
188. Williams, D.W.; Liebhold, A.M. Influence of Weather on the Synchrony of Gypsy Moth (Lepidoptera: Lymantriidae) Outbreaks in New England. *Environ. Entomol.* **1995**, *24*, 987–995. [CrossRef]
189. Drake, W.E. Evaluation of an approach to improve acorn production during thinning. In Proceedings of the Eighth Biennial Southern Silvicultural Research Conference, Auburn, AL, USA, 1–3 November 1994; U.S. Department of Agriculture, Forest Service, Northeastern Forest Experiment Station: Radnor, PA, USA, 1995; pp. 429–441.
190. Hough, J.A.; Pimentel, D. Influence of Host Foliage on Development, Survival, and Fecundity of the Gypsy Moth. *Environ. Entomol.* **1978**, *7*, 97–102.
191. Gottschalk, K.W. Gypsy moth effects on mast production. In *Proceedings of Southern Appalachian Mast Management Workshop, Knoxville, TN, USA, 14–16 August 1989*; McGee, C.E., Ed.; University of Tennessee: Knoxville, TN, USA, 1989; pp. 42–50.
192. Forbush, E.H.; Fernald, C.H. *The Gypsy Moth: Porthetria dispar (linn.). A Report of the Work of Destroying the Insect in the Commonwealth of Massachusetts, Together with an Account of Its History and Habits Both in Massachusetts and Europe*; Wright & Potter Printing Company: Boston, MA, USA, 1896.
193. Christisen, D.M. Yield of Seed by Oaks in the Missouri Ozarks. *J. For.* **1955**, *53*, 439–441.
194. Gibson, L.P. *Insects That Damage Red Oak Acorns*; Research Paper NE-492; U.S. Department of Agriculture, Forest Service, Northeastern Research Station: Newtown Square, PA, USA, 1982.
195. Riccardi, C.L.; McCarthy, B.C.; Long, R.P. Oak seed production, weevil (Coleoptera: Curculionidae) populations, and predation rates in mixed-oak forests of southeast Ohio. In Proceedings of the 14th Central Hardwood Forest Conference, Wooster, OH, USA, 16–19 March 2004; Yaussy, D.L., Hix, D.M., Long, R.P., Goebel, C.P., Eds.; U.S. Department of Agriculture, Forest Service, Northeastern Research Station: Newtown Square, PA, USA, 2004; pp. 10–21.
196. Miller, D.R.; Schlarbaum, S.E. Acorn Fall and Weeviling in a Northern Red Oak Seedling Orchard. *J. Entomol. Sci.* **2005**, *40*, 31–38. [CrossRef]
197. Lazic, D.; Hipp, A.L.; Carlson, J.E.; Gailing, O. Use of Genomic Resources to Assess Adaptive Divergence and Introgression in Oaks. *Forests* **2021**, *12*, 690. [CrossRef]
198. Plomion, C.; Martin, F. Oak genomics is proving its worth. *New Phytol.* **2020**, *226*, 943–946. [CrossRef]
199. Gailing, O.; Hipp, A.L.; Plomion, C.; Carlson, J.E. Oak Population Genomics. In *Population Genomics*; Springer: Cham, Switzerland, 2021; pp. 1–37.
200. Pellicer, J.; Leitch, I.J. The Plant DNA C-values database (release 7.1): An updated online repository of plant genome size data for comparative studies. *New Phytol.* **2019**, *226*, 301–305. [CrossRef]
201. Bai, C.; Alverson, W.S.; Follansbee, A.; Waller, D.M. New reports of nuclear DNA content for 407 vascular plant taxa from the United States. *Ann. Bot.* **2012**, *110*, 1623–1629. [CrossRef]
202. Chen, S.C.; Cannon, C.H.; Kua, C.S.; Liu, J.J.; Galbraith, D.W. Genome size variation in the Fagaceae and its implications for trees. *Tree Genet. Genomes* **2014**, *10*, 977–988. [CrossRef]
203. Favre, J.M.; Brown, S. A flow cytometric evaluation of the nuclear DNA content and GC percent in genomes of European oak species. *Ann. Sci. For.* **1996**, *53*, 915–917. [CrossRef]
204. Horjales, M.; Redondo, N.; Rodríguez, M. Cantidades de DNA nuclear en árbóreas y arbustos. *NACC Nova Acta Cient. Compost. Biol.* **2003**, *13*, 20–33.
205. Olszewska, M.J.; Osiecka, R. The relationship between 2C DNA content, systematic position, and the level of nuclear DNA endoreduplication during differentiation of root parenchyma in some dicotyledonous shrubs and trees: Comparison with herbaceous species. *Biochem. Physiol. Pflanz.* **1984**, *179*, 641–657. [CrossRef]

206. Pustahija, F.; Brown, S.C.; Bogunić, F.; Bašić, N.; Muratović, E.; Ollier, S.; Hidalgo, O.; Bourge, M.; Stevanović, V.; Siljak-Yakovlev, S. Small genomes dominate in plants growing on serpentine soils in West Balkans, an exhaustive study of 8 habitats covering 308 taxa. *Plant Soil* **2013**, *373*, 427–453. [CrossRef]
207. Zoldos, V.; Papes, D.; Brown, S.C.; Panaud, O.; Siljak-Yakovlev, S. Genome size and base composition of seven *Quercus* species: Inter-and intra-population variation. *Genome* **1998**, *41*, 162–168. [CrossRef]
208. Bodénès, C.; Chancerel, E.; Ehrenmann, F.; Kremer, A.; Plomion, C. High-density linkage mapping and distribution of segregation distortion regions in the oak genome. *DNA Res.* **2016**, *23*, 115–124. [CrossRef] [PubMed]
209. Konar, A.; Choudhury, O.; Bullis, R.; Fiedler, L.; Kruser, J.M.; Stephens, M.T.; Romero-Severson, J. High-quality genetic mapping with ddRADseq in the non-model tree *Quercus rubra*. *BMC Genom.* **2017**, *18*, 417. [CrossRef]
210. Bodénès, C.; Chancerel, E.; Gailing, O.; Vendramin, G.G.; Bagnoli, F.; Durand, J.; Goicoechea, P.G.; Soliani, C.; Villani, F.; Mattioni, C.; et al. Comparative mapping in the Fagaceae and beyond with EST-SSRs. *BMC Plant Biol.* **2012**, *12*, 153. [CrossRef]
211. Gailing, O.; Bodénès, C.; Finkeldey, R.; Kremer, A.; Plomion, C. Genetic mapping of EST-derived simple sequence repeats (EST-SSRs) to identify QTL for leaf morphological characters in a *Quercus robur* full-sib family. *Tree Genet. Genomes* **2013**, *9*, 1361–1367. [CrossRef]
212. Leroy, T.; Louvet, J.-M.; Lalanne, C.; Le Provost, G.; Labadie, K.; Aury, J.-M.; Delzon, S.; Plomion, C.; Kremer, A. Adaptive introgression as a driver of local adaptation to climate in European white oaks. *New Phytol.* **2020**, *226*, 1171–1182. [CrossRef]
213. Scotti-Saintagne, C.; Bodenes, C.; Barreneche, T.; Bertocchi, E.; Plomion, C.; Kremer, A. Detection of quantitative trait loci controlling bud burst and height growth in *Quercus robur* L. *Theor. Appl. Genet.* **2004**, *109*, 1648–1659. [CrossRef]
214. Gailing, O. QTL analysis of leaf morphological characters in a *Quercus robur* full-sib family (*Q. robur* × *Q. robur* ssp. *slavonica). Plant Biol.* **2008**, *10*, 624–634. [CrossRef]
215. Gailing, O.; Kremer, A.; Steiner, W.; Hattemer, H.H.; Finkeldey, R. Results on quantitative trait loci for flushing date in oaks can be transferred to different segregating progenies. *Plant Biol.* **2005**, *7*, 516–525. [CrossRef] [PubMed]
216. Gailing, O.; Vornam, B.; Leinemann, L.; Finkeldey, R. Genetic and genomic approaches to assess adaptive genetic variation in plants: Forest trees as a model. *Physiol. Plant.* **2009**, *137*, 509–519. [CrossRef] [PubMed]
217. Brendel, O.; Le Thiec, D.; Scotti-Saintagne, C.; Bodénès, C.; Kremer, A.; Guehl, J.M. Quantitative trait loci controlling water use efficiency and related traits in *Quercus robur* L. *Tree Genet. Genomes* **2008**, *4*, 263–278. [CrossRef]
218. Parelle, J.; Zapater, M.; Scotti-Saintagne, C.; Kremer, A.; Jolivet, Y.; Dreyer, E.; Brendel, O. Quantitative trait loci of tolerance to waterlogging in a European oak (*Quercus robur* L.): Physiological relevance and temporal effect patterns. *Plant Cell Environ.* **2007**, *30*, 422–434. [CrossRef] [PubMed]
219. Caignard, T.; Delzon, S.; Bodénès, C.; Dencausse, B.; Kremer, A. Heritability and genetic architecture of reproduction-related traits in a temperate oak species. *Tree Genet. Genomes* **2019**, *15*, 1. [CrossRef] [PubMed]
220. Song, J.; Brendel, O.; Bodénès, C.; Plomion, C.; Kremer, A.; Colin, F. X-ray computed tomography to decipher the genetic architecture of tree branching traits: Oak as a case study. *Tree Genet. Genomes* **2017**, *13*, 1–15. [CrossRef]
221. Casasoli, M.; Derory, J.; Morera-Dutrey, C.; Brendel, O.; Porth, I.; Guehl, J.M.; Villani, F.; Kremer, A. Comparison of quantitative trait loci for adaptive traits between oak and chestnut based on an expressed sequence tag consensus map. *Genetics* **2006**, *172*, 533–546. [CrossRef] [PubMed]
222. Plomion, C.; Aury, J.M.; Amselem, J.; Leroy, T.; Murat, F.; Duplessis, S. Oak genome reveals facets of long lifespan. *Nat. Plants* **2018**, *4*, 440–452. [CrossRef] [PubMed]
223. Bartholomé, J.; Brachi, B.; Marçais, B.; Mougou-Hamdane, A.; Bodénès, C.; Plomion, C.; Robin, C.; Desprez-Loustau, M.L. The genetics of exapted resistance to two exotic pathogens in pedunculate oak. *New Phytol.* **2020**, *226*, 1088–1103. [CrossRef] [PubMed]
224. Kapoor, B.; Jenkins, J.; Schmutz, J.; Zhebentyayeva, T.; Kuelheim, C.; Coggeshall, M.; Heim, C.; Lasky, J.; Leites, L.; Islam-Faridi, N.; et al. Haplotype-resolved, chromosome-scale genome assembly of *Quercus rubra* L. *G3 Genes Genomes Genet.* **2023**, *13*, jkad209. [CrossRef] [PubMed]
225. Plomion, C.; Aury, J.M.; Amselem, J.; Alaeitabar, T.; Barbe, V.; Belser, C.; Bergès, H.; Bodénès, C.; Boudet, N.; Boury, C.; et al. Decoding the oak genome: Public release of sequence data, assembly, annotation and publication strategies. *Mol. Ecol. Resour.* **2016**, *16*, 254–265. [CrossRef]
226. Sork, V.L.; Fitz-Gibbon, S.T.; Puiu, D.; Crepeau, M.; Gugger, P.F.; Sherman, R.; Stevens, K.; Langley, C.H.; Pellegrini, M.; Salzberg, S.L. First draft assembly and annotation of the genome of a California endemic oak *Quercus lobata* Née (Fagaceae). *G3: Genes Genomes Genet.* **2016**, *6*, 3485–3495. [CrossRef]
227. Ramos, A.M.; Usié, A.; Barbosa, P.; Barros, P.M.; Capote, T.; Chaves, I.; Simões, F.; Abreu, I.; Carrasquinho, I.; Faro, C.; et al. The draft genome sequence of cork oak. *Sci. Data* **2018**, *5*, 180069. [CrossRef]
228. Quercus Robur Reference Genome Assembly dhQueRobu3.1, National Center for Biotechnology Information (NCBI), Accession PRJEB51283, Submitted by Wellcome Sanger Institute. Available online: https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_932294415.1 (accessed on 29 November 2023).
229. Quercus Glauca Reference Genome g3h1, National Center for Biotechnology Information (NCBI), Accession PRJNA435294, Submitted by Central South University of Forestry and Technology. Available online: https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_023736055.1/ (accessed on 29 November 2023).
230. Zhou, X.; Liu, N.; Jiang, X.; Qin, Z.; Farooq, T.H.; Cao, F.; Li, H. A chromosome-scale genome assembly of *Quercus gilva*: Insights into the evolution of *Quercus* section Cyclobalanopsis (Fagaceae). *Front. Plant Sci.* **2022**, *13*, 1012277. [CrossRef]

231. Ai, W.; Liu, Y.; Mei, M.; Zhang, X.; Tan, E.; Liu, H.; Han, X.; Zhan, H.; Lu, X. A chromosome-scale genome assembly of the Mongolian oak (*Quercus mongolica*). *Mol. Ecol. Resour.* **2022**, *22*, 2396–2410. [CrossRef] [PubMed]
232. Han, B.; Wang, L.; Xian, Y.; Xie, X.M.; Li, W.Q.; Zhao, Y.; Zhang, R.; Qin, X.; Li, D.-Z.; Jia, K.-H. A chromosome-level genome assembly of the Chinese cork oak (*Quercus variabilis*). *Front. Plant Sci.* **2022**, *13*, 1001583. [CrossRef]
233. Sork, V.L.; Cokus, S.J.; Fitz-Gibbon, S.T.; Zimin, A.V.; Puiu, D.; Garcia, J.A.; Gugger, P.F.; Henriquez, C.L.; Zhen, Y.; Lohmueller, K.E.; et al. High-quality genome and methylomes illustrate features underlying evolutionary success of oaks. *Nat. Commun.* **2022**, *13*, 2047. [CrossRef] [PubMed]
234. Wang, W.B.; He, X.F.; Yan, X.M.; Ma, B.; Lu, C.F.; Wu, J.; Zheng, Y.; Wang, W.H.; Xue, W.B.; Tian, X.C.; et al. Chromosome-scale genome assembly and insights into the metabolome and gene regulation of leaf color transition in an important oak species, *Quercus dentata*. *New Phytol.* **2023**, *238*, 2016–2032. [CrossRef]
235. Liu, D.; Xie, X.; Tong, B.; Zhou, C.; Qu, K.; Guo, H.; Zhao, Z.; El-Kassaby, Y.A.; Li, W.; Li, W. A high-quality genome assembly and annotation of *Quercus acutissima* Carruth. *Front. Plant Sci.* **2022**, *13*, 1068802. [CrossRef] [PubMed]
236. Rey, M.D.; Labella-Ortega, M.; Guerrero-Sánchez, V.M.; Carleial, R.; Castillejo, M.Á.; Ruggieri, V.; Jorrín-Novo, J.V. A first draft genome of holm oak (*Quercus ilex* subsp. *ballota*), the most representative species of the Mediterranean forest and the Spanish agrosylvopastoral ecosystem "dehesa". *Front. Mol. Biosci.* **2023**, *10*, 1242943. [CrossRef]
237. Quercus Aquifolioides Genome Assembly ASM1902251v1. Available online: https://www.ncbi.nlm.nih.gov/datasets/genome/GCA_019022515.1/ (accessed on 29 November 2023).
238. Kitts, P.A.; Church, D.M.; Thibaud-Nissen, F.; Choi, J.; Hem, V.; Sapojnikov, V.; Smith, R.G.; Tatusova, T.; Xiang, C.; Zherikov, A.; et al. Assembly: A resource for assembled genomes at NCBI. *Nucleic Acids Res.* **2016**, *44*, D73–D80. [CrossRef]
239. Figshare. Available online: https://figshare.com/ (accessed on 5 January 2023).
240. Goodstein, D.M.; Shu, S.; Howson, R.; Neupane, R.; Hayes, R.D.; Fazo, J.; Mitros, T.; Dirks, W.; Hellsten, U.; Putnam, N.; et al. Phytozome: A comparative platform for green plant genomics. *Nucleic Acids Res.* **2012**, *40*, D1178–D1186. [CrossRef]
241. Chen, M.; Ma, Y.; Wu, S.; Zheng, X.; Kang, H.; Sang, J.; Xu, X.; Hao, L.; Li, Z.; Gong, Z.; et al. Genome Warehouse: A public repository housing genome-scale data. *Genom. Proteom. Bioinform.* **2021**, *19*, 584–589. [CrossRef]
242. Chen, F.Z.; You, L.J.; Yang, F.; Na Wang, L.; Guo, X.Q.; Gao, F.; Hua, C.; Tan, C.; Fang, L.; Shan, R.Q.; et al. CNGBdb: China National Genebank database. *Yi Chuan Hered.* **2020**, *42*, 799–809.
243. Falk, T.; Herndon, N.; Grau, E.; Buehler, S.; Richter, P.; Zaman, S.; Baker, E.M.; Ramnath, R.; Ficklin, S.; Staton, M.; et al. Growing and cultivating the forest genomics database. *TreeGenes Database* **2018**, *2018*, bay084. [CrossRef]
244. Coyne, J.A.; Orr, H.A. Speciation: A catalogue and critique of species concepts. In *Philosophy of Biology: An Anthology*; John Wiley & Sons: Hoboken, NJ, USA, 2009; pp. 272–292.
245. Lotsy, J.P. Species or linneon. *Genetica* **1925**, *7*, 487–506. [CrossRef]
246. Petit, R.J.; Bodénès, C.; Ducousso, A.; Roussel, G.; Kremer, A. Hybridization as a mechanism of invasion in oaks. *New Phytol.* **2003**, *161*, 151–164. [CrossRef]
247. Curtu, A.L.; Gailing, O.; Finkeldey, R. Evidence for hybridization and introgression within a species—Rich oak (*Quercus* spp.) community. *BMC Evol Biol.* **2007**, *7*, 218. [CrossRef] [PubMed]
248. Khodwekar, S.; Gailing, O. Evidence for environment-dependent introgression of adaptive genes between two red oak species with different drought adaptations. *Am. J. Bot.* **2017**, *104*, 1088–1098. [CrossRef] [PubMed]
249. Oney-Birol, S.; Fitz-Gibbon, S.; Chen, J.M.; Gugger, P.F.; Sork, V.L. Assessment of shared alleles in drought-associated candidate genes among southern California white oak species (*Quercus* sect. *Quercus*). *BMC Genet.* **2018**, *19*, 12. [CrossRef] [PubMed]
250. Cavender-Bares, J.; Gonzalez-Rodriguez, A.; Eaton, D.A.R.; Hipp, A.A.L.; Beulke, A.; Manos, P.S. Phylogeny and biogeography of the American live oaks (*Quercus* subsection *Virentes*): A genomic and population genetics approach. *Mol. Ecol.* **2015**, *24*, 3668–3687. [CrossRef] [PubMed]
251. Eaton, D.A.R.; Hipp, A.L.; Gonzalez-Rodriguez, A.; Cavender-Bares, J. Historical introgression among the American live oaks and the comparative nature of tests for introgression. *Evolution* **2015**, *69*, 2587–2601. [CrossRef] [PubMed]
252. Aldrich, P.; Cavender-Bares, J. Quercus. In *Wild Crop Relatives: Genomic and Breeding Resources, Forest Trees*; Kole, C., Ed.; Springer: Berlin, Germany, 2011; pp. 89–129.
253. Sullivan, A.R.; Owusu, S.A.; Weber, J.A.; Hipp, A.L.; Gailing, O. Hybridization and divergent selection in multispecies oak communities. *Bot. J. Linn. Soc.* **2016**, *181*, 99–114. [CrossRef]
254. Dodd, R.S.; Afzal-Rafii, Z. Selection and dispersal in a multispecies oak hybrid zone. *Evolution* **2004**, *58*, 261–269. [PubMed]
255. Lepais, O.; Gerber, S. Reproductive patterns shape introgression dynamics and species succession within the European white oak complex. *Evolution* **2011**, *65*, 156–170. [CrossRef]
256. Kim, B.Y.; Wei, X.Z.; Fitz-Gibbon, S.; Lohmueller, K.E.; Ortego, J.; Gugger, P.F.; Sork, V.L. RADseq data reveal ancient, but not pervasive, introgression between Californian tree and scrub oak species (*Quercus* sect. *Quercus*: Fagaceae). *Mol. Ecol.* **2018**, *27*, 4556–4571. [CrossRef]
257. Curtu, A.L.; Gailing, O.; Finkeldey, R. Patterns of contemporary hybridization inferred from paternity analysis in a four-oak-species forest. *BMC Evol. Biol.* **2009**, *9*, 284. [CrossRef]
258. Gailing, O.; Zhang, R. Experimental evidence for selection against hybrids between two interfertile red oak species. *Silvae Genet.* **2018**, *67*, 106–110. [CrossRef]

259. Scotti-Saintagne, C.; Mariette, S.; Porth, I.; Goicoechea, P.G.; Barreneche, T.; Bodénès, C.; Burg, K.; Kremer, A. Genome scanning of interspecific differentiation between two closely related oak species (*Quercus robur* L. and *Q. petraea* (Matt.) Liebl.). *Genetics* **2004**, *168*, 1615–1626. [CrossRef] [PubMed]
260. Goicoechea, P.G.; Petit, R.J.; Kremer, A. Detecting the footprints of divergent selection in oaks with linked markers. *Heredity* **2012**, *109*, 361–371. [CrossRef] [PubMed]
261. Goicoechea, P.; Herrán, A.; Durand, J.; Bodénès, C.; Plomion, C.; Kremer, A. A linkage disequilibrium perspective on the genetic mosaic of speciation in two hybridizing Mediterranean white oaks. *Heredity* **2015**, *114*, 373–386. [CrossRef] [PubMed]
262. Via, S.; West, J. The genetic mosaic suggests a new role for hitchhiking in ecological speciation. *Mol. Ecol.* **2008**, *17*, 4334–4345. [CrossRef]
263. Via, S. Natural selection in action during speciation. *Proc. Natl. Acad. Sci. USA* **2009**, *106*, 9939–9946. [CrossRef] [PubMed]
264. Via, S. Divergence hitchhiking and the spread of genomic isolation during ecological speciation-with-gene-flow. *Philos. Trans. R. Soc. B Biol. Sci.* **2012**, *367*, 451–460. [CrossRef]
265. Lind-Riehl, J.; Gailing, O. Adaptive variation and introgression of a CONSTANS-like gene in North American red oaks. *Forests* **2017**, *8*, 3. [CrossRef]
266. Bradshaw, A.D. Evolutionary significance of phenotype plasticity in plants. *Adv. Genet.* **1965**, *13*, 115–155.
267. Davis, M.B.; Shaw, R.G. Range shifts and adaptive responses to Quaternary climate change. *Science* **2001**, *292*, 673–679. [CrossRef] [PubMed]
268. Gram, W.K.; Sork, V.L. Association between environmental heterogeneity in forest tree populations. *Ecology* **2001**, *82*, 2012–2021. [CrossRef]
269. Aitken, S.N.; Yeaman, S.; Holliday, J.A.; Wang, T.; Curtis-McLane, S. Adaptation, migration or extirpation: Climate change outcomes for tree populations. *Evol. Appl.* **2008**, *1*, 95–111. [CrossRef] [PubMed]
270. Chevin, L.-M.; Lande, R.; Mace, G.M. Adaptation, plasticity, and extinction in a changing environment: Towards a predictive theory. *PLoS Biol.* **2010**, *8*, e1000357. [CrossRef] [PubMed]
271. Huang, Y.-N.; Zhang, H.; Rogers, S.; Coggeshall, M.; Woeste, K. White oak growth after 23 years in a three-site provenance/progeny trial on a latitudinal gradient in Indiana. *For. Sci.* **2016**, *62*, 99–106. [CrossRef]
272. Alexandre, H.; Truffaut, L.; Klein, E.; Ducousso, A.; Chancerel, E.; Lesur, I.; Dencausse, B.; Louvet, J.-M.; Nepveu, G.; Torres-Ruiz, J.M.; et al. How does contemporary selection shape oak phenotypes? *Evol. Appl.* **2020**, *13*, 2772–2790. [CrossRef] [PubMed]
273. Matyas, C. Modeling climate change effects with provenance test data. *Tree Physiol.* **1994**, *14*, 797–804. [CrossRef]
274. Burianek, V.; Benedikova, M.; Kyselakova, J. Evaluation of twenty-years-old pedunculate and sessile oak provenance trial. *For. Sci.* **2011**, *57*, 153–169. [CrossRef]
275. Kapeller, S.; Lexer, M.J.; Geburek, T.; Hiebl, J.; Schueler, S. Intraspecific variation in climate response of Norway spruce in the eastern Alpine range: Selecting appropriate provenances for future climate. *For. Ecol. Manag.* **2012**, *271*, 46–57. [CrossRef]
276. Rellstab, C.; Zoller, S.; Walthert, L.; Lesur, I.; Pluess, A.; Graf, R.; Bodenes, C.; Sperisen, C.; Kremer, A.; Gugerli, A. Signatures of local adaptation in candidate genes of oaks (*Quercus* spp.) with respect to present and future climatic conditions. *Mol. Ecol.* **2016**, *25*, 5907–5924. [CrossRef]
277. Didier, B.D.; Lebourgeois, F.; Ponton, S.; Musch, B.; Ducousso, A. Which oak provenances for the 22nd century in Western Europe? Dendroclimatology in common gardens. *PLoS ONE* **2020**, *15*, e0234583.
278. Zohner, C.M.; Renner, S.S. Common garden comparison of the leaf-out phenology of woody species from different native climates, combined with herbarium records, forecasts long-term change. *Ecol. Lett.* **2014**, *17*, 1016–1025. [CrossRef]
279. Vieitez, A.M.; Corredoira, E.; Martínez, M.T.; San-José, M.C.; Sánchez, C.; Valladares, S.; Vidal, N.; Ballester, A. Application of biotechnological tools to *Quercus* improvement. *Eur. J. For. Res.* **2012**, *131*, 519–539. [CrossRef]
280. Savill, P.S.; Kanowski, P.J. Tree improvement programs for European oaks: Goals and strategies. *Ann. Sci. For.* **1993**, *50* (Suppl. S1), 368–383. [CrossRef]
281. Bacilieri, R.; Labbé, T.; Kremer, A. Intraspecific genetic structure in a mixed population of *Quercus petraea* (Matt.) Liebl. and *Quercus robur* L. *Heredity* **1994**, *73*, 130–141. [CrossRef]
282. Sáenz-Romero, C.; Lamy, J.; Ducousso, A.; Musch, B.; Ehrenmann, F.; Delzon, S.; Cavers, S.; Chałupka, W.; Dağdaş, S.; Hansen, J.K.; et al. Adaptative and plastic response of *Quercus petraea* populations to climate across Europe. *Glob. Change Biol.* **2017**, *23*, 2831–2847. [CrossRef] [PubMed]
283. Sork, V.L.; Koop, A.; de la Fuente, M.A.; Foster, P.; Raveill, J. Patterns of Genetic Variation in Woody Plant Species in the Missouri Ozark Forest Ecosystem Project. In Proceedings of the Missouri Ozark Forest Ecosystem Project Symposium: An Experimental Approach to Landscape Research, St. Louis, MO, USA, 3–5 June 1997; Brookshire, B.L., Shifley, L., Stephen, R., Eds.; Gen. Tech. Rep. NC-193. USDA Forest Service, North Central Forest Experiment Station: St. Paul, MN, USA, 1997; pp. 231–247.
284. Gram, W.K.; Sork, V.L. Population density as a predictor of genetic variation for woody plant species. *Conserv. Biol.* **1999**, *13*, 1079–1087. [CrossRef]
285. Rink, G.; Coggeshall, M.V. Geographic variation in white oak acorn volume. In Proceedings of the 3rd North Central Tree Improvement Conference, Wooster, OH, USA, 17–19 August 1983; Guries, R.P., Ed.; North Central Tree Improvement Association: Fargo, ND, USA, 1987; pp. 24–53.
286. Kormanik, P.P.; Sung, S.-J.; Kormanik, T.L.; Zarnoch, S.J.; Schlarbaum, S. Heritability of first-order-lateral roots in five Quercus species: Effect on 1-0 seedling quality evaluation. In Proceedings of the Second Meeting of Working Party 2.08.05, Genetics of

Quercus, of the International Union of Forest Research Organizations, State College, PA, USA, 12–17 October 1997; Steiner, K.C., Ed.; University Park: State College, PA, USA, 1997; pp. 194–200.
287. Craft, K.J.; Ashley, M.V. Population differentiation among three species of white oak in northeastern Illinois. *Can. J. For. Res.* **2006**, *36*, 206–215. [CrossRef]
288. Meier, A.; Saunders, M.R. Epicormic development in pole-size white oak (Quercus alba L.) progeny tests three years following crown release. In Proceedings of the 18th Biennial Southern Silvicultural Research Conference, Knoxville, TN, USA, 2–5 March 2015; Schweitzer, C.J., Clatterbuck, W.K., Oswalt, C.M., Eds.; e-Gen. Tech. Rep. SRS-212. USDA Forest Service, Southern Research Station: Asheville, NC, USA, 2016; pp. 395–404.
289. Wheeler, N.C.; Steiner, K.C.; Schlarbaum, S.E.; Neale, D.B. The evolution of forest genetics and tree improvement research in the United States. *J. For.* **2015**, *113*, 500–510. [CrossRef]
290. Schlarbaum, S.E. Growth trends and geographic variation in a Quercus alba progeny test. *Ann. Sci. For.* **1993**, *50*, 425s–429s. [CrossRef]
291. O'Connor, P.A.; Coggeshall, M.V. White oak seed source performance across multiple sites in Indiana through age. In *Proceedings, 17th Central Hardwood Forest Conference, Lexington, KY, USA, 5–7 April 2010*; Fei, S., Lhotka, J.M., Stringer, J.W., Gottschalk, K.W., Miller, G.W., Eds.; Gen. Tech. Rep. NRS-P-78; USDA Forest Service, Northern Research Station: Newtown Square, PA, USA, 2010; pp. 358–363.
292. Schlarbaum, S.E. Problems and prospects for forest tree improvement research in the United States. In *Forest Genetics and Sustainability*; Springer: Dordrecht, The Netherlands, 1999; pp. 223–233.
293. Clark, S.L.; Schweitzer, C.J. Sustaining oak forests in the 21st century through science-based management. In *Proceedings of the 2017 Oak Symposium, Knoxville, TN, USA, 24–26 October 2017*; No. SRS-237; Southern Research Station, USDA Forest Service: Lexington, KY, USA, 2019.
294. DeWald, L.E.; Hackworth, Z.J.; Nelson, C.D. White oak genetics and tree improvement program (WOGTIP): Range-wide collaborative effort and early results. In Proceedings of the 36th South Forest Tree Improvement Conference, Athens, GA, USA (Virtual), 7–9 June 2021; Merkle, S.A., Levi, E.M., Eds.; pp. 22–23. Available online: http://www.sftic.org (accessed on 29 November 2023).
295. Chalupa, V. Vegetative propagation of oak (*Quercus robur* and *Q petraea*) by cutting and tissue culture. *Ann. Sci. For.* **1993**, *50* (Suppl. S1), 295s–307s. [CrossRef]
296. Amissah, J.N.; Paolillo, D.J., Jr.; Bassuk, N. Adventitious Root Formation in Stem Cuttings of *Quercus bicolor* and *Quercus macrocarpa* and Its Relationship to Stem Anatomy. *J. Am. Soc. Hort. Sci.* **2008**, *133*, 479–486. [CrossRef]
297. Amissah, J.N.; Bassuk, N. Cutting Back Stock Plants Promotes Adventitious Rooting of Stems of *Quercus bicolor* and *Quercus macrocarpa*. *J. Environ. Hort.* **2009**, *27*, 159–165.
298. Álvarez, R.; Alonso, P.; Cortizo, M.; Celestino, C.; Hernández, I.; Toribio, M.; Ordás, R.J. Genetic transformation of selected mature cork oak (*Quercus suber* L.) trees. *Plant Cell Rep.* **2004**, *23*, 218–223. [CrossRef]
299. Sánchez, N.; Manzanera, J.A.; Pintos, B.; Bueno, M.A. Agrobacterium-mediated transformation of cork oak (*Quercus suber* L.) somatic embryos. *New Forest.* **2005**, *29*, 169–176. [CrossRef]
300. Álvarez, R.; Álvarez, J.M.; Humara, J.M.; Revilla, Á.; Ordás, R.J. Genetic transformation of cork oak (*Quercus suber* L.) for herbicide resistance. *Biotechnol. Lett.* **2009**, *31*, 1477–1483. [CrossRef]
301. Vidal, N.; Mallón, R.; Valladares, S.; Meijomín, A.M.; Vieitez, A.M. Regeneration of transgenic plants by Agrobacterium-mediated transformation of somatic embryos of juvenile and mature *Quercus robur*. *Plant Cell Rep.* **2010**, *29*, 1411–1422. [CrossRef] [PubMed]
302. Mallón, R.; Valladares, S.; Corredoira, E.; Vieitez, A.M.; Vidal, N. Overexpression of the chestnut CsTL1 gene coding for a thaumatin-like protein in somatic embryos of *Quercus robur*. *Plant Cell Tissue Organ Cult.* **2014**, *116*, 141–151. [CrossRef]
303. García-Casado, G.; Collada, C.; Allona, I.; Soto, A.; Casado, R.; Rodriguez-Cerezo, E.; Gomez, L.; Aragoncillo, C. Characterization of an apoplastic basic thaumatin-like protein from recalcitrant chestnut seeds. *Physiol. Plant* **2000**, *110*, 172–180. [CrossRef]
304. Cano, V.; Martínez, M.T.; San José, M.C.; Couselo, J.L.; Varas, E.; Bouza-Morcillo, L.; Toribio, M.; Corredoira, E. Regeneration of transgenic plants by *Agrobacterium*-mediated transformation of *Quercus ilex* L. somatic embryos with the gene CsTL. *New For.* **2020**, *51*, 1003–1021. [CrossRef]
305. Serrazina, S.; Martínez, M.T.; Cano, V.; Malhó, R.; Costa, R.L.; Corredoira, E. Genetic Transformation of Quercus ilex Somatic Embryos with a Gnk2-like Protein That Reveals a Putative Anti-Oomycete Action. *Plants* **2022**, *11*, 304. [CrossRef]
306. Sawano, Y.; Miyakawa, T.; Yamazaki, H.; Tanokura, M.; Hatano, K. Purification, characterization, and molecular gene cloning of an antifungal protein from *Ginkgo biloba* seeds. *Biol. Chem.* **2007**, *388*, 273–280. [CrossRef]
307. Merkle, S.A.; Parrott, W.A.; Flinn, B.S. Morphogenic aspects of somatic embryogenesis. In *In Vitro Embryogenesis in Plants*; Thorpe, T.A., Ed.; Kluwer Academic Publisher: Dordrecht, The Netherlands, 1995; pp. 155–203.
308. Merkle, S.A.; Nairn, C.J. Hardwood tree biotechnology. *Vitr. Cell Dev. Biol. Plant* **2005**, *41*, 602–619. [CrossRef]
309. Vieitez, A.M.; Corredoira, E.; Ballester, A.; Muñoz, F.; Durán, J.; Ibarra, M. In vitro regeneration of the important North American oak species *Quercus alba*, *Quercus bicolor* and *Quercus rubra*. *Plant Cell Tissue Organ Cult.* **2009**, *98*, 135–145. [CrossRef]
310. Corredoira, E.; San-José, M.C.; Vieitez, A.M. Induction of somatic embryogenesis from different explants of shoot cultures derived from young *Quercus alba* trees. *Trees* **2012**, *26*, 881–891. [CrossRef]
311. Andrade, G.M.; Nairn, C.J.; Huong, T.L.; Merkle, S.A. Sexually mature transgenic American chestnut trees via embryogenic suspension-based transformation. *Plant Cell Rep.* **2009**, *28*, 1385–1397. [CrossRef] [PubMed]

312. Filichkin, S.A.; Meilan, R.; Busov, V.B.; Ma, C.; Brunner, A.M.; Strauss, S.H. Alcohol-inducible gene expression in transgenic Populus. *Plant Cell Rep.* **2006**, *25*, 660–667. [CrossRef] [PubMed]
313. Sakvarelidze, L.; Tao, Z.; Bush, M.; Roberts, G.R.; Leader, D.J.; Doonan, J.H.; Rawsthorne, S. Coupling the GAL4 UAS system with alcR for versatile cell type-specific chemically inducible gene expression in *Arabidopsis*. *Plant Biotechnol. J.* **2007**, *5*, 465–476. [CrossRef] [PubMed]
314. Tull, A.R.; Gladfelter, H.; Pampolini, F.; Rieske, L.; Nelson, C.D.; Merkle, S. Development of a New Genetic Transformation System for White and Green Ash Using Embryogenic Cultures. *Forests* **2022**, *13*, 671. [CrossRef]
315. Ecke, S.; Dempewolf, J.; Frey, J.; Schwaller, A.; Endres, E.; Klemmt, H.-J.; Tiede, D.; Seifert, T. UAV-Based Forest Health Monitoring: A Systematic Review. *Remote Sens.* **2022**, *14*, 13. [CrossRef]
316. Guo, W.; Carroll, M.E.; Singh, A.; Swetnam, T.L.; Merchant, N.; Sarkar, S.; Singh, A.K.; Ganapathysubramanian, B. UAS-Based Plant Phenotyping for Research and Breeding Applications. *Plant Phenomics* **2021**, *2021*, 9840192. [CrossRef] [PubMed]
317. Beloiu, M.; Heinzmann, L.; Rehush, N.; Gessler, A.; Griess, V.C. Individual Tree-Crown Detection and Species Identification in Heterogeneous Forests Using Aerial RGB Imagery and Deep Learning. *Remote Sens.* **2023**, *15*, 5. [CrossRef]
318. Chen, Q.; Gao, T.; Zhu, J.; Wu, F.; Li, X.; Lu, D.; Yu, F. Individual Tree Segmentation and Tree Height Estimation Using Leaf-Off and Leaf-On UAV-LiDAR Data in Dense Deciduous Forests. *Remote Sens.* **2022**, *14*, 2787. [CrossRef]
319. Rodríguez-Puerta, F.; Gómez-García, E.; Martín-García, S.; Pérez-Rodríguez, F.; Prada, E. UAV-Based LiDAR Scanning for Individual Tree Detection and Height Measurement in Young Forest Permanent Trials. *Remote Sens.* **2022**, *14*, 170. [CrossRef]
320. Borges, M.V.V.; de Oliveira Garcia, J.; Batista, T.S.; Silva, A.N.M.; Baio, F.H.R.; da Silva Junior, C.A.; de Azevedo, G.B.; de Oliveira Sousa Azevedo, G.T.; Teodoro, L.P.R.; Teodoro, P.E. High-throughput phenotyping of two plant-size traits of *Eucalyptus* species using neural networks. *J. For. Res.* **2022**, *33*, 591–599. [CrossRef]
321. Sagan, V.; Maimaitijiang, M.; Sidike, P.; Eblimit, K.; Peterson, K.T.; Hartling, S.; Esposito, F.; Khanal, K.; Newcomb, M.; Pauli, D.; et al. UAV-Based High Resolution Thermal Imaging for Vegetation Monitoring, and Plant Phenotyping Using ICI 8640 P, FLIR Vue Pro R 640, and thermoMap Cameras. *Remote Sens.* **2019**, *11*, 330. [CrossRef]
322. Da Cunha Neto, E.M.; Rex, F.E.; Veras, H.F.P.; Moura, M.M.; Sanquetta, C.R.; Käfer, P.S.; Sanquetta, M.N.I.; Zambrano, A.M.A.; Broadbent, E.N.; Corte, A.P.D. Using high-density UAV-Lidar for deriving tree height of Araucaria Angustifolia in an Urban Atlantic Rain Forest. *Urban For. Urban Green.* **2021**, *63*, 127197. [CrossRef]
323. Krůček, M.; Král, K.; Cushman, K.C.; Missarov, A.; Kellner, J.R. Supervised Segmentation of Ultra-High-Density Drone Lidar for Large-Area Mapping of Individual Trees. *Remote Sens.* **2020**, *12*, 3260. [CrossRef]
324. Mazis, A.; Choudhury, S.D.; Morgan, P.B.; Stoerger, V.; Hiller, J.; Ge, Y.; Awada, T. Application of high-throughput plant phenotyping for assessing biophysical traits and drought response in two oak species under controlled environment. *For. Ecol. Manag.* **2020**, *465*, 118101. [CrossRef]
325. Sapes, G.; Lapadat, C.; Schweiger, A.K.; Juzwik, J.; Montgomery, R.; Gholizadeh, H.; Townsend, P.A.; Gamon, J.A.; Cavender-Bares, J. Canopy spectral reflectance detects oak wilt at the landscape scale using phylogenetic discrimination. *Remote Sens. Environ.* **2022**, *273*, 112961. [CrossRef]
326. Green Forests Work. Available online: https://www.greenforestswork.org/ (accessed on 29 November 2023).
327. iTREE. Available online: https://www.itreetools.org/ (accessed on 29 November 2023).
328. The Trillion Trees Initiative. Available online: https://www.1t.org (accessed on 29 November 2023).
329. The Nature Conservancy's Billion Trees Campaign. Available online: https://www.nature.org/en-us/get-involved/how-to-help/plant-a-billion/ (accessed on 29 November 2023).
330. Trees for the Future. Available online: https://trees.org/ (accessed on 29 November 2023).
331. The United Nations Forum on Forests. Available online: www.un.org/esa/forests/category/climate-change (accessed on 29 November 2023).
332. Steinkellner, H.; Fluch, S.; Turetschek, E.; Lexer, C.; Streiff, R.; Kremer, A.; Glössl, J. Identification and characterization of (GA/CT)n-microsatellite loci from Quercus petraea. *Plant Mol. Biol.* **1997**, *33*, 1093–1096. [CrossRef]
333. Kampfer, S.; Lexer, C.; Glössl, J.; Steinkellner, H. Characterization of (GA)n microsatellite loci from *Quercus robur*. *Hereditas* **1998**, *129*, 183–186. [CrossRef]
334. Bruschi, P.; Venderamin, G.G.; Bussotti, F.; Grossoni, P. Morphological and molecular diversity among Italian populations of Quercus petraea. *Ann. Bot.* **2003**, *91*, 707–716. [CrossRef]
335. Sebastiani, F.; Carnevale, S.; Vendramin, G.G. A new set of mono- and dinucleotide chloroplast microsatellites in Fagaceae. *Mol. Ecol. Notes* **2004**, *4*, 259–261. [CrossRef]
336. Durand, J.; Bodénès, C.; Chancerel, E.; Frigero, J.-M.; Vendramin, G.G.; Sebastiani, F.; Buonamici, A.; Gailing, O.; Koelewijn, H.P.; Villani, F.; et al. A fast and cost-effective approach to develop and map EST-SSR markers: Oak as a case study. *BMC Genom.* **2010**, *11*, 570. [CrossRef] [PubMed]
337. Guichoux, E.; Lagache, L.; Wagner, S.; Léger, P.; Petit, R.J. Two highly validated multiplexes (12-plex and 8-plex) for species delimitation and parentage analysis in oaks (*Quercus* spp.). *Mol. Ecol. Resour.* **2011**, *11*, 578–585. [CrossRef]
338. Staton, M.; Best, T.; Khodwekar, S.; Owusu, S.; Xu, T.; Xu, Y.; Jennings, T.; Cronn, R.; Arumuganathan, A.K.; Coggeshall, M.; et al. Preliminary genomic characterization of ten hardwood tree species from multiplexed low coverage whole genome sequencing. *PLoS ONE* **2015**, *10*, e0145031. [CrossRef]

339. Antonecchia, G.; Fortini, P.; Lepais, O.; Gerber, S.; Legér, P.; Scippa, G.S.; Viscosi, V. Genetic structure of a natural oak community in central Italy: Evidence of gene flow between three sympatric white oak species (Quercus, Fagaceae). *Ann. For. Res.* **2015**, *58*, 205–216. [CrossRef]
340. Chmielewski, M.; Meyza, K.; Chybicki, I.J.; Dzialuk, A.; Litkowiec, M.; Burczyk, J. Chloroplast microsatellites as a tool for phylogeographic studies: The case of white oaks in Poland. *Iforest-Biogeosciences For.* **2015**, *8*, 765. [CrossRef]
341. Ortego, J.; Noguerales, V.; Gugger, P.F.; Sork, V.L. Evolutionary and demographic history of the Californian scrub white oak species complex: An integrative approach. *Mol. Ecol.* **2015**, *24*, 6188–6208. [CrossRef]
342. Thunder, R.G. Effects of Thinning Regimes on Genetic Variation of White Oak (*Quercus alba* L.) in Upland Oak Forests of Eastern Kentucky. Master's Thesis, University of Kentucky, Lexington, KY, USA, 2020.
343. Di Pietro, R.; Conte, A.L.; Di Marzio, P.; Fortini, P.; Farris, E.; Gianguzzi, L.; Müller, M.; Rosati, L.; Spampinato, G.; Gailing, O. Does the genetic diversity among pubescent white oaks in southern Italy, Sicily and Sardinia islands support the current taxonomic classification? *Eur. J. For. Res.* **2021**, *140*, 355–371. [CrossRef]
344. Padutov, V.E.; Baranov, O.Y.; Kagan, D.I.; Razumova, O.A.; Veinberga, I.; Baumanis, I.; Ruņģis, D.E. Analysis of Latvian and Belarusian Oak (*Quercus robur* L.) Population Provenance and Genetic Structure Using. Chloroplast Markers. *Proc. Latv. Acad. Sci.* **2021**, *75*, 248–253. [CrossRef]
345. Spence, E.S.; Fant, J.B.; Gailing, O.; Griffith, M.P.; Havens, K.; Hipp, A.L.; Kadav, P.; Kramer, A.; Thompson, P.; Toppila, R.; et al. Comparing genetic diversity in three threatened oaks. *Forests* **2021**, *12*, 561. [CrossRef]
346. Klápště, J.; Kremer, A.; Burg, K.; Garnier-Géré, P.; El-Dien, O.G.; Ratcliffe, B.; El-Kassaby, Y.A.; Porth, I. *Quercus species* divergence is driven by natural selection on evolutionarily less integrated traits. *Heredity* **2021**, *126*, 366–382. [CrossRef] [PubMed]
347. Dvořák, J.; Korecký, J.; Faltinová, Z.; Zádrapová, D. Genetic diversity of sessile oak populations in the Czech Republic. *J. For. Sci.* **2022**, *68*, 8–18. [CrossRef]
348. Phillips, D.H.; Burdekin, D.A. *Diseases of Forest and Ornamental Trees*; Macmillan: Basingstoke, UK, 1992.
349. Lombardo, J.A.; McCarthy, B.C. Silvicultural Treatment Effects on Oak Seed Production and Predation by Acorn Weevils in Southeastern Ohio. *For. Ecol. Manag.* **2008**, *255*, 2566–2576. [CrossRef]