

Editorial

Tree Genetics: Molecular and Functional Characterization of Genes

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Forests represent one of the most important ecosystems on Earth, covering approximately 30% of the total global land area. Forest ecosystems are found in most biome types and harbor a large proportion of the global diversity both in terms of species and habitats. Furthermore, they are also essential for the provision of a range of products and ecological services that are important to human wellbeing, e.g., renewable materials for several industry sectors (construction, pulp and paper, etc.), the mitigation of excess air pollutants, and CO₂ storage.

Forest trees and ecosystems are being threatened by climate change due to fluctuations in the frequency and intensity of heat and drought (extreme events), and the emergence of new pathogens and pests.

How trees will respond to climate change is thus a very relevant question both in the contexts of natural forests and tree plantations, even if recent findings highlight the need to move from a tree-based approach (tree as biological unit) to more complex systems, in which the understanding of forest decline and dieback (ecosystem level) can be better explained by abiotic and biotic interactions than the effects of a single climatic event.

To achieve deeper knowledge on these issues, plant molecular biology approaches leading to genomics descriptions and gene-to-function-centered studies are crucial. Such studies have already disclosed the genetic basis of various useful traits [1,2], but this information has limitedly been utilized in tree improvement and conservation. Indeed, breeding woody perennials is primarily bottlenecked by genomics and reproductive biology features [1], but these limitations can be at least partially solved with high-throughput genomics-assisted selection and phenotyping. The increasing amount of morphological, physiological, and genetic data may find practical applications in forest management, and in next-generation breeding programs to enhance forest health, ecosystem services, and sustainable production.

Hence, the Special Issue “Tree Genetics: Molecular and Functional Characterization of Genes” aimed to collect woody species gene-centered studies, with a special emphasis on functions related to trees’ tolerance and resilience to global changes.

This collection contains 10 research papers and two reviews. In general, 9 out of the 10 research papers report the identification and/or characterization of genes involved in a very wide set of biological facets: growth promotion/optimization, reproductive biology, wood production, and responses to abiotic and biotic stresses.

As a positive consequence of the new technical approaches in -omics research [1] and the continuous decrease in sequencing and other molecular biology techniques costs, the papers do not merely focus on model species. Indeed, six papers focus on broadleaved trees and four on conifers, including economically relevant species for a plethora of different uses, but also rare/endangered species [3] and ecologically important trees [4,5]. The variety of different species studied by the research papers belonging to this Special Issue



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perfectly respond to the invitation reported in [2], to extend the research fields in forest genetics to a broader number of species.

In particular, [6] analyzes *Camellia oleifera*, which is used for oil production; [7] *Liriodendron sino-americanum*, a relevant ornamental and afforestation species; and [3] *Handeliidendron bodinieri*, a rare and endangered species, which is also important for bio-energy, landscaping, and water and soil conservation. The study of [4] focuses on *Picea likiangensis*, one of the dominant tree species in the subalpine forest of southwest China, with an important ecological role in soil and water conservation and carbon storage; [8] reports findings on *Pinus massoniana*, a relevant timber tree, as well as loblolly and slash pines studied in [9]. *Chosenia arbutifolia* [10] is used as a raw material for technological aims and for landscape planting in China. Studies on two economically relevant species, a woody perennial shrub, *Camelia sinensis* [11], and a tree, *Hevea brasiliensis* [12], are also covered in this issue. Finally, [5] involves the Japanese larch, *Larix kaempferi*.

Reproductive biology, *sensu lato*, is the topic most represented in this Special Issue, with a total of five papers. In [6], transcriptome sequencing was used to study the male sterility caused by stamen petalody in *Camellia oleifera*, whose molecular regulation mechanism remains unclear. The results showed that four MADS transcription factor genes are predicted to be involved to different extents. These results lay a solid foundation for the selection of *C. oleifera* varieties and provide suitable references for future genetic breeding strategies.

In [7], the role of MiRNAs during callus growth and differentiation is investigated, leading to the hypothesis of a putative role of MiR397 in mitosis: its overexpression might delay callus proliferation, while overexpressing could accelerate callus proliferation.

Ref. [3] studies the molecular mechanism of stamen abortion underlying sex differentiation, using the *H. bodinieri* features of unisexual flowers with aborted stamens in female trees, which can be used as a model to study unisexual flower development in tree species. The results showed the differential accumulation of RNA belonging to 14 genes related to another development and meiosis, providing a theoretical basis for future research. The study of [12] reports the identification of three polyubiquitin genes for *H. brasiliensis*, as the replacement of the CaMV35S promoter by endogenous polyubiquitin promoters might improve the genetic transformation efficiency of this species. Since no endogenous polyubiquitin promoters in rubber tree were reported, those identified in [12] will expand the availability of molecular tools for driving the transgene expression in genetic engineering.

Ref. [5] reports the functional characterization in Japanese larch of a flowering promoting DEFICIENS-AGAMOUS-LIKE 1 (DAL1) gene, whose exact role in the life-cycle is still not completely understood. With a genetic transformation approach, the research showed that DAL1 accelerates the life-cycle progression in Arabidopsis by promoting the transition of meristem fate, providing more and novel functional information about the conifer age-related gene DAL1.

Two research papers investigate the role of specific genes in the response of trees to pathogens: the function of thaumatin-like proteins (TLP), as most of them exhibit antifungal activity, was investigated in [4]; four TLP genes were isolated, identified, and characterized, and their role in defense response demonstrated in *Picea likiangensis*.

The characterization of genes involved in the production of diterpene resin acids (DRAs), major components of pine oleoresin, effectively contributing to counteracting the invasion of insects and pathogenic microorganisms, is the topic of [9]; the paper uses RNAseq data to identify members of the subfamily CYP720B of cytochrome P450s involved in the catalysis of diterpene products into DRAs. The combination of qRT-PCR and biochemical data provides a valuable resource for a better understanding of the biological role of individual CYP720Bs in the production of DRA component and resistance to pathogens.

Ref. [8] analyzes in *Pinus massoniana* the role of a MYB gene involved in the secondary cell wall (SCW) biosynthesis. The use of transgenic lines showed that PmMYB4 targets lignin biosynthetic genes, and its overexpression increases lignin deposition, SCW thickness, and the expression of genes involved in SCW formation.

Single-molecular real-time sequencing (SMRT) technology based on the PacBio platform was used in [10] to fully sequence the transcriptome of *Chosenia arbutifolia*. Since molecular and genomic data are scarce for this species, this paper provides a very useful background and reference for functional genomic research on Salicaceae.

Ref. [11] identified and characterized 30 mature miR166s and twelve pre-miR166s in tea plants. MicroRNA166 (miR166) is a highly conserved plant miRNA that plays a crucial role in plant growth, and its resistance to various abiotic stresses had not previously been comprehensively identified and analyzed.

Traversari et al. [1] review the current knowledge on the molecular mechanisms triggering in conifers the transition between the production of cells with the typical features of earlywood and latewood. Since -omics resources, e.g., genomes and transcriptomes, are laying the basis for the comprehension of wood formation dynamics, boosting both breeding and gene-editing approaches, the review highlights the importance of xylem plasticity traits and wood formation dynamics of conifers within a changing environment.

The review from Baldi and La Porta [2] focuses on the molecular response of conifer adaptations to low water availability, describing the advantages and limitations of the approaches used in this field and the main results obtained in recent years. Furthermore, recommendations for future research are also offered, in particular regarding the study of a broader selection of resilient species and genera.

As Guest Editors, we believe that this Special Issue offers a meaningful collection of research papers and reviews regarding different aspects of tree genomics research, as well as offering interesting outlooks on current trends and future directions in woody perennial species' molecular genetics within a changing environment.

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

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