

Genetics and Improvement of Forest Trees

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Forest tree improvement has mainly been implemented to enhance the productivity of artificial forests. However, given the drastically changing global environment, improvement of various traits related to environmental adaptability is more essential than ever.

Plant genome research has revealed the genetic background of various useful traits. Abundant genomic and genetic information has accumulated for several important forest tree species. Such information not only enables rapid improvement of new traits, but also greatly contributes to forest tree breeding programs, including interpretation of the results thereof. However, there are few cases in which genetic information has been used effectively for forest tree improvement.

Tree improvement involves many processes, from determining the target tree species to setting breeding goals, establishing breeding strategies, and producing seeds. Each of these processes requires specific genetic information. Research on the phylogeny and genetic diversity of target species can provide information of fundamental importance at the beginning of a tree improvement program and for evaluating its results. Knowledge of the genes controlling the heritability and physiology of traits is essential. Accumulated genetic information can be used directly for marker-assisted selection (MAS) or genomic selection (GS) of target traits, facilitating more rapid tree improvement.

This special issue focuses on genetic information, including trait heritability and the physiological mechanisms thereof, which facilitates tree improvement. Nineteen papers are included reporting genetic approaches to improving various species, including conifers, broad-leaf trees, and bamboo.

Of the 19 papers, 5 deal with species phylogeny and the phylogeography of woody species. Li et al. [1] developed retrotransposon-based markers for Bamboo (*Phyllostachys* spp.), which are important natural resources, especially in Asia. The taxonomy and genetics of this group are complex. Therefore, this research should aid future studies. Research on within-species genetic diversity focuses mainly on conservation issues. However, this is also an essential issue for forest tree improvement, especially the derivation of efficacious improvement strategies. Kitamura et al. [2] (*Abies sachalinensis* F.Schmidt) and Chen et al. [3] (*Larix kaempferi* (Lamb.) Carr.) both discuss genetic variation in marginal populations. Understanding the genetic diversity of such populations will be useful for estimating their adaptability under changing environmental conditions. Inanaga et al. [4] report on the genetic diversity of *Thujaopsis dolabrata* (Thunb. ex L. f.) Siebold & Zucc., which is an important traditional species in Japanese forestry. Cai et al. [5] report on the genetic diversity and structure of *Cryptomeria japonica* var. *sinensis* (*Cryptomeria fortunei* (Hooibrenk)), which is endemic to China. These studies not only reveal the phylogeny of these species, but are also useful for evaluating the genetic resources available for further improvement thereof. They also provide useful information for determining the genetic consequences of tree improvement. Mukasyaf et al. [6] revealed the population genetic effects of adding *Pinus thunbergii* Parl. seedlings from pine wood nematode-resistant stock to existing forests.

Several papers discuss the inheritance of trees and relationship between genotype and environment, which is important to understand for forest tree improvement. Carignano et al. [7] report genetic variability in drought resistance among *Eucalyptus* clones and indicate



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the possibility of early selection in the nursery. Two papers evaluate selected *P. thunbergii* clones in terms of pine wood nematode resistance [8,9]. Iki et al. [8] report that the cumulative temperature after nematode infection does not affect the resistance ranking of progeny seedlings of nematode-resistant pine wood clones. Matsunaga et al. [9] examine the stability of traits in progeny seedlings moved to a different area from that in which they were selected. Tsuyama et al. [10] report the results of a 10-year provenance trial of *A. sachalinensis* using multivariate random forests, a machine learning method. Matsushita et al. [11] examine the growth-promoting effects of the light environment and girdling treatment on female cones in larch seed orchards. Takashima et al. [12] develop an infrared thermography/chlorophyll fluorescence technology for rapid evaluation of the response to drought stress of *C. japonica*. All of these papers not only provide specific selection criteria, but may also stimulate further research on the genes controlling these traits.

Four papers comprehensively analyze the physiological pathway of trait expression; this was made possible by recent advances in metabolomics and transcriptome analysis. Kurita et al. [13] examine genes promoting male strobilus formation after gibberellin treatment in *C. japonica*. Yang et al. [14] reveal candidate genes related to wood formation in *C. fortunei*. Cao et al. [15] study genes controlling wood properties in *Cunninghamia lanceolata* (Lamb.) Hook., especially heartwood color. Yang et al. [16] assess genes associated with the accumulation of tea oil in the leaves of *Camellia oleifera*. These four papers show the usefulness of genomic research for expediting genetic improvement of tree species with long lifespans.

Among the major targets of contemporary genetics research are MAS for specific traits and GS for quantitative trait loci. Lebedev et al. [17] provide a detailed review of GS and emphasize the need for advanced research in this field. Finally, two papers report on practical research. Moriguchi et al. [18] present the successful results of MAS of male sterility in *C. japonica*. Nagano et al. [19] report advanced results of GS in the same species. Both studies were successful because they used vast amounts of accumulated genetic information. Molecular breeding requires intensive research on the target species.

All of the papers published in this special issue provide cutting-edge genetic information on tree genetics and suggest research directions for future tree improvement. Tree improvement efforts are expected to be facilitated by research progress in various research fields.

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