

Preface

Twenty-five years ago I attended an IUFRO Meeting in Segovia (Spain) entitled "Biotechnology of Trees". Only a few papers in that conference included molecular approaches to study tree biology. From that time, rapid developments in plant molecular biology and sequencing capacity have revolutionized the way we currently study physiological processes in plants, including trees (Tsai, Harding, & Cooke, 2018). A crucial advance was the sequencing of the poplar genome (*Populus trichocarpa*) over 10 years ago (Tuskan et al., 2006). Afterwards, with the development of second-generation high-throughput sequencing, the genomes of an increasing number of angiosperm trees have been sequenced and it has even been possible to complete drafts for the megagenomes of several gymnosperm species (De la Torre et al., 2014; Street, Chapter 1; Cañas et al., Chapter 2). Overall, the reviews included in this book largely reflect the extraordinary impact that the above-mentioned technologies have had to accelerate the exponential progress in our current understanding of essential processes in tree biology.

The aim of this book is to present an overview of recent advances in the molecular physiology and biotechnology of forest trees. The 10 chapters of the book cover important aspects of fundamental tree biology which are addressed by leading scientists in the field. The authors present the current status and future directions in research related to structural and functional genomics, nutrition, growth and development, wood and cell wall regulation, stress tolerance, and the use of trees for phytoremediation purposes. A brief introduction to the contents is presented below.

In Chapter 1, Street presents the current sequencing technologies and how they are used for different applications in the genomic analysis of forest trees. The decreasing cost of high-throughput sequencing has facilitated the routine characterization of transcriptomes by RNA sequencing, studies of gene expression variation, and the resequencing of genomes (Ingvarsson, Hvidsten, & Street, 2016). Useful guidelines are provided for genome assembly, validation, annotation, transcriptome assembly, and profiling as well as genomic approaches for epigenetic and population studies. New approaches are addressed to the understanding of adaptive genetic variation in natural populations.

To elucidate the function of key genes and networks controlling essential processes a variety of functional genomics approaches are now available.

Cañas et al. consider present-day technologies and online resources for functional genomic studies in conifers (Chapter 2). Recent methods have been developed to investigate how metabolic processes are organized in specialized tissues and cell types (Cañas et al., 2017). Homologous and heterologous systems are used for gene validation and characterization of regulatory regions. Recently, platforms for functional analysis in transgenic conifers have also been established via somatic embryogenesis, a technology that is described in Chapter 5.

Trees acquire nutrients to incorporate essential elements that are needed to complete their life cycles. Because of their low abundance in the soil, trees have established symbiotic associations to enhance nutrient use efficiency. Membrane proteins involved in nutrient transport between fungi and colonized roots constitute the so-called “transportome” (García, Doidy, Zimmermann, Wipf, & Courty, 2016). In Chapter 3, Becquer et al. reviewed the recent progress in understanding how ectomycorrhizas contribute to tree nutrition. The molecular mechanisms involved in the transport of macronutrients, micronutrients, and water are examined in the mutualistic interaction with their fungal partners. The evolution and ecological relevance of the transportome are also considered.

Nitrogen is an essential macronutrient and frequently a major limiting factor for tree growth. In addition to uptake and assimilation from the soil, internal nitrogen cycling is largely influencing the efficient use of nitrogen in woody plant species exhibiting long life cycles with annual periods of seasonal growth and development (Babst & Coleman, 2018). In Chapter 4, Li and Coleman present an updated description of the molecular and physiological basis of nitrogen cycling in forest and fruit trees but with a special focus on *Populus*, a model tree in which most of the recent knowledge has been generated. Major players involved in nitrogen cycling are described as well as potential mechanisms controlling this process and its environmental regulation.

The development of single cells to mature embryos is a complex process that is strictly regulated. Tree embryogenesis is a developmental programme of paramount importance from a scientific and applied point of view. In Chapter 5, von Arnold et al. provided an updated overview of the developmental patterning and its regulation during zygotic and somatic embryogenesis in conifers. Recent advances include the identification and functional analyses of key genes involved in the process (Alvarez et al., 2015). This knowledge is of great interest in fundamental tree biology but also may have an immediate biotechnological application because

somatic embryogenesis in combination with cryopreservation is one of the most relevant technologies for mass propagation of conifer trees.

The relationships and coordinated regulation of shoot apical, axillary, and cambial meristems determine tree growth and shape. Meristematic activities are largely influenced by environmental signals and seasonal changes adapting tree species to changes in their living habitats (Brunner, Evans, Hsu, & Sheng, 2014). Using *Populus* as a model, Teixeira et al. review the coordination of meristematic activity during the transition to secondary growth and wood formation (Chapter 6). The roles of signalling proteins, sugars, and hormones in long-distance communication between apical and vascular meristems are examined and discussed. Genes involved in the molecular regulation of meristematic activity by photoperiod and temperature have been identified. However, further work is necessary to unravel the complex pathways involved in long-distance signalling as well as the molecular components of the responses in the target tissues.

Wood, the most abundant lignocellulosic biomass, plays essential structural and functional roles in plants and represents an important raw material for many different purposes. Genome-wide analysis has been made to identify key genes involved in the biosynthesis of wood components in forest trees (Carocha et al., 2015). In Chapter 7, Camargo et al. reviewed the recent advances to elucidate the mechanisms of wood formation in trees, highlighting the similarities and differences found in the secondary xylem differentiation described in herbaceous model plants. The functional analysis of the regulatory gene networks governing wood formation has revealed a high level of complexity involving sophisticated mechanisms of control and cross-regulation.

Plant cell wall composition and organization change during development and in response to environmental cues (Harding et al., 2018). Although of low abundance in lignocellulosic biomass, the pectin fraction of the cell wall usually has negative effects in the postprocessing of woody plant biomass for paper production or saccharification. Harding and Tsai discussed how pectin interacts with other components of the cell wall during cell expansion and the lignification process (Chapter 8). A better knowledge of pectin biology is needed to improve our current understanding of cell wall organization and function. Recent findings in this research area are providing new insights into the biotechnological manipulation of pectin biosynthesis and degradation.

Poplar has been extensively used to study gene function by its amenability to transformation and easy generation of transgenic lines for molecular and physiological analyses. Trees with increased tolerance to a wide range

of environmental stresses are needed to cope with a changing climate and at the same time maintaining the productivity of forest and fruit plantations (Merino et al., 2014). Transgenic approaches to develop and understand drought tolerance in poplar are reviewed in Chapter 9. Transgenic poplars with enhanced nitrogen assimilation also exhibit increased tolerance to drought stress (Molina-Rueda & Kirby, 2015). It has been found that genes involved in the protection against reactive oxygen species appear to be critical in the observed tolerance to drought. However, further studies will be necessary to investigate the connection between nitrogen metabolism and enhanced stress tolerance.

Human activities are consubstantial with the release of a vast variety of pollutants into the environment. The use of plants to restore clean environmental conditions is based on their favourable and unique characteristics to extract, store, and even metabolize a wide range of pollutants. Gómez et al. examined the potential of trees in phytoremediation of contaminated areas (Chapter 10). Some fast-growing trees used as phytoremediators include additional advantages such as longevity, the production of high levels of biomass, complex pathways in secondary metabolism, and stress tolerance. Nowadays, the phytoremediation capacity of selected genotypes can be accelerated and improved using advances in genomics and biotechnology. On the other hand, tree plantations for cleaning up polluted areas represent a valuable source of feedstocks for biorefineries and bioenergy applications.

I am extremely grateful to all authors for contributing with their excellent reviews to this volume. We are confident that the book will be a useful reference for researchers and professionals interested in an updated monography on the functional genomics of forest trees. We also hope that the book will be useful for advanced students and young researchers interested in the molecular aspects of tree biology. Finally, I want to thank the kind invitation of Professors Jacquot and Gadal to coordinate this project.

References

- Alvarez, J. M., Sohlberg, J., Engström, P., Zhu, T., Englund, M., Moschou, P. N., et al. (2015). The WUSCHEL-RELATED HOMEODOMAIN 3 gene PaWOX3 regulates lateral organ formation in Norway spruce. *The New Phytologist*, 208, 1078–1088.
- Babst, B. A., & Coleman, G. D. (2018). Seasonal nitrogen cycling in temperate trees: Transport and regulatory mechanisms are key missing links. *Plant Science*, 270, 268–277.
- Brunner, A. M., Evans, L. M., Hsu, C. Y., & Sheng, X. (2014). Vernalization and the chilling requirement to exit bud dormancy: Shared or separate regulation? *Frontiers in Plant Science*, 5, 732.
- Cañas, R. A., Li, Z., Pascual, M. B., Castro-Rodríguez, V., Ávila, C., Sterck, L., et al. (2017). The gene expression landscape of pine seedling tissues. *The Plant Journal*, 91, 1064–1087.

- Carocha, V., Soler, M., Hefer, C., Cassan-Wang, H., Fevèreiro, P., Myburg, A. A., et al. (2015). Genome-wide analysis of the lignin toolbox of *Eucalyptus grandis*. *The New Phytologist*, 206, 1297–1313.
- De la Torre, A., Birol, I., Bousquet, J., Ingvarsson, P., Jansson, S., Jones, S. J. M., et al. (2014). Insights into conifer giga-genomes. *Plant Physiology*, 166, 1724–1732.
- García, K., Doidy, J., Zimmermann, S. D., Wipf, D., & Courty, P. E. (2016). Take a trip through the plant and fungal transportome of mycorrhiza. *Trends in Plant Science*, 21, 937–950.
- Harding, S. A., Hu, H., Nyamdari, B., Xue, L. J., Naran, R., & Tsai, C. J. (2018). Tubulins, rhythms and cell walls in poplar leaves: It's all in timing. *Tree Physiology*, 38, 397–408.
- Ingvarsson, P. K., Hvidsten, T. R., & Street, N. R. (2016). Towards integration of population and comparative genomics in forest trees. *The New Phytologist*, 212, 338–344.
- Merino, I., Contreras, A., Jing, Z. P., Gallardo, F., Cánovas, F. M., & Gómez, L. (2014). Plantation forestry under global warming: Hybrid poplars with improved thermotolerance provide new insights on the in vivo function of small heat shock protein chaperones. *Plant Physiology*, 164, 978–991.
- Molina-Rueda, J. J., & Kirby, E. G. (2015). Transgenic poplar expressing the pine GS1a show alterations in nitrogen homeostasis during drought. *Plant Physiology and Biochemistry*, 94, 181–190.
- Tsai, C. J., Harding, S. A., & Cooke, J. E. K. (2018). Branching out: A new era of investigating physiological processes in forest trees using genomic tools. *Tree Physiology*, 38, 303–310.
- Taskan, G. A., Difazio, S., Jansson, S., Bohlmann, J., Grigoriev, I., Hellsten, U., et al. (2006). The genome of black cottonwood, *Populus trichocarpa* (Torr. & Gray). *Science*, 313, 1596–1604.