PREFACE

Trees form a polyphyletic group that includes a variety of plant species that have independently evolved specific features such as great size, longevity and long generation time and woodiness. Trees are of major importance to human society. They provide a wide array of ecosystem services that confer benefits to people, including, for example, the production of goods such as fruits, timber, biomass fuels and precursors to many industrial and pharmaceutical products, the sequestration of carbon (mitigating climate change) and the prevention of soil erosion. Natural forests, as well as intensively managed forest tree plantations and fruit tree orchards, support the economy of many countries worldwide, providing employment especially for rural populations. Last but not least, forests also offer habitats for flora and fauna that are an essential part of the functioning of terrestrial ecosystems.

Owing to the rapidly evolving tools and methods in genomics and bioinformatics, our understanding of the structure, functioning and evolution of tree genomes is progressing at an accelerated pace. This thematic volume, 'Genomes of trees', illustrates areas where progress in forest and fruit tree genomics has been made over the past 10 years, since the first tree genome sequence (poplar) was published. The knowledge gained from research performed in this area is expected to lead to important improvements in terms of genetic resource characterisation, management and valorisation in breeding programmes, deliveringhigh quality products, with enhanced robustness to a changing environment.

In the first two chapters, David Chagné (Whole genome sequencing of fruit tree species) and Geneviève Parent et al. (Forest tree genomics: review of progress) highlight the acceleration of delivery of reference genome sequences for several forest and fruit tree species, thanks to new sequencing technologies and despite the challenge of coping with sometimes very large genomes. They underline that these new resources have already allowed a better understanding of genome evolution in plants and given access to new and powerful tools to study their biology, their adaptation to biotic and abiotic cues and to facilitate their breeding. The third and fourth chapters review how genomics could meet the breeding and conservation challenges of the twenty-first century, especially considering that breeders need to be more efficient in improving the traits of interest to increase productivity, develop genetic resources that can adapt to a changing environment and

be resistant to disease and pests. In Chapter 3, (Acceleration of forest and fruit tree domestication by genomic selection, by Fikret Isik et al.) the authors consider how genomics could be used to design novel tree-breeding schemes, while in Chapter 4 (Population and conservation genomics in forest and fruit trees, by Filippos Aravanopoulos et al.) they explore how genomics could improve the characterisation of genetic resources diversity and conservation strategies and increase our ability to select and prioritise conservation targets. The three following chapters illustrate functions that are unique to these long-lived and large-size organisms: their stature, their ability to synchronise phenological events with climatic conditions, and their plasticity in response to environmental changes, thus allowing them to subsist in a spatially and temporally highly heterogeneous environments. In Chapter 5 (The genetics and genomics of tree architecture) Evelyne Costes and Jean-Marc Gion report that genomic resources and progress in phenotyping technologies, have lead to significant advances in the understanding of the genetic, physiological and molecular determinants of tree architecture plasticity in response to environmental changes. In Chapter 6, (The genetic control of bud-break in trees) Albert Abbott et al. highlight our current state of knowledge about the molecular mechanisms underlying the timing of floral and vegetative bud-break, helping to improve our understanding of how trees coordinate their annual growth, development and reproduction with the environmental cycle. In Chapter 7, (Tree responses to environmental cues) Ingo Ensminger et al. give a very complete review of the current knowledge on the physiological responses and associated molecular regulation pathways of trees to drought, temperature and photoperiod, thus completing the emerging picture from the two former chapters. In the last chapter (Chapter 8, Molecular signatures of adaptation and selection in forest trees) Juan-Pablo Jaramillo-Correa et al. elegantly summarise forward-genetic approaches (i.e. from phenotype to gene function) currently used in forest trees to identify genes/alleles that are important for adaptation.

With the continuing decrease of cost and development of higher throughput sequencing methods, the next decade will continue to see a growing number of species (including wild relatives of highly domesticated fruit tree species) being sequenced and the discovery of their variants. Major challenges are then to: (1) exploit this new wealth of data in order to detect naturally occurring variations that matter for productivity, quality and adaptation and (2) design innovative conservation and breeding strategies to help these long-lived and sessile organisms cope with the rapidly increasing biotic

and abiotic threats during their lifetime, while still providing the provisioning services for which they have been planted. Genomics opens the doors to the development of these applications in forestry and fruit tree production, and thus should contribute to sustain economic growth in rural areas.

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