

# Plant Genetics and Genomics: Crops and Models

Volume 8

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Editors

# Genetics and Genomics of *Populus*

 Springer

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ISBN 978-1-4419-1540-5                      e-ISBN 978-1-4419-1541-2  
DOI 10.1007/978-1-4419-1541-2  
Springer New York Dordrecht Heidelberg London

Library of Congress Control Number: 2009943301

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Printed on acid-free paper

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# Preface

Trees are truly amazing! Woody species underpin vital terrestrial ecosystems ranging from the Amazon rainforests to the Krummholz forests that grow on harsh mountaintop environments, to the vast boreal forests that ring the northern hemisphere. Forest trees also present a complex array of evolutionary novelties, including the ability to measure and anticipate the changing seasons (perennial growth), and the ability to produce massive, woody bodies. Indeed, forest trees include the oldest (*Pinus longaeva*) and largest (*Sequoiadendron giganteum*) sexually producing, non-clonal species. Among species with clonal reproduction, it has been suggested that the massive “Pando” grove of *Populus tremuloides* in Utah may be the largest organism in the world.

Forest trees also provide important benefits and commodities. Trees provide lumber and wood products, pulp and paper, and are a major energy source for many developing countries. Trees also play a key role in the major biogeochemical cycles, including water, oxygen, and nitrogen. Notably, forests are second only to oceans in the biological sequestration of carbon, and forests are recognized for their vital role in regulating the concentration of the greenhouse gas, CO<sub>2</sub>. At the same time, forests are threatened by land clearing for development and agriculture, introduced pathogens and insects, and by climate change.

A fundamental need encompassing all of these scientific, economic, and management issues is a better understanding of the basic biology of forest trees. One proven strategy for biological research is the development of so-called model organisms, in which an organism is identified that both presents biological traits of interests for study, and for which key experimental tools can be developed. Increasingly, the basis for modern model species development often revolves around genomics. In this regard, the ultimate resource is the determination of the full genome sequence of the organism, which both reveals the entire complement of genes and allows development of advanced genomic tools indexed to the genome.

As the power of genetic model systems for biological research became increasingly obvious, the need for a good tree model system grew. Gradually, *Populus* – a genus consisting of over 30 species with a wide geographic distribution – developed into the prime model system for tree research. *Populus* have many fundamental differences to *Arabidopsis* and other current plant model species. With regards to life habit, *Populus* species are ecologically dominant species, have long life spans,

and form large woody bodies. They have extended juvenile phases, are dioecious and therefore obligate outbreeders, and some species are often found in extensive clones. Through their relatively long life spans *Populus* are exposed to extreme abiotic conditions and have numerous antagonistic and symbiotic interactions with other organisms. However, from a phylogenetic point of view *Populus* and *Arabidopsis* are relatively closely related organisms – for example they are more closely related than *Arabidopsis* and tobacco. This phylogenetic relatedness makes comparisons of gene content and function in *Arabidopsis* and *Populus* relatively straightforward.

Trees are found among many phylogenetic groups. It can not be excluded that the last common ancestor of today's angiosperms and gymnosperms was woody, and transition from herbaceous to tree life habit (or tree to herbaceous) is apparently relatively simple in evolutionary terms. This suggests that the genetic differences underlying the defining characteristics of forest trees could ultimately be homologous, but are highly plastic and easily modified to produce the wide array of organisms called “trees.” Undoubtedly, the tree life habit is rather different from the herb life habit and the unique selection pressures acting on trees versus herbaceous plants are at least in part responsible for variation in different characters. With the advent of *Populus* as a full-fledged model system for plant genetic and genomics, tools are now available for plant researchers to explore these fascinating aspects of tree biology. Tools and approaches are currently being developed for *Populus* that address genetic variation of traits at the levels of species, populations, and gene function. Importantly, most forest trees, including *Populus spp.*, are characterized by high levels of genetic variation, making them highly amenable to population genomics approaches. Indeed, approaches such as association mapping that exploit natural genetic variation in outcrossing species that are now being applied to *Populus* have more in common with human genetics than crop genetics.

Several key innovations in the evolution of land plants that are largely lacking in *Arabidopsis* and other herbaceous annual models can be studied in *Populus*. These include processes underlying perennial growth and seasonality (for example in cambial activity, leaf senescence and dormancy), extensive wood formation, as well as many processes relating to biotic interactions. There are also research areas, not yet well developed, where *Populus* holds great promise as a model system. For example, studies in ecosystem genomics are supported by the recent sequencing of *Populus* symbionts (*Laccaria bicolor* and *Glomus intraradices*) and a pathogen (*Melampsora larici-populina*). With regards to developmental traits, juvenile to mature transitions may be better studied in a tree versus herbaceous plant, and it is also possible that epigenetic processes may be of increased importance in an organism with a long time span. Therefore, we expect that in the decade to come, many discoveries will be made in *Populus* that will impact plant science in general.

Although the *Populus* genetics and genomics community started to grow in the nineties, the decision to sequence the *Populus* genome in the winter of 2001/2002 prompted additional researchers to choose *Populus* for their studies. The authors of this book is a blend of researchers that have spent most of their research career on *Populus* and those that have moved to *Populus* from other model systems. The chapters describe (for both experienced *Populus* researchers and newcomers to the

field) both genetic and genomic approaches for *Populus* and some of the interesting biology that has been elucidated using genomics. Notably, research on *Populus* forms a useful complement to research on *Arabidopsis*. In fact, many plant species found in nature are – in terms of the life history and genetics – more similar to *Populus* than to *Arabidopsis*. Thus the genetic and genomic strategies and tools developed by the *Populus* community may serve as inspiration for researchers working in other, less well developed, systems.

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