

FOREST TREE GENOME RESEARCH

This special issue of forest Genetics includes five papers which were originally presented at the Forest Tree genome Mapping Workshop at the Plant Genome III Meeting in San Diego, California, USA on January 17, 1995. The annual Plant Genome meeting is organized by Dr. Jerome Miksche (USDA/ARS) and others in response to the enormous growth in plant genome research particularly in crops such as corn, rice, and wheat. I have organized a special workshop on Forest Tree genomes at each of the Plant Genome meetings. These workshops are attended by forest tree genome researchers from throughout the world and have become an important event for information exchange within the community.

This first paper by Hipkins, Krutovskii, and Strauss (Organelle Genomes in Conifers: Structure, Evolution, and Diversity) summarizes the considerable body of knowledge on the chloroplast and mitochondrial genomes. The next two papers are case studies for two important tree species. Bradshaw and Grattapaglia (QTL Mapping in Interspecific Hybrids of Forest Trees) discuss approaches used to identify QTLs for many different traits in interspecific *Populus* and *Eucalyptus* hybrids. They demonstrate that genes of very large effect can easily be identified. Neale, Kinlaw and Sewell (Genetic Mapping and DNA Sequencing in Loblolly Pine) describe a basic genome research program in loblolly pine whose primary goal is to understand pine genome organization and evolution through genetic mapping and DNA sequencing. The paper by O'Malley and McKeand (Marker Assisted Selection for Breeding Value in Forest Trees) is an in-depth discussion of how marker breeding might be applied in forest tree breeding. They specifically show how marker breeding would be used for within family selection in subline breeding. Finally, Davis and Lawrence (Strategies to Identify Genes Involved in Forest Tree Defense) describe how a technique called anti-sense technology can be used to identify the genes most important in determining defense against pathogens in forest trees. This approach is fundamentally different than the mapping approaches previously described but could be highly complementary. In all, I hope that this series of papers gives the reader a concise introduction to genome research in forest trees and provides a sense how this research will enhance efforts to better manage gene resources and breed forest trees.

I would like to dedicate this issue of Forest Genetics to Dr. Jerome Miksche upon his retirement for his significant contributions to forest tree genome research. Jerry was a pioneer in forest tree molecular genetics. His work in the 1960s on DNA reassociation kinetics in conifers was among the first explorations in the pine genome. Later Jerry served as a Project Leader at the North Central Forest Experiment Station in Rhinelander, Wisconsin and as the Head of the Botany Department at North Carolina State University. The last stop in Jerry's career was as Program Director for the USDA/ARS/NRI Plant Genome Program. Jerry was instrumental in ensuring that forest trees were included as target species in the Plant Genome Competitive grants Program and also were a part of the Plant Genome Database Project. The forest tree genome research community owes a great debt of gratitude to Jerry for his active support and promotion of tree genome research.

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