FOREST GENETICS AND TREE BREEDING IN THE AGE OF GENOMICS – IUFRO CONFERENCE

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BACKGROUND

Significant progress has been made in forest genetics research and tree breeding in the last three decades. Many breeding programs in the world have achieved substantial genetic gains in productivity, pest resistance and wood quality. Genetically improved plantations from breeding programs have had and continue to make significant impacts on forest productivity, wood supplies, and sustainability of forest resources. As some breeding programs are moving into advanced generations, it was timely to review the up-to-date progress and evaluate current strategies in breeding, selection, deployment, and genetic resources management. As a vast amount of new information has been accumulated in biotechnology and genomics in recent years, it is critical to explore opportunities on how to incorporate these tools into forest genetics research and tree breeding programs.

The *Forest Genetics and Tree Breeding in the Age of Genomics* conference was held from November 1–5, 2004 in Charleston, South Carolina, USA. The conference was organized as a joint conference with multiple working parties related to breeding and genetic resource management of IUFRO Division 2, and over 120 papers and posters were presented. This international conference brought together geneticists, breeders, applied and basic scientists, managers and professional foresters to exchange the latest information on forest genetics and tree breeding, with special focus on potential application

of bio-technology and genomics in the future. Given that the topics were important, timely, and pertinent to scientists worldwide, a total of 231 people from 22 countries participated. The conference included invited, contributed presentations, and poster presentations.

CONFERENCE TOPICS

The purpose of this conference was to update the progress in major areas of breeding and genetic resource management and to explore opportunities for integration of new biotechnology and genomics information to develop optimum strategies. There were seven general sessions and 12 concurrent sessions with leading scientists from each relevant field invited to speak in each session.

The general sessions included: Session I: Advances in Breeding and Tree Improvement Programs (Moderator: Steve McKeand); Session II: Advances and Challenges of Clonal Forestry (Moderator: Floyd Bridgwater); Session III: Advances in Forest Biotechnology (Moderator: Dave Canavera); Session IV: Advances in Genomics and Applications for Tree Breeding (Moderator: Jerry Tuskan); Session V: Genetic Diversity and Gene Conservation (Moderator: Per Ståhl). Session VI: Wood Quality Improvement (Moderator: Dick Daniels); Session VII: Productivity and Gain Prediction (Moderator: Sue Carson).

The main topics of the concurrent sessions were: Advances in Tree Breeding Programs (Moderator: Tim Mullin), Strategies for Clone and Family Testing and Selection (Moderator: Dudley Huber), Advances in SE Technology and Clonal Forestry (Moderator: Kamal Chowdhury), Population Genomics (Moderator: Row-land Burdon), Genetic Diversity and Gene Conservation (Moderators: Judy Loo and Sally Aitken), Progeny Testing and Selection (Moderator: Tom Byram), Genetic Analysis and Modeling (Moderator: Randy Johnson), Advances in Reproductive Biology and Seed Orchards (Moderators: Barry Goldfarb and Clem Lambeth), Advances in Genomics and Applications in Forestry (Moderators: Les Pearson

Figure 1. Partial attendees of the conference.

and Matias Kirst), Advances in Resistance Breeding (Moderator: Dana Nelson), Advances in Breeding Strategies (Moderator: Mark Dieters), Social Aspects of Clonal Forestry (Moderator: Bob Kellison), Wood Quality Improvement (Moderator: Alex Clark), and Applications of Genomics (Moderator: Christine Dean).

As a part of the conference, an optional field trip was organized to visit MeadWestvaco Corporation and ArborGen. At MeadWestvaco, participants saw all aspects of breeding and tree improvement with loblolly pine (*Pinus taeda*), including breeding facilities, progeny and clone testing, vegetative propagation, greenhouse, seed orchards, nursery, and improved pine plantations. At ArborGen, forest biotechnology and genomics research was displayed, including genetic transformation, somatic embryogenesis, and gene discovery.

GENERAL CONCLUSIONS

Advances in Tree Breeding Programs: Tree breeders provided overviews of the major tree breeding programs in the world and updates on the breeding strategies of advanced generations, clonal testing and selection strategies, top-grafting for accelerated breeding and genetic gain predictions. Significant progress has been made in forest genetics research and tree breeding in the last three decades. Many breeding programs in the world have progressed

rapidly from provenance testing to advanced-generation breeding. Substantial genetic gains have been achieved for most tree species in adaptation, productivity, pest resistance, and wood quality. Genetically improved plantations from breeding programs have had and continue to make significant impacts on forest productivity, wood supplies, and sustainability of forest resources. Deployment of genetically improved genotypes, whether they originated from open-pollinated seed orchards or mass control-pollinated full-sib families, has been a standard practice for some species in many parts of the world. Recent progress in vegetative propagation in rooted cuttings and somatic embryogenesis has made possible the operational

Figure 2. Conference attendees visited loblolly pine progeny tests (left) and nursery production.
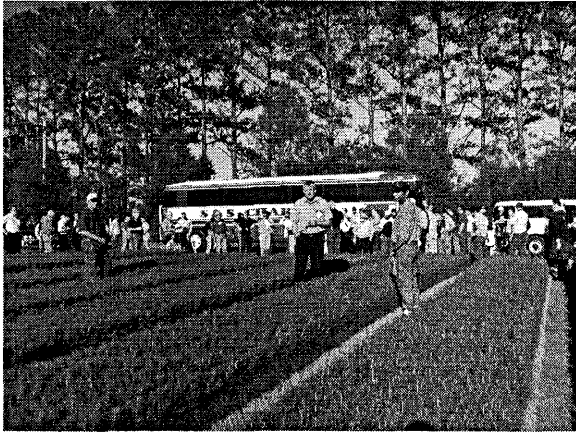
deployment of clones in forest plantations. New breeding strategies and selection and testing methods are being developed to improve breeding efficiency to capture much greater genetic gains in tree breeding programs. However, the traditional breeding programs are being challenged by the overwhelming level of new information in bio-technology and genomics. It is critical to explore opportunities on how to incorporate these tools into forest genetics research and tree breeding programs.

Advances in Biotechnology/Genomics and Integration with Breeding: New advances in somatic embryogenesis (SE) technology have had a great impact in recent years on the deployment of genetic materials for several major breeding programs. SE has also offered great opportunities for genetic transformation and production of clonal forestry with improved productivity, reduced disease, and enhanced wood quality in plantations. Major break-throughs in genomics research have been in genome sequencing, genotyping with markers (including SNPs, SSRs etc.), transcript profiling (DNA microarrays and RT-PCR), and metabolite profiling. Based on the up-to-date information, conference participants explored opportunities for integration of new genomics and biotechnology into major areas of breeding and genetic resource management.

Key biotechnology challenges are successful transformation systems for major species, gene expression, risk analysis and public acceptance. Although great progress has been made in quantitative trait locus (QTL) mapping for trees, limitations in markers and trait variation and low-resolution mapping have restricted the application to breeding. Association mapping, with gene space scan, abundant marker and trait variation and high resolution mapping of QTL, may be more promising for integration with breeding. For successful implementation of marker assisted breeding, we need to improve high through-put genotyping, high-resolution framework mapping, and reliable experimental approaches for tree phenotyping. Genetic diversity and gene conservation were discussed for implications on breeding, biotech-nology, deployment and forest resources management.

Additional Information: The full conference proceedings can be accessed online at http://www.ncsu.edu/feop/iufro_genetics2004/proc eed-ings.pdf.
Li, B. & McKeand, S., eds.: Forest Genetics and Tree Breeding in the Age of Genomics: Progress and Future. Proceedings of IUFRO Joint Conference of Division 2, November 1–5, 2004, Charleston, South Carolina, USA.