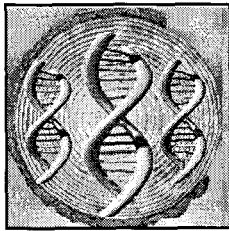


WOOD, BREEDING, BIOTECHNOLOGY AND INDUSTRIAL EXPECTATIONS WBB CONFERENCE

C. Plomion¹, C. Cahalan² & M. P. Reviron¹

¹ INRA, Equipe de Génétique et Amélioration des Arbres Forestiers, F-33 610 Cestas, France

² School of Agricultural and Forest Sciences, University of Wales, Bangor, Gwynedd, LL57 2UW, United Kingdom.
plomion@pierroton.inra.fr



PREFACE

The last 10 years have witnessed considerable progress in molecular biology, transgenesis and genomics, and in the assessment of wood and end-product properties. Genetic improvement programmes for wood properties and other characteristics of economic and ecological importance, which have traditionally focused on phenotypic assessments (e.g. of wood density, volume and adaptive traits), may in future be mainly concerned with new traits and/or genes that make it possible to reduce the cost of breeding. The possibility has also emerged of the mass propagation of forest trees by somatic embryogenesis, for the rapid deployment of superior genotypes.

The *Wood, Breeding, Biotechnology and Industrial Expectations (WBB)* conference was held from 11–14 June 2001 in Bordeaux (France). *WBB* was organized by INRA (Equipe de Génétique et Amélioration des Arbres Forestiers), and sponsored by the following organizations: The European Union (QLAM-2000-00226), INRA (bureau des colloques), AFOCEL, CTBA, Conseil Régional d'Aquitaine and Smurfit Comptoir du Pin. This multidisciplinary conference assembled 210 scientists from state institutions, universities and industry in 28 countries, covering a wide spectrum of expertise in genetics, biotechnology and wood sciences. *WBB* was a joint meeting between a group of European Union funded projects dealing with the general topic of the conference (Wood, Breeding and Biotechnology), the 9th Conifer Biotechnology Working Group and the IUFRO 5.01.02 and 2.04.00 working parties.

The objectives of *WBB* were: (1) to provide a forum for presentations on and discussion of the introduction of biotechnologies (molecular and cellular biology, somatic embryogenesis, molecular genetics) and wood quality traits into tree breeding programs; (2) to identify, with the participants from industry, the main topics which need further investigation in order to meet both the increasing demand for wood and the environmental standards expected of wood processing industries; (3) to provide an opportunity for numerous contacts and new collaborations between participants.

Ten invited papers by first class scientists and 89 voluntary papers were presented. A total of 72 posters were also presented. The abstracts are available at <http://www.pierroton.inra.fr/WBB/index.html>. Eight scientists from CEECs (Central and Eastern European Countries) and other developing countries received fundings to attend the

conference.

The conference was divided into nine sessions. Sessions 2/3/4/5 and sessions 6/7/8 were held in parallel. Sessions 1 and 9 were plenary sessions.

Session 1 (keynotes) Chairs: N. Borralho & J. Aitken

Application of new technology to meet the requirements of the wood chain industry. This introductory session provided a thorough overview of current knowledge and future foci of forest tree breeding and biotechnology.

Session 2 Chairs: C. Matheson & H. Pereira

Methods for the assessment of wood and fibre properties. Non-destructive evaluation and recent progress in the rapid assessment of wood and fibre properties. Modelling wood properties at different scales (wood of standing trees, engineered wood products).

Session 3 Chairs: F. Zamudio & B. Karlsson

Natural variation and quantitative genetics of wood and fibre properties; connection between silviculture and wood properties. Inheritance and genetic variability of wood properties; genotype-environment interactions; age-age relationships; genetic relationships between adaptation, growth and form traits, and wood properties; interaction between forestry practices and genetic variation.

Session 4 Chairs: D. Cown & G. Chantre

Wood and fibre properties for particular end uses. Relationships between basic wood properties and the performance of end products; impact of wood properties on processing; inheritance and genetic variation of end product properties; economic weights.

Session 5 Chairs: E. Ritter & M. Sewell

Genetic mapping, QTL detection, candidate genes and proteins, exploitation of macro and micro-syteny.

Session 6 Chairs: P. Gupta & S. von Arnold

Somatic embryogenesis and tissue culture. Recent advances in clonal propagation, including the opportunity offered by cryo-conservation. Propagation systems to produce plants of high quality.

Session 7 Chairs: F. Canovas & M. Becwar

Molecular biology and genetic engineering.

Session 8 Chairs: B. Vendramin & Z. Kaya

Molecular diversity and application of molecular markers

for seed and plant material certification.

Session 9 Chairs: C. Cahalan & W. Boerjan
Genome analysis; conclusions and perspectives

SESSION REPORTS

Session 1

Seven keynote talks were given the first day of the conference in a plenary session. These provided a thorough overview of current knowledge and future foci of forest tree breeding and biotechnology. T. Richardson (New Zealand) summarized the genetic tools (gene mapping, transcriptomics, comparative genomics and genetic engineering) which can be used to reveal the genetic control of wood and fibre properties, and to select for elite trees at early ages. J. Aitken (New Zealand) reviewed the use of somatic embryogenesis for large-scale clonal testing and propagation of elite material. She showed how this technique is applied to *Pinus radiata* in a commercial environment. C. Raymond (Australia) presented new methods developed for assessing wood properties of eucalypts (*Eucalyptus* spp.) and emphasized the need to identify key wood properties and their economic weights, and to define breeding objectives for particular markets and products. R. Wimmer (Austria) dedicated his presentation to the effect of environmental factors, particularly temperature and water availability, on wood and fibre properties. D. Carraway (US) considered the application of biotechnology to the sustainable production of high quality wood, and called on research scientists and the forest industries to engage with the public in discussions about the use of biotechnology. H. Höfte (France) showed how *Arabidopsis* genomics is being used to dissect the main mechanisms of wood formation, and how this model species can be used to identify key genes in trees. Finally, B. Sundberg (Sweden) closed the session by summarizing the important advances being made in the understanding of wood formation in poplar (*Populus*) using EST and microarray analysis.

Session 2

In session 2, 13 authors gave papers describing indirect methods for assessing wood and fibre properties. Methods were presented for density, microfibril angle, stiffness/module of elasticity, decay resistance, early/latewood ratio, heartwood proportion, compression wood content and distribution, fibre dimensions, lignin quality and composition, and pulp yield. Results obtained from the use of novel equipment (Rigidimeter, Silviscan), validation of methods (sound wave velocity, ultrasonic vibration, X-ray densitometry, electrical capacitance, near infrared analysis, analytical pyrolysis), and modelling were shown. Measurements were made at different scales, from the standing tree to the end product, in a range of species including pines (*Pinus* spp.), spruces (*Picea* spp.), eucalypts and poplars. The results are promising, and suggest that equipment and methods for large scale screening of wood properties in breeding programmes and wood-using industries (e.g. for log grading) will soon be available.

Session 3

The 11 presentations given in session 3 were concerned with

describing natural variation and estimating genetic parameters of wood and fibre properties. All studies were on conifer species (*Picea abies*, *Pinus radiata*, *Pinus nigra* and *Pinus sylvestris*, *Pseudotsuga menziesii*, *Larix* spp.). The most frequently measured wood properties were density and microfibril or grain angle, although three presentations gave results for other traits including fibre dimensions and quality, chemical composition and wood colour. Results were shown for genetic coefficients of variation, environmental effects, heritabilities, G × E interactions, age variations, the effects of inbreeding, and genetic correlations between wood properties and growth traits. In a number of studies, heritabilities for wood properties were high but genetic coefficients of variation were low, the reverse of the situation for growth traits. For example, wood density of *Picea abies* showed high heritability and good stability over environments, but a low genetic coefficient of variation and a negative genetic correlation with growth. Microfibril angle in *Picea abies* seemed easier to include in breeding programmes (high heritability and genetic coefficient of variation, no G × E interactions, no correlation with growth), although cambial age effects must be investigated. The implications for tree breeding for wood properties were discussed.

Session 4

Session 4 (five speakers) was mainly concerned with the application of knowledge of basic wood properties to tree breeding programmes and to meeting the needs of industry. For example, in New Zealand (*Pinus radiata*) and Canada (*Tsuga heterophylla*), researchers have constructed large data bases on genetic parameters of basic wood properties and their potential value as predictors of end product performance. While juvenile wood content is a major concern in fast growing species, important selection traits for sawn timber seemed to be stiffness (MOE), density, microfibril angle and strength (MOR). Fibre length, coarseness and cell wall dimensions are important for pulp yield and paper quality. Multitrait selection indices with different economic weights are being studied and optimised. One author pointed out that it is more important for wood-using industry to eliminate the worst trees than to identify those which are best for particular purposes.

Session 5

In this session, 11 scientists presented papers on the usefulness of molecular markers for enhancing tree breeding programmes. Most of the results presented were for wood quality traits in economically important conifers. Saturated genetic maps have been constructed using different types of markers (RAPD, AFLP, SSR, EST). Wood mechanical (e.g. wood splitting), chemical (e.g. lignin content) and anatomical (e.g. microfibril angle) traits have been measured and linked with molecular markers using QTL mapping strategies or bulk segregant analysis. In the near future, both strategies should be validated in different genetic backgrounds, environments and species.

Session 6

Results from all stages of somatic embryogenesis in a large range of species were presented in 15 talks. Cell tracking systems give a good understanding of the dynamics of

proliferating immature somatic embryos. The importance of the role of plant growth regulators in somatic embryogenesis was emphasized. Several examples illustrated the opportunity of enhancing the process by the use of unusual or unusually low concentrations of PGR. The prominent role of water availability in embryo maturation in a wide range of *Pinus* species was reaffirmed. Long term (up to 15 year) follow-up research in *Abies alba* and *Picea abies* illustrated the well-established fact (although it is one which still needs to be emphasized) that somatic embryos give rise to trees which grow normally.

Session 7

A total of 18 talks was given in this session. The differential display technique "cDNA-AFLP" allows efficient identification of candidate genes regulated in differentiating xylem sampled from reaction wood. Results from a completed EU project showed that polyamines and DNA methylation are good indicators of the phase change between juvenile and mature states and of the concomitant loss of morphogenic ability. The progress in transgenesis of woody plants has been widely illustrated, showing overall good success in a wide range of economically important species and that transgenesis is an important tool for physiological analysis. Some interesting work on eucalypts showed that genes implicated in meristem function in woody plants are the same as those in herbaceous plants, but that they are regulated differently. The overall conclusion of this session was that genetic engineering, molecular biology and more traditional research fields such as physiology should be integrated in order to develop a better understanding of tree growth and development.

Session 8

This session (6 speakers) was mostly dedicated to papers on the use of molecular markers (nuclear or chloroplast) for describing geographic variation of genetic diversity in forest tree species, and for certifying forest tree material. RAPDs, AFLPs, nuclear or chloroplast SSRs can be used to screen populations for describing genetic diversity (examples were given for *Cedrus* and *Pinus* species) and to describe the human impact on this diversity (e.g. *Pinus brutia* in Turkey). Markers such as species specific alleles (e.g. AFLPs in *Cedrus* spp.) or markers specific to a geographic area within a species (nuclear or chloroplast SSRs in *Pinus pinaster*) can be a powerful tool in these kinds of study. Once developed, these specific markers can be used to detect hybridation between species and to certify the provenance or origin of seeds and plants.

Session 9

In this plenary session a variety of research topics was addressed by 11 speakers. Topics included the use of DNA markers to trace dead or living wood, the different types of markers available in tree species and their mutation rates, levels and distribution of variability, genome structure, and the molecular genetics of wood quality. Scientists are trying to identify key genes controlling economically important traits, with the ultimate aim of designing efficient molecular breeding strategies for a range of tree species. As a speaker said, we know what we want, but we do not know always what we are doing: genomics is sometimes mindless but

extraordinary powerful!

Finally, three keynote talks were given. T. Zhang (Canada) reviewed the major challenges faced by breeders trying to incorporate wood quality traits into tree breeding programs. B. Sutton (Canada) described the efforts being made by a private company to deliver genetically improved material using somatic embryogenesis, and R. Sederoff (US) concluded this final session by considering a genomic approach to wood formation in loblolly pine (*Pinus taeda*).

CONCLUDING REMARKS

About 40 of the papers (reviews and original articles) presented at the conference will be included in a special issue of *Annals of Forest Science* (AFS). All manuscripts have been peer reviewed according to the editorial rules of AFS.

The objectives of the conference were fulfilled.

It provided an excellent forum for presentations on and discussions of the introduction of biotechnologies (molecular and cellular biology, somatic embryogenesis, molecular genetics) and wood quality traits into tree breeding programs. It is clear that:

- the industrial need for a supply of high quality, uniform raw material is being addressed by the development of conventional breeding and advances in the application of biotechnology.
- consumer concerns must also be dealt with. On the one hand, consumers have learned to demand environmentally safe products from the existing chemical pulp and paper industry. Increasing knowledge of wood structure and genetics allows targeted modification of various chemical components of raw materials, potentially leading to improved processing and product quality. On the other hand, the potential use of genetically modified trees has raised some questions about sustainable plantation development.

It provided for effective exploitation of the results gathered during the course of previous and current EU projects, by transferring the knowledge gained in these projects into the industrial sector. Indeed, a total of 32 participants were from the industrial sector and organisations closely linked with industry (e.g. CSIRO, Forest Research, AFOCEL). Biotechnological tools are being more and more frequently applied to forest tree breeding and major research efforts in the area of tree gene discovery are underway in the US, New Zealand, Canada and Australia. The results presented in this conference should also catalyze investment in forestry biotechnology within the European Union.

The conference also allowed participants:

- to share and compare the results obtained by scientists worldwide;
- to identify the main topics which need further investigation in order to meet both the increasing demand for wood and the environmental standards expected of wood processing industries;
- to take advantage of an opportunity for numerous informal contacts.

Finally the international role of the conference was secured, with 62 % of the participants coming from abroad.

Acknowledgement. This conference would not have been possible without the assistance of the wonderful staff and students of INRA Pierroton and great support from Valérie and Marc-Antoine. For help with the preparatory work for the conference, we thank Laure Eschbasher, Christine Charlot, Danièle Pouvreau, Isabelle Lebayon, Marc Pâque, Luc

Harvengt, the members of the GENIALITY group, the international organizing and scientific committees and the chair persons. Finally, we thank the conference sponsors: The European Union (QLAM-2000-00226), INRA (bureau des colloques), AFOCEL, CTBA, Conseil Régional d'Aquitaine and Smurfit Comptoir du Pin, for their financial support.

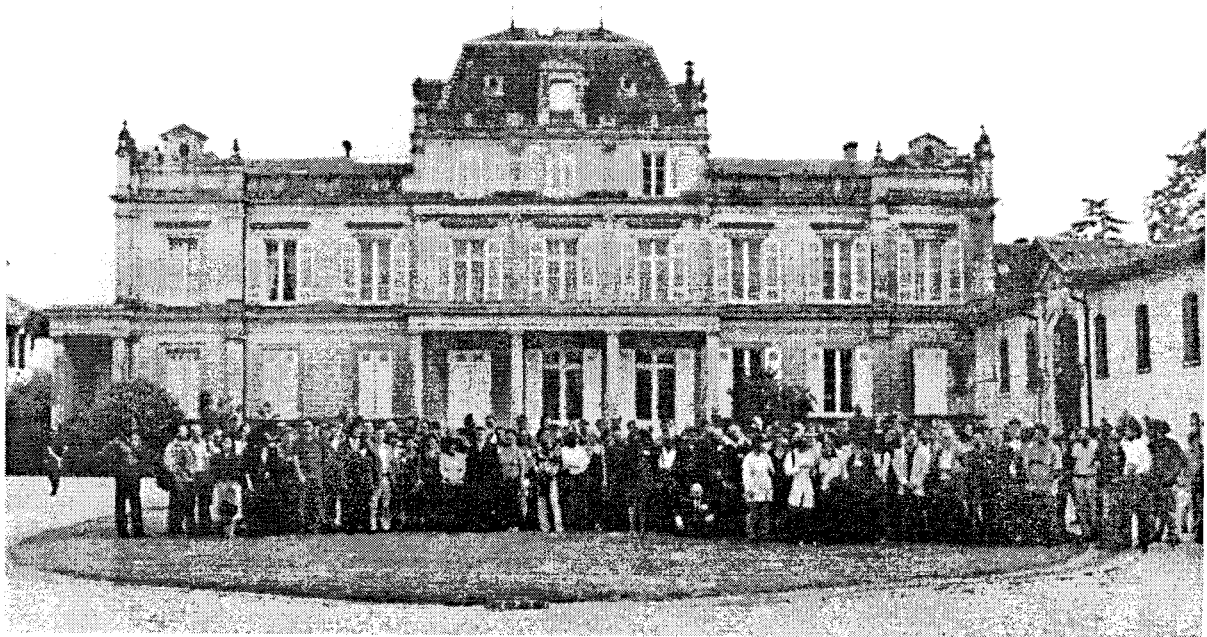


Figure 1. Participants of the Wwb Conference.