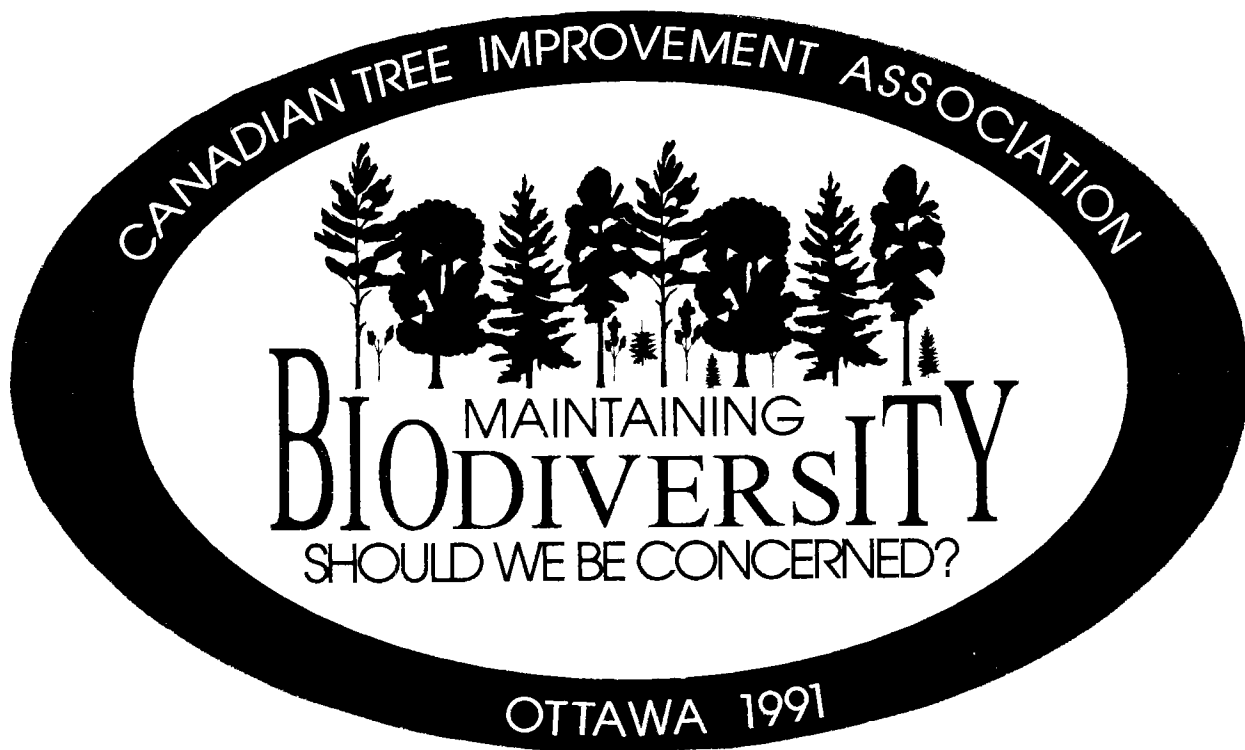


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PROCEEDINGS OF THE TWENTY-THIRD
MEETING AND ACTIVITY REPORTS OF THE
CANADIAN TREE IMPROVEMENT ASSOCIATION



COMPTES RENDUS DE LA VINGT-TROISIÈME
CONFÉRENCE ET DES ACTIVITÉS DE L'ASSOCIATION
CANADIENNE POUR L'AMÉLIORATION DES ARBRES

Catalogue No. Fo18-1/1991-1E
ISBN 0-662-18950-7

PROCEEDINGS
OF THE
TWENTY-THIRD MEETING
OF THE
CANADIAN TREE IMPROVEMENT
ASSOCIATION

**MAINTAINING BIODIVERSITY
"SHOULD WE BE CONCERNED?"**

Held in
Ottawa, Ontario
August 19-23, 1991

Editors:

S. Magnussen, J. Lavereau & T.J. Boyle

COMPTES RENDUS
DE LA
VINGT-TROISIÈME CONFÉRENCE
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L'ASSOCIATION CANADIENNE
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*MAINTENIR LA BIODIVERSITÉ,
"DEVRAIT-IL VOUS
CONCERNER?"*

Ottawa (Ontario)
du 19 au 23 août 1991

Rédacteurs:

S. Magnussen, J. Lavereau et T.J. Boyle

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K0J 1J0**

Produced by

**Forestry Canada
for the
Canadian Tree Improvement Association
Ottawa, 1991**

Sponsors

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**Forêts Canada
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Ottawa, 1991**

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PART I

THE CONFERENCE

ABSTRACTS OF

INVITED SYMPOSIA PAPERS¹

¹ Full length papers will appear in a dedicated issue of the Forestry Chronicle.

BIODIVERSITY AND FORESTRY

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Understanding genetic structure, dynamics, diversity, and management for a few plant species is a lifetime career. Understanding species association, interspecific dynamics, diversity, and management for a few associations is a lifetime career. Understanding the relationship between intra- and inter-species associations and its structure, dynamics, diversity, and management for a few species in a few paradigm associations is a lifetime career. Yet, we are faced with unprecedented pressures on habitats, species, and gene systems. To understand and manage biodiversity requires a broader perspective than our fragmented forested profession now has.

BIODIVERSITY IN CANADIAN FORESTRY

T.J.B. Boyle

**Forestry Canada
Science and Sustainable Development Directorate
Fuller Building, 3rd Floor
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The current state of knowledge of the biodiversity in Canadian forests is examined, together with an assessment of current conservation programs, both *in situ* and *ex situ*. Research results and ongoing research related to forest biodiversity being undertaken in Canada are discussed. Gaps in present knowledge that are identified. Possible impacts of various domestic and international initiatives of forest biodiversity and forest management are discussed.

INTERNATIONAL ASPECTS OF BIODIVERSITY

J.T. Williams

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Major new initiatives and strategic planning are underway on international work on biodiversity, especially in relation to the United Nations Conference on the Environment and Development to be held in 1992. An outline is given on how work on conservation and utilization of plant genetic resources has progressed over the past 25 years, and how current efforts need to be modified in the light of new scientific developments. For trees, more emphasis needs to be placed on *ex situ* conservation in order to back sustainable production forestry, prevent further loss of biological diversity, and to support ITTO's goal for 2000 as the date by which all internationally traded tropical timber would have to be derived from sustainable sources.

RATIONALE FOR PRESERVING CROP GENETIC DIVERSITY

B. Fraleigh

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Genetic erosion is a term used to describe loss of variability in crop gene pools. Genetic vulnerability refers to the narrow genetic base of varieties grown in the field. Genetic resources centres were established worldwide to counteract the effect of these factors by preserving crop genetic diversity and by facilitating its use in research and plant breeding.

THE POTENTIAL EFFECTS OF GLOBAL CLIMATE CHANGE ON THE BIODIVERSITY OF WOODY PLANTS

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Climatologists predict a doubling of atmospheric CO₂ during the next 100 years. Climate models vary in predicting how doubling CO₂ will affect North American climate, but generally agree on three points: mean summer and winter temperature will increase between 2° and 5°C, temperature changes will be greater at high latitude and mid-continental regions will experience lower rainfall. The effect of these phenomena on biodiversity is likely to be dramatic. Predictions of species range shifts in response to climate change vary from 250 to 500 km. These predicted future ranges are non-overlapping with current range limits for many trees. Historical evidence of species range movements following the Pleistocene indicate that tree species migrated at rates between 10 and 45 km per century. These estimates probably approximate maximum migration rates for trees. The movement of trees through the modern landscape may be slowed by as much as 50% because of habitat reduction and fragmentation. This model predicts that trees will not come to climatic equilibrium for at least a millennium. Differential migration rates between species will result in new contacts between species with unpredictable ramifications. Insects and microbial pathogens should respond to climatic warming faster than long-lived trees. Predicted increases in the incidence of drought should increase plant stress and thereby increase the frequency of insect outbreaks and disease. In addition, it is predicted that exotic weeds will expand their ranges to become pests where they currently are not. These simple models of species response are further complicated by numerous additional factors for which there is little information. For instance, elevated CO₂ increases water-use efficiency and enhances growth in many plants. However, response to elevated CO₂ varies among species. Thus reproductive and competitive abilities of species may shift within their current habitats. While one could move trees to compensate for their response lag to climate change, the knowledge to predict how far species can safely be moved is lacking. Much needs to be learned with respect to the exact climatic variables that limit individual species' ranges. Finally, range shifts and disease may exert a strong selective pressure on tree populations. While it remains to be seen which species will survive under these diverse selective pressures, we can target species that are likely to be vulnerable based on range size and habitat specificity.

BIOTECHNOLOGY AND BIODIVERSITY - THE INTERRELATIONSHIPS

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Although the two current high profile scientific fields of biotechnology and biodiversity have extremely different scientific foundations and philosophies, they are still closely interrelated. Forest biotechnology to be useful is dependent on the availability and maintenance of a broad genetic foundation. Such a foundation is best achieved over time by maintaining the biological diversity of natural systems. In contrast, it is conceivable that with the release of genetically engineering organisms, natural biological diversity could be negatively impacted. The possibility of such an influence will be discussed. Finally, the politics of the relationship between these two emerging scientific fields will be briefly reviewed.

**BREEDING STRATEGIES IN A CHANGING CLIMATE
AND IMPLICATIONS FOR GENETIC DIVERSITY**

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Most global climate models predict a rapid increase in temperature over the next few decades as a result of elevated levels of CO₂ and other greenhouse gases. Although the resolution of the existing models is not sufficient to predict specific weather patterns for Canada's Maritimes Region, the predicted rate of change is such that forest tree populations will be unable to adapt fully to future conditions. If conventional rotation lengths are planned, presently adapted seedlings will be poorly adapted to the new conditions by the time of harvest. A three-pronged approach is proposed to mitigate the impact of climate change in the Maritimes: development of short rotation clonal forestry, testing and breeding for stability of genotypes over a range of climatic conditions and collections, storage and testing of native and non-native materials of potential value.

*ABSTRACTS OF
WORKSHOP CONTRIBUTIONS*

Population Genetics

Chaired by Dr. F.C. Yeh, University of Alberta

**DOMESTICATION AND GENETIC DIVERSITY - SHOULD WE BE
CONCERNED?**

Y.A. El-Kassaby

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Despite the fact that forest trees are in their early stages of domestication, there has been little direct evaluation of the genetic diversity throughout this process. The dynamic changes in the genetic structure of wild conifers were monitored through several bottlenecks, namely: phenotypic selection, seed orchards, seed processing and storage methods, and seedling production. The genetic structure of phenotypically vs. randomly selected individuals of two conifers with known contrasting diversity levels is compared. The biology and management methods practiced in seed orchards are evaluated, and seed extraction and storage procedures are assessed to evaluate common practices on biological peculiarity. Finally, the cultural practices of container nurseries were monitored and their impact on the genetic structure of future forests is evaluated.

GENETIC DIVERSITY OF CANADIAN HARDWOODS: IMPLICATIONS FOR CONSERVATION

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and

John Mackay

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Hardwoods occupy a large portion of several forest ecosystems found in Canada. Collectively, they have long been the neglected child in Canadian forest genetics and tree improvement. Even though the ecological status of many Canadian hardwoods is relatively well known, their genetic diversity, genecology, mating system and population structure remain to be deciphered. Abundant natural regeneration for several species, high costs associated with seedling production and plantation establishment, low demand from the pulp and paper sector, and lack of strategies in dealing with the numerous private owners of the southern Canadian forest have refrained the industry and the governments from investing into basic biological and genetic research of hardwoods species. However, this situation is changing rapidly and new interests have emerged for genetic improvement and conservation of hardwoods species. Fast growing species such as red alder, trembling aspen or birch can be found as major components of the mixed boreal forest, and are becoming economically important. In the southern part of eastern Canada, the rich mixed hardwood forest contains numerous major and minor species of high economic value. Most of these forests have suffered from intensive harvesting during the past 200 years, and some are affected by declines. We review our current knowledge of the organization of genetic diversity in the few Canadian hardwood species that have been studied. Studies derived from the analyses of quantitative characters showed extensive genetic variation that could be used in improvement programs. Biochemical markers such as isozymes have shown that the levels of genetic diversity and population structure were quite similar to those reported for conifer species. Programs aimed at studying population genetic aspects of hardwoods and establishing conservation and improvement programs are currently developed nationwide. New strategies at the DNA level that could help monitor genetic diversity of these species will be discussed.

TREE BIODIVERSITY AND THE PRESERVATION OF NEWFOUNDLAND PINES

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Red pine, *Pinus resinosa* Ait., is a rare species in Newfoundland with an extant population of less than 10,000 trees located in 20 small stands that are clustered in 2 main population centres on an Island with an area of about 115,000 km². The decline of red pine, the extinction of natural populations is an ecological and economical concern on an Island with a limited biodiversity in tree species, and a limited resource base for commercial exploitation. Native pines have an important ecological role on dry sties that cannot support productive forests of other species. Seedlings from a sample of trees from most of the extant natural populations are being established at several "safe" sites to preserve the Island's gene pool. However, molecular genetic studies that are underway to characterize genetic variation suggest that Newfoundland populations of red pine remain largely undifferentiated from mainland populations. Ecological studies on seed production indicate that reproductive success in red pine populations from the interior of the Island is comparable to that of mainland populations. Adverse spring weather during flowering and pollination period (in coastal populations), natural successional trends, overcutting, and fire suppression are among the factors that may limit red pine's success as a naturally occurring species on the Island. In this article, we use Newfoundland's red pine population as an example for broader discussion of concepts in population ecology and genetics that can guide our approach to the conservation and genetic management of species with fragmented distributions and small population sizes.

GENETIC CONSEQUENCES OF FOREST FRAGMENTATION FOR SUGAR MAPLE POPULATIONS

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Forest fragmentation, the dissection of large continuous forests into small spatially discrete forest patches, is a global phenomenon. However, little is known about its affects on the genetic structure of forest tree populations. Data from natural populations of different sizes have been used to provide some insight into this question, suggesting that fragmentation may result in reduced genetic variation and increased population differentiation. Recent data from sugar maple populations, in both fragmented and continuous forests, indicate that such extrapolation may be unjustified. Small forest patches were found to exhibit elevated levels of within population and within individual variation. These data suggest mechanisms that are important in generating and partitioning genetic variation within fragmented forests.

GENETIC CONSEQUENCES OF *IN SITU* AND *EX SITU* CONSERVATION OF FOREST TREES

Rong-Cai Yang and Francis C. Yeh

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To counteract the accelerating loss of genetic diversity crucial for current and future tree improvement, forest genetic resources have been either conserved *in situ* in their natural ecosystems (undisturbed reservoirs) or exploited and maintained in controlled (*ex situ*) environments (breeding arboreta, seed orchards, and test plantations). What is the best means of conserving genetic resources has been the subject of debate and the focus of research. This paper first reviews previous studies on population structures of forest tree species in the context of their impact on the choice of conservation methods. Using available theory and isozyme data, we address the following issues: What are the features of population structure that differentiate *in situ* and *ex situ* conservation? How does knowledge pertaining to the genetic structure of a natural population help to implement an efficient and practical strategy for *ex situ* conservation and/or tree improvement? Does the presence of multilocus structure of a population suggest a different strategy? Do *ex situ* conserved populations provide enough genetic variation for future tree improvement? What is the practicality of implementing an *in situ* conservation program? The second part of this paper deals with the monitoring of genetic changes in conserved populations. Do *in situ* and *ex situ* conservation lead to different genetic structures of populations? The answer to this question can be found in two ways: prediction of long-term behaviour and direct measurement of genetic variation in conserved populations. Both prediction from simple genetic models and empirical studies show that genetic diversity in *ex situ* conserved populations decreases considerably over generations, compared with the natural populations. We conclude that while *ex situ* conservation is a convenient operational program for short-term tree improvement, *in situ* conservation is essential to explore new genetic variation to meet the changing environments in the future.

*ABSTRACTS OF
WORKSHOP CONTRIBUTIONS*

Wood Quality

Chaired by J. Gonzalez, Forintek

ALLOCATION OF VARIANCE IN RELATIVE DENSITY OF WOOD FROM NORTHWESTERN CONIFERS

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and

L. Jozsa and J. Gonzalez
Forintek Canada Corp., Vancouver, B.C.

Relative density is a complex trait reflecting contributions from earlywood and latewood density and their proportions. Distribution of variance among 15 components of variance was compared for species with markedly different patterns of wood formation and for different ages. The species analysed were Douglas-fir, Sitka spruce, western larch, western red cedar, and yellow cypress.

EFFECT OF SPACING ON WOOD DENSITY ESTIMATION IN EARLY TESTING OF DOUGLAS-FIR

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A partial six-parent diallel of Douglas-fir [*Pseudotsuga menziesii* (Mirb.) Franco] planted at two spacings (15 x 15 and 15 x 30 cm) was destructively measured three years after germination. The objective of the study was to determine the extent of genetic control on yearly ring width (RW) and density (RD) as affected by spacing. The total phenotypic variance of yearly RW and RD were partitioned into genetic, environmental (spacing), genetic-spacing and random error effects to permit the determination of heritability and genotype x spacing interaction. Significant genetic [general (GCA) and specific (SCA) combining abilities], spacing, and spacing x GCA effects were obtained. The SCA variance component was larger than that for GCA, however, the relationship between SCA and GCA variance components showed a consistent decline of SCA over the three studied years. Conversely, the GCA effect was virtually non-existent in the first year and steadily increased over the three year period. Although only six parents were studied, significant GCA x spacing effects were observed. The implications of this interaction on early testing is discussed.

GENETIC AND PHENOTYPIC RELATIONSHIPS BETWEEN GROWTH AND WOOD RELATIVE DENSITY OF INTERIOR SPRUCE

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Juvenile wood relative density (RD) was assessed by the maximum-moisture content (MMC) method in 40 open-pollinated families of interior spruce growing in two 15-year-old progeny tests of north-central British Columbia to examine: (1) the magnitude of family differences; (2) phenotypic, genetic and family mean correlations between RD and growth traits, and; (3) develop an approach for using these parameters for the prediction of parental breeding values. Differences among the 40 families for mean RD were large (0.38 to 0.44), as indicated by high individual ($h^2_f = 0.47 \pm 0.03$) and family mean ($h^2_f = 0.67 \pm 0.11$) heritabilities. Genetic correlations between both height growth and diameter growth and RD were near zero, whereas phenotypic correlations were significant ($P < 0.05$) at -0.40 and -0.46, respectively. Family differences using the Pilodyn (PIN) apparatus as an indirect measure of RD were significant ($P < 0.05$) and exhibited a moderate family heritability (0.48 ± 0.25). The genetic correlation between PIN and RD as assessed by the MMC method was -0.80 ± 0.10 . Family selection for RD using PIN data was expected to be 67% as efficient as direct family selection for RD based on the MMC values. Parental breeding value predictions for height growth and RD, using the PIN at age 15, indicate that no reduction in RD from family selection is likely. Moreover, it appears that the selection of families with high positive breeding values for both traits is possible.

SPECIFIC GRAVITY — ANOTHER SELECTION TRAIT FOR A HYBRID POPLAR CLONAL SCREENING PROGRAM?

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Specific gravity is of key importance in forest product manufacture because it has a major effect on both quality and yield of pulp, energy, and solid wood products. The hybrid poplar tree improvement program in eastern Ontario uses multiple-stage clonal selection. New clones are selected for Septoria canker resistance, good rooting ability and photoperiodic adaption, and fast early growth. To investigate the potential of including wood quality as a fifth selection trait, two studies were recently undertaken.

In the first study, specific gravity was evaluated for thirty randomly selected individuals from seven hybrid poplar families to explore variability in the trait. Height, root collar diameter, and Septoria canker severity were also measured to determine correlations between these traits and specific gravity. Two samples for wood quality testing were taken from each stem: one at 10% of the distance from whorl to butt and another at 10% of the

distance from whorl to tip. Specific gravity was determined on a green volume basis using the volume by water immersion method. Moisture content was determined gravimetrically on an oven-dried basis. Results showed significant ($p=0.0001$) differences between families with those of *P. deltoides* x *maximowiczii* parentage ranking first, second, and third with respect to specific gravity. Families with *P. deltoides* x *nigra* parentage were generally more resistant to canker. Variability within and between families was high. Coefficients of variation ranged from 28.4 for family 2253 to 87.1 for family 2296.

To determine the best place for wood quality selection within the multiple-stage program, a second study investigated juvenile:mature correlations in specific gravity. Sample cores were cut from disks taken at the centre of each internode for ten eleven-year-old trees of clone DN74. Ring widths and densities were recorded for each sample using the X-ray densitometry method. Whole-tree specific gravity at two or three years of age will be compared to that of rotation age material.

*ABSTRACTS OF
WORKSHOP CONTRIBUTIONS*

**Tree Seeds:
Crown Management for
Cone Production**

Chaired by R. Smith, Forestry Canada, Maritimes Region

CROWN MANAGEMENT — ARE WE APPLYING WHAT WE KNOW?

Ron Smith
Forestry Canada - Maritimes

Past and ongoing research on crown management in conifers was reviewed. While there is a good information base on the spatial (crown-shoot-bud) patterns of reproductive and vegetative bud development in conifers, as well as the temporal patterns (initiation/differentiation), little is known about the physiological control mechanisms. Consequently, virtually all of the research into crown management conducted to-date has focused on empirical measurements.

Crown management studies in black and white spruce in the Maritimes were reviewed in the context of developing a crown management regime as part of a seed orchard management system. Response to topping treatments was affected by the timing, frequency, and severity of topping, as well as tree species and age. Potential problems associated with topping such as changes in sexual zonation within the crown, and affects on seed and pollen cone production while present, have not been shown to be of major consequence in spruce trees receiving regular, light toppings.

Crown management should be combined with cone induction and other cultural practices in both conventional seed orchards as well as non-conventional orchards e.g., meadow orchards and breeding halls.

DEVELOPMENT OF THE CROWN AND OF THE PATTERN OF CONE DISTRIBUTION: THE STARTING POINT FOR CROWN MANAGEMENT FOR SUSTAINED CONE PRODUCTION

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To understand patterns of cone distribution in the crowns of common genera one must first understand the various patterns of development of the structure of the crown. These patterns of development involve (i) character of the structures, such as morphological nature of short and long shoots, proportion of performed and neoformed extension of shoots, or proportion of proleptic and sylleptic branching; (ii) orientation of shoots, whether inherently orthotropic or plagiotropic, or plagiotropic by imposition; (iii) amount of development, such as differences in shoot lengths down crowns or inward on branches; and (iv) timing of events, such as budburst, the period of steady shoot elongation, and bud formation, and rate of shoot elongation. Although some patterns occur in several genera, others are monogeneric, or are expressed to varying extent in different genera. The crown of each genus, and sometimes species, must be understood as developing in a distinct way. Development of the long-shoot crown structure of

Pinus strobus, *P. monticola*, *P. resinosa* and *P. ponderosa* may be considered simple. Crown structure of *Pinus banksiana* and *P. contorta* is more complex because of multinodality, with intermediate whorls of preformed branches decreasing in initial vigour acropetally while main whorls of branches decrease in vigour of extension basipetally. Crown structure of *Picea* is also made complex by the many preformed "interwhorl" branches that decrease in vigour basipetally. Young *Picea* may exhibit some neoformed extension, but later, all extension is preformed. *Larix* crowns have great complexity not only because of production of short shoots and long shoots, both vastly different in character from those of *Pinus*, but also because of retention into old age of a propensity for large proportions of neoformed extension of long shoots, and, in younger trees, production of sylleptic branches. These varying patterns are related to how cones are borne in the crowns and along the individual shoots. In each genus distinct patterns of cone distribution become evident as crowns bear cones for the first time and then increase their capacity for cone bearing. Again, complexity of patterns of distribution vary with genus, and probably, as in *Pinus*, with species. If one is to manipulate crowns with the objective of sustaining cone production, one must take into account the patterns evident in structural development and in both seed-cone and pollen-cone distribution.

CROWN RESPONSES AND STROBILI PRODUCTION IN TOP-PRUNED JACK PINE SEED ORCHARD TREES

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The effects of top-pruning were examined on 9-year-old jack pine seed orchard trees over a three year period. In 1987, light topping removed the developing current leader and the 1986 main-stem internode: severe topping removed the leader, two years of previous growth and the 1984 internode. A single replacement stem developed on lightly topped trees the year following treatment. Multiple replacement stems occurred on severely topped trees but required 3 years to develop. Senescence of older branches at the bottom of the crown was reduced by topping. Production of seed strobili on lightly topped trees was unaffected in the following 3 years but on severe trees, production remained significantly lower than control trees. Seed strobili production increased on the uppermost branches of topped trees at the expense of pollen strobili.

*ABSTRACTS OF
WORKSHOP CONTRIBUTIONS*

**Biotechnology in Tree Improvement
and Impact on Biodiversity**

Chaired by P.J. Charest, Forestry Canada, PNFI

ASPECTS OF BIOTECHNOLOGY AND BIODIVERSITY

Pierre J. Charest

Project Leader

Molecular Genetics and Tissue Culture

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Biotechnology can be related to genetic biodiversity in many ways and it can be seen as a help or as a threat. Help can be found in applications such as tissue culture for germplasm preservation or DNA fingerprinting for characterization of genetic biodiversity. Threat can be envisioned with the use of clonal forestry by reducing biodiversity or with genetic engineering by potential of genetic pollution. However, the overall goal of biotechnology is to increase artificial forest productivity so that natural forests can be left untouched. Consequently, preserving natural biodiversity. During the course of this workshop, an overview of research trends in Canada and abroad will be given, with some insights on integrated pest management. There will be a presentation on the use of tissue culture in a tree improvement program and on the use of molecular biology to analyze biodiversity. As an example of clonal propagation, an overview will be presented of the accelerated tree improvement program of J.D. Irving Co. Ltd. Finally, there will be a subjective view of the impacts of biotechnology related to genetic engineering on forest ecosystems.

OVERVIEW OF RESEARCH TRENDS IN BIOTECHNOLOGY IN CANADA AND ABROAD

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Biotechnology research done in Canada has been pioneering the areas related to forestry in the world. Good success stories exist with the large scale field application of *Bacillus thuringiensis* against spruce budworm and the use of viruses for the control of other insects. Biotechnology research related to trees has made tremendous advances in the areas of conifer somatic embryogenesis (spruce and larches) and cryopreservation of these tissues. Major efforts are being put together in Canada by Silvagen and by J.D. Irving Co. Ltd. to develop the somatic embryogenesis to a commercial level. In addition, work done at PNFI has pioneered the area of regeneration of tree species from larch protoplasts (single cells). Genetic engineering has been successful in producing transgenic poplar trees that are now undergoing fielding testing and environmental impact assessments. Moreover, a breakthrough with a marker gene (b-glucuronidase) in the regeneration of somatic embryos of white spruce has been achieved and lead the way to exciting molecular biology spruce species.

APPLICATION OF SOMATIC EMBRYOGENESIS IN TREE IMPROVEMENT PROGRAMS

**Ben Sutton, Dane Roberts, Fiona Webster, Steve Grossnickle,
John Major, Ann Eastman¹**

**Forest Biotechnology Centre
British Columbia Research Corporation
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¹ Petawawa National Forestry Institute, Forestry Canada, Chalk River, Ontario

Somatic embryogenesis (SE) is a tissue culture system with the potential to rapidly multiply improved seed and accelerate its introduction into operational reforestation. In addition, since it is possible to store clonal material in a regenerative state for extended periods, it allows for clonal selection and subsequent clonal forestry. This presentation covers the basic properties of the tissue culture system and the results of a range of assessments for phenotypic quality and genetic stability of material produced from SE. Its application in tree improvement and the implications for biodiversity are discussed in the context of forestry in British Columbia.

A NOVEL APPLICATION OF MOLECULAR TECHNOLOGIES FOR ASSESSMENT OF BIODIVERSITY

Bob Rutledge

**Petawawa National Forestry Institute
Chalk River, Ontario
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Recent breakthroughs in the understanding of gene function have led molecular biology into a revolutionary period, which is providing an unprecedented understanding of the molecular basis for the regulation of cellular development and intracellular signal transduction. These discoveries are now providing the foundation for what can be best described as a unified molecular theory for cellular function and development (Science 251, page 1176 (1991)). In addition to resolving the fundamental aspects of cellular differentiation, is an intriguing opportunity to address the basic mechanisms underlying morphological character, in a manner that is potentially applicable to both tree breeding and the assessment of population biodiversity.

Our molecular genetics group at PNFI has utilized the Polymerase Chain Reaction (PCR) to isolate and character segments of several conifer gene families, including homologs to the flower homeotic genes and myb-related genes. We have confirmed that conifers do possess homologous genes, and that these genes comprised very large gene families containing 20-50 genes each. Although our major objective is to examine the role of these genes in the regulation of embryo development, an examination of variation within these gene families within a population, may provide an opportunity to directly evaluate the genetic

component determining morphological variations between individuals. Specifically, based upon the demonstrated importance of TAF (trans acting factors) genes in morphology suggests that study into the variation of the type and composition of these genes within a population, may provide important insights into the molecular basis for biodiversity within a specific tree species.

ACCELERATED TREE IMPROVEMENT PROGRAM: INTEGRATING NEW TECHNOLOGIES

G.W. Adams

**J.D. Irving, Limited, Sussex Tree Nursery
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Accelerated breeding techniques for black spruce have been developed to the stage where they are being incorporated into the tree improvement program. Clonal propagation by rooted cuttings or possibly somatic embryogenesis may soon be economically justifiable as control-pollinated seed becomes available from second generation selections. The full length paper discusses accelerated breeding techniques and clonal propagation and how they may be utilized in long-term breeding and production strategies for black spruce.

IMPACT OF BIOTECHNOLOGY ON FOREST ECOSYSTEMS

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The impact of biotechnology on forest ecosystems is discussed. The application of biotechnology in Canadian forests will bring about characteristics of high-yield forestry. Desirable impacts of biotechnology are increased forest productivity, reduced pressure on forest lands, and increased forest management. Undesirable impacts of biotechnology include pest adaptations to new pesticides, non-target pest emergence, reduction of biodiversity, genetic pollution and new evolutionary tracts. In order to minimize the negative impact of biotechnology policies controlling the use of biotechnology in Canadian forests should be enacted. These policies should emphasize the understanding of the ecological effects of biotechnology and integrated forest management.

*ABSTRACTS OF
WORKSHOP CONTRIBUTIONS*

**North American Quantitative
Forest Genetics Group**

Chaired by J. Loo-Dinkins, Forestry Canada, Maritimes Region

MINIMUM CLONE NUMBERS REQUIRED IN PRODUCTION SEED-ORCHARDS AND CLONAL PLANTATIONS

W.J. Libby

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When estimating minimum and optimum numbers of clones for deployment in clonal forestry, the following considerations seem important: (1) Risk to a random genotype from biotic and/or physical damage; (2) The level of unacceptable loss; (3) Diversity among the deployed clones; (4) Gain changes with changed selection differential; (5) Stability in both WIMP and MOMS configurations; (6) Rotation time from planting to harvest; (7) Management comprehension and efficiencies; (8) The extent and reliability of test knowledge; and (9) Both professional and public resistance to small numbers of clones.

Zygotic offspring (including vegetatively multiplied propagules) may be deployed either as families (family forestry) or as orchard-run mixtures (classical tree-improvement). For the zygotic offspring of either cp or op seed-orchards, compared to deployed clones, (1) risk to a random genotype will be similar although not identical; (2) if planting density is greater, more loss will be acceptable; (3) because recombination produces a central tendency, overall diversity will be less although greater extremes will occur; (4) gain will generally be less; (5) average stability of the recombinant zygotic propagules will be less than that of clones selected for stability in either WIMP or MOMS configurations; (6) because of within-clone uniformity, rotation times may be slightly shorter with clones in MOMS but similar in WIMPs; (7) management comprehension and efficiencies are much reduced; (8) clonal maturation will erode the reliability of clonal tests while pollen changes or uncertainty will erode cp and op test reliability; and (9) professional public resistance may be somewhat less.

BREEDING FOR CLONAL MIXTURES

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Since no resistances are absolute, nor can safety be assured by increasing the number of clones. Serial breeding for resistance can only lead to arms races with rapidly evolving pests, and to epidemics when virulence evolves. An alternative is to induce a genetic dynamic within pathogen/pest populations that forces non-epidemic behavior. One way to do this is to use clonal mixtures with widely different resistances that require such wide pest adaptations that generalist pests are less fit than specialists. By breeding multiple populations for differences, and using clonal mixtures from them, super-pests may never evolve. Alternative deployment strategies are possible. Therefore, while increasing the number of random clones may not increase security, increasing differences among clones could.

TIME TO FAILURE IN CLONAL POPULATIONS OF FOREST TREES

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The appropriate number of clones to deploy in clonal plantations is a major concern of managers involved with clonal forestry. Although there are a number of characteristics of clonal plantations for which considerations involving numbers of clones are important, a particularly relevant aspect is risk of catastrophic loss due to an unanticipated physical or biotic agent. Even though a clone may not succumb to such an agent for some time after its introduction, it almost assuredly will eventually fall victim to an attack or occurrence of a destructive agent. Analyses of distributions for times to failure for a clone or mixtures of clones thus are useful for evaluating the effect of numbers of clones on the risk of population failure. A model for time to failure is presented and the effect of increasing the numbers of clones in mixtures on the probability of population failure is discussed. Cases are explored showing how increases in numbers of clones can result in either increased or decreased chances for population failure.

ALLOZYME DIVERSITY OF NATURAL STANDS VERSUS SEED ORCHARD LOBLOLLY PINE

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The maintenance of genetic diversity in the breeding population of any commercially valuable species should be a top priority of any breeding program. This may be especially critical for forest tree improvement programs since trees are often reintroduced into highly heterogeneous natural environments. Thus, it is important to determine how much of the native gene pool is maintained in commercial seed orchards. Genetic diversity at 21 polymorphic allozyme loci are compared between 16 natural populations from the eastern range of loblolly pine (*Pinus taeda*) and two loblolly pine seed orchards. Of the 21 loci 19 (90.4%) are polymorphic in each of the two orchards. Relative to the natural populations 83.6% and 88.2% of the genetic diversity and 62.3% and 60.9% of the 69 alleles observed in the natural populations were maintained in the two orchards. Every allele that was missing from the orchards had an average frequency across the 16 natural populations of less than 10%. The majority (66%) of the absent alleles had mean frequencies of less than 1% in the eastern range of loblolly pine.

BIOLOGY TO POLICY: CASTING PEARLS TO SWINE

J.V. Hood

Ontario Ministry of Natural Resources

Increased international exchange of forest tree seeds and cuttings led to, in the 1960's-70's, the first "official" guidelines for movement and/or trade. The growing use of vegetative propagules with tree species other than Poplars induced Sweden and Germany to put into place regulations governing the production and trade of clonal material in 1982 and '85 respectively. Denmark, Belgium, New Zealand, Canada and Ontario have since followed suit with either policy, guidelines, a proposal or a discussion paper. Pertinent details of these efforts, primarily as they pertain to clonal forestry, are compared and contrasted.

*ABSTRACTS OF
POSTER EXHIBITS*

**VARIABILITÉ GÉNÉTIQUE DE POPULATIONS D'ÉPINETTE
BLANCHE (*PICEA GLAUCA* (MOENCH)) INTÉGRÉES DANS LE
PROGRAMME D'AMÉLIORATION DU QUÉBEC**

Mireille Despons, Ariane Plourde, Jean Beaulieu et Gaétan Daoust

**Génétique et Amélioration des Arbres
Centre de Foresterie des Laurentides
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La préservation du patrimoine génétique préoccupe grandement les responsables des programmes d'amélioration des essences forestières. C'est dans cette optique qu'on a vérifié si les sélections qu'impliquent ces programmes ont entraîné une baisse de la variabilité chez l'épinette blanche au Québec. La structure et la variabilité génétique de 2 populations naturelles ont été comparées à celles observées dans 3 provenances, ainsi qu'à un groupe d'individus du croisement diallèle. Les résultats obtenus par l'analyse électrophorétique de 7 systèmes enzymatiques indiquent globalement le maintien de la variabilité parmi les provenances. Malgré une réduction importante de l'effectif, les individus impliqués dans la plan de croisement diallèle montrent des taux d'hétérozygotie et de polymorphisme très élevés suggérant un effet d'hétérose.

DIVERSITY OF THE MITOCHONDRIAL GENOME OF *LARIX*

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Despite their ecological and commercial importance, conifer mitochondrial genome organization, complexity, and diversity is not well known. As descendants of some of the most primitive land plants, conifers have unique physiology and genetics. We have isolated total genomic DNA from several *Larix* species to examine the diversity of the mitochondrial genome, using hybridization with wheat mitochondrial gene probes for restriction fragment length polymorphism (RFLP) analysis. Our results indicate that several *Larix* species can be differentiated by specific RFLP's when hybridized with a wheat mitochondrial gene probe. Wheat mitochondrial gene probes are also being used in heterologous hybridization experiments to study the complexity of *Larix leptolepis*

mitochondrial genes and to evaluate the effect of *in vitro* embryogenic cell culture on individual mitochondrial gene structure and organization.

BIOCHEMICAL MARKERS AS PROBES IN SCREENING BIODIVERSITY IN WILLOW (*SALIX* L.) INTENSIVE FORESTRY

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University of Toronto**

As the potential for short rotation willow plantations is increasing, both the intensity of the culture and its dependency on clonal stock impose questions regarding the maintenance of genetic biodiversity in *Salix*. One of the most efficient ways of investigating and studying biodiversity is the use of biochemical markers to characterize species, populations and individuals. We report the development of 27 enzyme systems for *Salix*, which encode for at least 50 isoenzymic genes that can be used as markers. Optimal electrophoretic techniques, source tissues for enzymes, gel and electrode buffers, starch compositions, running conditions and staining procedures are presented. The validity of enzyme markers in the assessment and evaluation of biodiversity is discussed.

CHLOROPLAST DNA POLYMORPHISM IN SOME TREE FORM WILLOWS (*SALIX*) DETECTED BY DIGOXIGENIN LABELED NONISOTOPIC PROBES

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Chloroplast DNA (cpDNA) fragment polymorphism in some willow ssp. was visualized by digoxigenin labeled nonradioactive probes. Some critical parameters have been determined that are important for optimizing the sensitivity and avoiding non specific banding background of digoxigenin system. Compared to ^{32}P labeled probe, digoxigenin labeled DNA was more efficient in detecting chloroplast DNA in *Salix*. Interspecific cpDNA polymorphism were evident between diploid species and tetraploid species. RFLPs were identified that differentiate diploids and tetraploids. Intraspecific conservation of RFLPs was confirmed by examining trees from different sites across the species natural range. A mislabeled accession of *S. alba* L. was delineated based on its unique variants detected by different combinations of enzyme digestion and probe hybridization. *S. alba* L. and *S. pentandra* L. share the same chloroplast genome which implies a same progenitor involved in the process of their polyploidization.

DNA POLYMORPHISM IN *SALIX* AMPLIFIED BY PCR WITH ARBITRARY PRIMERS

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Newly developed, random amplified polymorphic DNA (RAPD) markers are well suited for genetic mapping, for DNA fingerprinting and for plant breeding applications. The present study demonstrates that these RAPD markers are also useful for the study of species relationships in *Salix*. DNAs from twelve willow species were amplified by polymerase chain reaction with seven arbitrary primers. Polymorphism was evident among species. Species kinship was inferred based on RAPD polymorphisms.

MULTILOCUS STRUCTURE IN *PINUS CONTORTA*

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We studied non-random associations (Gametic disequilibria, GD) between alleles at different allozyme loci for 66 populations from three sub-species, and elucidated the contribution of GD to development of multilocus structure in *Pinus contorta*. For each population, the distribution of number of heterozygous loci in two randomly chosen gametes was established and compared with the expectation without GD. The total and average variances over populations were partitioned into single-locus and two-locus effects of population structure. GD were important and accounted for a major part of structuring in *P. contorta*.

CLIMATES OF ONTARIO AND GENETIC VARIATION

Dennis Joyce and Don MacIver

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The principle guiding the choice of seed source for successful establishment of artificially regenerated forests is simple; match the environment of seed origin to that of the deployment environment. In areas where environmental gradients are steep, such as boreal Ontario, movement of seed must be carefully controlled to ensure the use of well-adapted stock. The Ontario Ministry of Natural Resources and Environment Canada are working together to update information on climatic gradients in Ontario. This information is to be used in the management of seed collection and deployment in Ontario.

SITKA SPRUCE IN A CHANGED CLIMATE

J.P. Hall

**Forestry Canada
Science and Sustainable Development Directorate
Ottawa, Ontario**

This poster is based on previously published data on several provenances of Sitka spruce growing in western Newfoundland. Sitka spruce survived and grew poorly compared to local black spruce, but in plantations with the best survival and growth, the tallest tree in each replicate was usually a Sitka spruce, and the tree-to-tree variation in height of Sitka spruce was much greater than black spruce. The climates of the seed origin and plantation are compared. The difference in mean annual temperature between the seed origin and planting site is about 2.5°C, well within the ranges predicted by climate models although the temperature change is in the opposite direction.

Trees have reacted strongly to the seed transfer, over half of them have died, many more have survived as 'cabbages' barely reaching a height of 50 cm in 25 years. A small proportion, probably about 5%, however, grew rapidly and are tolerant to local climate, insect and disease conditions as the native black spruce. The data demonstrate that conifers have an extremely variable genotype as befits a group of organisms with a long geological past and wide distribution. Conifers may be very adaptable to future changes in climate and the indications are that a land race is developing in western Newfoundland in response to what is in effect a changed climate. This may represent one view of our forests in the future.

ADAPTIVE VARIATION AMONG JACK PINE POPULATIONS NORTH OF LAKE SUPERIOR

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An intensive short-term provenance study was used to determine the patterns of adaptive variation displayed by jack pine (*Pinus banksiana* Lamb.) throughout a portion of its range in north-central Ontario. Seed from 64 populations was planted in common gardens tests in three environments and ten traits relating to phenology and growth rate were examined. Seed origin was a significant source of variation for most individual seedling traits in all trials. The first principal component was associated with growth potential, while the second was more closely related to drought resistance. Multiple regression analysis of principal component scores indicated that latitude, longitude, total precipitation, and maximum temperature explained some of the variation seen among populations.

EFFECT OF TREE SPACING, CONE STORAGE, YEAR OF COLLECTION, AND PRECHILLING ON GERMINATION OF *PICEA GLAUCA* (MOENCH) VOSS SEED

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Cones were collected late August in 1984 and 1988 from 13 open-pollinated white spruce trees growing in a demonstration seed production area at the Petawawa National Forestry Institute. Trees were at spacings of 1.2, 2.4, or 4.9 m. Seeds were extracted from cones after 2 or 6 weeks of storage. For each of the 2- and 6-week cone storage periods, four 100-seed samples were prechilled and four others were non-prechilled. The objective of this study was to evaluate the effect of cone storage and prechilling on seed germination for white spruce from cones collected at the time of seed dissemination from individual trees in two different years.

Seed were more mature at collection time in 1988 than in 1984 as evidenced by the germination results. Non-prechilled seeds from cones stored for two weeks averaged 30 and 61% germination in 1984 and 1988, respectively. Seeds from cones stored for 6 weeks in 1984 matured during the storage (up to 60% germination) whereas those in 1988 did not. Prechilling of seed after two weeks of storage increased germination percentage from 30 to 60%, and from 61 to 87% in 1984 and 1988, respectively. This was an indication that seed dormancy was present in both years. Prechilling of seed after 6 weeks of storage increased germination from 60 to 95% and 64 to 89% in 1984 and 1988, respectively. Thus, dormancy remained high after 6 weeks of storage. Analyses of variance indicated that all factors (year of collection, cone storage, seed treatment, tree spacing, and individual trees) were significant in explaining the percentage of germination. However, tree spacing explained little of the variation in the data (0.2%); seed treatment, cone storage, individual trees, year of collection, and the error term explained 39, 15, 16, 8 and 22%, respectively, of the variability in germination percentage.

EFFECT OF SITE AND FAMILY ON BLACK SPRUCE (*PICEA MARIANA* (MILL. B.S.P.)) SEED GERMINATION AND CONE MORPHOMETRIC CHARACTERISTICS

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Cones were collected from each of three trees in each of nine families located in two black spruce (*Picea mariana* (Mill.) B.S.P.) seedling seed orchards in early September 1990. Trees in the Three Brooks and Second Falls orchards, located in northwestern New Brunswick, were used for the collection. The objectives of the study were to determine: i) the effect of site and family on cone morphometric characteristics such as cone length, full-seed yield, total seed yield, and total number of fertile scales; and ii) the effect of site, family, and trees within family on seed germination and rate of germination. Four replicates of 50 seeds per tree for each family and for each site were used to evaluate seed germination percentage and germination rate (Czabator Peak Value = PV).

Analyses of variance of germination percentage and PV indicated that site, family, and individual trees within each family, as well as the interaction site*family, were all significant. Site had the highest F-value with family second and trees within family last. Cones from the Three Brooks orchard were the longest (36 vs 31 mm), had the most fertile scales (46 vs 42) and yielded the most seed (full and empty; 53 vs 47); however, seed from the Three Brooks orchard had the lowest germination percentage and PV. Among the various cone characteristics studied, only cone length differed among families.

This study indicates that the location of an orchard may play a major role in seed germination percentage and germination rate. In addition, cone size may not be a good indicator of seed quality.

VARIATION MORPHOMÉTRIQUE DES CONES DE PINS BLANCS AU QUÉBEC

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Université de Montréal

Les résultats d'une étude de la variation morphométrique des cônes de pins blancs (*Pinus strobus* L.) sont présentés. Le but est de vérifier l'existence de divergences régionales.

Dix populations originant de quatre régions du Québec ont été échantillonnées. Huit caractéristiques ont été mesurées sur les cônes. Des techniques d'analyse multidimensionnelle ont été utilisées.

Les quatre régions diffèrent entre elles. Celle d'Anticosti est la plus divergente du groupe, suivie de celle d'Abitibi. Les régions St-Laurent et Outaouais ne sont pas semblables bien que les conditions pédoclimatiques générales soient similaires.

Il est proposé que ces différences soient le reflet d'une adaptation à des conditions locales particulières. La répartition spatiale des populations peut aussi jouer un rôle.

MORPHOMETRIC VARIATION IN WHITE PINE CONES FROM QUEBEC

Results from a study of the morphometrics of eastern white pine (*Pinus strobus* L.) cones are presented. The aim was to identify regional differences.

Ten populations from four regions in Québec were sampled in 1989. Eight cone traits were measured. Multivariate analyses were used in order to identify trends.

The four regions samples are significantly different. Anticosti island population is the most divergent one followed by the Abitibi population. The St-Lawrence and Ottawa river regions are different despite the fact that their climate and ecological conditions are relatively similar.

We believe that the differences are mainly due to adaptation to local conditions, but spatial distribution may also be involved.

INDUCTION FLORALE CHEZ *PICEA GLAUCA* ET *P. ABIES*

Gaétan Daoust ing. f., Ariane Plourde Ph.D., Jean Beaulieu ing.f., M.Sc.

**Génétique et amélioration des arbres
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Afin d'accélérer la production de semences forestières et la réalisation de notre programme de croisements dirigés chez *Picea glauca* (Moench) Voss et *P. abies* (L.) Karst., des essais de stimulation de la floraison ont été réalisés en 1990 dans nos parcs d'hybridation. Vingt clones de *P. glauca* âgés de 10 à 13 ans et 15 clones de *P. abies* âgés de 7 ans ont reçu divers traitements. Les traitements 1 et 2 consistaient à injecter 100 mg de AG₄/7 seul ou avec 10 mg de ANA (demi-dose pour *P. abies*). Le traitement témoin ne contenait que le l'alcool utilisé comme solvant pour les autres traitements. Les données recueillies au printemps 1991, soit le nombre de strobiles femelles et mâles par verticille ont été analysées. Nous présenterons les résultats et les conclusions de cette expérience.

PHENOLOGY OF NATIVE AND EXOTIC *LARIX* MILL. SPECIES IN NEW BRUNSWICK

Cyndy Carswell

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Several provenances of eight species of *Larix* Mill. were planted in the UNB Larch Arboretum in 1988. This provides a unique opportunity to study phenological responses of each provenance to the conditions (temperature and photoperiod) at a common site. The responses, such as, time of growth initiation, occurrence of late shoots and time of growth cessation, will give an indication of genetic differentiation within and among species, and adaptation to the local environment.

BRANCH BENDING ON 8 YEAR OLD EUROPEAN AND JAPANESE LARCH GRAFTS INDUCES MALE FLOWERING

Cathy Nielsen and Hilary Veen

**Fast Growing Forests
Ontario Ministry of Natural Resources
Brockville, Ontario**

Lower branches of European larch grafts were bent downwards in early spring of 1989 and kept in position until October of the same year. The following spring numbers of male and female cones were analyzed. Branch bending had a highly significant effect on male flower production ($P > 0.0001$), but did not effect female flowering. The same treatment applied to Japanese larch in 1990 produced similar results. This treatment can be used operationally to obtain pollen from selected clones.

POLLEN CONTAMINATION IN THE ISLAND LAKE SEED ORCHARD

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Our field site is at the Island Lake Tree Improvement Area (ILTIA), Chapleau, N. Ont. We began work during the 1990 pollination season and continued in 1991. Our work was preceded in 1989 by the pollen contamination study of Dr. R.H. Ho (OFRI-OMNR).

Objectives:

- To study the aerobiophysics of pollen dispersal, i.e. the source of pollen, its dispersal characteristics and its mode of deposition
- To modify models of particle dispersal to simulate pollen flow in seed orchards
- To test and modify the model for use by seed orchard managers and designers to reduce pollen contamination

Methods:

- We look at the source of pollen in three different ways: we are testing the feasibility of attempting to determine the number of pollen shed per tree/unit area; we look at the 'effective' source strength of contaminant pollen at the upwind edge of the orchard; and we release tracer particles upwind of the orchard (pollens exotic to Chapleau). We are also looking at the meteorological "trigger" mechanisms which initiate pollen dispersal (e.g. temperature, humidity, etc.)
- The dispersal of pollen is traced by: measuring wind flow patterns within the orchard using anemometers; setting sticky slides within the orchard to monitor pollen deposition; and using the tracer particles to show dispersal directions
- The deposition of pollen is measured on the ground, on branches and on seed cones to determine the overall pollen budget

- In 1991 we have initiated a set of studies to look at diurnal and nocturnal variation of pollen flow.

Summary of Results:

- Pollination is a short-time process (e.g. fig. 1) which is climatically controlled and predictable
- Preliminary results from 1991 indicate rain to be an important factor in pollen deposition (including deposition to seed cones)
- Results so far indicate the distance of pollen dispersal into the seed orchard and thus give an indication of management techniques useful to reduce contamination (e.g. buffer zones; fig. 2)

DEVELOPMENT OF HYBRID POPLAR CLONES IN EASTERN ONTARIO

S. Strobl

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Since 1976, approximately 2,260 hectares of hybrid poplar have been planted in eastern Ontario through a cooperative program between the Ontario Ministry of Natural Resources and Domtar Incorporated. New clones are continually required for the annual planting program. Interspecific breeding produces several thousand seedlings annually and multiple-stage clonal selection is used to select new clones for planting. Nursery tests identify clones which are resistant to *Septoria* canker, have good rooting ability, and photoperiodic adaption, and fast early growth. Promising clones are tested on field sites to identify "plastic" clones. Top-ranking "plastic" clones are planted in blocks to obtain yield estimates. Finally, new clones for plantation establishment are identified.

DEVELOPMENT AND EVALUATION OF HIGH YIELDING WILLOWS FOR ENERGY PRODUCTION

L. Zsuffa, B. Beatson, R.L. Gambles, W.A. Kenney, B.J. Vanstone

**Forest Genetics Laboratory
University of Toronto**

Genetic and breeding research, aimed at the development of high yielding willow clones by selection and hybridization of North American species, was undertaken by the Forest Genetics Laboratory, University of Toronto.

A series of four clonal screening trials containing intra- and interspecific crosses of *Salix* species, was established in 1986 and 1987. The purpose of these trials was to provide information for the screening of superior clones (based on biomass production, growth habit and disease resistance).

In 1990, all trials were assessed for biomass production. The results of this harvest indicate that the yields produced by the best of the North American clones equal and often surpass those produced by willows in Swedish and United Kingdom programmes (where willows have been bred for several hundred years). Since these clones represent a first attempt at selection and breeding, the prospects for improving North American willow are excellent.

JUVENILE GENETIC EVALUATION OF LODGEPOLE PINE AND ITS IMPLICATIONS IN EARLY SELECTION

Xiaming Wu and Francis C. Yeh

**Department of Forest Science
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A retrospective study was initiated for lodgepole pine (*Pinus contorta* spp. *latifolia*). Genetic performance of 121 open-pollinated families was assessed for two growing seasons in the greenhouse. Genetic parameters (heritability and genetic correlation) for growth, bud, branch, and biomass characters were estimated. The potential of predicting mature performance using single and/or composite juvenile characters is presented.

TECHNOLOGY DEVELOPMENT FOR AN ACCELERATED BREEDING PROGRAM

Cathy Nielsen and Hilary Veen

**Fast Growing Forests
Ontario Ministry of Natural Resources
Brockville, Ontario**

Tree improvement efforts in Eastern Ontario are concentrated primarily on white pine, Norway spruce and the larches. Technology development efforts at the G. Howard Ferguson Forest Station in Kemptville, Ontario, are focused on accelerating the breeding and testing process for each of these species. Fall grafting is utilized for white pine plus trees that are difficult to access and to supplement the winter grafting program. Growing grafts under environmentally controlled conditions and applying compressed growth cycles increases growth and reduces the time to onset of flowering. Flower induction treatments are applied to obtain early and abundant flowering once the grafts have reached a size of 1.0 to 1.5 m in height so that controlled crosses can be carried out as soon as possible. Early progeny testing in the form of nursery screening trials allows early roguing of the production population and promotes the selection of superior genotypes at the earliest possible time. Vegetative propagation facilitates the early reproduction of superior material in a shorter time period as compared to conventional seed orchards.

GENETIC RESISTANCE TO THE WHITE PINE WEEVIL IN SITKA SPRUCE

Cheng C. Ying

**Forest Science Research Branch
B.C. Ministry of Forests**

Fifteen-year records of weevil attacks in Sitka spruce provenance trials revealed large differences among provenances in percent of trees attacked and number of attacks per tree. This provenance variation in weevil attack was repeated in a clonal test suggesting a genetic basis in weevil resistance. On the average, provenances from the high weevil hazard zone and also those from the hybridization (white Sitka spruce) zone showed a high level of resistance to weevil attack. Two provenances, Haney and Big Qualicum, which showed high resistance to weevil and were also fast growing are recommended as seed sources for reforestation at sites in the high weevil hazard zone.