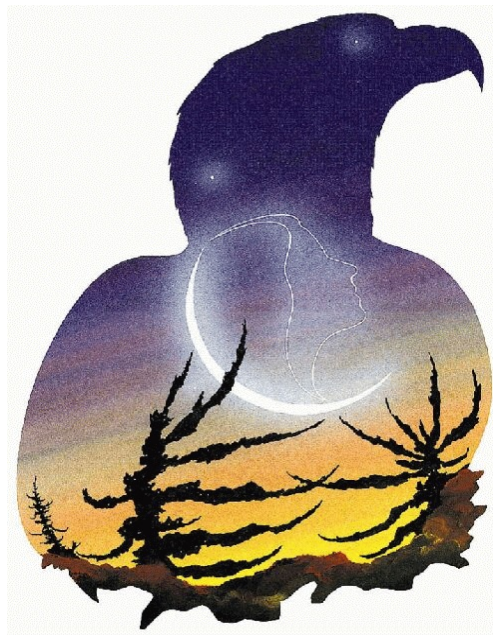


**PROCEEDINGS OF THE TWENTY-SEVENTH MEETING  
OF THE  
CANADIAN TREE IMPROVEMENT ASSOCIATION**

PART 1 Minutes and Members' Reports  
PART 2 Symposium

*Genetic Resource Management: Building Strategies  
for the New  
Millennium*



*Aménagement  
des ressources  
génétiques:*

*développement de stratégies pour le prochain millénum*

**COMPTES RENDUS DU VINGT-SEPTIÈME CONGRÈS  
DE  
L'ASSOCIATION CANADIENNE POUR  
L'AMÉLIORATION DES ARBRES**

1<sup>re</sup> PARTIE Procès-verbaux et rapports des membres  
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## Conference Logo

The conference logo was designed by David Johnson. David is a well known Ojibway artist living in the Peterborough, Ontario area. He was asked to develop a logo that is symbolic of native views of natural diversity and living in balance with nature. David's describes the symbolism within the logo in this way:

"This design is inspired by native symbolism and colour.

The eagle is the main theme of the logo. I chose the eagle because of the many teachings I have been given about the eagle. The eagle has thousands of feathers upon its body. Yet no two feathers are alike. Each is shaped and formed according to what is required. Some of the feathers are stiff, sharp, and cutting. Others are pliable and soft. This kind of diversity is essential so that the eagle can stay warm, stay cool, stay dry, line its nest, and fly.

Another teaching of the eagle is that it has the ability to see further than other animals and is therefore symbolic of great vision, the kind of vision that is needed to secure our future.

The face in the sky represents Mother Earth. We must treat the earth with the same respect that we would our mother. The line of her hair juxtaposed against the circle of the moon reminds me of the yin & yang symbol of balance.

I felt that the design must be freeform to set itself apart from our concept of a conventional logo. The white pines were incorporated into the design because they are the epitome of freeform."



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PROCEEDINGS  
OF THE  
TWENTY-SEVENTH MEETING  
OF THE  
**CANADIAN TREE IMPROVEMENT  
ASSOCIATION**

PART 1

Minutes and members' reports

**GENETIC RESOURCE MANAGEMENT:  
BUILDING STRATEGIES  
FOR THE NEW MILLENNIUM**

Sault Ste. Marie, Ontario  
August 15-17, 2000

Editor  
J.D. Simpson

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COMPTES RENDUS  
DU  
VINGT-SEPTIÈME CONGRÈS  
DE  
**L' ASSOCIATION CANADIENNE POUR  
L' AMÉLIORATION DES ARBRES**

1<sup>re</sup> PARTIE

Procès-verbaux et rapports des membres

**AMÉNAGEMENT DES RESSOURCES  
GÉNÉTIQUES: DÉVELOPPEMENT  
DE STRATÉGIES POUR LE  
PROCHAIN MILLÉNIUM**

Sault Ste. Marie, Ontario  
15-17 août 2000

Rédacteur  
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Michel Villeneuve  
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Dr. S. Y. Zhang  
Forintek Canada Ltd.  
319 rue Franquet  
Sainte-Foy, Québec  
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BUSINESS MEETING MINUTES

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Sally John	Isabella Point Forestry Ltd. Salt Spring Island, BC
Barry Linehan	Forest Resources & Agrifoods Grand Falls, NF
Pengxin Lu	Ministry of Natural Resources Sault Ste. Marie, ON
Pierre Périnet	Forêt Québec Sainte-Foy, Qc
Diane Renaud	Weldwood of Canada Ltd. Hinton, AB
Kermit Ritland	University of British Columbia Vancouver, BC
Daryl Sandee	Weyerhaeuser Prince Albert, SK
Denise Tousignant	Forêt Québec Sainte-Foy, Qc
Richard Trudel	Institut Armand-Frappier Laval, Qc
Deb Weedon	Millar Western Forest Products Ltd. Whitecourt, AB
Motion:	That the nominated Active Members be duly elected.
Moved by:	Bruce Dancik
Seconded by:	Al Gordon
Carried.	

### 310.3 Corresponding Membership

The following names were presented:

Harvinder Cheema	University of Toronto Toronto, ON
Abrolhossein Lohrasebi	University of British Columbia Vancouver, BC

Motion: That the nominated Corresponding Members be duly elected.  
 Moved by: Jerry Klein  
 Seconded by: Leonard Barnhardt  
 Carried.

**311 Chair's Report**

On behalf of the Ontario Ministry of Natural Resources and Forest Genetics Ontario, I would like to thank you for participating in the 27<sup>th</sup> meeting of the Canadian Tree Improvement Association. Hosting this meeting has offered the opportunity to foster discussions about resource management issues that our profession is being asked to address. In the coming century, the pendulum of forest genetic programs has, and will continue to oscillate between an emphasis on economic benefits derived from tree breeding and conservation concerns. The challenge to our profession is to promote a dynamic balance between conservation and use of genetic resources.

The supportive comments by the participants suggest that the meeting was a success. The keys to this success were two fold: the excellence of both invited and voluntary presentations, and the active participation of a number of people in organizing the event. I would like to take this opportunity to thank the members of the organizing committee: Peter Gagnon, Vic Wearn, Ann Foggia, Randy Ford, Paul Charrette, Cathy Nielsen, Pengxin Lu, Bob Sinclair, and Marilyn Cherry. I would also like to thank David Johnson for an exceptional logo for the conference.

**312 Treasurer's Report**

Since the last meeting Linda DeVerno transferred from Fredericton to Ottawa. Tannis Beardmore agreed to fill this position. The financial statement for the period of July 30, 1997 to July 31, 2000 was prepared by Treasurer Tannis Beardmore and tabled for information and acceptance by the membership (see Attachment #1). The statement shows a balance of \$15,893.15 in the Association's account and GIC's totalling \$24,000.00.

Motion: That the financial statement be accepted as presented.  
 Moved by: Jerry Klen  
 Seconded by: Dave Reid  
 Carried.

**313 Financial Contributions**

Bowater Pulp and Paper Canada Inc.  
 Clergue Forest Management  
 Domtar Forest Resources  
 Forest Genetics Ontario  
 Forintek Canada Corporation  
 Natural Resources Canada  
 New North Greenhouses  
 Ontario Ministry of Natural Resources  
 Tembec Incorporated  
 Weyerhaeuser Canada Ltd.

Motion: That the CTIA/ACAA executive of the 27<sup>th</sup> meeting express our sincere appreciation to these contributors.  
 Moved by: Bruce Dancik  
 Seconded by: John Major  
 Carried.

### 314 Editor's Report

The proceedings were printed and distributed during April 1998 to all active members, honorary members, Canadian universities and libraries, registrants and financial contributors of the 26<sup>th</sup> meeting. Two hundred and seventy-five proceedings were mailed.

A letter advising of the theme of the 26<sup>th</sup> biennial meeting, the proceeding context, and a request for a twenty dollar donation to obtain a copy was sent to all corresponding members, USA addresses and international addresses. As a result, proceedings were mailed to 17 Canadian, 10 USA and 24 international addresses. About 65 copies remain on inventory.

### 315 Education Committee

To promote students' knowledge and understanding in tree improvement activities and forest genetics research, the forestry faculties of Canadian universities were encouraged to nominate a student to attend the 27<sup>th</sup> CTIA/ACAA meeting. Sponsorship of these students is paid by the executive committee of each biennial meeting through registration fees. Paul Charrette reported that the following students received the award which provided all meeting costs including registration, accommodation, tours, and travel:

Kirstin Campbell	University of Northern British Columbia
Joanna Carlisle	University of New Brunswick
Juan Pablo Jaramillo-Correa	Université Laval
Jean-Francois Morin	Université de Moncton
Susan Nykoluk	University of Northern British Columbia
Steve Sarazin	Lakehead University
Christopher Stephenson	University of British Columbia

### 316 Working Group Reports

#### 316.1 Tree Seed Working Group

Ron Smith moderated the Tree Seed Working Group's (TSWG) afternoon workshop "The Role of *Ex-Situ* Germ Plasm Storage in Gene Conservation" on August 14, 2000.

Immediately following the workshop, the Tree Seed Working Group held its Business Meeting. Five issues of the TSWG News Bulletin (Nos. 27-31) were produced since the last meeting on August 18, 1997 in Sainte-Foy. Editor Ron Smith (CFS - Atlantic) indicated he plans to step down and hopes someone will come forward to fill the position. He also announced that Howard Frame had resigned as Chairperson due to a change in employment duties. Dave Kolotelo agreed to become the new Chairperson.

Thanks go to Ron for editing, printing, and mailing of our News Bulletin.

#### 316.2 Wood Quality Working Group

There being no activity since the last meeting in Sainte-Foy, 1997 no report was given.

Alvin Yanchuk  
BC Forest Service, Victoria  
Chair, CTIA Wood Quality Working Group

### **317 Business Arising from Previous Meetings**

#### **305.2 Update and Publish Constitution and Bylaws**

Dale reported this had been completed and the updated version was mailed to all Active members with the Proceedings of the 26<sup>th</sup> meeting.

#### **305.3 Registration of CTIA/ACAA**

Dale reported that he had made contacts in New Brunswick and Ottawa. CTIA/ACAA has to be incorporated first before it can be registered. He felt incorporation was not necessary. General discussion pointed out that the name should be registered not the organization.

Motion: That the Executive Secretary take the necessary steps to register the name nationally.  
 Moved by: Sally John  
 Seconded by: Ron Smith  
 Carried.

#### **305.4 Bursary**

Michel Villeneuve suggested at the 26<sup>th</sup> Business Meeting that CTIA/ACAA could consider establishing an award for students who write or present a paper on tree improvement/genetics. He developed a "Student Recognition Award Proposal" which Chairperson Dennis read aloud (Attachment # 2).

Motion: That the proposal be accepted.  
 Moved by: Michel Villeneuve  
 Seconded by: Arianne Plourde  
 Defeated.

The concept was favorably accepted but it was deemed necessary that additional refinement to the proposal was necessary. One point was concern about differences in quality between BSc, MSc and PhD students. It was recommended that the incoming executive refine the proposal and present it again at the next business meeting.

### **318 New Business**

#### **318.1 Official Gavel**

Michel Villeneuve suggested the Association should have an "official" gavel.

Motion: That Michel will coordinate the crafting of a gavel using wood of improved species from each province.  
 Moved by: Michel Villeneuve  
 Seconded by: John Major  
 Carried.

### **318.2 Change Name of Association**

Al Gordon suggested the Association change its name to better reflect “the times.” Sally John suggested the word “Genetics” be part of the name.

Motion: That CTIA/ACAA change its name to Forest Genetics Association of Canada/Association genetique forestière du Canada.

Moved by: Jerry Klein

Seconded by: Al Gordon

After consulting the Constitution and Bylaws it was revealed that at least 20 members must vote affirmatively and not less than two-thirds of those present and voting. Since only 20 members were present it was felt wise to adjourn this portion of the meeting and complete it at the Banquet where more members would be present.

Two names were moved and voted on just prior to the Banquet: Forest Genetics Association of Canada and Forest Genetics and Tree Improvement Association of Canada. Both suggestions failed to receive 20 affirmative votes. Therefore, it was recommended the incoming executive deal with this issue.

### **319 Future Meetings**

#### **319.1 Location of 2002 Meeting**

Motion: CTIA/ACAA hold its next meeting in Edmonton, Alberta hosted by Alberta Land and Forest Service, the forest industry and University of Alberta.

Moved by: Bruce Dancik

Seconded by: Michel Villeneuve

Carried.

#### **319.2 Location of the 2004 Meeting**

Motion: British Columbia Ministry of Forests host the meeting in Okanagan, BC.

Moved by: Dave Reid

Seconded by: Sally John

Carried.

#### **319.3 Location of the 2006 Meeting**

Motion: That the meeting be held in Atlantic Canada.

Moved by: Kathy Tosh

Seconded by: Ariane Plourde

Carried.



**320 Election of New Executive**

The following slate of officers will serve as the executive for the next CTIA/ACAA meeting:

Chairperson:	Bruce Dancik University of Alberta
Vice-Chairperson: Symposium	Leonard Barnhardt Alberta Land and Forest Service
Vice-Chairperson: Local arrangements	Florance Niemi Daishowa-Marubeni Int. Ltd.
Treasurer:	Tannis Beardmore Canadian Forest Service
Editor:	Dale Simpson Canadian Forest Service
Executive Secretary:	Dale Simpson Canadian Forest Service

**321 Adjournment**

Motion: That the 27<sup>th</sup> business meeting of the CTIA/ACAA be adjourned.  
Moved by: Sally John

**Attachment # 1**

CTIA/ACAA  
Financial Statement  
July 30, 1997 - July 31, 2000

**Cash balance July 30, 1997** **\$4,539.99**

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**Credit:**

Interest (account)	1 164.11
Interest (GIC)	1 799.59
Purchase of Proceedings	413.49
Reimbursement of monies borrowed for the 26 <sup>th</sup> CTIA meeting	5 000.00
CFS financing for publishing the 26 <sup>th</sup> CTIA Proceedings	7 973.95
Surplus from 26 <sup>th</sup> CTIA meeting	3 532.64
GIC matured (deposited directly into account, Nov. '97)	5 000.00
GIC matured (deposited directly into account, Nov. '97)	10 000.00
GIC matured (deposited directly into account, April '99)	16 000.00

**Total Credit:** **\$50 883.78**

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**Guaranteed Investment Certificates (as of July 1997):**

GIC principal	10 000.00
GIC principal	8 000.00
GIC principal	5 000.00

**Total GICs:** **23 000.00**

**Guaranteed Investment Certificates (as of August 2000):**

GIC principal	8 000.00
GIC principal	16 000.00

**Total GICs:** **\$24 000.00**

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**Debits:**

Envelopes	203.55
Printing of 26 <sup>th</sup> Proceedings	6 279.00
Printing of Constitution and By-laws	699.20
CFS (postage for mailing Proceedings)	284.16
Purchase of cheques	22.17
Address labels	42.54
Purchase of GIC (April '98)	16 000.00
Purchase of GIC (August '00)	16 000.00

**Total Debits:** **\$39 530.62**

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**Cash Balance July 31, 2000\*** **\$15,893.15**

**Invested GIC Balance** **\$24,000.00**

**TOTAL HOLDINGS** **\$39,893.15**

\* (Credits - Debits) + (July 30, 1997 cash balance): **\$11,353.16 + \$4,539.99**

## **Attachment # 2**

CTIA/ACAA –Terms of reference for a new award program, to be adopted at the business meeting of August 16, 2000

It is suggested that the Association adopts a resolution to create a recognition award for students who write a paper or essay on their research (proposal or results) or on any tree improvement/genetics topic (ref.: art. 305.4 in minutes of 26<sup>th</sup> business meeting).

It is proposed that the award be called the CTIA Student Paper Award. Students of Bachelors, Masters or PhD programs are eligible.

### **AIM**

To complement the sponsorship program, which allows students (one per forestry faculty in Canadian universities) to attend the CTIA/ACAA meeting at no cost (travel, registration, accommodation and tours).

### **FORMAT**

The conferring of the award coincides with the biennial or triennial meeting of the Association. The summer preceding the meeting (traditionally held in August), an announcement is made in each of the Canadian forestry universities. An appropriate professor at each one is contacted to foster participation.

Interested students have to submit a paper or essay, on a subject pertaining to the mandate of CTIA/ACAA. A maximum of 3 tables and figures can be included, but the total must not exceed 12 pages (double-spaced), including bibliography (single-spaced). Recommended font is Arial 10 points or equivalent. Format will follow that of the Canadian Journal of Forest Research. The paper/essay can be written in English or French, with abstracts in both languages.

### **DEADLINE**

Papers/essays (original + 3 copies) must be submitted no later than the 15<sup>th</sup> of January in the year of the meeting. The mailing address will be specified in the announcement.

### **REVIEW COMMITTEE**

The review committee is composed of a chairman (named at each business meeting for the following term), and of 2 or 3 active or honorary members of the Association.

### **EVALUATION CRITERIA**

Compliance with format requirements, organisation of the manuscript, originality, grammar, spelling, adequate use of tables, figures and references.

### **AWARD**

The award is paid through the holdings of the Association. Up to two prizes will be awarded (\$ 1000, \$ 500). The author of the winning paper is invited to present it at the following meeting and all expenses (travel, registration, accommodation and tours) are paid through the holdings of the CTIA/ACAA.



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ACTIVITY REPORTS  
FROM ACTIVE MEMBERS

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## THE STATUS OF TREE IMPROVEMENT IN NEWFOUNDLAND AND LABRADOR

**Basil English and Barry Linehan**

**Dept. of Forest Resources and Agrifoods  
P.O. Box 2006, Fortis Building  
Corner Brook, NF  
A2H 6J8**

The Newfoundland Forest Service has in place tree improvement programs for three species, all of them native conifers: black spruce (*Picea mariana* (Mill.) B.S.P.), white spruce (*Picea glauca* (Moench) Voss) and eastern larch (*Larix laricina* (Du Roi) K. Koch). Six first generation seed orchards have been established, two per species. One orchard per species will serve the reforestation needs of the Northern Peninsula/Labrador breeding zone. The other will produce seed for the southern part of insular Newfoundland (i.e., the Main Island breeding zone). The three Northern Peninsula/Labrador orchards are located at Pynn's Brook on Newfoundland's west coast. The Main Island orchards are located at Wooddale Provincial Tree Nursery in central Newfoundland. While the production facilities have been geographically separated, all breeding work is being carried out at Wooddale. Work is also being carried out to ensure we have secure supplies of red pine (*Pinus resinosa* Ait.) and white pine (*Pinus strobus* L.) seed to meet future reforestation needs.

### BLACK SPRUCE PROGRAM STATUS

The black spruce orchards, both of which are of seedling origin, were established in the early 1990's. As of 2000, they are beginning to produce small quantities of female cones without benefit of any particular cone enhancement techniques. The black spruce family tests established at the same time (1993) were not scheduled to receive their first measurement until age 10. However, this precocious cone production may cause us to accelerate our measurement schedule, providing us with data for an early, light roguing.

For some time we have been concerned about the small number of families in our black spruce programs, a situation that could, if left unchecked, limit our freedom to rogue rigorously and obtain the greatest possible genetic gain. Therefore, in 1997 we selected an additional 40 plus trees, 20 per program, from CFS-established range-wide black spruce provenance trials. These will feed directly into the second generation production/breeding programs. As well, we have made additional plus tree selections from wild stands and, with the support of our Maritime colleagues, obtained seed from a number of PEI and New Brunswick plus trees. These will be used in a new series of family tests to be established in the fall of 2000.

In anticipation of second generation breeding requirements, we have selected black spruce polycross pollen donors from one of the range-wide black spruce provenance trials mentioned above. Scions have been collected and grafted, and a polycross pollen donor garden has been established at Wooddale.

### WHITE SPRUCE PROGRAM STATUS

Over the past several years we have concentrated our greatest effort on the white spruce breeding program. In 1998, polycross pollen donors were selected. Pollen has been collected annually from these trees and used to carry out polycrosses. Enough polycrosses have now been done that we hope to establish our first series of polycross progeny tests in 2001. As well, scions were taken from the polycross pollen donors in 1998 and a grafted polycross pollen donor garden was established at Wooddale. Also since 1998, we have been

collecting pollen from within the white spruce orchards and using it for specific crosses. The first series of selection plantations will be established within the next two years.

The white spruce orchards, both of which are clonal, were established over a period of several years in the early 1990's. Many of the clones have begun to bear cones (hence, the opportunity to conduct the breeding work described above) and we anticipate a sizable cone crop any time now. The first topping activities were carried out in 1999.

#### EASTERN LARCH PROGRAM STATUS

Due to a lack of demand for larch planting stock, the decision has been made to focus our resources on the more important reforestation species. Therefore, breeding work on the two eastern larch programs has been temporarily deferred. The two orchards, both of which are of clonal origin, are receiving basic maintenance (including, fertilization, grass control and topping) but no breeding work is being contemplated at this time. That being said, polycross pollen donor trees were selected in 1998. Scions were taken from these and a polycross donor garden has been established at Wooddale to facilitate future breeding work.

#### TESTING, TRIALS AND TRAINING

In an effort to gain some hands-on experience with GA<sub>4/7</sub> before using it at an operational scale, we carried out a GA trial in our Main Island white spruce orchard in 1999. Several application rate and date combinations were tested. Although the results are not yet compiled, the numbers of female flowers we detected on the treated trees in the spring of 2000 leave no doubt as to the efficacy of GA<sub>4/7</sub> in enhancing white spruce cone crops.

In 1998 we carried out a similar GA<sub>4/7</sub> trial on red pine in the windbreaks surrounding the bareroot fields at Wooddale. The goal is to develop the windbreaks as a seed collection area. Red pine, though native to Newfoundland, is very uncommon and the acquisition of enough local seed to sustain our reforestation needs is a perennial problem. Unfortunately, we had no success in enhancing cone production, probably due to the immaturity of the trees. This year, once again, there are few maturing cones on the red pine. However, we have noted a very sizable cone crop coming on stream for 2001. Perhaps it is time to repeat the trial.

Breeding work is very new to us. Until several years ago, all our effort was going into first generation plus tree selection and orchard establishment. In anticipation of increased flowering activity, particularly in the white spruce orchards, and the need to start moving ahead on the breeding side of the program, we invited Ron Smith, a tree improvement expert with the Canadian Forest Service, Fredericton, NB to visit Wooddale and help us evaluate our existing resources, identify our needs and assist us in mapping out a strategy. As well, key staff toured the tree improvement facilities in the Maritimes. We learned a great deal and, we believe, have made tremendous progress over the past few years as a consequence. We gratefully acknowledge the assistance of Kathy Tosh and the staff at Kingsclear, (NB), Howard Frame and the staff at Debert, (NS) and Ron Smith.

#### WHITE PINE GENE CONSERVATION

White pine is a species in decline in Newfoundland. Though once relatively common, it was decimated by unregulated harvesting at the turn of the 19<sup>th</sup> century and has been under unrelenting pressure from white pine blister rust since then. Between 1998 and 2000 the Provincial Tree Improvement Committee coordinated the establishment of a clonal white pine seed orchard / gene conservation garden at Wooddale. Scions were taken from more than 200 mature, healthy white pine from all across the island range of the species. It is hoped that the new orchard will provide us with a secure, reliable source of high quality native seed and protect against the loss of genetic diversity should local pine populations become extinct over time.



## COOPERATIVE TREE BREEDING IN NOVA SCOTIA

Howard Frame and David Steeves

Department of Natural Resources  
Tree Breeding Centre  
P. O. Box 190  
Debert, NS  
B0M 1G0

**Keywords:** *Picea mariana*, *P. glauca*, *P. rubens*, *P. abies*, *Pinus strobus*, seed orchards, breeding

The Nova Scotia Tree Improvement Working Group (NSTIWG) was established in 1977 and is the coordinating body for tree improvement in Nova Scotia. Active members include the Department of Natural Resources, Bowater Mersey Paper Company Limited, Kimberly-Clark Nova Scotia Inc., Stora Forest Industries, and J.D. Irving Limited. The Canadian Forest Service has provided support services as well as technical and scientific expertise since the program's inception. Meetings are held in the spring and fall of each year to review progress and plans, while day-to-day activities are coordinated by the Department of Natural Resources. Species of interest include black spruce (*Picea mariana* (Mill.) B.S.P.), white spruce (*P. glauca* (Moench) Voss), red spruce (*P. rubens* Sarg.), Norway spruce (*P. abies* (L.) Karst.) and white pine (*Pinus strobus* L.). There are currently about 17 million trees planted annually in Nova Scotia.

### SEED ORCHARD PRODUCTION

White spruce clonal orchards have consistently overproduced to the point where cones have often been left unharvested. Two red spruce clonal orchards have been able to supply sufficient seed for the provinces' reforestation requirements. Rogued first-generation black spruce seedling seed orchards have produced sufficient seed to meet reforestation requirements. The second-generation black spruce orchards have not produced seed yet. Clonal Norway spruce orchards yielded a five-year supply of seed in 1998; the first seed collection of this magnitude.

### BREEDING

Second generation selection (family plus within-family) of black spruce is complete based on 10-year measurements made in three 1990 family test series. Approximately 400 selections have been included in the F<sub>2</sub> breeding population. Twenty-five percent of the second-generation selections were successfully polycrossed in 1999, nine pair-mates were also completed.

As for the white, red, and Norway spruce breeding programs, the first generation white and red are virtually complete. Norway spruce continues to be a challenge with only about 25 percent of the selections represented in polycross tests. The Norway spruce program was combined with the New Brunswick program in 1998 with breeding and testing shared between the provinces.

## FIELD TESTING

Polycross progeny test series were established in 1997 and 1999 for white and red spruce. A second Norway spruce polycross test series was outplanted in 1999. Cooperators are outplanting the first 2<sup>nd</sup> generation black spruce polycross test series in 2000.

Since the last update, the “first round” of testing our first generation black spruce families was completed with the measurement of nine-year heights in three 1990 series of half-sib family tests. Narrow-sense individual-tree heritabilities ( $h^2_i$ ) among these three series ranged from 0.20 to 0.44 and family heritabilities ( $h^2_f$ ) from 0.64 to 0.80. Recommendations were made to complete the initial roguing of the seedling seed orchards which will result in the removal of roughly 50% of the genotypes. A summary of the estimates of genetic gain from this “first round” of roguing has yet to be completed.

Fifteen-year-height and breast height diameter were measured in two 1985 black spruce family test series. Information derived from these data, which is pending, will provide age trends in the genetic parameters and will be used to begin a “second round” of seed orchard roguing.

The initial assessment of the clones constituting the first generation white and red spruce and white pine breeding populations commenced with height measurement of five series of white spruce, one of red spruce, and the first of two series of white pine progeny tests. Measurement details and heritabilities estimated to date are shown in Table 1. Predicted breeding values will be used to conduct an initial roguing of about one-third of the tested clones from our clonal seed orchards.

Table 1. Clonal progeny test series measured to date with heritability estimates where available

Species	Series	Progeny Type	Trait Measured	$h^2_i$	$h^2_f$
White spruce	PT91/1	Polycross	8-year Height	0.07	0.53
	PT91/2	“	“	0.10	0.67
	PT92/2	“	7-year Height	n/a	n/a
	PT93/1	“	“	0.17	0.65
	PT93/2	“	“	0.10	0.61
Red Spruce	PT91/3	“	8-year Height	0.11	0.63
White Pine	PT92/1	Open-pollinated	“	n/a	n/a

## FOREST GENETICS, BIOTECHNOLOGY AND MOLECULAR TREE BREEDING RESEARCH AT DALHOUSIE UNIVERSITY

Om P. Rajora

Department of Biology  
Life Sciences Centre  
Dalhousie University  
Halifax, NS  
B3H 4J1

**Keywords:** molecular, population, and conservation genetics; genome mapping, quantitative trait loci mapping of growth and adaptive traits, pedigree reconstruction and molecular breeding; EST, microsatellite DNA, AFLP, RAPD, SNP, SCAR, STS and allozyme markers; gene discovery; genetic implications of silvicultural practices, forest fragmentation and small population size; conservation, restoration and sustainable management of forest genetic resources; gene dispersal, minimum viable population size and indicators of population viability

A program in forest genetics and biotechnology has been initiated in the Department of Biology, Dalhousie University, with the establishment of StoraEnso Senior and Junior Chairs in Forest Genetics and Biotechnology in 2000. A generous donation from StoraEnso Port Hawkesbury Ltd. made the establishment of these chairs possible. Dr. Om Rajora has been appointed as the Senior Chair and Dr. Christophe Herbinger as the Junior Chair.

### FOREST GENETICS AND BIOTECHNOLOGY PROGRAM

The program will focus on molecular, population and conservation genetics, biotechnology, genome mapping, qualitative and quantitative trait loci mapping and molecular breeding, conservation and sustainable management of forest genetic resources, particularly those of conifers. The new forest genetics and biotechnology program at Dalhousie University will provide a missing component to a larger program in resource and conservation genetics and biotechnology in the Department of Biology. The program will be conducted in collaboration with Canadian Forest Service, Fredericton; StoraEnso Port Hawkesbury Ltd.; Tree Breeding Centre, Nova Scotia Department of Natural Resources; Nova Scotia Tree Improvement Working Group industry members (StoraEnso Port Hawkesbury Ltd., Bowater Mersey Paper Company, Kimberly Clark Worldwide Inc., JD Irving, Limited), Faculty of Forestry and Environmental Management, University of New Brunswick; New Brunswick Department of Natural Resources and Energy; New Brunswick Tree Improvement Council; Ontario Ministry of Natural Resources; National Research Council Institute of Marine BioSciences; and Royal Institute of Technology, Sweden.

### PUBLICATIONS

Buchert, G.P.; Rajora, O.P.; Hood, J.V.; Dancik, B.P. 1997. Effects of harvesting on genetic diversity in old-growth eastern white pine (*Pinus strobus* L.) in Ontario, Canada. *Conserv. Biol.* 11: 747-758.

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## TREE IMPROVEMENT ON PRINCE EDWARD ISLAND

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**Keywords:** seed orchards, progeny tests, provenance trials, hardwood research and gene pool conservation

The PEI Forestry Division, recently renamed the Natural Resources Division, continues to focus its tree improvement efforts on four major reforestation species: black spruce (*Picea mariana* (Mill.) BSP), white spruce (*Picea glauca* (Moench) Voss), eastern larch (*Larix laricina* (Du Roi) K. Koch.) and eastern white pine (*Pinus strobus* L.). Secondary species include red spruce (*Picea rubens* Sarg.), balsam fir (*Abies balsamea* (L.) Mill.), yellow birch (*Betula alleghaniensis* Britton.), red oak (*Quercus rubra* L.), white ash (*Fraxinus americana* L.), black ash (*Fraxinus nigra* Marsh.), and hop-hornbeam (*Ostrya virginiana* (Mill.) K. Koch). Provenance trials are underway to identify suitable seed sources for a number of native and non-native species.

### SEED ORCHARDS

First generation seed orchards are complete with the exception of red spruce. A second generation black spruce orchard has been established using selections from family tests. Plans for the establishment of a hybrid larch orchard will go ahead in 2001. Improved seed is now available from the eastern larch, white spruce, and eastern white pine first generation orchards as well as the rogued black spruce seedling seed orchard. Balsam fir, red spruce, and second generation black spruce orchards have not yet produced significant amounts of seed.

### PROGENY TESTS

The first series of white spruce progeny tests was established in 1997. Polycrossing carried out in 1998 produced seed for the second series of tests to be out-planted in 2000. Pollen was collected in the white spruce clone bank spring 2000 for future pair-mating.

The eastern white pine and eastern larch selections in our tree improvement program will be tested through open pollinated progeny tests. The eastern larch test was established in 1997 and the eastern white pine test will be planted in 2002. Results from these tests will be used to rogue the orchards.

### PROVENANCE TESTS

Two pine provenance tests were established in 1998. The first was an eastern white pine test which included seed sources from PEI, Nova Scotia, New Brunswick, Ontario, Tennessee, and Germany. The second was a Corsican pine (*Pinus nigra* var. *maritima*) test which included six Corsican pine sources from the Thetford Forest in England as well as local pine species for comparison.

A Norway Spruce provenance test will be planted in 2001 and will compare the growth of local populations of unknown origin with seed sources from Maine, Nova Scotia, Ontario, and Germany.

## HARDWOOD RESEARCH/GENE POOL CONSERVATION

The existing hardwood trials are being monitored and maintained. Our most successful yellow birch and red oak spacing trials were established in strip cuts and continue to grow at an impressive rate.

Red oak provenance tests will be established in spring 2000. Seed sources are from PEI, Nova Scotia, and New Brunswick.

Largetooth aspen (*Populus grandidentata* Michx.) shows potential as a riparian zone afforestation species along waterways. In addition, there is interest in its potential as a lumber species. We are studying the feasibility of growing largetooth aspen from seed for these purposes. Up to 15 largetooth aspen will be selected and propagated to establish a seed collection area for the future.

The Natural Resources Division is continuing research into the growth patterns of ground hemlock (*Taxus canadensis* Marsh.) for medicinal purposes. Early results of these studies have been used to produce guidelines for the sustainable harvest of this valuable shrub.

Gene pool conservation efforts continue for black ash and ironwood. Progress is moving slowly due to unavailability of seed and time constraints.

## J.D. IRVING, LIMITED – TREE IMPROVEMENT SUMMARY

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**Keywords:** spruce species, jack pine, white pine, tree breeding, seed orchards, clonal propagation, somatic embryogenesis

### STATUS OF BREEDING PROGRAMS AND ORCHARD PRODUCTION

J.D. Irving, Limited (JDI) participates in breeding and testing programs with the New Brunswick Tree Improvement Council (NBTIC) and the Nova Scotia Tree Improvement Working Group (NSTIWG) as well as operating independent testing programs. The company manages a total of 100 ha of clonal seed orchards including white spruce (*Picea glauca* (Moench) Voss ) (first and second generation), black spruce (*Picea mariana* (Mill.) B.S.P.) (first and second generation), Norway spruce (*Picea abies* (L.) Karst), red spruce (*Picea rubens* Sarg.), jack pine (*Pinus banksiana* Lamb.) (first and second generation), white pine (*Pinus strobus* L.) and eastern larch (*Larix laricina* (Du Roi) K. Koch). Breeding and progeny testing associated with first generation orchards of white spruce, black spruce and jack pine is complete and genetic roguing is in progress. Breeding and testing of red spruce and Norway spruce is still underway and work with eastern larch is not a priority at present. Second generation orchards of black spruce and jack pine were established from selections made in NBTIC open-pollinated family tests and the breeding and testing work for these orchards is nearly completed. Establishment of a second generation white spruce orchard based on individuals selected in NBTIC full-sib tests began in 2000.

Annual reforestation stock production for the company is 18 million seedlings and seed orchards have been filling this requirement since the early 1990's for all species with the exception of Norway spruce and red spruce. Difficulty is still being experienced in obtaining good cone crops of Norway spruce and flower induction is being used routinely. Vegetative propagation of controlled crosses of this species is proceeding. A seed orchard of red spruce was not established until 1992 and cone production has begun. Second generation orchard seed production for black spruce and jack pine increase each year and since 1996, sufficient jack pine seed has been harvested to satisfy nursery stock production requirements.

The white pine breeding program, initiated in 1997, is proceeding well. Approximately 125 selections were made in New Brunswick and selections from Nova Scotia, Prince Edward Island and Québec will be incorporated in polycross testing. A seed orchard of New Brunswick plus trees was established in 1998.

### VEGETATIVE PROPAGATION AND TESTING

Vegetative propagation activities were initially focussed on bulking up full-sib second generation black spruce families. In the past two years, emphasis has shifted to crosses among tested first generation white spruce selections as well as crosses among white pine weevil resistant Norway spruce. Rooted cutting production is currently between 1 and 1.5 million annually with future production increases anticipated.

Clonal testing programs have been initiated again with black spruce but now emphasizing white spruce and Norway spruce. Control-pollinated families are produced among tested individuals and clonal lines are initiated by somatic embryogenesis. The clonal lines are cryostored and sufficient somatic seedlings are

produced for establishing clonal field tests. Approximately 250 to 350 clones are established in field tests annually. Groups of clones will be selected for operational production as field test results become available.

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## NEW BRUNSWICK TREE IMPROVEMENT COUNCIL UPDATE

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**Keywords:** breeding, second generation, seed orchard, black spruce, jack pine, white spruce, tamarack

The New Brunswick Tree Improvement Council (NBTIC) completed its 24<sup>th</sup> year of operation in 2000. NBTIC has completed breeding and testing of first generation white spruce (*Picea glauca* (Moench) Voss) and tamarack (*Larix laricina* (Mill.) Karst.) and has started selection of second generation white spruce clones. Testing of second generation black spruce (*Picea mariana* (Mill.) BSP) and jack pine (*Pinus banksiana* Lamb.) is continuing. First generation orchards are providing enough seed for all reforestation stock. By the year 2001, all black spruce and jack pine seedlings will be grown from second generation seed.

### SEED ORCHARDS AND SEED PRODUCTION

Since 1978, seed orchards have been established by the industrial members of NBTIC who operate reforestation programs on freehold land, as well as by the New Brunswick Department of Natural Resources and Energy (NBDNRE) who is responsible for planting programs on Crown land. Over 130 ha of black spruce and jack pine seedling seed orchards were planted over a 10-year period ending in 1987. Clonal seed orchards, primarily of white spruce and tamarack, were also established over this time period, with over 60 ha planted.

Second generation orchard establishment of black spruce and jack pine began in 1989, with three agencies participating. Orchard establishment is now complete for these species with a total of 34.5 ha. The first planting of the second generation white spruce orchard was in 2000. Three agencies will be participating in the establishment of second generation white spruce orchards.

Seed production was lowest in 1997 with a total yield of 4.2 million seed most of which was jack pine (3.7 million). The good news about this collection was that the jack pine was collected from second generation orchards. In 1998, cone production increased significantly with a total of 29 000 l of cones and a yield of over 106 million seed. Black spruce first and second generation orchards yielded 31 million and 9.6 million seed, respectively. Second generation jack pine orchards also yielded 6.8 million seed. Cone production was good in the white spruce orchards in 1998 with 14 500 l yielding over 56 million seed. As expected cone production was down in 1999 with just over 5 200 l collected, 4 700 l from jack pine orchards.

### BREEDING

The Council conducts a complimentary breeding program which began in 1987 with white spruce and tamarack. A polycross, consisting of a mix of 20 unrelated pollens, is used to estimate breeding values. Pair-mating, involving specific crosses, is conducted to produce material from which selections will be made for the next generation. Polycrossing of second generation black spruce and jack pine has made tremendous progress since the start of the breeding program. This is partly due to polycrossing *in situ* on

selections in the family tests as well as the considerable experience that Council members have gained over the 10 years of breeding work. Pair-mating of black spruce and jack pine commenced in 1994 and 1996, respectively and will produce material for third cycle selections. Table 1 summarizes breeding progress for all species. Pair-mating of tamarack was discontinued due to reduced interest in planting.

Table 1. Summary of breeding progress

Species	Polycross		Pair-mate	
	No. Completed	% Completed	No. Completed	% Completed
White spruce	398	96%	501	96%
Tamarack	253	94%	60	-
Black spruce	348	85%	244	50%
Jack pine	348	86%	218	45%

The Council continues to follow the breeding strategy for black spruce that was adopted in 1993. Clones have been uniformly deployed to breeding groups and breeding is conducted in a positive assortative manner based on breeding values generated from nursery tests. A total of 15 sub-lines have been established for black spruce and 13 for jack pine. Breeding continues in the elite sub-line of black spruce and a clonal test from elite crosses was planted in 1999.

#### SELECTION PROGRESS

Trees were selected in family tests for inclusion into the second generation breeding population. Top performing families were identified based on 10-year height for black spruce and 7-year height for jack pine. Candidate trees were initially identified based on height growth, phenotypically graded in the family tests, and the final selection made from each family based on a combination of superior phenotypic and metric traits. Selection of second generation is complete for black spruce and jack pine with a total of 400 and 402 selections, respectively.

The next species that the Council has started second generation selections in is white spruce. The white spruce strategy is slightly different in that second generation selections originate from selection plantations. The first selections from these 48 tree blocks were made in the fall of 1998. These selections were based on results from 10-year progeny test measurements. A total of 66 of 400 trees have been selected to date.

#### TESTING AND DATA ANALYSIS

Testing continues to be an important component of the NBTIC program. Over the past 24 years, 246 tests were planted on over 284 ha. Over the past 12 years, progeny tests have been established to assess the performance of white spruce and tamarack plus trees and second generation black spruce and jack pine selections. Progeny testing of white spruce and tamarack will be completed in 2001, as well as the establishment of white spruce selection plantations from pair-mate breeding. Establishment of polycross tests of second generation black spruce and jack pine is 77% complete for both species.

Other testing highlights over the past 3 years include the establishment of the first series of a full-sib black spruce clonal test. Rooted cuttings, derived from controlled crosses within an elite black spruce sub-line, were grown over 2 years and outplanted on 4 sites. The purpose of this test is to quantify gains that could be realized from clonal deployment.

Another "first" for the Council was the establishment of the first series of full-sib progeny tests of black spruce and jack pine. Both series tested crosses from 4 of the 20 sub-lines. Third generation selections will be made from these tests in 10 years.

The data analyst position has continued to be funded by the Council members. Over the past 3 years the data analyst, Bryce McInnis, has analyzed 14 progeny tests, 6 family tests, 2 stand tests, and 1 gain test for a total of 23 tests. Results from 20-year measurements of a series of black spruce and jack pine family tests produced some very interesting gain estimates. In the black spruce series, selecting the top 25% of families would result in a volume gain of 13.4% and the top 50% of the families resulted in a gain of 9.2%. The jack pine series gain results were very similar with the top 25% of families having a volume gain of 13% as compared to the family mean and the top 50% having a gain of 8%.

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**TREE IMPROVEMENT PROGRESS BY THE NEW BRUNSWICK  
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**Keywords:** cross-pollinations, progeny tests, seed orchards

The tree improvement program conducted by the Province of New Brunswick (NB) is celebrating its 26<sup>th</sup> year of operation. Our efforts continue to focus on the main reforestation species: white spruce (*Picea glauca* (Moench) Voss), black spruce (*Picea mariana* (Mill.) BSP), and jack pine (*Pinus banksiana* Lamb.). Interest in planting tamarack (*Larix laricina* (Mill.) Karst.) has diminished substantially in the past several years largely as a result of the larch canker. Secondary species for tree improvement include balsam fir (*Abies balsamea* (L.) Mill.), Norway spruce (*Picea abies* (L.) Karst), and red spruce (*Picea rubens* Sarg.)

#### TREE BREEDING AND TESTING

The New Brunswick Department of Natural Resources & Energy (DNRE) is a member of the New Brunswick Tree Improvement Council (NBTIC), a group of cooperators including DNRE, the federal government, and eight large industrial companies located in NB. All tree improvement work in the province is co-ordinated by the NBDNRE and all co-operators share in the workload.

In the past three years, we have planted another series each of black spruce and jack pine progeny tests. There are over 300 families planted for each of these two species. Progeny testing is over 75 % complete. In 1999, a black spruce full-sib clonal test was planted, the first ever for NBTIC. Material was generated from 17 crosses within the elite sub-line. Cuttings were taken from the seedlings over a 2-year period until enough material had been produced to plant 4 tests, one ha each in size.

In 2000, both a jack pine and black spruce full-sib test were planted. These two test series came from full-sib crossing done within sub-lines established for each species. These tests will be used for making 3<sup>rd</sup> generation selections in 10 years. There should be enough seed from breeding conducted in 2000 to establish a full-sib test series for each species in 2001.

#### SEED ORCHARDS

All second generation selections have been identified for black spruce and jack pine, and in 1998, we began selecting second generation material for white spruce. These are being done in selection plantations. Sixty-five trees have been selected in the last two years from 46 different families. This will continue until we have made 400 or so selections.

In 1998, our white spruce clonal orchards were rogued again, removing another 9 clones, making a total of 27 clones removed out of 99 clones planted (27% removal). We are continuing to establish new

orchards. Table 1 summarizes orchard establishment for DNRE. A Norway spruce seed production area was also planted using seed originating from the Istebna area of Poland.

Table 1. Seed orchards established by DNRE

Species	Generation	Type	Establishment Year	Area (ha)
White spruce	1 <sup>st</sup> Gen.	CSO <sup>1</sup>	1985-1987	9.0
	1 <sup>st</sup> Gen. OV <sup>2</sup>	SSO <sup>3</sup>	1978-1982	8.6
	2 <sup>nd</sup> Gen.	CSO	2000	2.0
Black spruce	1 <sup>st</sup> Gen.	SSO	1980-1987	32.0
	2 <sup>nd</sup> Gen.	CSO	1989-1997	11.8
Jack pine	1 <sup>st</sup> Gen.	SSO	1979-1986	25.0
	2 <sup>nd</sup> Gen.	CSO	1992-1998	7.9
Tamarack	1 <sup>st</sup> Gen.	CSO	1984-1986	8.0
Balsam fir	1 <sup>st</sup> Gen.	CSO	1990-1992	2.7
Red spruce	2 <sup>nd</sup> Gen.	CSO	1999	2.0
Norway spruce	1 <sup>st</sup> Gen.	CSO	1999	2.0
	-	SPA <sup>4</sup>	1998	2.0

<sup>1</sup> clonal seed orchard <sup>2</sup> Ottawa Valley <sup>3</sup> seedling seed orchard <sup>4</sup> seed production area

#### CONE COLLECTION IN ORCHARDS

The second generation orchards are beginning to produce more and more cones. Below is a table showing the production from second generation orchards and also what we harvested from first generation orchards.

Table 2. Cone collection and seed yield from orchards from 1997 to 1999

Species	Orchard	1997		1998		1999	
		Cones (l)	Seed (kg)	Cones (l)	Seed (kg)	Cones (l)	Seed (kg)
Jack pine	1 <sup>st</sup> Gen.SSO	-	-	-	-	2 856	16.4
	2 <sup>nd</sup> Gen.CSO	246	1.2	763	5.3	1 181	7.95
Black spruce	1 <sup>st</sup> Gen.SSO	-	-	1 100	8.3	-	-
	2 <sup>nd</sup> Gen.CSO	200	.001	760	4.2	143	0.22
White spruce	1 <sup>st</sup> Gen.CSO	-	-	1 046	16.3	-	-
	1 <sup>st</sup> Gen.SSO	-	-	154	2.0	-	-
Balsam fir	1 <sup>st</sup> Gen.CSO	-	-	86	0.78	-	-

## TREE HEALTH AND WOOD FORMATION RESEARCH AT THE UNIVERSITY OF NEW BRUNSWICK

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**Keywords:** biochemistry, cambium, coniferin, dormancy, proteinases, tree health, wood formation

Research since 1996 has addressed fundamental questions of tree physiology in three categories: 1) the physiology of the healthy tree, 2) regulation of the annual cycle of growth and dormancy, and 3) regulation of wood formation biochemistry. The research has been supported primarily by the Natural Sciences and Engineering Research Council of Canada with minor support for graduate students from the Canadian Forest Service – Atlantic Forestry Centre.

Additional activities, not described further below, have included organizing in 1999 an international conference on the cell and molecular biology of wood formation, publishing the proceedings of that conference (Savidge *et al.* 2000), and establishment of the first plantation trials of *Ginkgo biloba* L. (China provenance) and *Castanea dentata* (Marsh.) Borkh. (Maine provenances) in northeastern New Brunswick.

### THE PHYSIOLOGY OF THE HEALTHY TREE

Past research into tree health has tended to focus on overt phenotypic symptoms displayed following insect and disease damage, or in response to acid rain and ozone. However, the health status of a tree is not unlike that of a human being. When outward symptoms indicating reduced resistance or tree decline have become obvious it is because hidden biochemical changes deleterious to normal healthy metabolism were activated earlier (Savidge 1997). Unless there is reliable technology in place for early detection of impending problems, remedial silviculture is limited to harvesting and cleaning, and there is no solid scientific basis for justifying when to harvest old growth. Our research has focused on identifying and indexing early-warning biochemical indicators diagnostic of reduced resistance and decadence, thus enabling differentiation between healthy and unhealthy trees. Progress has been summarized elsewhere (Steeves and Savidge 2000).

### REGULATION OF SEASONAL CAMBIAL GROWTH AND DORMANCY

Seasonal tree growth is normal to the temperate zones and has bearing not only on forest productivity but also on species fitness, particularly in relation to climate change and tolerance of out-of-season stresses. Our research is the first to identify an enzyme in perennial plants not at all present during dormancy but present throughout the growing period, pointing to a control mechanism at the level of gene expression (Förster *et al.* 1999; Savidge *et al.* 1998; Savidge and Förster 1998).

## REGULATION OF WOOD FORMATION BIOCHEMISTRY

There is a definite need in forestry to recognize the visible phenotype, whether it be forest, tree, log or individual fibre, for what it is; a biosynthetic end product manifesting genotype X environment interactions at the sub-cellular levels of catalysis and regulation. Current understanding of the biochemistry underlying cambial growth remains rudimentary for common end products such as cellulose, lignins and the hemicelluloses, and is almost non-existent for the substances engendering heartwood formation and resistance to insects and decay. Not until the non-visible determinants of growth, development and functioning in trees are well understood can a scientific basis for the management of wood supply, wood quality and forest ecosystem health be in place. Providing a solid scientific foundation is what we are trying to do in my research program (Forneris and Savidge 2000; Förster *et al.* 1998, 1999, 2000; Iliev and Savidge 1999, 2000; Leitch and Savidge 1999, 2000; Savidge *et al.* 1998; Savidge and Förster 1999).

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## ECOLOGY AND MANAGEMENT OF SEED AND CONE INSECTS

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Research on host-insect interactions, insect behavior, and population dynamics of the spruce cone maggots (*Strobilomyia neanthracina* Michelsen and *S. appalachensis* Michelsen) was conducted in collaboration with colleagues with Canadian Forest Service-Sault Ste. Marie, the University of New Brunswick and the British Columbia Ministry of Forests. Our main objective is to develop ecologically-based and environmentally sound methods of pest management, with emphasis on the cone maggots which can destroy >99% of spruce seeds in some years. Laura Fidgen (MSc, University of New Brunswick, 1999) quantified the influences of natural factors on the stage-specific survival of the black spruce cone maggot, *Strobilomyia appalachensis*. For this species, as well as *S. neanthracina* which attacks white spruce, mortality of larvae and pupae in the soil was high, chiefly due to arthropod predators (Fidgen *et al.* 1999; Sweeney *et al.* unpublished). This suggests that arthropod predators (e.g., ants, carabid beetles) should be conserved in seed orchards whenever possible. We also observed that rainfall triggered dispersal of cone maggots from cones to the soil and found that this behavior was adaptive and resulted in less larval death from predation and desiccation (Sweeney and Gesner 1999). Death from parasitism was variable and generally low (Fidgen *et al.* 1999) and the parasitoid species were very similar to those found for a sibling European species, *S. anthracina* (Brockhoff and Kenis 1997) suggesting that a classical biological control strategy would have little potential for success. Cone maggot survival was also significantly affected by size of the cone crop and its fluctuation from year-to-year. Competition among maggots increased when cones were sparse: as the number of larvae per cone increased, survival and pupal weight decreased (Sweeney and Quiring 1998). Cone fly egg-lay and seed consumption were greater in larger cones than in smaller cones (Fidgen *et al.* 1998; McCready and Sweeney 1999). The bias towards infesting larger cones results not only in greater survival of the maggot but also greater impact on spruce seed production because the number of viable seeds usually increase with cone size.

Studies in collaboration with Robb Bennett (B.C. Ministry of Forests) resulted in the first direct evidence for use of a host-marking pheromone by a cone fly (Quiring *et al.* 1998). The female cone fly uses her mouthparts to mark the surface of the cone following egg-lay; subsequent females are deterred from laying eggs in marked cones. This results in the cone flies spacing their eggs among the cones, thereby reducing larval competition (good for the maggot) but resulting in a greater number of cones infested than if egg lay were random or clumped (bad for seed production because 1 larva causes about 70% seed loss). The botanical insecticide, neem, was tested for control of cone maggot by stem-injection in white spruce and black spruce in 1998 and 1999, respectively. Despite good results with the application of neem by stem-injection techniques for control of sawflies and other defoliators on spruce (Helson *et al.* 1999), the neem did not provide adequate protection of spruce seed against maggot damage. Further testing with neem as a foliar application is planned for 2000.

Work on the impact of alternative silviculture treatments on the diversity and abundance of ground beetles began in 1999, in collaboration with John Major, Alex Mosseler and Tony Thomas (CFS-Atlantic) (Major *et al.* 1999). Preliminary results indicate that beetle species composition and richness differs significantly among silviculture regimes and that certain species are more sensitive to human impact than others.

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**FOREST GENETICS RESEARCH AT THE CANADIAN FOREST SERVICE -  
ATLANTIC FORESTRY CENTRE**

**R.F. Smith, J.M. Bonga, S.I. Cameron, M. Grant,  
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Research in forest genetics at the Atlantic Forestry Centre continues to be conducted under the aegis of several programs, most of which falls under two major networks, Biodiversity and Biotechnology. The following report focuses mostly on activities within the Biotechnology Network.

**PHYSIOLOGY AND GENETIC ENGINEERING OF WOOD FORMATION  
C.H.A. Little**

Research on hormonal control of shoot growth and enhancement of wood quantity and quality using genetic engineering continued in collaboration with personnel at: 1) Swedish University of Agricultural Sciences, Umeå, Sweden, 2) Växjö University, Växjö, Sweden, and 3) University of New Brunswick, Fredericton, NB.

Recent research on hormonal control of shoot growth has focused on the interaction of ethylene and gibberellins (GAs) with indole-3-acetic acid (IAA). It was demonstrated that, for elongating shoots of *Pinus sylvestris*: 1) both the shoot apex and the developing needle fascicles are major sources of the IAA present in the stem, whereas stem GAs originate primarily in the needle fascicles, 2) GAs and IAA are required for both shoot elongation and cambial growth, and 3) GAs act directly in the control of shoot growth, rather than indirectly through affecting the IAA concentration (Wang *et al.* 1997). Eklund *et al.* (1998) showed that neither latewood formation nor cambial dormancy in *Picea abies* stems was associated with decreased cambial region concentrations of IAA or oxygen. In 1-year-old shoots of *Abies balsamea*, the cambial region was the major source of endogenous ethylene and ethylene derived from ringing with Ethrel mobilized carbohydrates to the ringing site (Eklund and Little 1997, 1998). Cambial region ethylene evolution from *Abies balsamea* shoots was enhanced when compression wood was being formed and the enhancement was related to compression wood formation *per se* rather than the associated increase in cambial growth (Little and Eklund 1998, 1999). Enhanced ethylene production in stems of IAA-overproducing transgenic tobacco plants was associated with increased peroxidase activity and lignin content, as well as with altered lignin composition (Sitbon *et al.* 1999). Work was initiated on: 1) understanding how and where ethylene is metabolized in *Pinus sylvestris* shoots (Tiltu *et al.* 1998), 2) the possibility of using *Arabidopsis thaliana* as a model system for studying cambial development and function (MacDonald and Little 1998), and 3) the characterization of a cambial region-specific promoter in hybrid aspen shoots for future genetic engineering studies (Hertzberg *et al.* 1998; Johansson *et al.* 1998). Finally, reviews were prepared on: 1) altering growth and development in *Populus* using genetic engineering (Sundberg *et al.* 1997), 2) the roles of IAA, GA, ethylene, cytokinin, and abscisic acid in regulating the rate of cambial growth and the differentiation of xylem and phloem in conifer stems (Little 1999), and 3) progress was made in elucidating genetic mechanisms determining the identity of meristematic cells and the fates of their derivatives, current approaches for identifying and characterizing key genes and

promoters involved in these mechanisms, and genes known to have regulatory roles in the shoot and root apical meristems, particularly in *Arabidopsis*, which may also have relevance for the cambial meristem (Olsson and Little 2000).

#### SOMATIC EMBRYOGENESIS OF CONIFERS, STABILITY OF EMBRYOGENIC CLONES, AND CLONAL FORESTRY

Y.S. Park, J.M. Bonga and I. MacEacheron

Research on somatic embryogenesis (SE) of conifers includes eastern white pine (*Pinus strobus* L.), jack pine (*P. banksiana* Lamb.), and white spruce (*Picea glauca* (Moench) Voss). The purpose of this work is to develop and improve SE techniques to a level that is sufficiently advanced for implementation in operational clonal forestry programs.

Somatic embryogenesis initiation in eastern white pine was optimized by the manipulation of plant growth regulator (PGR) concentrations in the culture medium. Modified Litvay's medium supplemented with lower than routinely used PGR concentrations increased initiation of established embryogenic cultures from approximately 20 to 53%. The original developmental stage of zygotic embryos had a great effect on SE induction. The optimum stage was the pre- to shortly post-cleavage stage. A substantial genetic influence on initiation of SE was indicated by a significant variance component due to families. Genotype x collection date and genotype x media interactions had a large influence on initiation of SE. The PGR levels in the culture medium prior to maturation had a significant effect on the subsequent production of mature somatic embryos. Embryogenic tissue initiated and proliferated on medium with a low level of PGR consistently produced a high number of somatic embryos, indicating that optimized initiation protocol also enhanced somatic embryo production. Somatic embryos of 93 embryogenic lines (representing 5 families), that were initiated on media with different PGR concentrations, were converted to plants at an overall frequency of 76% and grown in the greenhouse. With improved protocols, application of *P. strobus* SE in commercial clonal forestry is feasible as an alternative to traditional seed orchards.

SE on jack pine continued, but the species is still recalcitrant for SE induction. Since the initial success in 1995 (Park *et al.* 1999), we were unable to obtain SE in two subsequent years. However, progress has been made during 1998 and 1999 by obtaining 14 and 40 new clone lines, respectively. This represents less than a 1% induction rate, which is too low for operational programs at this time.

As a complimentary part of a study examining genetic stability of cryopreserved clones based on developmental and morphological traits (Park *et al.* 1998), trees were regenerated from six white spruce embryogenic clones after cryopreservation for 3 and 4 years. Genetic stability was evaluated using randomly amplified polymorphic DNA (RAPD) fingerprints. Somaclonal variation was detected in some *in vitro* embryogenic cultures 2 and 12 months after they were re-established following cryopreservation, but not in the corresponding regenerated trees. These results suggest that trees regenerated from cryopreserved cultures in subsequent years are primarily genetically stable in the genomic regions tested and variation observed due to the *in vitro* culture process rarely affects trees regenerated from normally maturing and germinating somatic embryos. However, trees regenerated from somatic embryos that matured or germinated abnormally in *in vitro* culture exhibited altered RAPD fragment patterns (DeVerno *et al.* 1999).

#### CONIFER REPRODUCTIVE BIOLOGY

Ron Smith and Laurie Yeates

Research within the conifer reproductive biology project continued to focus on both the physiological and molecular components of cone initiation and development. Trials to induce flowering on young (<5 year-old) putatively transformed black spruce emblings that had been grown under various accelerated growth regimes were unsuccessful in that none of the trees produced any reproductive structures. Preliminary conclusions from this work indicate that these transformed emblings did not exhibit the precocious

flowering often observed in herbaceous species following transformation with similar, e.g., homologous, genes.

Results from cone induction trials using GA and Paclobutrazol were published (Smith 1998) and the results were used to initiate additional field and greenhouse trials. These follow-up trials were established to provide the materials required for a new study on the molecular characterization of developing black spruce meristems.

#### GENETICS OF GROUND HEMLOCK (*Taxus canadensis*)

Stewart Cameron, Ron Smith and Laurie Yeates

Yew species throughout the world, contain a family of compounds called taxanes. First discovered in the bark of Pacific yew (*Taxus brevifolia* Nutt.), several of these taxanes are now in considerable demand for the production of anti-cancer drugs, the best known of these being Taxol<sup>®</sup>. The high value and significant demand for these compounds has resulted in considerable harvesting pressure on yew species worldwide. Demand for yew biomass has recently expanded to include ground hemlock (*T. Canadensis* Marsh.).

Ground hemlock is a wide-ranging but not overly abundant woodland understory shrub. It can occur in large populations but it is just as likely to be found as isolated plants or in small, widely spaced groups of plants. The ecological importance of ground hemlock as a food source for many wildlife species is well documented. The shrub also produces significant amounts of paclitaxel (active ingredient in Taxol<sup>®</sup>) and several other taxanes, thereby making ground hemlock a potentially valuable commercial resource as well. Although *T. canadensis* occurs across the northern USA and from Ontario eastward, there are no good inventory data on plant populations in any province (Ontario, Québec, New Brunswick, Nova Scotia, and Newfoundland) except Prince Edward Island. Consequently, no information exists on the impact of biomass collection, timber harvesting, or land conversion, which are presumed to be the main threats to *Taxus* abundance. Given that relatively little is known about the biology, ecology or genetics of ground hemlock, and in order to try to help avoid potential over-harvesting from wild populations, CFS-Atlantic initiated a genetics program for ground hemlock in 1997.

This program is comprised of studies in: 1) quantifying levels of genetic variation, 2) developing/refining propagation techniques, and 3) increasing taxane yields from selected genotypes.

During the past three years, approximately 1 200 clones from over 350 locations throughout the natural range of *T. canadensis* have been sampled. We have had the cooperation of over 40 individuals and agencies in, among other things, finding sampling sites, facilitating contacting landowners, and assisting in sampling. Rooted cuttings from these 1 200 clones are being grown in our nursery and will be used to establish a series of range-wide nursery provenance trials. The first of these trials is scheduled for outplanting in the spring of 2001.

Nursery and greenhouse studies have also been conducted. Preliminary estimates of the levels of genotypic variation in traits such as rooting percentage, biomass - root and shoot growth, gas exchange properties (photosynthesis and respiration), and capacity for free growth, have been obtained. Work is also underway to quantify levels of variation in taxane production among clones and to optimize existing tissue culture methodologies, e.g., somatic embryogenesis and/or organogenesis.

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**BIODIVERSITY RESEARCH AT CANADIAN FOREST SERVICE -  
ATLANTIC FORESTRY CENTRE, 1997-2000**

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**Keywords:** climate change, adaptation, genetic diversity, cold hardiness, drought tolerance, elevated CO<sub>2</sub>, G x E, *Picea mariana*, *Picea rubens*, hybrids, *Pinus rigida*, provenance, genetic variation, ecological restoration, population viability, gas exchange, water relations, allometry, adaptive traits, inbreeding, fitness, gene conservation, *Quercus macrocarpa*, *Fagus grandifolia*, *Tsuga canadensis*, *Juglans cinerea*, National Tree Seed Centre, seed certification

**RED SPRUCE ECOSYSTEM BIODIVERSITY PROJECT  
John Major, Alex Mosseler, Debi Barsi and Moira Campbell**

In 1999, a large 60 ha silvicultural impact test was established at the Acadia Research Forest (ARF) to demonstrate the impacts of various forest harvesting regimes on biodiversity in general and on the maintenance of long-lived, shade-tolerant, late-successional species such as red spruce (*Picea rubens* Sarg.) in particular. Research on this site involves a multi-disciplinary approach where geneticists, entomologists, ecologists, and silviculturists are studying various aspects of harvesting impacts on biodiversity conservation. This larger biodiversity study provides the context for assessing a range-wide genetic sample of red spruce.

**RED SPRUCE RESTORATION  
Alex Mosseler**

Work on red spruce continued with a focus on development of a set of reproductive and genetic indicators for monitoring population viability and status. A second and more recent focus has been on red spruce dominated old-growth forest: its status and value with respect to conservation of genetic resources. With regard to the latter, the Canadian Forest Service (CFS) is sponsoring a national conference in October 2001 on "*Old growth forests in Canada: a science perspective*" which we hope will help guide the forest sector with respect to policy development on old-growth forests and their role in biodiversity conservation.

The CFS-Atlantic Forestry Centre organized seed collections across much of the Canadian range during the good cone crop of 1996 to assess the reproductive and genetic status of red spruce across the northern margins of its geographic range. In 1999, with collaboration from the Ontario Ministry of Natural Resources (OMNR), a sample of 120 red spruce seedlots (12 trees from 10 natural populations) from across the Canadian range was established at the GURD Tree Improvement Area south of Lake Nipissing, Ontario. This test was established under a thinned red pine (*Pinus resinosa* Ait.) plantation, to serve as a nurse crop, and on an adjacent clear-cut to demonstrate the effects of shelter on red spruce survival and growth. Tembec Inc. appears poised to take control of the former OMNR GURD Tree

Improvement Area and is now investing its resources to rehabilitate this area as a repository of forest genetic resources. Tembec Inc. recently funded a second round of strip thinning of red pine plantations on this site to prepare a nurse crop for another series of red spruce underplanting tests aimed at developing an enhanced red spruce gene pool or seed source for restoration purposes.

A similar genetic test was established in 1999 on the ARF near Fredericton, New Brunswick in a large scale, 60 ha silvicultural study aimed at demonstrating the effects of retention forestry systems on red spruce survival and growth. This test included four treatments: control, clear cut, selection cut, and strip cut) replicated twice on two different sites within the ARF.

Range-wide red spruce provenance tests, established across eastern and central Canada by the CFS 40 years ago, were measured for height and diameter following recent thinnings. Cones were collected from the test at the Petawawa Research Forest in 2000 to assess both growth performance and aspects of reproductive fitness. These tests will be managed and maintained as seed sources for restoration of red spruce in Ontario.

## GENETIC DIVERSITY AND REPRODUCTIVE SUCCESS

Alex Mosseler

Work continues on conservation of the native Canadian gene pool of pitch pine (*Pinus rigida* Mill.). Several Canadian range-wide genetic tests have been established in collaboration with OMNR staff in eastern Ontario and in connection with the Southern Ontario Forest Gene Conservation Association.

## MOLECULAR GENETICS

Alex Mosseler and John Major

One of the most significant events for tree improvement and genetics in the Maritimes has been the recent establishment of the STORA/ENSO Chair for Forest Genetics and Biotechnology in the Biology Department at Dalhousie University, Halifax. Dr. Om Rajora, formerly with the University of Alberta, was the successful candidate for the Senior Chair. Collaboration with Om Rajora and Dalhousie University continues in several areas, including: 1) red spruce and black spruce genomics, 2) micro-satellite marker development, and 3) genetic diversity studies of red spruce and pitch pine. The collaboration recently culminated in the awarding of a NSERC Strategic Grant aimed at "Genome and QTL mapping of traits related to growth and adaptation to climate change in black spruce".

## ADAPTIVE GENETIC VARIATION AND RESPONSE TO CLIMATE CHANGE

John Major

Greenhouse gas levels are expected to double during this century and alter prevailing environmental conditions, which alters physiological components of tree productivity. It was hypothesized that there would be significant species X genotype interactions with the projected climate change. A number of studies have been conducted to examine the potential importance of species and genetic x atmospheric CO<sub>2</sub> and genetic x soil drought interactions in black spruce (*Picea mariana* (Mill.) BSP), red spruce, and their hybrids using seed sources from across their sympatric range (Ontario, New Brunswick, and Nova Scotia). Significant results for instance, show that freezing vulnerability increases under elevated CO<sub>2</sub> conditions and that red spruce seems particularly susceptible to damage. Also, red spruce allocates 40% more biomass to roots than black spruce.

## BUR OAK

Judy Loo and Donnie McPhee

A bur oak (*Quercus macrocarpa* Michx.) project on gene conservation and restoration was completed in 2000. Bur oak is an uncommon species in New Brunswick with a small and declining distribution. We conducted a survey to determine how the present distribution compares with the species distribution in the published literature. The survey revealed that much of the original range within the province is now devoid of the species and those populations that remain tend to be threatened because of cottage development, pasturing, or road building.

New Brunswick populations of bur oak are at least 230 km distant from the nearest isolated population in Maine and 750 km from the edge of the continuous range. Thus small and shrinking populations in New Brunswick were considered to be genetically vulnerable. An isozyme study was undertaken to assess the genetic diversity in New Brunswick populations relative to that of other isolated populations, fringe populations on the edge of the range, and populations occurring well within the species range.

The analysis indicated that the populations in New Brunswick, though small and threatened by human activities, have maintained levels of genetic diversity that are comparable to those of populations within the continuous range. There was no evidence of unique alleles within the New Brunswick populations, implying that the isolation is relatively recent.

A concurrent test involved establishing restoration plantings in areas where bur oak might have been expected to occur prior to the landscape level disturbances over the past 200 years. Bur oak seed was successfully stored over the winter and germinated under greenhouse conditions. Outplanting was carried out in two successive years, and except for an area that unexpectedly became a pasture, survival of seedlings in the field has exceeded 90%.

## BEECH RESTORATION

Judy Loo

A second project, undertaken by graduate student Jamie Simpson, during the past two years involves putative resistance to beech bark disease (*Nectria coccinea*). We are searching for a vegetative propagation procedure that will allow us to establish a "source material orchard" for potential restoration efforts. Almost all the beech (*Fagus grandifolia* Ehrh.) in the Maritime provinces is heavily damaged by beech bark disease which is caused by an exotic fungal pathogen which only occurs in association with a scale insect (*Cryptococcus fagisuga*). There are indications that occasional disease-free trees, found in heavily diseased stands, are resistant to the scale insect that transports the disease. We are locating disease-free trees in diseased stands in southern New Brunswick for vegetative propagation trials. We are attempting three propagation methods: tissue culture using buds, forced suckering from severed roots in a greenhouse, and rooting cuttings taken from suckers. Limited success has been achieved with both the tissue culture and the suckering from severed roots and we have not yet had plants survive through a winter dormancy period.

## HEMLOCK

Judy Loo, Kathleen Forbes, and Donnie McPhee

A new project undertaken in 2000 is an isozyme survey of twelve old hemlock (*Tsuga canadensis* (L.) Carrière) stands in the Maritime provinces. The purpose of the study is to compare levels of genetic diversity between old trees in the stands scattered across the Maritimes and young regenerating trees in the understory. Regeneration is frequently identified as a problem in old hemlock stands. Often it is scattered in small isolated patches within the stands. Our hypothesis is that the level of genetic diversity

remains at a healthy level on the old cohort but genetic diversity is reduced in the younger cohort due to increased isolation among stands and reduced regeneration success within the stands.

### BUTTERNUT CONSERVATION

Tannis Beardmore, Kathleen Forbes and Garry Scheer

Butternut (*Juglans cinerea* L.) trees produce recalcitrant seed and the recommended storage conditions are temperatures of +5 to -5°C under high relative humidities (i.e., 80–90%), with viability ranging from 6 months to 2 years. Butternut survival in North America is threatened by the fungus *Sirococcus clavigignenti-juglandacearum*. To date, there is no control for this fungal disease and long-term seed storage, to ensure survival of the species, is not a viable option. We have developed methodologies for the long-term cryogenic storage of butternut embryonic axes and have initiated, in 2000, a long-term cryogenic storage experiment using butternut embryonic axes from one New Brunswick population. In addition, we are trying to elucidate the biochemical mechanism(s) that are responsible for the development of the embryonic axes' increased tolerance to low (i.e., -10 and -20°C) and cryogenic (-196°C) temperatures. Our results suggest that cryogenic storage of embryonic axes may be a viable method for butternut *ex situ* conservation.

The ad hoc group, New Brunswick Gene Conservation Working Group, has identified butternut as requiring specific gene conservation measures based on three factors: 1) there is no or an uncertain seed source, 2) there is a serious threat from disease (butternut canker), and 3) the frequency of the species is decreasing. However, we do not possess the knowledge required to develop an effective *ex* and *in situ* conservation strategy at this time. As members of the ad hoc group, we are in the process of examining a number of factors which must be addressed before a butternut conservation strategy can be produced. These factors are to: 1) Identify butternut populations in New Brunswick (NB). A summary report identified a large number of locations based on data from several sources. 2) Assess the prevalence of butternut canker in NB and estimate mortality due to the canker. Assessment of NB populations will also allow for identification of putative resistant butternuts. 3) Examine the genetic diversity of NB butternuts. There is concern that there may be a hybrid component (based on nut morphology) in some NB butternut populations. Before we develop an *ex situ* conservation program, we need to determine which trees/populations have a hybrid component. Also, assessing the genetic variation in NB butternut populations will allow us to preserve material that best represents the existing genetic variation.

### NATIONAL FOREST GENETIC RESOURCES CENTRE

Dale Simpson and Bernard Daigle

The Centre consists of three sections: National Tree Seed Centre, OECD seed certification, and genetics experiment databases.

Seed Centre staff have been very active and productive since the Centre was transferred from the Petawawa Research Forest in 1996. Staff are comprised of one full-time technician supplemented with a summer student and occasional casual help. Activities have focused on collecting/acquiring seed, germination testing, providing seed as per requests, and developmental research. Since 1996, almost 500 seedlots have been collected, about 1 000 seedlots acquired, over 2 500 germination tests conducted, and 1 800 seedlots provided for research. Collections have focused on species in the Maritime provinces while acquisitions have consisted of donations by provincial governments from across Canada. This has resulted in a stronger inventory of native species. The intent is to store samples from throughout the ranges of as many native tree and major shrub species as possible. Work is in progress on expanding the *ex situ* conservation collection. This includes seedlots from endangered, threatened, and unique populations as well as other seedlots exhibiting high viability. Germination testing is focusing on eliminating the backlog so information will be current for most all species. Germination test data have been evaluated for a number of species and curves developed in an effort to evaluate long-term storage

potential and to develop testing frequencies. Several undergraduate forestry students completed theses. Red oak (*Quercus rubra*) acorns stored in mason jars without peat germinated best after 12 months in storage at 4° C (Burry 1999) however after 18 and 24 months acorns stored in mason jars with peat germinated best. Removal of the pericarp significantly improved germination of 22-year-old white ash (*Fraxinus americana*) seed stored at 4° C and -20° C (Knox 2000). A storage experiment was initiated for pussy willow (*Salix discolor*), Bebb willow (*S. bebbiana*) and red-topped willow (*S. eriocephala*). Seed of each species at two moisture contents was stored at four temperatures (4° C, -20° C, -80° C and -196° C). After 12 months germination has declined the most for seed stored at 4° C. A catalogue listing seedlots available upon request for research was published in 1998 (Simpson and Daigle, 1998). A cryogenic facility is managed to store plant tissue for conservation and research purposes.

Canada is one of 21 countries participating in the "OECD Scheme for the Control of Forest Reproductive Material Moving in International Trade." The CFS is the designated authority of the Government of Canada for the administration of the Scheme. The Scheme is applied to seed which is sold primarily to European countries. Seed from natural populations, principally from British Columbia, is certified as to provenance. In order for seed to be certified, a representative from CFS must inspect the collection operation and extraction/cleaning of the seed to ensure standards are maintained. When the inspector is satisfied all procedures have been properly followed certificates and labels are issued. The labels are attached to the sealed containers of seed and a certificate accompanies each seedlot that is sold. The process protects the purchaser by guaranteeing the authenticity of a seedlot. A new scheme was developed in the mid 1990's but unfortunately its unanimous approval has been delayed due to inclusion of genetically modified organisms.

A database of genetics experiments established by CFS in the Maritime provinces was completed. It contains information for each experiment such as species, year and location planted, experimental design and layout, and maintenance and measurement activities. This complements a similar database for the Petawawa genetics program. It is hoped to have these databases online.

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## AMÉLIORATION GÉNÉTIQUE DES ARBRES FORESTIERS À LA DIRECTION DE LA RECHERCHE FORESTIÈRE

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### AMÉLIORATION GÉNÉTIQUE DU PIN GRIS, DU PIN LODGEPOLE, DU PIN SYLVESTRE ET DU PIN PONDEROSA Roger Beaudoin

Les éclaircies génétiques des vergers de semis de pin gris (*Pinus banksiana* Lamb.) et de certains tests de descendance se sont poursuivies en 1997 et 1998. Des prescriptions d'éclaircie ont été faites en 1997 pour trois vergers et un test de descendance, en 1998 et 1999 pour deux tests de descendance. Jusqu'à ce jour, 10 des 12 vergers établis ont été éclaircis de même que quatre tests de descendance. Les gains génétiques calculés en hauteur à 10 ans pour des variétés issues des vergers et des tests éclaircis varient de 1,9 à 5,5 % lorsque les graines sont récoltées sur l'ensemble des descendance conservées dans le verger.

Dans le but de délimiter le territoire d'utilisation des semences des vergers à graines de première génération et d'autres sources recommandées, nous avons testé la fiabilité du modèle de transfert de Máttyás et Yeatman (1992), à partir de tests de provenances et de descendance réalisés au Québec. Le modèle semble assez fiable et nous comptons l'utiliser pour délimiter le territoire d'utilisation des semences de pin gris.

L'éclaircie génétique d'un test de provenances de pin lodgepole (*Pinus contorta* Dougl.) a été faite en 1997. Des données ont été prises sur les dégâts causés aux arbres, sur certains sites, par le nodulier du pin gris (*Petrova albicapitana* (Busck)) et le nodulier du pin (*Synanthedon pini* (Kellicott)). L'accroissement en hauteur des arbres dominants, dans trois tests de provenances de pin lodgepole, a été comparé à celui de l'épinette de Norvège (*Picea abies* (L.) Karst). Sur certains sites, l'accroissement en hauteur après 20 ans est semblable pour les deux espèces.

L'éclaircie génétique d'un verger à graines de semis de pin sylvestre (*Pinus sylvestris* L.) a été réalisée en 1999. L'identification et la description de symptômes de perte de dominance apicale ont été menées sur plusieurs sites. Des analyses foliaires et pédologiques ont été faites ainsi que l'examen microscopique d'aiguilles afin de confirmer l'hypothèse que la perte de dominance apicale, qui cause la mauvaise forme de l'arbre, serait principalement attribuable à une déficience en bore dans le sol.

L'évaluation de quelques provenances de pin ponderosa (*Pinus ponderosa* Laws.) a été réalisée à l'âge de 12 ans sur trois sites d'expérimentation ; les résultats ont été publiés en 1997 (note de recherche forestière n° 79). Le territoire d'utilisation se situe dans la partie sud du Québec. Nous émettons l'hypothèse que les provenances situées dans la partie Nord de l'aire de distribution du pin ponderosa (Colombie-Britannique) donneraient un meilleur rendement que celles déjà introduites.



## SÉLECTION D'ARBRES FEUILLUS POUR LEUR RÉSISTANCE AUX MALADIES

Marie-Josée Mottet

**Mots-clés:** *Populus*, *Septoria musiva*, chancre septorien

Depuis 1986, en plus des observations en plantation, la méthode employée pour évaluer la sensibilité des clones et semis de peuplier au chancre septorien (*Septoria musiva* Peck) consiste à inoculer artificiellement le pathogène en pépinière. En 1999, plus de 400 nouveaux clones ont été testés en pépinière. Dans le but d'évaluer l'expansion potentielle de cette maladie dans d'autres régions, un dispositif expérimental a été établi au printemps 2000 afin de mesurer la capacité de *S. musiva* à se développer dans le domaine bioclimatique 3. De plus, des études ont été entreprises sur l'insolation hivernale afin de préciser les facteurs environnementaux impliqués et de développer une méthode pour sélectionner plus rapidement des clones résistants.

## AMÉLIORATION GÉNÉTIQUE DE L'ÉPINETTE BLANCHE

Marie-Josée Mottet et André Rainville

Le programme d'amélioration génétique de l'épinette blanche est divisé en trois volets. Le premier vise à déterminer la valeur génétique des clones présents dans les vergers à graines de première génération. Le second constitue le cœur du programme d'amélioration: le matériel sélectionné dans les tests de provenances et de descendances de la première génération est utilisé dans des croisements dirigés pour développer les générations futures. Le troisième volet est exploratoire et vise à développer des variétés hybrides entre l'épinette blanche et d'autres espèces d'épinette.

Dans le premier volet, la mise en place de tests de descendances reliés aux vergers à graines de première génération se poursuit. Entre les années 1998 et 2000, 18 tests reliés à six vergers à graines ont été établis dans les différentes régions reboisées avec cette espèce. On prévoit finaliser l'installation des tests des trois derniers vergers à tester d'ici trois ans. Pour le premier verger évalué (Wendover), les résultats du test précoce âgé de trois ans ont permis de faire un classement préliminaire des clones. De plus, pour répondre au besoin en sources de semences adaptées aux régions plus nordiques, trois tests de provenances ont été installés en 1999 dans le domaine bioclimatique 6.

Dans le second volet, 35 arbres ayant des valeurs en croisements nulles ont été reproduits par greffage pour servir de géniteurs dans les croisements dirigés visant à évaluer l'aptitude générale à la combinaison (AGC) des arbres sélectionnés dans les prochaines générations. Les 1 000 greffes produites ont été plantées au printemps de 1999 dans la pépinière de la Station forestière de Duchesnay.

Les 3 000 greffes plantées au même endroit en 1996 ont été cultivées en 1998 et 1999 ; elles représentent 460 arbres sélectionnés dans les tests de descendances uniparentales des années '70-'80 et serviront de géniteurs pour développer le matériel de la prochaine génération d'amélioration. Dans la même période, des carottes de bois ont aussi été prélevées sur la majorité des arbres sélectionnés dans les tests afin de déterminer la densité du bois, et permettre ainsi de réduire la population d'arbres sélectionnés à 240.

Les cinq tests de descendances établis en 1997, issus d'un test de croisements multiples entre les 100 premiers arbres sélectionnés par le SCF, ainsi que les deux plantations de sélection établies en 1996, issues de croisements dirigés biparentaux entre ces mêmes 100 arbres, ont été mesurés à l'automne de 1998. L'analyse des données est en cours.

Au printemps de 1999, on a complété ces deux dernières plantations de sélection par l'ajout de nouvelles descendances biparentales. On a aussi procédé à l'installation d'un troisième test, constitué du même matériel, dans la région de Matane (canton Asselin).

Dans le troisième volet, deux tests ont été établis en 1998 avec des descendances issues des croisements effectués entre l'épinette blanche locale et d'autres espèces comme l'épinette blanche de l'Ouest et l'épinette de Sitka.

### AMÉLIORATION GÉNÉTIQUE DU PEUPLIER

Pierre Périnet

**Mots-clés:** *Populus*, hybridation, croisement, test clonal, test de descendances

Dans le contexte du rendement accru, les arbres à croissance rapide peuvent contribuer à l'augmentation de la productivité forestière. Au cours des dernières années, l'industrie forestière, particulièrement celle des panneaux OSB qui est en plein essor, continue de s'intéresser à la plantation de peupliers hybrides. La récolte d'arbres de plus de 20 ans dans un test à Saint-Ours permettra au laboratoire Forintek d'étudier les caractéristiques de plusieurs clones de peupliers hybrides (*Populus* spp.) pour la fabrication de panneaux.

En 1998, des croisements artificiels ont été réalisés en serre pour la région du Bas-Saint-Laurent-Gaspésie produisant plus de 25 000 semis répartis dans 287 croisements entre des espèces et hybrides des sections *Leuce*, *Aigeiros* et *Tacamahaca*. Les plants obtenus seront établis en trois tests de descendances au printemps 2000. De plus, une soixantaine de croisements d'hybridation intraspécifique ont été réalisés *in situ* chez le peuplier deltoïde (*Populus deltoides* Bartr. ex Marsh.).

En 1998, cinq tests clonaux ont été établis à La Sarre, Cabano, Lac des Pins, Godmanchester et Val-Brillant et une plantation de démonstration à Dablon. En 1999, seize tests de collection ou d'introduction ont été établis dans les cantons de Packington, Tessier et Jetté au Bas-Saint-Laurent. Deux tests clonaux ont été plantés en Estrie et dans l'Outaouais et un test au Lac-Saint-Jean.

Depuis 1969, plus de 4 000 clones ont été évalués dont 2 760 sélectionnés dans des tests de descendances ou de provenances, 575 en peuplement naturel et 759 introduits principalement d'Europe et d'Ontario. De plus, 80 tests de provenances et de descendances et 108 tests clonaux ont été mis en place au Québec. Plus de 7 800 croisements ont été tentés dont 1 381 ont donné au-delà de 129 000 semis. Une cinquantaine de clones de peuplier hybrides sont maintenant recommandés pour les différentes régions écologiques du Québec et multipliés dans les pépinières de Forêt Québec.

### AMÉLIORATION GÉNÉTIQUE DES FEUILLUS À BOIS NOBLE

André Rainville

**Mots-clés:** Amélioration génétique, croisements dirigés, feuillus nobles, sélection d'arbres, greffage

Pour le chêne rouge (*Quercus rubra* L.), à l'automne de 1998, on a mesuré quatre des cinq tests de provenances-descendances plantés en 1993 et comprenant des provenances de toute l'aire de distribution du chêne rouge au Québec. Les données ont été analysées et les résultats seront publiés. À l'automne de 1999, on a mesuré les trois tests établis en 1995 avec des provenances américaines (ce qui en restait après le gel en pépinière). Finalement, toujours en 1999, on a réalisé des tailles de formation et procédé à une évaluation de leur effet sur la qualité des arbres et sur l'expression du potentiel génétique dans deux tests établis en 1993.

Chez le frêne blanc (*Fraxinus americana* L.), on a récolté les semences de 65 arbres à l'automne de 1998, représentant une quinzaine de provenances du Québec, et d'une quinzaine d'arbres en 1999; elles serviront à l'établissement de tests de provenances-descendances de l'espèce. On a procédé à leur stratification à la pépinière de Berthierville durant l'hiver 1999-2000. À l'automne de 1998, on a converti

une plantation de conservation située à Saint-Ours en verger à graines après identification du sexe des arbres. Finalement, on a analysé en 1998 les mesures prises à l'automne de 1996 dans les trois tests de provenances de frêne de Pennsylvanie (*Fraxinus pennsylvanica* Marsh.) (provenances de l'Ontario surtout) âgés de 10 ans, et situés à Lotbinière, La Patrie et Rigaud. Les résultats seront bientôt publiés.

Aucun nouvel essai de croisement dirigé entre le bouleau jaune (*Betula alleghaniensis* Britt.) et le bouleau à papier (*B. papyrifera* Marsh.), avec la technique du pollen mentor et du pollen pionnier, n'a été réalisé. Les arbres des deux tests de descendance établis en 1996 à La Tuque, sur terrain forestier, ont par contre été mesurés; les données seront analysées en 2000, et les résultats publiés. Chez le bouleau à papier, le titulaire a collaboré à une revue de littérature sur l'espèce, réalisée pour le compte de l'IQAFF, ce qui a permis de bien camper la stratégie d'amélioration. Finalement, des observations ont été prises sur la forme et la croissance de descendance issues de croisements dirigés, établies à Saint-Germain de Grantham.

Les travaux réalisés chez les espèces de deuxième priorité se limitent au noyer cendré (*Juglans cinerea* L.) et à l'érable à sucre (*Acer saccharum* Marsh.). Pour la première, les inspections phytosanitaires ont été faites à nouveau en 1998 et 1999 dans les quatre plantations de conservation de noyer cendré établies en 1996; les analyses sont en cours et la compilation des résultats des quatre dernières années sera publiée en 2000. En 1998 et 1999, on a également procédé à des essais de contrôle des populations de mulots dans quatre plantations d'érable à sucre, avec la collaboration de Denis Robitaille (sylviculture des plantations de feuillus).

## AMÉLIORATION GÉNÉTIQUE DE L'ÉPINETTE NOIRE

Michel Villeneuve

Au cours des trois dernières années, les grandes orientations de recherche se sont maintenues. La voie clonale est toujours en développement avec l'implantation de nouveaux dispositifs expérimentaux: six tests dont les plants sont issus de bouturage (144 clones) ou d'embryogenèse somatique (55 clones) ont été mis en terre. Huit autres dispositifs expérimentaux (croisements dirigés pour le programme d'amélioration, étude des idéotypes de cimes étroites, plan factoriel et hybridation entre *Picea mariana* (Mill.) B.S.P. et *P. rubens* Sarg.) ont été installés.

Neuf nouvelles prescriptions d'éclaircies génétiques de vergers à graines ont été produites. Les gains en hauteur calculés varient de 2,6 % à 9,5 %. L'intensité de l'éclaircie est encore limitée par l'objectif de production de graines de chaque verger.

Nous avons commencé à sélectionner des individus d'élite dans les tests de descendance de 1<sup>re</sup> génération, afin de constituer de nouveaux vergers à graines et de mettre en place les populations d'amélioration pour la génération suivante. Des boutures sont prélevées en juillet sur les arbres sélectionnés afin de les multiplier. Trois zones d'amélioration ont été couvertes; les deux dernières seront faites en 2000 et 2001. Les clones d'élite donnent un gain moyen de croissance en hauteur de l'ordre de 20 %.

Certains tests précoces en pépinière ont été conservés et éclaircis systématiquement; ils servent à diverses fins, dont des études sur la reproduction et la réalisation de croisements F2 ou de rétro-croisements dont le pedigree sera connu sur trois générations.

AMÉLIORATION GÉNÉTIQUE DES MÉLÈZES (*Larix* spp.) ET  
DE L'ÉPINETTE DE NORVÈGE  
Ante Stipanovic

**Mots-clés:** éclaircie génétique, croisement dirigé, tests de descendance, tests de provenances

Une nouvelle étude concernant l'introduction de mélèzes sur différents sites (sol sableux, sol argileux) en Abitibi a été mise en marche en 1998. Dix-huit provenances composées de mélèze d'Europe, de Sibérie et d'hybrides MEU x MEJ sont incluses dans cette étude.

Onze nouveaux tests de descendance ont été installés durant les trois dernières années, dans le but d'évaluer les qualités génétiques des arbres semenciers dans les vergers à graines ou des arbres géniteurs utilisés pour les croisements dirigés. Les prescriptions ont été réalisées pour l'éclaircie génétique dans le verger à graines de mélèze laricin de Rémigny (Abitibi). Un gain génétique en volume de 2,5% est calculé à partir des données de dix ans recueillies dans trois tests de descendance qui accompagnent ce verger à graines. Le faible gain génétique est dû à la nécessité de garder un nombre suffisant de semenciers pour satisfaire les besoins en production de graines. Les éclaircies génétiques ont été pratiquées aussi dans quatre autres tests de descendance de mélèze d'Europe, afin de les transformer en sources de graines génétiquement améliorées.

En 1998, nous avons effectué une pollinisation par polymix des clones de mélèze d'Europe dans notre verger expérimental sous abri. Nous avons obtenu 23 descendance qui permettront d'évaluer l'AGC de clones de mélèze d'Europe sélectionnés pour la deuxième génération d'amélioration. Le même travail a été effectué au printemps 1999 sur les clones sélectionnés de mélèze du Japon. En même temps, cinq nouveaux croisements spécifiques entre le mélèze d'Europe et le mélèze du Japon ont été réalisés. Les graines obtenues en 1998 et 1999 ont été semées et les tests sont planifiés pour l'année 2001 et 2002. Seize descendance originaires du verger à graines «Unity», propriété de la compagnie «Plum Creek» (Maine, USA), ont été ajoutées aux descendance obtenues en 1998. Cette collaboration permettra l'échange de résultats qui serviront à déterminer la zone d'utilisation des graines et les performances génétiques des clones sélectionnés, utilisés dans les vergers à graines.

Le projet d'amélioration génétique d'épinette de Norvège se déroule en étroite collaboration avec M. Gaëtan Daoust du Service canadien des forêts. Ainsi, une étude qui englobe près de 250 descendance a été mise en marche avec l'installation de neuf tests dans trois zones d'amélioration. Les premiers résultats obtenus par l'analyse des données de cinq tests indiquent un gain génétique pour la croissance en hauteur de 10 à 23%.

Une série de trois tests composés de 200 familles issues de croisements dirigés a été mise en marche en 1997. Les dispositifs, installés au printemps 2000, permettront de sélectionner des arbres pour la prochaine génération d'amélioration de l'épinette de Norvège.

Deux études, dont le but est d'évaluer la rusticité de certaines provenances et leurs performances en forêt boréale, ont été mises en marche en 1998 et 1999 en collaboration avec la région 02 de Forêt Québec et la Commission scolaire Harricana d'Amos. Une étude similaire incluant aussi les sources de graines d'épinette blanche a été initiée au printemps 2000 en collaboration avec la compagnie Cartons Saint-Laurent.

La collaboration efficace entre les deux organismes se poursuit aussi dans le domaine de la pollinisation dirigée des clones sélectionnés et la production de variétés d'épinette de Norvège dont la résistance au charançon de pin blanc est améliorée.

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## **RECHERCHE ET DÉVELOPPEMENT SUR LA REPRODUCTION DES ARBRES AU QUÉBEC**

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La recherche sur la reproduction des arbres se situe à l'interface des programmes d'amélioration génétique et de la production des plants destinés au reboisement. Cette recherche permet de multiplier en grand nombre les arbres d'élites sélectionnés afin de maximiser leur utilisation et ainsi rentabiliser l'investissement en amélioration génétique. Ces travaux se divisent en deux approches complémentaires ayant chacune leur place dans le reboisement : la reproduction sexuée et asexuée. Plus particulièrement, les travaux de recherche sur la reproduction sexuée consistent à maximiser la production de graines (en quantité et en qualité génétique et morfo-physiologique) dans les vergers à graines de première et de deuxième génération, à développer des méthodes de récolte et de conservation du pollen ainsi que de pollinisation artificielle et à développer des conditions de germination adéquates des graines en pépinière. Par ailleurs, lorsque l'espèce s'y prête bien, que la qualité génétique des arbres le justifie, et à plus forte raison, que le nombre de graines est limitant, la reproduction asexuée devient une voie à privilégier pour produire des plants. La recherche dans ce secteur vise essentiellement à développer les conditions de culture des pieds-mères et d'enracinement des boutures, Pour concrétiser l'investissement déjà réalisé et produire les plants qui vont exprimer tout ce potentiel, il faut mettre au point des techniques simples et peu coûteuses qui vont permettre d'obtenir un très grand nombre de propagules. Dans un autre ordre, des travaux de recherche axés sur la répression des insectes nuisibles dans les vergers à graines sont réalisés afin de protéger les investissements en matière de cônes et de semences destinés à la production de plants génétiquement améliorés.

### **AMÉNAGEMENT DES VERGERS À GRAINES DE DEUXIÈME GÉNÉRATION Stéphan Mercier**

Nous avons élaboré au cours des trois dernières années un nouveau concept d'aménagement pour les vergers à graines de deuxième génération. En effet, en plus des vergers sous abri, nous avons développé le principe des vergers entre brise-vent rapprochés, qui réussit à créer un microclimat accélérant le développement des inflorescences de manière à réduire, voire éliminer la contamination pollinique. Un suivi des inflorescences et des conditions climatiques se font quotidiennement afin de comparer les différentes stratégies d'aménagement. Nous avons rédigé un document dressant une comparaison des coûts liés aux différentes stratégies d'aménagement des vergers à graines de deuxième génération. La technique de pollinisation de masse à l'aide du pistolet électro-statique a été peaufinée, de sorte qu'elle est maintenant opérationnelle à grande échelle. D'autres travaux de développement ont également porté sur la mise au point d'un aspirateur servant à la récolte de pollen dans les vergers, en vue des travaux de

pollinisation de masse. Par ailleurs, nous suivons l'étalement de la floraison des arbres présents dans les vergers en vue de déterminer un mode de gestion permettant de réduire les inconvénients liés à ce

phénomène. D'autres travaux de R-D ont complété ce projet, notamment la mise au point d'une technique provoquant l'avortement des cônes, ainsi que l'induction florale à peu de frais.

#### RECHERCHE ET DÉVELOPPEMENT SUR LES GRAINES D'ARBRES FEUILLUS Stéphane Mercier

La recherche sur les graines des arbres feuillus est regroupée dans deux projets. Le premier vise à mettre au point une technique de désinfection des noix de *Juglans* sp. contre le chancre à la tige (*Sirococcus*). Les différentes techniques de désinfection diffèrent selon l'espèce concernée, en raison des caractéristiques morpho-physiologiques propres à chacune des espèces. Le second s'attaque à la levée de dormance des graines de certains arbres, qui empêche la production de plants à grande échelle. Nous avons réussi à mettre au point une technique de stratification efficace pour lever la dormance des graines de *Prunus serotina* (Ehrh.) et de *Fraxinus americana* L.. Toutefois, il nous reste à mettre au point une technique pour lever la dormance des graines de *Tilia americana* L., phénomène qui limite très fortement la production de plants de cette espèce.

#### RECHERCHE ET DÉVELOPPEMENT SUR LE POLLEN ET LES GRAINES RÉSINEUSES Fabienne Colas

##### Conservation du pollen des arbres forestiers

Nous avons évalué la qualité de la conservation de pollens gardés dans la banque depuis 5 ans. Les résultats ont montré que la viabilité de lots de pollen d'épinettes (*Picea* sp.) et de pins (*Pinus* sp.) se maintient à des taux très élevés. Ainsi, nous considérons que notre technique de conservation des pollens d'épinettes et de pins est fiable et répond aux besoins des chercheurs pour ces espèces. Nous poursuivrons l'évaluation de la conservation à long terme au cours des prochaines années. Le développement de la pollinisation de masse entraîne la récolte de quantités massives de pollen, et l'espace d'entreposage devient limitant. Nous développerons donc des méthodes de conservation pour des lots de pollen de gros volumes (de 500 ml à 1 litre) pour minimiser l'espace requis pour la conservation. Les travaux de développement concernent maintenant les pollens de mélèzes (*Larix* sp.) et de peupliers (*Populus* sp.). Ces deux genres présentent des problématiques différentes, mais les besoins en pollen sont grandissants, ce qui justifie les efforts de recherches.

##### Qualité de la germination des graines d'épinette blanche et de pin blanc en pépinière

La stratification des graines d'épinette blanche [*Picea glauca* (Moench) Voss.] et de pin blanc (*Pinus strobus* L.) est maintenant opérationnelle. La méthode a évolué vers la stratification en sac, inspirée de la méthode développée en Colombie-Britannique. Par ailleurs, nous avons montré l'influence de la grosseur de la graine sur le gabarit des plants. Ce résultat a abouti à un criblage systématique des graines au Centre de semences forestières de Berthier. L'homogénéité du criblage a été étudiée à l'aide du logiciel *Winseed*<sup>®</sup>. Des ajustements sont encore à prévoir.

Le test de germination des graines de pin blanc donne souvent des résultats non reproductibles. Nous étudions actuellement la modification des conditions du test pour en améliorer la reproductibilité.

## Lutte intégrée contre les agents pathogènes portés par les graines forestières

Dans le cadre de l'amélioration de la germination des graines en pépinière, nous envisageons d'enrober les graines. Or, des essais ont montré que les graines résineuses sont porteuses de champignons pathogènes comme *Fusarium* et *Phoma*. De plus, l'ancienne méthode de stratification en multicouches provoquait la prolifération de ces champignons. Il s'agissait donc de développer une technique rapide et peu coûteuse pour éliminer les champignons de la surface des graines. Nous avons adapté une méthode de désinfection des graines à l'aide de peroxyde d'hydrogène. Elle est appliquée opérationnellement au pin blanc, mais suite à nos essais, nous ne l'avons pas étendue à l'épinette blanche.

## MULTIPLICATION VÉGÉTATIVE PAR BOUTURAGE Denise Tousignant

### Bouturage du mélèze hybride

Les espèces à croissance rapide suscitent de plus en plus d'intérêt au Québec. Le bouturage des mélèzes hybride (*Larix x marschlinsii* Coaz., entre autres) s'avère une voie de multiplication privilégiée en raison de la pénurie de graines. Depuis 1998, nous développons un nouveau système de bouturage sous tunnel pour le mélèze hybride, avec brumisation (« mist »), associé au forçage des pieds-mères dans un tunnel chauffé, de février à mai. Les succès positifs obtenus à ce jour ont mené à une première production de 100 000 boutures en 1999, puis de près d'un million de boutures en 2000, à la pépinière de Saint-Modeste.

Dans leur premier volet, nos recherches ont pour but de mettre au point le régime de culture des pieds-mères de mélèze. Cultivés en bacs, ils produisent actuellement de 20 à 25 boutures à un an, et plus de 40 boutures à deux ans. Le vieillissement des pieds-mères s'exprime par une croissance plagiotrope des boutures. L'étude de ce phénomène, ainsi que des traitements culturaux pour le corriger ou l'éviter, est l'un des sujets prioritaires cette année. Après deux ans, les pieds-mères ne montrent encore aucun symptôme de vieillissement. La poursuite des recherches permettra d'évaluer la durée de vie utile des pieds-mères et, donc, le facteur de multiplication du système de bouturage que nous mettons au point. Un second volet de nos recherches a étudié le stade optimal pour la récolte des boutures de mélèze. Nous travaillons maintenant à optimiser les conditions à grande échelle. L'uniformité de la brumisation d'eau est un facteur critique pour le succès des opérations. Une fois enracinées, les boutures de mélèzes sont repiquées en pépinière, à racines nues ou en récipients à parois ajourées, et cultivées pendant 1 à 2 ans avant d'être livrées au reboisement. Un nouveau projet commence en 2000, visant à optimiser la régie de culture des plants de mélèzes en pépinière (collaboration avec B.-M. Gingras et M. Lamhamedi, de la Direction de la recherche forestière).

### Bouturage de l'érable à sucre

L'augmentation de la teneur en sucre de la sève d'érable offrirait des bénéfices économiques importants pour les acériculteurs, car les volumes de sève à faire évaporer, pour obtenir une même quantité de sirop, seraient réduits. Grâce à des marqueurs génétiques, on réussit maintenant à identifier, même à un jeune âge, les arbres qui ont un bagage génétique rendant leur sève plus sucrée (J. Bousquet et collaborateurs, données non publiées). Les jeunes érables à sucre (*Acer saccharum* Marsh.) ont l'avantage d'être plus faciles à bouturer que les arbres adultes, mais la technique propre à cette espèce n'est pas au point.

En 1999, nous avons débuté des recherches sur le bouturage de jeunes érables à sucre de 7 ans. Les premiers résultats ont atteint jusqu'à 75 % d'enracinement. La reprise de croissance des boutures enracinées semble toutefois difficile. La teneur en eau de la tige et le nombre d'écailles du bourgeon terminal sont des marqueurs phénologiques prometteurs pour suivre le développement jeunes pousses



sur l'arbre. Les conditions environnementales ont un grand impact sur l'enracinement des boutures. Nous avons également observé d'importantes variations clonales du taux d'enracinement. L'étude des facteurs environnementaux qui influencent l'enracinement et la survie à long terme des boutures se poursuit.

**RECHERCHE ET DÉVELOPPEMENT SUR LES INSECTES RAVAGEURS DES CÔNES  
ET DES GRAINES AU QUÉBEC**  
Richard Trudel

Les vergers à graines sont des sites propices pour l'établissement et le développement de populations d'insectes nuisibles. Ces ravageurs s'attaquent aux cônes et aux graines, entraînant ainsi une réduction significative de la récolte de semences servant à la production de semis génétiquement améliorés. Il devient donc impératif d'acquérir des connaissances et de développer des outils de lutte afin de limiter les dégâts occasionnés par ces insectes.

Écologie reproductive de la Pyrale des cônes du sapin

La pyrale des cônes du sapin [*Dioryctria abietivorella* (Grote)], est un insecte qui occasionne d'importants dégâts dans les vergers à graines au Québec. De récentes études ont permis mettre en évidence des mécanismes de sélection des sites de ponte lors de la période de reproduction des femelles. La présence de dommages sur les cônes semble être étroitement liée avec la présence d'œufs sur ceux-ci. On peut supposer que les substances de nature terpénique émanant des cônes endommagés sont à l'origine de leur pouvoir attractif. Dans le cadre de cette étude, un plus grand nombre d'œufs ont été retrouvés sur des cônes sévèrement endommagés que sur des cônes sains. Des études ultérieures pourraient nous amener à développer des pièges servant à capturer des femelles de pyrale des cônes du sapin en période de reproduction.

Utilisation du Diméthoate 480® dans le contrôle des insectes des cônes

Les insectes des cônes et des graines demeurent des ravageurs pour lesquels il existe très peu d'alternative pour leur contrôle. Du fait que ces insectes passent une grande partie de leur vie dans les cônes, il est très difficile de les atteindre via des méthodes de lutte conventionnelles. Le Diméthoate 480® est un insecticide systémique pouvant circuler dans toutes les structures de l'arbre en passant par le réseau de vascularisation de la plante. Des tests ont été réalisés avec le Diméthoate 480® l'été dernier, au cours duquel le produit fut utilisé par application au sol dans un verger d'épinette blanche [*Picea glauca* (Moench) Voss]. Des résultats intéressants ont été notés dans le contrôle de la mouche granivore de l'épinette *Strobilomyia neanthracina* Michelsen et de la tordeuse des graines de l'épinette *Cydia strobilella* L.. Des études sont en cours afin d'identifier le mode d'utilisation du produit le plus efficace, soit la pulvérisation, l'injection au tronc ou l'application au sol.

Piégeage du Scolyte des cônes du pin blanc à l'aide d'une phéromone sexuelle

Le scolyte des cônes du pin blanc [*Conophthorus coniperda* (Schwartz)], est une menace pour la rentabilité des vergers à graines de pin blanc au Québec. Des études approfondies de l'insecte par des chercheurs ont permis de caractériser la phéromone sexuelle de ces femelles. Cette phéromone sert donc actuellement à piéger des mâles de scolyte des cônes du pin blanc en période d'accouplement. Les expériences réalisées par le passé ont permis d'identifier les paramètres optimaux (couleur et type de piège, position dans l'arbre, ...) afin d'obtenir de bons succès de piégeage. Notre étude vise à évaluer l'effet du piégeage massif sur le niveau de perturbation reproductive de l'espèce et le niveau de protection des cônes. Une étude est actuellement en cours où différents traitement de densité de piégeage sont testés afin d'identifier lequel procure le meilleur niveau de protection contre ce ravageur.

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## RECENT ADVANCES IN MOLECULAR FOREST GENETICS AND SOMATIC EMBRYOGENESIS

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Since 1997, year of our previous report, training of graduate students and postdoctoral fellows has been again one of our main activities. Our university group is well integrated with the forest genetics group at Canadian Forest Service-Québec (CFS-Québec), allowing students and postdocs to gain experience in various research environments and allowing more efficient use and exchange of markers, pedigree populations and field experiments.

### PAST POSTDOCTORAL FELLOWS AND GRADUATE STUDENTS

Under the supervision of J. Bousquet, Dr. Daniel Perry, from the University of Minnesota, completed his postdoc in developing STS markers of expressed genes for various conifers and after a period of time at University of British Columbia, he is now a scientist at the Canadian Grain Commission in Winnipeg. Dr. Zhou Yi, from the University of Beijing, completed his postdoc under the co-supervision of Dr. Nathalie Isabel (CFS-Québec) in the area of conifer genome mapping and he is now a research associate at Texas A&M University. Dr. Ahmed Koubaa, from the Université du Québec at Trois-Rivières, also completed his postdoc on the study of variation in mature wood density in black spruce (*Picea mariana* (Mill.) B.S.P.) under the co-supervision of Drs. N. Isabel and J. Beaulieu (CFS-Québec) and Tony Zhang (Forintek Canada). He is now a college teacher in forestry. Dr. Martin Perron completed his PhD on the molecular population genetics of the hybrid zone between black spruce and red spruce (*Picea rubens* Sarg.). He is now a postdoctoral fellow with J. Beaulieu at CFS-Québec. Dr. Sylvie Richard completed her PhD under the co-supervision of Dr. Armand Séguin (CFS-Québec), studying the patterns of gene expression of stress-resistance genes in conifers. She is now a scientist at Agriculture Canada. Dr. Jerome Laroche completed his PhD, studying the molecular evolution of plant mitochondrial genes. He is now a scientist in human genomics for SignalGene Inc. Dr. Marie-Josée Laberge completed her PhD under the co-supervision of Dr. Serge Payette (CEN-U.Laval), studying the molecular ecology of old black spruce clones at the tree limit in Northern Québec. She is now a scientist at Parks Canada. Mrs. Sauphie Senneville completed her MSc under the co-supervision of J. Beaulieu at CFS-Québec, studying the population genetics of *Taxus canadensis*. She is now a scientist for DNA Landmarks Inc. Mr. Ricardo Morin also completed his MSc under the co-supervision of J. Beaulieu at CFS-Québec, studying the genetic diversity of the endangered *Juglans cinerea*. Mrs. Alice Roy, previously the coordinator of our molecular genetics laboratory, left us for a research position at the Human Genome Center of M.I.T. while Mr. François Laroche moved to the position of coordinator of the Forest Biology Research Centre, being replaced by Mr. Nicolas Tremblay (MSc, McGill University).

Under the supervision of F.M. Tremblay, Dr. Marika Delalonde, from the University of Montpellier, completed her postdoc on the characterization of endogenous phytohormones during spruce somatic embryogenesis. She returned to France to work as a scientist for AFOCEL. Dr. Edwige Cazaux, from the University of Montpellier, completed a postdoc on somatic embryo encapsulation before returning to France. Dr. Cazaux's work was continued by Dr. Elizabeth Garin, from the University of Montpellier, who completed her postdoc before returning to France as a scientist for AFOCEL. Dr. Yvan L'Homme from McGill University completed his postdoc on the study of different classes of retrotransposons in spruce. He is now working as a college professor. Dr. Le Van Quy, with a PhD from the Université de Paris-Orsay, pursued his postdoc on the genetic transformation of white spruce (*Picea glauca* (Moench) Voss).

#### CURRENT POSTDOCTORAL FELLOWS AND GRADUATE STUDENTS

Among the new postdoctoral fellows, Dr. Christophe Andalo, from the Université de Paris-Orsay, joined us in 1999 and under the co-supervision of J. Beaulieu (CFS-Québec), he is actively developing models of seed source adaptation in relation to seed source and climate change for white spruce. Dr. Niloufar Madjidian, from the University of Montpellier, also joined us in 1999 and under the co-supervision of N. Isabel (CFS-Québec), is engaged in mapping conifer genomes and developing new AFLP and SSCP markers. Drs. M. Delalonde and E. Garin (see above) returned to our laboratories to complete their postdoctoral work, respectively on the characterization of endogenous growth regulators in the spruce somatic embryogenesis system and on somatic embryo encapsulation.

Graduate students include Mrs. Marie Bouillé, at the PhD level, who is studying the molecular phylogeny of the genus *Picea* and the coalescence of alleles at STS loci of expressed genes at the intra- and interspecific levels. Mr. Juan Pablo Jaramillo-Correa, at the PhD level, is conducting comparative studies of the modes and tempo of variation at allozyme loci, STS loci, mitochondrial DNA and quantitative characters in white spruce under the co-supervision of J. Beaulieu (CFS-Québec). Under the co-supervision of Dr. Camille Gervais (MEF-Québec), Mr. Stéphane Plante is completing his PhD dissertation on the recognition of rare taxa in the genus *Bidens* from the analysis of morphological, cytological and molecular characters. Mrs. Isabelle Gamache initiated her PhD under the co-supervision of Dr. Serge Payette (CEN-U.Laval), and she is studying in black spruce the patterns of variation along a latitudinal transect extending to the tree limit using STS markers of expressed genes. Mr. Claude Bomal should complete his PhD in 2000 on the desiccation of spruce somatic embryos while Mr. Abdelmalek El Meskaoui is expected to complete his PhD on the environmental control of spruce somatic embryogenesis. Mr. Driss Iraki is also at the stage of completing his PhD thesis on the effects and biochemistry of carbohydrates during the different stages of somatic embryogenesis. Mrs. Betty Pelgas should also complete her MSc in 2000 on the genetic transformation of larch (*Larix* sp.). Mrs. Isabelle Gosselin is completing her MSc under the co-supervision of N. Isabel (CFS-Québec). Her studies estimated a consensus genome map in white spruce using dominant and co-dominant markers.

#### MOLECULAR POPULATION GENOMICS

Over the past three years, much of the work in molecular population genomics has focused on developing new co-dominant STS markers of expressed genes for conifers for use in molecular population genetics and estimating consensus genome maps. Dominant and co-dominant STS markers of expressed genes have been developed and sequenced for black spruce, white spruce and Norway spruce (*Picea abies* (L.) Karst), their inheritance has been characterized and they were also tested in various other conifers (Perry and Bousquet 1998a, b; Perry *et al.* 1999) (supported by NSERC-Strategic and NCE-Forest Sustainable Management Network). They have been used to estimate the genetic diversity and the mating system parameters in black spruce stands from layering after clear-cut or from seeds after fire where no difference was observed (Perry and Bousquet 2000). They have been used to compare the genetic diversity between black spruce and red spruce, where a significant loss of variation was found for red spruce, suggesting red spruce to be recently derived from black spruce on the geological time scale (Perron *et al.* 2000).

Following initial evidence in black spruce (Isabel *et al.* 1995), we have further demonstrated with our colleagues from CFS-Québec the important biases in gene diversity parameters derived from dominant RAPD markers in white pine (*Pinus strobus* L.) (Isabel *et al.* 1997, 1999). We have also shown how extensive natural hybridization and introgression was between black spruce and red spruce, by surveying many populations from the sympatric and allopatric areas using RAPD species-specific markers, and shown the biases in using morphological criteria for such a purpose (Perron and Bousquet 1997) (supported by MRN-Québec, NSERC and FCAR of Québec). Current work involves estimation of the population structure in the hybrid zone using mitochondrial DNA markers (N. Tremblay and J. Bousquet) as well as comparative analysis of the population structure of white spruce using allozymes, STS and mtDNA markers, and adaptive characters (J. Jamillo-Correa, J. Beaulieu, N. Tremblay, M. Deslauriers and J. Bousquet). Studies aimed at evaluating the genetic diversity of more minor ecosystem components have been completed, in collaboration with our colleagues from CFS-Québec and financial support from CFS and FCAR. Notably, we have shown that the genetic diversity of *Juglans cinerea* and *Taxus canadensis* is depauperated and the implications for conservation have been discussed (Morin *et al.* 2000, Senneville *et al.* 2000). Finally, we have completed, with colleagues from the Centre d'Études nordiques (Univ. Laval), evaluation of the genetic diversity of very old black spruce layering clones discovered much further north than the actual tree limit in New Québec, with some of them aged near 2 000 years. Surprisingly, the diversity of these empetroid clones was as high as that detected in more southern populations suggesting this marginal population to be the remnant of a once much larger population at the peak of the warmest period of the Holocene, 3 000 years ago (Laberge *et al.* 2000).

#### EVOLUTIONARY GENOMICS

Studies conducted during the past two years in the area of molecular biosystematics and evolutionary genomics have been supported by grants from NSERC and FCAR of Québec. Our studies aimed at estimating the modes and tempos of evolution of mitochondrial introns and exons of angiosperms have been completed, with a sampling of over 170 distinct DNA sequences distributed among 15 genes (Laroche *et al.* 1997). Notably, intron sequences have been shown to vary as much as synonymous sites of exon sequences, and mitochondrial *CoxI* genes of poplar, birch and other woody angiosperms were shown to evolve much slower than similar gene sequences in annual plants (Laroche and Bousquet 1999), paralleling such a contrast observed for the chloroplast gene *rbcL* from gymnosperms and angiosperms (Bousquet *et al.* 1992). Therefore, on the geological time scale, woody taxa such as trees are evolving more slowly than annuals and this is likely attributable to longer generation time, larger population sizes and slower speciation rate due to archaic reproductive isolation mechanisms.

At a much finer scale, the molecular phylogeny and phylogeography of the genus *Fraxinus* has been established using internal transcribed spacer sequences (ITS1 & ITS2) of nuclear ribosomal DNA for about 30 taxa (Jeandroz *et al.* 1997). This was the first complete phylogeny deduced from DNA sequences for a tree genus. Intraspecific variation was minimal and closely related hybridizing taxa showed a small divergence at the DNA level. Much higher diversity was observed among sections. The origin of the genus was determined to be in North America, with two latter events of intercontinental migration towards Asia. More recent work at this level involves the estimation of the phylogeny and phylogeography of the nitrogen-fixing genus *Alnus*, in collaboration with scientists from CNRS-France and the University of Lyon I (Navarro *et al.* 2000). Current work involves the estimation of the phylogeny of the genus *Picea* from ITS as well as single-copy nuclear gene sequences, and the study of the coalescence of allelic variants determined by sequencing within and between spruce species (Bouillé and Bousquet).

#### MOLECULAR BREEDING AND QUANTITATIVE GENETICS

A collaborative project involving the development of marker-aided selection for mature wood density in eastern spruces has been pursued and further supported by grants from NSERC and the Québec Ministry of Natural Resources and active collaboration with CFS-Québec (N. Isabel and J. Beaulieu), Forintek Canada (Tony Zhang), the Québec Ministry of Natural Resources (M. Villeneuve), J.D. Irving, Limited (G. Adams) and Fraser Papers Inc. Results on spatial and temporal variation of wood density in black spruce

are being published (Koubaa *et al.* 2000a,b) and mapping of multiple spruce genomes is well underway (I. Gosselin, N. Madjidian, N. Isabel, J. Beaulieu and J. Bousquet). A similar study supported by the Québec Ministry of Natural Resources on marker-aided selection for sap sugar content in sugar maple has also been completed (Larochelle *et al.* 1998, Roy *et al.* 1998).

Studies conducted in collaboration with CFS-Québec (J. Beaulieu and P. Li) on the development of multivariate approaches for the risk assessment of seed source movements in white spruce have been completed (Li *et al.* 1997). Briefly, two large breeding zones have been delineated and validated for Québec. Latitude appeared as the main factor of population differentiation and more geographic differentiation was observed for phenological traits than for growth characters. Work is underway on assessing the effects of climate change on adaptation in the same species (C. Andalo, J. Beaulieu and J. Bousquet).

#### SOMACLONAL VARIATION

Populations of white spruce raised *in vitro* following somatic embryogenesis typically show a low incidence of somaclonal variation (Tremblay *et al.*, 1999). The different phenotypic variations encountered following somatic embryogenesis were characterized. Furthermore, it was possible to link somaclonal variation to the genotype and the time in maintenance. One of the few spontaneous changes observed, the *variegata* phenotype, was previously shown through ultrastructural studies to harbour extensively modified cells with immature chloroplasts (Isabel *et al.* 1996). These mutants shared a single RAPD marker out of hundreds screened, but the sequence of the DNA fragment did not show any homology to known genes or intergenic regions. The presence of the fragment could be related to the relative abundance of nuclear and chloroplast genomes in the modified *variegata* phenotypes (Isabel *et al.* 1996). More recently, we have used the conservation of reverse transcriptase and integrase domains among retroelements to amplify by PCR three well-known types of these mobile genetic elements in black and white spruce (L'Homme *et al.* 2000). Genomic Southern hybridizations revealed the complexity and high copy number of LTR retrotransposons in black and white spruce, which might be implicated in somaclonal variation following somatic embryogenesis.

#### PHYSIOLOGY AND SOMATIC EMBRYOGENESIS

With the financial support of the Québec Ministry of Natural Resources and the Québec Ministry of Industry, Trade, Science and Technology in partnership with three industrial seedling producers, CPPFQ Enr., PAMPEV Inc. and BECHEDOR Inc. various research projects have continued to focus on white spruce and black spruce somatic embryogenesis to which were added hybrid larches (*Larix X* spp.) and Norway spruce.

Different components of the culture medium were studied to improve embryo production and quality. Previously, we had shown that glutamine could be used as the sole nitrogen source to support embryo maturation (Khlifi and Tremblay 1995 and see our 1997 report for other references). The beneficial effect of an increased sucrose concentration in the maturation medium was also shown to be caused by its complete and rapid hydrolysis under the enzymatic action of the cells. Furthermore, the experiments showed that sucrose and later on glucose and fructose were not utilized by the cells during maturation but might act on maturation mainly through an increase in the osmotic pressure of the medium. Recent investigations indicated that the effect of sucrose on embryo maturation is not essentially linked to the osmotic pressure and that the presence of sucrose and of its hydrolysis during maturation is important (Iraki and Tremblay 2000). The positive effects of sucrose on embryo maturation and subsequent development into plants were related to an increased abundance of some storage proteins but not of the carbohydrate content of the embryos. Other investigations conducted on the desiccation of black spruce and white spruce somatic embryos have shown that they can survive desiccation but survival was dependent on the relative humidity treatment (Bomal and Tremblay 1999). An adequate control of the

water loss was also shown to be necessary to subsequent embryo germination. When water loss was well controlled, desiccated embryos germinated in a comparable way to fresh embryos. A protocol based on desiccation and cryopreservation of somatic embryos was also defined to allow long-term preservation of somatic embryos either for direct plant regeneration or for germplasm storage (Bomal and Tremblay 2000).

The role of the *in vitro* gaseous micro environment was also investigated. It was found that a confined micro environment, characterized by an accumulation of CO<sub>2</sub> and C<sub>2</sub>H<sub>4</sub> together with an O<sub>2</sub> consumption, promoted a higher production and uniformity of somatic embryos than a vented micro environment (El Meskaoui *et al.* 1999). The beneficial effects of gases was tentatively explained by their action on ethylene biosynthesis. This gaseous phytohormone was therefore further studied through the addition of either promoter or inhibitor of this hormone as well as through C<sub>2</sub>H<sub>4</sub> enrichment (El Meskaoui *et al.* 2000; El Meskaoui and Tremblay 2000a). Furthermore, the relationship of C<sub>2</sub>H<sub>4</sub> and the capacity of embryogenic tissue lines to produce embryos was studied using black spruce embryogenic lines with different maturation capacities (El Meskaoui and Tremblay 2000b). The analysis of C<sub>2</sub>H<sub>4</sub> biosynthesis and that of its immediate precursor (ACC) together with the utilization of molecules known to alter C<sub>2</sub>H<sub>4</sub> metabolism showed that C<sub>2</sub>H<sub>4</sub> is implicated in somatic embryogenesis of black spruce and that the low capacity lines had excess C<sub>2</sub>H<sub>4</sub> production.

Besides our work on somatic embryogenesis, a study was conducted where somatic seedlings from different clones were compared in morphology, growth, physiology, anatomy, and ultrastructure (Lamhamedi *et al.* 2000). It was found that within the same family and under similar cultural and growth conditions, several clones differed significantly from the zygotic seedlings in height, root-collar diameter, needle dry mass, branch density, shoot and root dry mass, and length of needles. Microscopy showed differences in tannin distribution among clones while analysis of macronutrients N, P and K showed considerable variations within family in their use efficiency.

## GENE TRANSFORMATION

With the financial support of the Québec Ministry of Natural Resources, investigations were also conducted to understand the factors involved in the genetic transformation of white spruce. Using embryogenic suspension culture as a study system, different factors such as the culture conditions of the cells prior to bombardment and the age of the suspension have been tested (unpublished). Previously, transgenic tissues were obtained (Belles-Isles *et al.* 1995) and plants were regenerated. They are currently growing under greenhouse conditions for further testing. In parallel, a transformation protocol was also developed using *Agrobacterium tumefaciens*, which led to stable transformation and plant regeneration from white spruce (Van Quy *et al.* 2000).

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**ADVANCED GENETICS AND BIODIVERSITY RESEARCH AT THE CANADIAN  
FOREST SERVICE, LAURENTIAN FORESTRY CENTRE**

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**Keywords:** white spruce, black spruce, eastern white pine, Canada yew, butternut, *Picea glauca*, *Picea mariana*, *Pinus strobus*, *Taxus canadensis*, *Juglans cinerea*, seed zones delineation, genotype x environment interaction, climate change, frost tolerance, RAPD, isozymes, genomic mapping, genetic markers, somatic embryogenesis, Canadian biotechnology strategy

This report summarizes the progress of the Canadian Forest Service - Québec research in forest genetics and biodiversity for the period 1997-2000. During this period, efforts have continued to focus on three spruce species as well as on eastern white pine for which tree improvement programs are carried out in Québec. Two other economically less important species, butternut (*Juglans cinerea* L.) and Canada yew (*Taxus canadensis* Marsh.), also required our attention. The first is currently severely affected by the butternut canker (*Sirococcus clavigignenti-juglandacearum*) in the United States and the pathogen is spreading across southeastern Canada. The second might soon be under harvesting pressure due to the presence of a taxane in its foliage, which may be used in anti-cancer drugs. Studies were carried out to obtain a baseline estimate of genetic diversity and population structure in both species.

In September 1999, a meeting was organized to present the progress made for all tree breeding programs in Québec during the last decades. It provided us with an opportunity to give talks on the contributions made by the Canadian Forest Service (CFS) over the years.

Research accomplishments were made possible with the generous contributions of dedicated collaborators who deserve our thanks. They are: Serge Légaré, René Pâquet, Magella Gauthier, Jean-Paul Bilodeau, Yves Dubuc, Dominique Fournier, Suzanne Gagnon, Manuel Lamothe, Nicolas Tremblay, Dr. Martin Perron, Dr. Christophe Andalo, Dr. Niloufar Madjidian and many summer students.

**RESEARCH ACTIVITIES ON THE GENETICS OF INDIGENOUS SPRUCES IN QUÉBEC**  
Jean Beaulieu

During the past two years, much effort has focused on two research projects: 1) estimating genetic parameters for quantitative traits in white spruce, and 2) delineating seed zones for black spruce. This last project, carried out in collaboration with Jean Bousquet of the Centre de recherche en biologie forestière, was funded by the Fonds forestier du Québec.

## White Spruce

After the Canadian government program review in 1995, it was decided that the white spruce (*Picea glauca* (Moench) Voss) breeding program under the responsibility of CFS in Québec would be transferred to the provincial government and the CFS would provide support during the next few years to the new breeders. Hence, over the last two years, second-generation progeny tests were established by the CFS and transferred to the Ministère des Ressources naturelles du Québec (MNRQ). These tests will provide selections for the next breeding cycle.

Furthermore, over the last few years, two complete diallel mating designs involving six parents each were carried out to estimate genetic parameters in white spruce. The first diallel mating design involved 6 trees selected for superior growth in the same population while the second one involved six trees from as many different populations. Three replicated full-sib progeny tests were established in 1999 using alpha-designs with three blocks of 5-tree row plots. Besides allowing us to obtain estimates of the genetic parameters for growth traits, these tests will permit us to compare genetic variances obtained from controlled crosses at the intra- and inter-population levels. Another partial diallel mating design involving trees selected for low, intermediate and high mature wood density was carried out. Two replicated full-sib progeny tests were established in 1998. Vegetative propagation of each seedling for four families was initiated in 1999 in order to establish new tests for identifying QTLs involved in mature wood density in white spruce.

Comparison of the performance of full-sib families made up of seedlings and rooted cuttings was continued. Trees in four replicated farm-field tests were measured each year and the best families identified. Four years after planting, the rooted cuttings were on average shorter than the seedlings, but the difference was not statistically significant. Recommendations were provided to the MNRQ for supplying the St-Modeste cutting centre with the best families. Six years after sowing, the best 25 full-sib families should give on average at least 30% to 40% genetic gain in height over an unimproved seed source.

Five new clonal tests including hundreds of clones obtained either by rooted cuttings or somatic embryogenesis were established over the last two years. Seedlings of the same full-sib families as well as of controls were also included in these tests in order to estimate the value of each clone. Increment cores were collected on more than 2 000 trees in a provenance-progeny test replicated on three sites. Wood density profiles were obtained using microdensitometry. Moreover, tree height and dbh were measured and a study of genotype x environment interaction was initiated. Data were also used to construct empirical models predicting climate change effect on white spruce populations growing in Québec with the active collaboration of C. Andalo (postdoctoral fellow) and J. Bousquet.

Two other genetic tests were established in 1999 to estimate whether seed source transfer might have any impact on the adaptive traits of local source progenies. Pseudo-geographical hybrids are compared with open-pollinated families originating from natural stands and with true geographical hybrids obtained by controlled crosses using a polymix.

## Black Spruce

Black spruce (*Picea mariana* (Mill.) B.S.P.) is the most planted species in Québec (over 50 million seedlings per year). While first-generation seed orchards are producing improved seeds, there is still a large proportion of seedlings currently planted coming from unimproved seed sources. Hence, there is a need to develop more precise seed zones and transfer rules. In 1997, a new project funded by the Fonds forestier du Québec and carried out in collaboration with Jean Bousquet from the Centre de recherche en biologie forestière to develop these new seed zones was initiated. Seeds from 90 open-pollinated families representing 30 provenances distributed between latitudes 45° and 51° and longitudes 64° and 80° were sown in the Laurentian Forestry Centre greenhouse. Geographic variation in frost tolerance was studied for one-year old seedlings using needles collected near the terminal bud. No differences were detected among the provenances, as black spruce is well adapted to frost. A scientific paper describing the methodology used and the results obtained is in preparation.

In 1999, a provenance-progeny test was established on three sites well differentiated for climatic conditions. Seedlings were measured after one growing season. This research is being pursued with Martin Perron's involvement as a postdoctoral fellow. Empirical models to delineate seed zones as well as to estimate impacts of climate change on black spruce populations will be developed in 2001 after phenological as well as phenotypic data have been collected.

## GÉNÉTIQUE DE L'ÉPINETTE DE NORVÈGE ET DU PIN BLANC Gaëtan Daoust

La collaboration étroite amorcée depuis 1984 avec M. Ante Stipanovic de la Direction de la recherche forestière (DRF) du ministère des Ressources naturelles du Québec (MRNQ) pour l'amélioration génétique de l'épinette de Norvège (*Picea abies* (L.) Karst) s'est poursuivie. Ainsi plusieurs dispositifs expérimentaux communs ont été établis. Parmi ceux-ci, il faut mentionner les trois tests de descendance (Série E390) établis en 1998 dans la zone d'amélioration du Saint-Laurent en collaboration avec les entreprises Tembec et Bowater ainsi qu'avec la région administrative de l'Estrie du MRNQ. Ces tests regroupent près de 250 descendance uni-parentales représentant plus de 35 provenances. Toujours en relation avec la Série E390 pour les zones d'amélioration des Appalaches et des Laurentides, les analyses effectuées sur les données recueillies dans les dispositifs mis en place en 1989 et en 1991 ont permis d'identifier des sources de semences présentant un gain génétique important pour la rusticité et la croissance en hauteur (10-23 %). Ces sources, disponibles en grande partie, permettront à la Direction de la production des semences et des plants (DPSP) du MRNQ d'utiliser des semences d'une grande qualité génétique pour le reboisement des zones écologiques similaires.

Au printemps 2000, trois tests de descendance bi-parentales (E408) comprenant près de 200 descendance ont été établis en collaboration avec la DPSP-MRNQ dans diverses régions du Québec. Ces tests permettront à long terme la sélection de matériel pour la prochaine génération d'amélioration génétique. Un test en champ établi à Valcartier en 1998 est jumelé à ces dispositifs.

En collaboration avec M. Luc Ouellet de la Fraser Papers Inc. du Nouveau-Brunswick, un test de descendance a été établi sur les terrains privés de l'entreprise afin d'évaluer divers groupes de descendance comprenant entre autres des descendance sélectionnées dans la zone d'amélioration des Appalaches (Série E390) qui offrent des gains génétiques pour la croissance en hauteur de 9 à 22 % à 8 ans.

Afin de répondre aux demandes de sources recommandées pour les régions nordiques de l'Ouest du Québec, des essais de provenances ont été établis dans le domaine écologique de la pessière près de Chibougamau. De même, un projet élaboré en collaboration avec la Commission scolaire Harricana permettra l'établissement de deux essais de provenances en Abitibi. D'autres essais ont également été initiés avec l'entreprise Cartons Saint-Laurent afin de sélectionner des sources de semences rustiques et bien adaptées à la région écologique de la sapinière à bouleau blanc de l'ouest.

Les travaux de recherche portant sur la résistance au charançon du pin blanc de la population d'amélioration, entrepris avec l'équipe du Dr Robert Lavallée, SCF-Québec, se sont poursuivis. Plus de 250 génotypes sont documentés et suivis en ce qui concerne les ravages causés par cet insecte. Les génotypes résistants identifiés par ces travaux ont été transférés aux entreprises J.D. Irving, Ltée et Fraser Papers Inc. ainsi qu'au ministère des Ressources naturelles et de l'Énergie du Nouveau-Brunswick pour inclusion dans leurs vergers à graines. Des semences de croisements contrôlés produites sur ces génotypes résistants sont utilisées dans des travaux d'embryogénèse somatique chez

J.D. Irving, Ltée et chez la Dre Francine Tremblay du Centre de recherche en biologie forestière à l'Université Laval. La DPSP-MRNQ effectue également des croisements contrôlés entre ces génotypes résistants afin de produire des semences pour alimenter le Centre de bouturage de Saint-Modeste.

Pour le pin blanc (*Pinus strobus* L.), le programme d'amélioration génétique demeure toujours sous la responsabilité du SCF-Québec. La dernière période a été consacrée à la mesure de la hauteur et du diamètre des arbres présents dans les trois tests de descendance de la Série E600-II, située à Notre-Dame-du-Laus, à Notre-Dame-du-Rosaire et à Grand-Mère. Ces données nous permettront au cours de la prochaine période de valider les sélections effectuées pour constituer la deuxième population d'amélioration. Cette deuxième population comprend plus de 150 génotypes représentant une cinquantaine de familles performantes dans le centre du Québec. Ces génotypes ont été sélectionnés et greffés en 1997-1998 et établis en parc d'hybridation en 1999. Parallèlement, des tests de descendance uni-parentales, comprenant la majorité des arbres sélectionnés en forêt naturelle et représentant la première population d'amélioration, ont été initiés afin d'évaluer leur aptitude générale à la combinaison. Ces tests seront établis le printemps prochain.

#### POPULATION GENETICS OF FOREST TREE SPECIES

Jean Beaulieu, Gaëtan Daoust, Marie Deslauriers and Nathalie Isabel

During the 1997-1999 period, two population genetics studies using isozyme markers were completed by Master's degree students supervised by Jean Bousquet from Université Laval and co-supervised by CFS scientists. The first one, carried out by Ricardo Morin, was on butternut, a species that is under strong pressure from the butternut canker in the United States. The pathogen was observed in Canada in the early 1990's and is now threatening populations growing in Canada. The main aim of this study was to obtain an estimate of the baseline genetic diversity in butternut before it is decimated by the fungus. Besides the Master's degree thesis, a scientific paper has been published (Morin *et al.* 2000). It was shown that butternut has a low level of genetic diversity in the northeastern part of its natural range. The second student completing her Master's degree was Sauphie Senneville. The objective of her study was to estimate the levels of genetic diversity and population structure in Canada yew before any sizeable effects resulting from harvesting of its foliage for taxane production began. It appears that Canada yew has a low level of genetic diversity and its populations are more differentiated than all the gymnosperms on average. A scientific paper was prepared and submitted (Senneville *et al.*).

The relevance of using dominant random amplified polymorphic DNA (RAPD) fingerprints for estimating population differentiation was investigated using haploid tissues from 75 eastern white pine individuals belonging to five populations. Results showed that estimates derived from dominant RAPD fingerprints were generally inflated. Furthermore, simulations showed that an increase in the number of loci sampled and in population sample size does not significantly alleviate the biases observed. Results were published (Isabel *et al.* 1999).

#### MOLECULAR BREEDING IN FOREST TREE SPECIES

Nathalie Isabel and Jean Beaulieu

Over the last two years, we have initiated a project for developing new molecular markers to study white and black spruce genomes and to develop marker-aided selection tools for economically important and adaptive traits in these two species of the genus *Picea*. Our objectives were to: 1) develop expressed gene markers as well as organellar DNA markers, 2) develop consensus maps at the intra- and interspecific levels for white and black spruce, and 3) follow up and complete a previous Canadian Biotechnology Strategy project for the search for molecular markers associated with somatic embryogenesis (SE) capacity for white spruce.

#### Genetic Marker Development

Primers were designed based on DNA sequences already published for other species. It was done with software in the public domain and in the GCG package. The primers were synthesized and are currently being tested on our pedigree material. This approach seems to be promising and our search continues in

the gene banks using genomic (including introns) and cDNA sequences. Computer as well as laboratory work was mainly carried out by Dominique Fournier.

Thanks to our collaboration with Jean Bousquet of Université Laval, we were also able to extend the number of polymorphic codominant PCR-based markers we had access to. This was done by submitting monomorphic sequence-tagged site (STS) markers on agarose developed by Perry and Bousquet (1998) to the single-stranded DNA conformation polymorphism (SSCP) method. Hence, we got access to 22 new highly polymorphic codominant PCR-based markers that will be used in our single-tree genetic maps for white and black spruce. Results for white spruce were presented at the International Plant & Animal Genome Conference, 8th Edition, in San Diego, CA (Isabel *et al.* 2000).

Mitochondrial DNA markers are being developed in collaboration with Jean Bousquet. This work is being done under his supervision by Nicolas Tremblay. As soon as these markers become available, we will have access to them for population genetics studies.

### Genomic Mapping

Our new codominant PCR-based markers were tested using megagametophyte arrays of two individual white spruce trees for which genetic maps are under construction. As these markers result from the amplification of coding DNA regions, they will provide anchor loci useful for developing intraspecific consensus maps. The first approximation consensus partial map for white spruce will be available in 2001. A student is completing her Master's degree and her research and results will be published in 2001 (Gosselin *et al.*, in preparation).

### Molecular Markers Associated With Traits of High Economic Value

In the past, SE initiation capacity was evaluated for 60 trees in our breeding population. A diallel mating design was carried out involving six trees; two of high, two of intermediate and two of low SE initiation capacity. Two full-sib families were chosen for the search for molecular markers associated with the SE trait. Two genetic maps have already been developed using dominant (RAPD) and codominant (STS) markers. Last year we began screening primers that generated the segregating markers for mapping. The work is being done on megagametophytes that were harvested when their corresponding zygotic embryos were submitted to SE. We are looking for strong correlations between embryo phenotypes (embryogenic or non embryogenic) and presence or absence of markers. We expect to complete this research by the end of 2000 for both families and publish the results in 2001.

The project for developing marker-aided selection for mature wood in white and black spruce has been pursued. Besides the breeding work presented earlier, results on spatial and temporal variation of wood density in black spruce have been published (Koubaa *et al.* 1999, 2000).

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## ONTARIO'S GENETIC RESOURCE MANAGEMENT PROGRAM

Barb Boysen, Paul Charrette, Randy Ford, Dennis Joyce<sup>1</sup> and Cathy Nielsen

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### OVERVIEW

Over the last couple of years, the Ontario Tree Improvement Board (OTIB) has gone through a reorganization, and has changed its name to Forest Genetics Ontario (FGO) to reflect the broad mandate of conservation of genetic diversity and tree improvement. The six original operational associations have been amalgamated into three regional associations that share the Ministry of Natural Resources' (MNR) regional boundaries. The MNR remains committed to scientific and technical support for operational programs. The MNR also supports the development of policy and planning guidelines that integrate genetic, species and ecosystem diversity conservation into forest management planning.

Most first generation seed orchards will be fully rogued within the next couple of years and the focus is shifting to optimizing seed production. Five-year strategic plans have been updated with a view to planning for second-generation breeding. Several programs are slated to start second generation efforts within the next two years. Under the guidance of the Forest Gene Conservation Association, the Southcentral Region has taken the lead on addressing operational genetic conservation.

In support of second generation breeding efforts, Forest Genetics Ontario is drawing on genecology research to begin refining breeding zone boundaries for black spruce and jack pine. The advanced-generation breeding strategy was developed for Ontario in 1994. However, there are always a number of unanticipated problems that arise when implementing any strategy. One jack pine (*Pinus banksiana* Lamb.) and one black spruce (*Picea mariana* (Mill.) B.S.P.) program have been selected as pilot second-generation breeding programs. These pilot programs are being used as learning tools to promote efficiency in all subsequent breeding programs. A series of technical reports will be issued regarding time commitments and financial costs of various activities required to implement second generation tree breeding. These reports will also contain recommendations for improving the efficiency of the activity.

Forest Genetics Ontario has also supported the development of a database management system to maintain records on trees selected as parents for second generation programs. The software assigns a provincial number to each selected tree and seedlot, and supports record keeping with regards to breeding program and breeding values for specified traits. Directories are available to record pollen collection details, identification of open-pollinated and control-pollinated seedlots.

### SUPERIOR - WOODS TREE IMPROVEMENT ASSOCIATION (SWTIA) Paul Charrette

#### First Generation

Abitibi-Consolidated Fort Frances Division completed marking and roguing in 3 orchards during the autumn of 1999 consisting of first roguing in the 4300 jack pine orchard and second roguing in the 4300 and 5300 black spruce orchards. McKenzie Forest Products completed marking and roguing of the

Goodie Lake North black spruce orchard (4300). The members of the 4400 jack pine program (Abitibi-Consolidated Fort Frances Division, Atikokan Forest Products, Bowater Pulp and Paper and Greenmantle Forest Inc.) cooperated in the marking and first roguing of the Sunshine Lake orchard.

This is the first year records of cone collections were requested from the members. In general it was not a good cone year. A total of 77 hl of cones was collected from SWTIA seed orchards in 1999.

#### Second Generation

Bowater completed field selection of the second-generation material in the Lake Nipigon West jack pine program. They also collected open-pollinated cones from many of the selections.

Lakehead University student Dan Rouillard and professor Bill Parker produced a new Arcview GIS extension and a manual for making use of Focal Point Seed Zone (FPSZ) information for black spruce and jack pine in Northwestern Ontario. Focal Point Seed Zones utilize information on patterns of adaptive variation for jack pine and black spruce from Northwestern Ontario and climatic information to generate maps of adaptive similarity for a location of a seed source or the location of a planting or seeding site. In the past, the information was made available in binder format that was developed for each of the old OTIB Zones (i.e. Zones 1, 2 and 3). The models in the new Arcview extension have been revised to include information from the Ontario Climate model. The software allows the user to select a species (jack pine or black spruce) and to select from two methods of generating a FPSZ map: 1) click on the desired location, or 2) enter the latitude and longitude for a location. The SWTIA industry members supported the reproduction and circulation of the software and manual to all users in Northwestern Ontario.

#### NORTHEAST SEED MANAGEMENT ASSOCIATION / NORTHSORE TREE IMPROVEMENT ASSOCIATION Randy Ford

The incorporation of Northeast Seed Management Association (NESMA) as a not for profit corporation was completed. A pollen processing and storage laboratory was established at the Aidie Creek Seed Orchard. Shiningtree Forest Inc., Timiskaming Forest Alliance Inc. and Tembec Industries Inc. (Kapuskasung) became members of NESMA.

#### First Generation

In addition to collecting data to support the final roguing of several first generation seed orchards, "topping" of orchard trees and subsequent cone collection has been the main activity in four jack pine and two black spruce seed orchards. It is estimated that the top was cut off more than 10 000 trees in these orchards. We have developed reasonably safe and efficient methods for cutting the tops off trees; even those greater than 5 meters tall. Annually, we use a model to determine whether our crown management efforts in the Ramore jack pine orchard are cost effective. In recent years it is consistently showing that crown management is worthwhile; scheduling of the initial and subsequent management is very important.

In the fall of 1999, 67 hl of jack pine and 21 hl of black spruce cones were collected. All of the partners are using orchard seed as their first choice when it is available. Annual cone collection plans are based on meeting the partner's need for seed. Our experience to date shows that for the most part cones collected in seed orchards yield more viable seeds per hl than cones from natural stands. We attribute this, at least in part, to the fact that mainly cones ripening in the year of collection are picked. We now use the cost per 1000 viable seeds as the basis for comparing the cost of seed collection rather than the cost per hl of cones.

## Second Generation

Tests for the pilot second-generation jack pine program were planted in the spring of 1998. The tests have been irrigated, fertilized and vegetation managed to ensure rapid establishment. Height and condition data were collected in the fall of 1999. The pilot second-generation black spruce program is attempting to complete the controlled pollinations. Pollen collections have begun for two additional second generation programs and controlled pollinations for those are scheduled to begin in 2001.

### FOREST GENE CONSERVATION ASSOCIATION Barb Boysen and Cathy Nielsen

The Forest Gene Conservation Association (FGCA) has been working with MNR and FGO to expand the mandate of the FGCA to include all of the Ministry's Southcentral Region. As part of this effort, the FGCA has revised its 5-year strategy and business plan for this expanded area, and submitted a request for additional OMNR support to address an expanded program. The MNR has agreed to provide a Regional Genetics Specialist to coordinate the program.

A seed certification program to ensure the use of biologically appropriate seed sources is being developed and tested for woody plant species used in reforestation and restoration in Ontario. The Richard Ivey Foundation has provided a grant for education, training, marketing and implementation projects associated with seed certification.

The FGCA is also involved in cooperative conservation work associated with white elm (*Ulmus americana* L.), pitch pine (*Pinus rigida* Mill.), butternut (*Juglans cinerea* L.), chestnut (*Castanea dentata* (Marsh.) Borkh.) and red spruce (*Picea rubens* Sarg.). The cooperative is also working with the MNR to insure genetic conservation principles are incorporated into silvicultural guidelines and to promote private landowner awareness of conservation concerns.

The FGCA has also revised the tree improvement programs within the FGCA strategy to address specific needs of the central Ontario Sustainable Forest License holders and Algonquin Forest Authority. The priorities include red pine (*Pinus resinosa* Ait.) seed management and a review of the white pine (*Pinus strobus* L.) breeding program.

## ONTARIO FOREST RESEARCH INSTITUTE

Marilyn Cherry, Pengxin Lu and Bob Sinclair

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The 5-year genecology trials installed for 5 species by the Ontario Forest Research Institute have been winding down; data collection is now complete for jack pine (*Pinus banksiana* Lamb.), black spruce (*Picea mariana* (Mill.) BSP), and white spruce (*Picea glauca* (Moench) Voss), and final measurements will be collected for white pine (*Pinus strobus* L.) and red oak (*Quercus rubra* L.) in 2000. For each species, approximately 100 populations spanning the species range within Ontario were planted at each of 3 sites in a randomized complete block design with 10-tree row plots in each of 4 reps per site following one year in the greenhouse. Data analysis of measured growth and adaptive traits is currently being carried out in relation to climatic information from each provenance. Results will be used in the development of species-specific breeding zones.

Research into white pine blister rust resistance is being revived. Blister rust testing was carried out many years ago in the province, involving native and exotic white pine species and their hybrids, but selections of resistant material were never made for operational purposes based on the results stemming from these former trials. A number of white pine seed orchards were installed, but never progeny tested. Plans are being made to collect, screen for blister rust resistance, and test a number of white pine genotypes.

Other areas of interest include the following: 1) in cooperation with Forest Genetics Ontario (FGO), research is being planned to exploit effective ways to increase genetic gains in Ontario's tree improvement programs, including refinement of breeding plans for each species, developing methodologies for advanced (generation?) genetic testing and data analysis, and evaluating realized gains, 2) we are also initiating a study into the genetic impacts of climate change on Ontario's forests, utilizing range-wide provenance trials previously established by the Canadian Forest Service as well as Ontario's genecology trials, which will link with studies being carried out in other provinces, and 3) we will also be involved with developing a species recovery plan for butternut (*Juglans cinerea* L.), which is severely threatened throughout its range by butternut canker (*Sirococcus clavigignenti-juglandacearum* V.M.G. Nair, Kostichka and Kuntz), an introduced pathogen.

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## **TREE GENETICS AND SEED ACTIVITIES AT THE PETAWAWA RESEARCH FOREST**

**P. Copis and B. Wang**

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### TREE GENETICS ACTIVITIES

Since the last CTIA report in 1997, activities have been directed towards the documentation of genetic resources at the Petawawa Research Forest (PRF), publishing information reports, conducting prescription maintenance of selected genetic test plantations, and in the utilization of resources for research studies.

Software development detailing the genetic resources of the PRF, including plantation locations, descriptive information, photographs, and available data, has been created and is available on CD (Kourtz, P. 1998. 'SunBurst' Program - A Forest Stand Viewer and Experiment Information System. Wildfire Management Inc., 80a Behnke Cres., Pembroke, ON, K8A 6W7).

An information report (Morgenstern and Copis 1999) was published. This report updates and consolidates results from three series of range-wide white spruce (*Picea glauca* (Moench) Voss) provenance trials established between the mid 1950's to late 1970's.

A co-operative effort between the Canadian Forest Service (PRF, Laurentian, and Atlantic), Ontario Ministry of Natural Resources, Alberta Forest Service, and B.C. Ministry of Forests is in preliminary stages which will take advantage of already established range-wide experiments for studies related to response to climate change. Common seedlots have been identified in a 20-year-old white spruce study that exists in twenty plantations from Alberta to Maine.

The conversion of numerous plantations of Norway spruce (*Picea abies* (L.) Karst.) at the PRF to develop elite areas for the purpose of cone/seed collection has started. Using time tested phenotypically rogued 60-year-old plantations as the mould, several others have been identified and phenotypic selections of weevil and frost resistant trees have been made. In three plantations, the removal of poor phenotypes has been accomplished. This will be an ongoing operation.

To note, the 'Petawawa Sunburst' - a rare genotype of white spruce (originating from a diallel experiment at PRF) in which the newly flushed spring foliage is bright yellow in colour, is the focus of a millennium project between the Great Lakes Forestry Centre and the City of Sault Ste. Marie, Ontario. A dedication tree has been moved to Sault Ste. Marie from the PRF.

### TREE SEED RELATED ACTIVITIES

Ben Wang joined the PRF in November 1997 when his Emeritus Research Scientist status was renewed by the Canadian Forest Service. His work objectives include providing scientific guidance and assistance in the evaluation, development, and marketing of PRF's genetic resources; to work in conjunction with CFS-Atlantic in Fredericton, maintaining contacts and activities with the Canadian and international seed community through involvement as a reviewer of research papers and providing information and



expert advice; to serve on the Advisory Board of the ASEAN Forest Tree Seed Centre in Thailand and as a Visiting Professor of the Liaoning Academy of Forest Science in China; to work with the PRF Forest Manager on the effect of seed tree age and silvicultural treatment on the germination and vigour of eastern white pine seeds; and to publish technical and scientific papers of reviews and past research results.

Working towards these objectives Ben has provided technical and scientific consultation to PRF staff on tree seed and forest genetics problems as well as to the Manager of the National Forest Genetic Resources Centre in Fredericton. In addition he has reviewed two reports on forest genetics for publication, a forest science proposal, journal papers, and books on subjects related to tree seeds.

Germination tests were conducted for eastern white pine seeds collected from a 165-year-old stand at PRF. Test results indicated that although the size of the seeds and their germinants were smaller as compared to those collected from a younger stand, there was no effect of seed tree age on the germination capacity or vigour.

Jack pine and eastern white pine seedlots from the Upper Ottawa Valley area were procured for family tests and gene plantations for the Liaoning Provincial Academy of Forest Science, China. Earlier provenance research with material provided by the former PNFI Seed Bank showed promising performance from the Upper Ottawa Valley seed source of both species.

On the publication side, several seed related papers have been authored or co-authored as well as having contributed to the 'IUFRO 2000 State-of-the-Knowledge review on tree seed physiology and technology'. Currently a survey of annual seed production and utilization in Canada with a view to writing a paper on "Tree seeds and reforestation in Canada, 1997-1999" has been undertaken in co-operation with a Consulting Geneticist, Dr. E.K. Morgenstern.

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## MANITOBA'S TREE IMPROVEMENT PROGRAMME

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**Keywords:** jack pine, black spruce, white spruce, co-operative

This report highlights the progress of tree improvement in Manitoba from 1998 – 2000. Tree Improvement programs have been established for jack pine (*Pinus banksiana* Lamb.), black spruce (*Picea mariana* (Mill) B.S.P.), and white spruce (*Picea glauca* (Moench) Voss). Co-operatives have been established with Tolko Manitoba, Pine Falls Paper Company, and Louisiana-Pacific Canada.

### JACK PINE

Based on 20-year family test measurements, 67 superior clones were added to the Hillside seed orchard in 1998. In 1999, 14 hl of cones were collected from the Hillside pedigree orchard. The orchard meets the seed demands for the breeding zone.

At the Interlake and Northern jack pine mass selection seed orchards a fourth and final roguing was completed in 1999. These orchards will meet the seed demands in the Interlake and Northern breeding zones.

### BLACK SPRUCE

A 7.4 ha seedling seed orchard was established in 1998 in co-operation with Tolko Manitoba in the Highrock Breeding Zone. A co-operative black spruce tree improvement program was signed with Louisiana-Pacific Canada Ltd. for the Mountain Breeding Zone. The selection of plus trees has been completed and two family test sites and a seed orchard site have been selected. The family test and orchard sites have been site prepared and will be planted in the spring of 2001.

The 10-year height measurements of the three family tests in the Lake Winnipeg East Breeding Zone were completed in 1998. Dr. J. Klein analyzed the family test data. The Brightstone seedling seed orchard was rogued in the summer of 1999 based on the family test analysis. In 1999 the four family tests in the Saskatchewan Breeding Zone were measured. Dr. J. Klein analyzed the 10-year height data and the results were used to rogue the Prospector seed orchard in the summer of 2000.

The Lake St. George mass selection seed orchard in the Interlake Breeding Zone was rogued in 1999 based on height measurements and ocular assessment.

## WHITE SPRUCE

A tree improvement co-operative was signed with Louisiana-Pacific for the Mountain Breeding Zone.

The 10-year family test height measurements were completed for the Mountain Breeding Zone in the fall of 1999. Dr. J. Klein analyzed the family test information and the Birds Hill clonal seed orchard was rogued in the spring of 2000.

The Saskatchewan River Breeding Zone container-breeding garden was converted to a soil based breeding orchard due to limited resources for managing a potted breeding garden.

## SUMMARY

Louisiana-Pacific Canada Ltd. entered into white spruce and black spruce co-operatives in the Mountain Breeding zone.

Improved jack pine seed is available to meet the seed requirements in three breeding zones.

The Birds Hill white spruce clonal seed orchard in the Mountain Breeding Zone, the Brightstone black spruce seedling seed orchard in the Winnipeg East Breeding Zone, and the Prospector black spruce seedling seed orchard in the Saskatchewan River Breeding Zone are nearing seed production.

Presently there are 7 provincial industry co-operatives with Louisiana-Pacific Ltd., Tolko Manitoba, and Pine Falls Paper Company.

## WEYERHAEUSER – TREE IMPROVEMENT IN SASKATCHEWAN

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**Keywords:** seed orchard, provenance trial, cross-pollinating, woodlot

### JACK PINE PROGRAM

A grafted first generation orchard is meeting all operational seed requirements. The two poorest clones were rogued from the orchard in 1999. A more significant roguing will occur once the trials containing full-sib crosses of orchard clones have been measured and analyzed. Excess seed is now being produced in the orchard and top management is being used in an attempt to control the height of orchard grafts.

Cross-pollinating in the first six of twelve sublines for the next generation is progressing well.

### WHITE SPRUCE PROGRAM

A grafted first generation orchard is now meeting all operational seed requirements. Mary Jo Godt and Jim Hamrick of the University of Georgia completed a genetic diversity study in 1999 designed to compare the orchard to a sample of wild stands. The unpublished report indicated no significant loss in diversity with the orchard population.

In 1976 the Canadian Forest Service established 12 white spruce Neldar provenance trials across Saskatchewan. These trials will be measured in the fall of 2000 to aid in determining the extent that seed from the orchard can be deployed across our Saskatchewan FMA's.

### ASPEN PROGRAM

A provenance trial was established in 1998 and will be measured in spring 2000. The Prairie Farm Rehabilitation Administration (PFRA) has two hybrid poplar trials established at our orchard site. Approximately 15 ha of our orchard site were planted using unimproved aspen seedlings in 1998. This plantation is designed to provide a hardwood woodlot demonstration.

## PFRA SHELTERBELT CENTRE - TREE IMPROVEMENT SUMMARY

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**Keywords:** shelterbelt, agroforestry, tree improvement, genetic diversity, Christmas tree, short rotation woody crop

The objectives of the tree improvement program at the PFRA Shelterbelt Centre are to develop genetically superior trees and shrubs for agroforestry planting in the prairie provinces of western Canada, *ex situ* conservation of woody plants and to study the diversity of prairie woody plants. The program focuses on poplar (*Populus* spp.), Scots pine (*Pinus sylvestris* L.), balsam fir (*Abies balsamea* (L.) Mill.), Siberian larch (*Larix sibirica* Ledeb.), green ash (*Fraxinus pennsylvanica* Marsh. var. *subintegerrima* (Vahl.) Fern.), sea buckthorn (*Hippophae rhamnoides* L.) and choke cherry (*Prunus virginiana* var. *melanocarpa* (A. Nells.) Sarg.).

### CHRISTMAS TREE IMPROVEMENT

An improvement program for the Saskatchewan Christmas Tree Growers Association was initiated in 1998. The objective is to develop genetically improved seed strains of Scots pine and balsam fir for the Christmas tree industry. Scots pine and balsam fir trees with superior needle colour and form were selected from shelterbelts and native stands. The plus trees were vegetatively propagated (vener grafting) and planted in two seed orchards.

### SIBERIAN LARCH

Improvement of Siberian larch has been under way since 1981. The objective of the larch program is to develop genetically improved seed sources for agroforestry planting in the prairies. The program has included provenance testing and evaluation of half-sib progeny throughout the Canadian prairies. A half-sib progeny test was evaluated in 1999. This planting is to be rogued in 2000 for use as a seed orchard. A five-year-old progeny test of selected native trees from the Altai Mountains in Siberia was evaluated.

### GREEN ASH

Provenance testing of green ash has identified several superior seed sources for shelterbelt planting. In 1998, five- and ten-year-old provenance tests were evaluated. The best sources originate from Bismarck, North Dakota; Delta, Manitoba; and the Qu'Appelle Valley in Saskatchewan. A 3 ha clonal seed orchard established in 1988 is producing seed. A seed propagated cultivar 'Plainsman' was released in 1998.

## POPLAR

The poplar improvement program at the Shelterbelt Centre continues to be a major activity. The Centre maintains an extensive clonal library which is added to annually. A breeding arboretum was established in 1988 to provide flower branches for controlled breeding. The arboretum includes 50 clones and is being expanded annually. Clonal testing of poplars has been conducted by the Shelterbelt Centre for over 50 years. The objective of the tests were to evaluate performance of clones in climate and soil conditions typical of the Canadian prairies. In 1998 and 1999 a series of tests of candidate clones from F1 populations of plains cottonwood (*Populus deltoides* Marsh. var. *occidentalis* Rydb.) was planted in plantations in Saskatchewan.

The Centre has initiated a hybrid poplar breeding strategy for the Canadian prairies emphasizing development of hardy, fast growing, insect and disease resistant hybrid poplar for use as short rotation woody crops. The strategy includes a combination of back-crossing of fast-growing *P. euramericana* (Dode) Guinier clones with plains cottonwood to improve growth rate and yield of plains cottonwood hybrids and production of F1 hybrids of hardy plains cottonwood with *P. nigra* L. and *P. trichocarpa* Torr & Gray. In addition, breeding efforts should attempt to produce intra and interspecific hybrid seedlots. First filial (F1) generation hybrid combinations will be attempted using primarily plains cottonwood from the PFRA Shelterbelt Centre poplar program and cottonwood selections assembled from native plains cottonwood populations. Because the Shelterbelt Centre has a large number of flowering clones that have been selected, the strategy will also use these candidate clones as parents in an advanced generation breeding matrix.

Plains cottonwood females serve as the basis for the breeding matrix. Selection of breeding materials is based on availability of flowering material, growth data, and insect and disease resistance ratings from existing test plantations. The breeding program goal is to produce 50 to 75 control-pollinated interspecific or advance generation families.

## SEA BUCKTHORN

Phenotypically superior female and male plants are being selected from planted shelterbelt populations. To broaden the genetic base for long-term breeding, sea buckthorn species from China, Russia, Finland and Germany have been introduced. A total of 100 accessions are located in a germplasm nursery at the Centre. New cultivars are in the final testing phase prior to release.

## CHOKER CHERRY

The Shelterbelt Centre is involved in improvement of choke cherry for fruit orchards and conservation planting. A population of 17,000 individuals representing 175 sources has been assembled, propagated and planted in tests in Saskatchewan and Manitoba. The project will provide valuable information on the genetic diversity of choke cherry in the prairies. In 1998, the cultivar 'Pickup's Pride' was released to the nursery trade through the Canadian Ornamental Plant Foundation.

## GENETIC DIVERSITY STUDIES

Woody plant populations in the Canadian prairies have been sampled, propagated and germplasm nurseries established for *ex situ* conservation of this plant material and for use in future biodiversity studies. The phenotypic diversity of four species from the *Elaeagnaceae* family including sea buckthorn, silver buffaloberry (*Shepherdia argentea* Nutt.), Russian olive (*Elaeagnus angustifolia* L.) and silverberry (*Elaeagnus commutata* Bernh. Ex Rydb.) growing in Saskatchewan landscapes were studied (Chowdry *et al.* 2000). The diversity of the four species was assessed by RAPD fragments. Estimates of

phenotypic diversity revealed that silver buffaloberry and sea buckthorn had relatively high phenotypic diversity whereas silverberry and Russian olive had low phenotypic diversity.

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**FOREST GENETICS, BIOTECHNOLOGY, TREE IMPROVEMENT AND  
MYCORRHIZAE RESEARCH AT THE UNIVERSITY OF ALBERTA**

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**Keywords:** molecular, population, evolutionary and conservation genetics; disease resistance, quantitative traits and genome mapping; speciation, biosystematics, phylogenetics and molecular evolution; RAPD, RFLP, microsatellite DNA, STS and allozyme markers; genetic implications of silvicultural practices, forest fragmentation and small population size; conservation, restoration and sustainable management of forest genetic resources; mycorrhizae

During the past three years, research activities continued primarily in the areas of molecular, population and conservation genetics, molecular evolution, speciation, biosystematics, phylogenetics, genetic implications of silvicultural management, molecular linkage mapping of disease resistance, qualitative and quantitative traits, identifying gender-specific DNA markers in poplars, and mycorrhizae. Rajora also initiated projects on studying genetic effects of natural disturbance (forest fires) and alternative harvesting and regeneration practices in white spruce (*Picea glauca* Moench (Voss) and black spruce (*Picea mariana* (Mill.) BSP). He also conducted projects on genetic effects of forest fragmentation and small population size and developing indicators for population viability and guidelines for restoration of forest genetic resources of declining conifer species in Ontario and the Maritimes. Dr. Om Rajora has resigned from his position at the University of Alberta to join Dalhousie University as the StoraEnso Senior Chair in Forest Genetics and Biotechnology.

MOLECULAR, POPULATION AND EVOLUTIONARY GENETICS, MOLECULAR EVOLUTION,  
SPECIATION AND BIOSYSTEMATICS

Allozyme studies

Studies on genetic diversity, population structure, and spatial genetic structure of eastern white pine (*Pinus strobus* L.) in virgin old-growth and second-growth stands in Ontario have been completed by using 54 allozyme loci (Buchert *et al.* 1997; Rajora *et al.* in prep.) The study on population genetic structure, variation, and evolution of Engelmann spruce (*Picea engelmannii* Parry), white spruce and their putative natural hybrid complex in Alberta has been completed and published (Rajora and Dancik 2000). Rajora and associates have also completed a study on genetic diversity and population genetic structure of black spruce from Manitoba. Endah Suwarni has completed her MSc program aimed at estimating pollen contamination, mating system, and genetic diversity in a *Pinus merkusii* Jungh & de Vriese seedling seed orchard (Suwarni *et al.* 1999, Suwarni *et al.* in prep.).



## Molecular Genetics

Rajora and Associates have developed and characterized microsatellite DNA markers from trembling aspen (*Populus tremuloides* Michx.) (Dayanandan *et al.* 1998; Rajora *et al.* 1999; Rahman *et al.* 2000) and determined their conservation and usefulness in 24 *Populus* L. and two *Salix* L. species (Rahman and Rajora in prep.). Data analysis for random amplified polymorphic DNA (RAPD) and cpDNA RFLP variation in trembling aspen selections from Alberta was completed (Rajora and associates). The study on genetic diversity of white spruce populations from ecologically distinct sites in Saskatchewan using RAPD markers was completed (Rajora in prep.). A study on microsatellite DNA and RAPD fingerprinting of hybrid poplar (*Populus x canadensis* Moench) cultivars and another study on microsatellite DNA somaclonal variation in tissue-cultured trembling aspen plants were completed by Rajora and associates (Manuscripts in preparation). Rajora and Associates have isolated, developed, and characterized microsatellite DNA markers from white spruce and black spruce, and determined their inheritance and linkage in white spruce controlled crosses and usefulness in related spruce species *Picea engelmannii*, *P. sitchensis* (Bong.) Carrière, *P. mariana*, *Picea rubens* Sarg. (red spruce), and *P. abies* (L.) Karst. (Rajora *et al.* in prep.). Microsatellite DNA markers that could differentiate between closely related *P. mariana* and *P. rubens* were identified. A fine-scale population and spatial genetic structure of eastern white pine old growth stands was determined and dynamics of stand establishment and gene dispersal within stands were estimated (Rajora *et al.* in prep.).

The study on population genetic structure and evolution of the *P. engelmannii* and *P. glauca* complex using RAPD analysis is progressing well and data are now being analyzed (Khasa and Dancik in preparation). The assessment of the magnitude of interspecific exchange of genes, in natural populations of white spruce and populations of Engelmann spruce from outside the sympatric zone, and populations that appeared to contain hybrid swarms, indicated the existence of bidirectional gene flow from the sympatric zone (Khasa *et al.* 1997). In collaboration with Dr. Ross Hodgetts of the University of Alberta (Department of Biological Sciences), Dancik and Khasa have developed and characterized microsatellite DNA markers for white spruce and other related species (*P. engelmannii* and *P. sitchensis*). These markers will also be tested on other spruce species. A study on population genetic diversity, breeding systems in *Larix lyallii* Parl. using microsatellites is underway in collaboration with Barry Jaquish of the B.C. Ministry of Forests. Microsatellite markers have been developed for larch using both database searches and cloning techniques (Khasa *et al.* 2000a, b). Two species-specific markers allow easy and rapid identification of alpine larch, western larch and their hybrids (Khasa *et al.* 2000c). Chris Todd is continuing his PhD study on acquisition of autotrophy during development of loblolly pine (*Pinus taeda* L.) seedlings under the supervision of Dr. David Gifford (Department of Biological Sciences, U of A) and Dancik.

## MOLECULAR MARKERS FOR DISEASE RESISTANCE, SEX DETERMINATION AND OTHER QUANTITATIVE TRAITS, AND GENOME MAPPING

Rajora in collaboration with Dr. Wout Boerjan (University of Gent, Belgium) and Marijke Steenackers (Institute for Forestry and Game Management, Geraardsbergen, Belgium) conducted a project on identifying and mapping markers for *Melampsora medusae* leaf rust resistance in *Populus deltoides* and its interspecific hybrids with *P. nigra* and *P. maximowiczii*. Both *in vitro* leaf disk and greenhouse inoculation methods were used to evaluate *Melampsora* leaf rust resistance. Data analysis is progressing well. Rajora and associates have also conducted a study to identify gender-specific DNA markers in trembling aspen. A study on genetic linkage mapping of microsatellite DNA and RAPD markers in a two-generation white spruce pedigree is in progress (Rajora).

## GENETIC IMPLICATIONS OF SILVICULTURAL PRACTICES, FOREST FIRES, FOREST FRAGMENTATION AND SMALL POPULATION SIZE, AND CONSERVATION, RESTORATION AND SUSTAINABLE MANAGEMENT OF FOREST GENETIC RESOURCES

Rajora primarily conducted several studies in this area on several conifer species. The studies on determining the impacts of silvicultural practices and phenotypic selection on genetic diversity in white spruce in Saskatchewan, and genetic diversity impacts of harvesting in old-growth and second growth eastern white pine stands in Ontario were completed using allozyme, RAPD, and microsatellite DNA markers (Buchert *et al.* 1997; Rajora 1999a,b,c; Rajora *et al.* 2000a; Rajora *et al.* in prep.). A study on determining genetic diversity effects of alternative silvicultural harvesting and regeneration practices and forest fires on black spruce in Manitoba using allozyme, STS, and microsatellite DNA markers, is nearing completion (Rajora and Associates). A project on determining genetic diversity inherent in pristine natural old-growth populations of white spruce and effects of forest fires and different harvesting intensities on genetic diversity, using microsatellite DNA markers, was initiated by Rajora and is progressing well. This project is part of a unique large multidisciplinary EMEND (Ecological Management Emulating Natural Disturbance) project in northern Alberta. Rajora in collaboration with Alex Mosseler (Canadian Forest Service, Fredericton) completed studies on genetic, reproductive, and mating behavior effects of forest fragmentation and small population size and developing indicators of population viability and guidelines for restoration of forest genetic resources of declining and remnant eastern white pine in Newfoundland and red spruce and pitch pine (*Pinus rigida* Mill.) in Ontario (Mosseler and Rajora 1998; Mosseler *et al.* 1999, 2000; Rajora *et al.* 1998, 2000b). Our group also continues its involvement in issues of biodiversity and sustainability of tropical forests (Khasa and Dancik 1997a,b).

### TREE IMPROVEMENT

Rajora continued field tests of the parents and F<sub>1</sub> progeny of the intraspecific *P. deltoides* and interspecific *P. deltoides* x *P. nigra* and *P. deltoides* x *P. maximowiczii* controlled crosses in Alberta. Khasa, Dancik and Associates have been involved in the selection of salt-alkaline tolerant tree species and genotypes for use in reclamation and revegetation of the composite tailings produced by the Canadian tar sands industry such as Syncrude and Suncor in the Northeastern Alberta (Hambling *et al.*, in prep.). Arlene Huybrechts is starting a MSc project on the potential for hybridization between native and exotic poplars in northern and central Alberta under supervision of Dr. Barb Thomas (Department of Biological Sciences, U of A) and Dr. Bruce Dancik.

### MYCORRHIZAL RESEARCH

Dancik, Lynne Sigler (University of Alberta Devonian Botanic Garden), Bill Ayer (Department of Chemistry) and Khasa have been awarded an NSERC strategic grant on Biotechnology of ectomycorrhizae in the Canadian Prairie Provinces. During the past 2.5 years of research, we have been able to select the most efficient ectomycorrhizal fungal strains for commercial softwoods in the prairie (Chakravarty *et al.* 2000a). Fungal metabolites have been isolated from ectomycorrhizal fungi, which have potentially antagonistic effects on pathogenic fungi such as *Fusarium moniliforme* and *F. oxysporum* (Chakravarty *et al.* 1999). With the latest isolation, separation, and structure elucidation techniques, new fungal metabolites (e.g. hebelophyllenes), have been discovered from liquid cultures of *Hebeloma longicaudum* (Wichlacz *et al.* 1999a, b). A CRD AI-Pac/NSERC grant was awarded in May 1999 aimed at enhancing the establishment of poplar strains by using specific mycorrhizae. The results have provided candidate beneficial microbial inoculants which offer promise for development of commercial inoculants for popliculture (Chakravarty *et al.* 2000b). We have also identified appropriate species of ectomycorrhizal fungi for use in the reclamation of saline-alkaline sites, such as the composite tailings produced by the Canadian tar sands industry (Kernaghan *et al.* 2000). Molecular characterization of the different ectomycorrhizal strains has been accomplished successfully by using PCR-RFLP and new taxon-specific primers are being developed (Kernaghan *et al.* in prep.).

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## GENETICS AND TREE IMPROVEMENT AT THE UNIVERSITY OF ALBERTA

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**Keywords:** quantitative and population genetics, conservation, early selection, tree improvement, balancing gain and diversity, introgression, genomic mapping, QTL and gene expression

During the past two years the following were accomplished: 1) doctoral student Ye Zhihong focused on investigations of coevolution in western gall rust (WGR) (*Endocronartium harknessii* (J.P. Moore) Y. Hiratsuka) with lodgepole pine (*Pinus contorta* Dougl.) and jack pine (*P. banksiana* Lamb) hosts based on morphology, RAPDs, and computer simulation, 2) doctoral student Aron Fazekas investigated the genetic structure and speciation in lodgepole pine using RAPDs and sequencing data, 3) doctoral student Deogratias Rweyongeza studied retrospective early genetic evaluation and selection in white spruce (*Picea glauca* (Moench) Voss) using seedling traits and seasonal growth curves, 4) doctoral student Li Changxi completed his degree based on a study of geographic variation, resistance breeding, host-fungus interaction, and QTL of WGR in lodgepole pine, 5) doctoral student Jonathan Cornelius examined the genetic effects of forest fragmentation in Costa Rica, and 6) M.Sc student Rose Guardamano worked on somatic embryogenesis and gene expression in jack pine and black spruce. We also initiated studies on the theoretical evaluation of balancing genetic gain and diversity in breeding.

We collaborated with the Alberta Land and Forest Service on the genetics and breeding of lodgepole pine and white spruce. Geographic variation patterns, heritabilities and genetic correlations, genetic gain predictions, geographic variation and host-fungus interaction in WGR incidence, retrospective early testing and selection, deployment of genotypes to balance genetic gain and diversity, and QTL mapping for resistance to WGR have been major components of our studies.

Considerable effort and time was spent to support POPGENE, the Microsoft Window-based user-friendly freeware for population genetic analysis. POPGENE started as a joint project between the University of Alberta (Francis Yeh and Rong-Cai Yang) and The Center for International Forestry Research (Tim Boyle). Current version (POPGENE 1.32) is distributed on the World Wide Web, <http://www.ualberta.ca/~fyeh/>.

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**GENETICS AND TREE IMPROVEMENT PROGRAM, 1997-2000  
ALBERTA LAND AND FOREST SERVICE**

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**Keywords:** tree breeding, provenance studies, species testing, seed orchards, progeny testing, selection, genetic diversity

This report summarizes the progress of the Alberta Land and Forest Service (L.F.S.) genetics and tree improvement program for the period of 1997–2000. A large part of the work was done in collaboration with forest industry, Alberta Agriculture, Food and Rural Development, University of Alberta, North Peace Applied Research Association, Canadian Forest Service, U.S. Forest Service, and BC Ministry of Forests.

#### PROGRAM DEVELOPMENT

The Alberta Forest Genetic Resources Council was formed in April 2000 to promote excellence in management of the forest genetic resources of Alberta. It was fostered by a productive partnership amongst government, industry, and the scientific community. The Council consists of a chair and 11 members representing broad interdisciplinary backgrounds. An inter-provincial agreement for scientific co-operation and genetic stock exchanges has also been signed with British Columbia (B.C.).

#### GENETIC IMPROVEMENT

##### Assembly of Breeding Stock

Geographic and superior parent tree selections made as part of L.F.S./Industry cooperative projects included 63 white spruce (*Picea glauca* (Moench) Voss), 92 black spruce (*Picea mariana* (Mill) B.S.P.), 110 lodgepole pine (*Pinus contorta* Dougl. Ex. Loud. var. *latifolia* Engelm.), 62 jack pine (*Pinus banksiana* Lamb.), 15 lodgepole/jack pine hybrids, and 3 Engelmann spruce (*Picea engelmannii* Parry ex Engelm.).

Companies participating in these projects included Alberta-Pacific Forest Industries Inc., ANC Timber Ltd., Blue Ridge Lumber (1981) Ltd., Canadian Forest Products Ltd., Manning Diversified Forest Products Ltd., Millar Western Forest Products Ltd., Northland Forest Products Ltd., Sunpine Forest Products Ltd., Vanderwell Contractors (1971) Ltd., Weldwood of Canada Ltd., and Weyerhaeuser Canada Ltd. Tolko Industries Ltd. (High Level Lumber Division) joined the cooperative tree improvement program in 1999.



From established provenance trials, 4 white spruce, 5 black spruce and 4 jack pine trees were selected. Grafting of 35, progeny-tested, superior lodgepole pine parents from the Alberta Plateau region of British Columbia was carried out.

### Genetic Testing

Survival and plant vigour assessments were completed on Breeding Region 'K1' (central and southern foothills) lodgepole pine progeny trials in 1997 at age two. The objective of the assessment was to provide early baseline information on establishment success and early performance of the two trials. Family differences in survival were not significant but family differences in vigour score were.

Two Siberian larch (*Larix sibirica* Ladeb.) progeny/provenance trials were assessed in 1997 at age 3 for height, survival, and vigour. The trials were established with material collected from an elevation transect in southern Siberia. The top performer in height growth in both trials was a 'local' bulk seedlot collected from old shelterbelt plantings in Alberta. Family variation in height and vigour score was significant at both sites. Climate related damage was common (loss of terminal shoot growth, terminal shoot dieback, chlorosis) but family differences were not significant at either trial.

White spruce progeny trials for Breeding Region 'D1' (boreal mixed wood) were measured in 1998 at age 16. Fifteen- and 16-year heights were measured and trees were assessed for white pine weevil damage. For the 3 sites combined, heritabilities for 15-year height were 0.24 (individual) and 0.72 (family). Site x family interaction was not significant. Fifteen-year height BLUPs were calculated and used for the genetic roguing of the Region 'D1' seedling seed orchard in 1999.

A series of Scots pine (*Pinus sylvestris* L.) field evaluation trials were commenced in 1998 to examine seasonal stability and uniformity of the materials for crown shape and needle colour for Christmas tree and amenity tree attributes. Test materials consisted of seedlings from open-pollinated bulk and single clone collection seedlots from a clonal seed orchard established at the Alberta Tree Improvement and Seed Centre (ATISC). Three trials have been established to date representing different seed crop years.

Development of experimental sites for the establishment of a series of lodgepole pine and white spruce progeny trials in northwestern Alberta was completed.

### Seed Orchards

A cooperative black spruce tree improvement project for Region 'L3' (northeast boreal mixedwood) was initiated between Northland Forest Products Ltd., Alberta-Pacific Forest Industries Inc., and the L.F.S. in 1999. Superior tree selections and graft production are underway with the establishment of a 400-ramet orchard projected for 2002.

Establishment of the Region 'G2' (Peace region) white spruce and Region 'J' lodgepole pine clonal orchards was commenced at North Star near Manning. Manning Diversified Forest Products, Tolko Industries Ltd. (High Level Division), and the L.F.S. are the current partners in the white spruce project. The lodgepole pine project partnership consists of L.F.S. and Manning Diversified Forest Products. The North Peace Applied Research Association will be responsible for local site management and maintenance of the orchards.

A clonal orchard for the white spruce parkland area was established at ATISC in 1999. The orchard consists of 35 parents selected from the wooded agricultural landbase within the Aspen Parkland Ecoregion of east central Alberta.

In 1999, the Region 'E' (northeast boreal) white spruce clonal orchard at ATISC produced its first substantial cone crop. The orchard yielded 16.1 kg of seed. The Region 'H' (northwest boreal) white spruce clonal orchard at ATISC also produced a sizeable cone crop in 1999 yielding 19.7 kg of seed.

In 1999, the second genetic roguing of the Region 'D1' (boreal mixedwood) white spruce seedling orchard was completed based on 15-year progeny trial results. Nearly 40 percent of the trees in the orchard were rogued and, of the 150 families originally represented in the orchard, the 50 lowest ranked in height growth were completely removed. This orchard produced its largest cone crop to date in 1999 yielding 213.4 kg of seed.

Both the Region 'E1' white spruce orchard planned in cooperation between the L.F.S. and Northland Forest Products Ltd. and the Region 'P1' jack pine orchard planned in cooperation between the L.F.S., Northland Forest Products Ltd., and Alberta-Pacific Forest Industries Inc. for northeastern Alberta are developed and graft establishment will begin in 2000. The 'E1' project will be a 500 ramet orchard located at ATISC and the 'P1' orchard will contain 550 ramets and be located at Wandering River.

#### Cone and Seed Insects and Diseases

A study of the disease cycle of spruce cone rust in the alternate host, common wintergreen (*Pyrola asarifolia*), was concluded in 1998. Pat Crane, a PhD candidate at the University of Alberta, conducted the study. The main finding was that moisture, particularly humidity, is the major determining factor in the development of the spore type (telia) that causes infection of spruce cones. Levels of cone rust observed in white spruce orchards at ATISC can be correlated to rainfall and relative humidity during the period when female strobili are receptive and susceptible to infection.

In 1997, a study was initiated to explore the use of synthetic pheromones and sticky traps as a means of monitoring important seed and cone insect pests in white spruce orchards. The species being monitored are the spruce cone maggot (*Strobilomyia neanthrancina*), spruce seed moth (*Cydia strobilella*), and fir cone worm (*Diorcyctria abietivorella*). Pheromone baited "wing" type sticky traps were deployed to capture male moths of the latter two species and non-baited yellow sticky traps were used to capture adult flies of the cone maggot (no pheromone has yet been developed for the maggot adult). Results are promising for the use of pheromone baited traps to forecast potential seed losses from *C. strobilella*. Rates of capture for each year appear to correlate with the percentage of cones infested. However, a comparison of captures between years indicates that capture rates are a function of cone crop size as well as infestation rate.

A trial to test the efficacy of Dimethoate 480 for control of spruce cone maggot was conducted in 1999 in the Region 'E' white spruce clonal seed orchard. The dimethoate treatment provided an estimated 88.9% control. In comparison, treated cones produced 14% more seeds per cone than non-treated cones. Additionally, seeds from treated cones were 3.4% heavier in weight and the seed germination rate was 4.0% higher than seed from non-treated cones.

## GENETICS AND TREE IMPROVEMENT RESEARCH

### Provenance Studies

A seven-year assessment of a Canada range-wide white spruce provenance trial at the Chinchaga River genetic site was completed in 1997. Thirty-six exotic and four Alberta seed sources were assessed for total height, survival, and overall tree condition. Of the five top ranking provenances in height, four are from Ontario and one is from Québec; the worst five are from Yukon, Manitoba, Saskatchewan and Ontario. Alberta seedlots fall in the middle ranks.

The Prairie Creek (southern foothills) Alberta-wide white spruce provenance trial was assessed at 21 years in 1997. Twenty-seven seed sources were evaluated for total height, dbh, survival, vigour, stem straightness, and white pine weevil incidence. A quadratic regression model fitting response to seed source elevation explained 60, 74, 26, and 56% of the total variation in dbh, height, survival, tree vigour, and stem straightness, respectively. Weevil incidence was positively and linearly correlated with longitude

and elevation.

In 1998, four other trials in the Alberta-wide white spruce provenance series were assessed at 21 years for the traits previously listed and, in 1999, 24-year assessments were completed on two trials and 21-year assessments on one trial. Thirteen field trials of this provenance study were established throughout Alberta and they are providing a valuable base of scientific information on the regional geographic variation of white spruce populations in Alberta. Two new spruce provenance trials were established during the report period. These trials include provenance collections of Engelmann spruce, white spruce, and white x Englemann natural hybrid provenances from Idaho, Montana, interior British Columbia, and southwestern Alberta.

Also in 1998, 3 USSR Siberian larch seed source trials were assessed at age 13 for survival, height, and dbh. Results indicate that optimal climate transfer distances from the seed origins in Russia to planting sites in Alberta did not differ significantly. Four Scots pine seed source trials, also of USSR seed origins, were assessed in 1999 at age 19. Height and dbh were measured and porcupine damage was assessed. Both of these studies are part of research collaboration with the U.S. Forest Service. The main objective of these studies is to evaluate population responses of the two species to climate gradients in North America.

Also in 1999, 6 lodgepole pine, jack pine and hybrid seed source trials were evaluated, three at age 15 and 3 at age 10. Height and dbh were measured and survival and overall tree condition were assessed. Three tamarack (*Larix laricina* (Du Roi) K. Koch) provenance trials were also assessed at 15 years from seeding for height, dbh, survival, and overall tree condition.

A 15-year-old black spruce provenance trial was assessed for provenance variation in height growth rhythm for current year leader growth. Data were also collected on 10, 13, 14 and 15-year heights and 14-year diameters. The study was carried out by Dr. S.D. Han who is a visiting professor at the University of Alberta. There were significant differences among provenances for all growth traits and some growth rhythm traits. Variation among growth traits was found to be related to frost-free period, growing degree-days, and elevation of provenance origin. The growth rhythms traits, however, showed better relationships to latitude, longitude, day-length, and negative degree-days of the provenance origins.

Two white birch (*Betula papyrifera* Marsh.) seed source trials were established in 1999. These contain 23 single tree collections from 3 provenances in east central Alberta and 3 bulk collections from northern and foothills regions of Alberta.

#### Climate Change and Genetic Variation of Forest Tree Species Populations

A project "Population responses of Alberta conifer tree species to predicted climate change and implications for reforestation" was initiated in 1999. The main objective of the project is to develop species and genetic population response functions for adaptation to climate and climate change. Species to be studied are white spruce, black spruce, lodgepole pine, jack pine, Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco), and tamarack. More than 1 000 weather stations from Alberta and the adjoining areas of neighbouring provinces and states with long-term observations were normalized, on a monthly basis, to the 1961-90 period for 4 primary weather variables (maximum temperature, minimum temperature, mean annual temperature, and precipitation). These four normalized variables were further extended to 13 derived variables for constructing climate prediction models for Alberta. By using climate prediction models and Alberta-wide provenance test data, provenance response functions to climate gradients will be developed as a first step to evaluating effects of climate change on provenance performance and genetic adaptation.

#### Selection, Mating Design and Genetic Diversity

A penalty index selection procedure was developed to maximize genetic gain while maintaining status

effective number (genetic diversity) at a desirable level. Formulations were developed for genetic gain and status number when penalty index procedure is applied to several selection sources. In simulations, the penalty index selection was verified by comparing to four other selection methods. Penalty index selection was simulated in two white spruce half-sib progeny tests. This method can be applied to cycling breeding populations or roguing existing seed orchards. In this study, it was also found that restricted phenotypic and combined index selection and family index selection can well approximate optimal selection in some situations. However, a combination of between and within-family selection is always the worst in improving genetic gain if comparing status effective number or inbreeding at the same level.

Another theoretical study examined the influences of different mating designs (single-pair, nested, factorial, and diallel) on the relatedness and status effective number in selection. Formulations were first developed to predict relatedness/status effective number in selection from populations generated under different mating designs. Numerical results were generated for: 1) investigating the interactions in status number with selection and population census structures of a mating design and 2) comparing the relative efficiencies in status number of different mating designs. Status number under a mating design is determined by the parent number, mating rate, initial population size, full-sib family size, etc. In general, single-pair mating most favoured status number in selection, followed by balanced factorial and diallel. Nested mating was the worst. Low mating rate (3-5) was suggested for nested, balanced factorial and diallel mating to yield high status number while providing extra key information for improving genetic gain.

#### Flowering and Cone Induction Studies

A flowering induction study was initiated in 1998 to develop experience in accelerated breeding of white and black spruce using potted grafts. Flowering induction with GA<sub>4/7</sub> treatments, following the protocol developed by the BC Ministry of Forests, was successful. The study was continued in 1999 with the focus on developing a protocol for a greenhouse environment out of synchronization with natural growth cycles. This would entail artificial chilling in the early fall to permit bud burst and cone induction during the winter, followed by artificial chilling to effect bud burst in the spring.

### GENETIC RESOURCES CONSERVATION

Genetic resources conservation is an integral part of all tree improvement projects in Alberta. Work has started on developing a comprehensive provincial genetic resources conservation strategy. *Ex situ* conservation of genetic stock in clone banks continued to be expanded. During the report period, a total of 1795 ramets were added to the spruce (1157), pine (513) and minor species (125) clone banks at ATISC.

### PLANT PROPAGATION, WOOD, SEED AND POLLEN TECHNOLOGY

#### Plant Propagation

During the report period, stock production consisted of 11 430 seedlings for rootstock, 55 560 seedlings for experimental trials, 11 160 seedlings for National Forestry Week and 5 321 grafts.

In 1998, 1 875 seedlings were produced for the Manning Area woodlot research and demonstration project. In 1999, 34 000 black spruce were produced as part of a seed use efficiency and container seedling production-greenhouse trial. In 2000, 9 760 lodgepole pine seedlings were grown for the Region "J" progeny trial and 7 740 white spruce seedlings for provenance and family testing of B.C., Québec, and Alberta material. An extra growth cycle per year was given to 1 858 grafts and 441 rootstock trees by providing an artificial chilling period in a growth chamber.

### Wood Technology

During the report period, relative density and fibre length measurements were completed on 461 parent trees. Of these, 161 were white spruce, 124 were lodgepole pine, 87 were black spruce, 63 were jack pine, and 26 were white x Engelmann spruce hybrids.

### Seed Technology

Over the report period, 481 seedlots were added to the genetics seed bank. The majority of entries were white spruce (218), jack pine (67), black spruce (63) and lodgepole pine (44). Other species seedlots added to the seed bank include tamarack (29) and Scots pine (23). The seed bank at ATISC presently contains 4 497 seedlots.

Reference seedlots, representing about 2% of seed bank entries, have been monitored for 19 years. Lodgepole pine seedlots have remained stable with a mean germination of 87% in 1981 and 87% in 2000. White spruce seedlots have declined slightly from a mean germination of 91% in 1981 to 86% in 2000. Mean germination of aspen (*Populus tremuloides* Michx.), plains cottonwood (*Populus deltoides* Bartr. ex Marsh. spp. *monilifera* (Ait.) Eckenw.) and balsam poplar (*Populus balsamifera* L.) have declined 26-33% after 9 years of storage.

Alberta and British Columbia Provincial Seed Centre staff met in May 1999 for a Seed Program Review meeting to discuss possibilities of standardizing seed testing protocol and methodology for the two provinces. A seed imbibition trial was carried out to investigate differences of seed hydration methods and germination dishes used by Alberta and British Columbia. This was the first step in determining germination testing differences between the two provinces. The National Tree Seed Centre, New Brunswick, participated as well and all data have been compiled.

### Pollen Technology

A temperature and humidity controlled forced-air pollen extractor was constructed in 1999 at ATISC. Pollen viability testing, including germination and electrical conductivity tests, program was started in preparation for commencement of controlled breeding.

## REFORESTATION SEED PROGRAM

A review of seed policy and legislation regarding the L.F.S.'s stewardship role is underway. Development of a comprehensive seed policy manual that covers all regulatory aspects of seed use and seed tracking from collection to deployment on public lands is ongoing. It will also include regulations for tree improvement initiatives, development and management of breeding programs, and incorporation of improved seed into forest management practices.

Operational reforestation seed collections averaged 1 730 kilograms per year for 1997, 1998, and 1999. The bulk of the collections were lodgepole pine (778 kg) and white spruce (831 kg). Annual seed withdrawals averaged 987 kg for seedling production and 1 006 kg for direct seeding projects over the same 3-year period. Approximately 700 withdrawals were completed each year. The provincial reforestation seed storage facility is located at ATISC and currently holds 1 489 seedlots for a total of 39 911 kg of seed.

## FOREST GENETICS RESEARCH AT THE UNIVERSITY OF BRITISH COLUMBIA, 1999

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**Key words:** management of genetic variance, resource use efficiency, fiber morphological traits, multiple population breeding,  $F_2$  genetic variance, red alder, Douglas-fir, lodgepole pine, interior spruce, western hemlock, genetic diversity, gene conservation, decision-making strategy

The research group in forest genetics headed by Dr. Gene Namkoong primarily focused on research and education in dynamics of evolution, maintenance, and management of genetic variance in forest trees. Another important area of investigation included genetics of wood and fiber quality in conifers. 1999 was perhaps the culmination of four decades of pioneering research in forest genetics by Dr. Gene Namkoong.



A symposium entitled 'Unifying Perspectives of Evolution, Conservation, and Breeding' in commemoration of Dr. Gene Namkoong's retirement after four decades of pioneering research in Forest Genetics, was held at the Forest Sciences Center, July 22-24, 1999. This symposium explored new directions in forest genetics research in population dynamics and evolution, tree breeding, and gene conservation, with an emphasis on biology at the population and species levels of organization. It focused on integrating evolutionary models of unstable systems, joint functions of genotype and environment effects, and multiple population structure of breeding to develop better designs for conservation and utilization of forest genetic resources.

Over 110 participants, representing over ten countries in Europe, Asia, and North and South America participated in the symposium. 24 invited lectures and 24 posters were presented at the meetings. As many

commented, "it was a very personally, and professionally energizing and uplifting" occasion for the Forest Genetics community around the world.

#### UTILIZATION AND MANAGEMENT OF RED ALDER GENETIC RESOURCES IN BRITISH COLUMBIA

Andreas Hamann, Mathew P. Koshy and Gene Namkoong

Genetic variation in both quantitative traits and allozymes, were investigated. Adaptation of red alder (*Alnus rubra* Bong.) provenances along environmental gradients was investigated with regression and multivariate analysis of growth and adaptive traits to see how closely variation is attuned to geographic variables. Multivariate analysis revealed complex associations of quantitative traits with the latitude, distance to the coast, and elevation of the seed source. Nei's genetic distance revealed a strong differentiation among island and mainland provenances at one allozyme locus. This differentiation can be interpreted as a result of migration from two different refugia since the last glaciation.

To further test the hypothesis of migration history since the last glaciation, we investigated allozyme polymorphisms in outlying populations that could have been potential refugia during the last ice age. Provenances from Vancouver Island, Queen Charlotte Islands, and Prince of Wales Island, Alaska represent possible coastal refugia, and populations in Idaho may be remnants of southern refugia. Genetic distances among these provenances corroborate our hypothesis of the existence of coastal refugia that at the end of the ice age formed a continuous coastal population from the Olympic Peninsula to Alaska. The Idaho population is genetically distinct, but their relation is unclear without further information of mainland provenances from California to Washington.

Based on provenance performance at four planting environments and climatic data for each provenance source environment, we investigated the degree of adaptation of the species to local environments, and used redundancy analysis to investigate the importance of different environmental clines. Significant genotype x environment interactions were found at the population and family level. Provenances close to each planting site showed superior performance in growth and survival, suggesting adaptation of red alder to local environments. Seed transfer guidelines and seed procurement zones were developed under the assumption of local optimality using methodology based on risk associated with seed transfer.

Estimated heritabilities for growth and adaptive traits were moderate with values between 0.30 and 0.50. Genetic gain in growth traits from individual selection would range from 25 to 35%. A methodology to remove spatially autocorrelated error variation in field experiments in order to increase heritabilities, gains from selection, and precision of parameter estimates was also developed.

Multiple populations for different climatic scenarios and different regions of British Columbia are derived from information on geneecology, risk associated with seed transfer, and genetic parameters. Six breeding populations of red alder, some with novel trait combinations, were found to be necessary to cope with possible effects of climatic warming in British Columbia. The feasibility of the strategy was tested with a breeding experiment involving 12 populations selected for growth, bud break, and leaf abscission using different selection intensities and directions.



MANAGING FOREST TREE GENETIC VARIANCE FOR CLIMATIC CHANGE - FIELD AND DNA MARKER  
BASED TESTING OF A NOVEL SYSTEM

Dan Perry, Mathew P. Koshy, Gene Namkoong, Carol Ritland and Kermit Ritland

This project continues the test of a novel system for generating higher genetic variance in populations for continued selection response and greater adaptability.  $F_0$ ,  $F_1$ , and  $F_2$  plants from a wide cross study of Douglas-fir provenances are evaluated for phenotypic traits in multiple field tests. DNA markers, such as, microsatellites and RAPDs, were used to investigate the identity of loci contributing to genetic variance in each parental population and the hybrids.

Of the 49 pairs of microsatellite primers tested, 15 markers were scored in 48 progeny per family, alongside the corresponding parents and grandparents. Several of the markers used were characterized by complex banding patterns and it was only possible to identify allelic variants because the material in question was of known decent (i.e., the result of controlled crosses). Null alleles were also present at many of these marker loci, although in some cases it was possible to reduce the occurrence of null alleles by modifying the PCR amplification conditions.

The utility of cDNA-based sequence-tagged-site (STS) markers, originally developed for black spruce, was also investigated. Although PCR amplification was consistently successful, only one locus (*Sb01*) was found to be polymorphic. This locus, encoding a putative aquaporin gene, was scored in the complete sets of progeny, parents, and grandparents.

Preliminary statistical analyses indicated strong support for linkage of one pair of microsatellite loci (C8 and G16; recombination frequency,  $\gamma = 0.134$ ) and also for a linked complex of four other microsatellite loci (G10, G12, G23, G39;  $\gamma = 0.001$  to 0.166 within the complex). Associations between marker alleles and quantitative trait values were also investigated. Randomization tests indicated a few instances where the differences in height observed between progeny groups as defined by allelic class were greater than might be expected by chance alone, but the expression of possible QTLs varied among years and among genetic backgrounds. These results are preliminary and further efforts to saturate the map using RAPD are in progress.

Third year field data showed higher within-family variation in the  $F_2$  generation in the two sites where the environmental conditions were harsher. In the fairly mild environment, the  $F_2$  didn't show higher variability, compared to  $F_0$  and  $F_1$ .

RESOURCE USE EFFICIENCY RESPONSE IN VARYING ENVIRONMENTS AND ITS ROLE IN THE  
MAINTENANCE OF GENETIC VARIATION IN FITNESS RELATED TRAITS  
IN LODGEPOLE PINE

Pia Smets, Mathew P. Koshy and Gene Namkoong

This study investigates genetic variation for resource-use efficiencies (RUE) in lodgepole pine (*Pinus contorta* Dougl.). Water-use efficiency (WUE) and nitrogen-use efficiency (NUE) were observed over a range of environments, created by controlled levels of available water and nitrogen, in 1-year-old seedlings of lodgepole pine families belonging to different provenances. Heritabilities for RUE and morphological traits were moderate to low across experimental environments, but were high in environments, where water and nitrogen were freely available. Response patterns of genotypes for these traits over environments were multi-dimensional, with significant crossover interactions resulting in rank change particularly among provenances. This finding implies that genotypes deal with experimental environments in different ways, which could partly be explained in the light of source environments. Provenances from the drier locations, for example, had the highest water-use efficiency in experimental environments that were both dry and nitrogen poor, and was apparently able to sacrifice NUE for WUE when necessary. However, provenances were not necessarily the most productive in terms of growth traits in the experimental environment most similar to their source environment. It was apparent that the breeder is not limited to specific seed sources to obtain adaptation to marginal sites. Neither is the choice of an appropriate seed source a guarantee for adaptation to extreme sites. Genetic correlations do not indicate conflicts between selection for growth and for adaptation. An alternative approach may be to focus on selection for increased plasticity.

Canonical correlation analysis of multiple trait performance suggests that if any relation of performance in different environments exists, then it is based on genotypes maintaining their rank order across environments. Rank changes among genotypes exist, but they are not systematic, i.e. similar behavior applying to groups of genotypes. Sources from dry and warm locations (i.e. low elevations) showed a consistently higher shoot root ratio in all experimental environments, and a particularly high WUE and low NUE under high nitrogen treatments (i.e. a larger growth potential). Genotypes with this particular expression in resource use efficiencies also performed significantly better in field plantations.

#### RAPID BREEDING FOR IMPROVEMENT OF TRACHEID PROPERTIES IN INTERIOR SPRUCE

Milosh Ivkovich, Mathew P. Koshy and Gene Namkoong

Tracheid morphology traits related to cross-sectional dimensions were analyzed in interior spruce (*Picea glauca* x *P. engelmannii*) and genetic parameters estimated. Traits included were ring width (RW), number of cells per ring (C/r), cell radial size (rCS), cell tangential size (tCS), mean double wall thickness (DW), mean ratio DW/CS (R), early-wood percentage (EW%), transition-wood percentage (TW%), late-wood percentage (LW%), modified Mork's index (MI), double wall thickness in early-wood (DWew), cell radial lumen in early-wood (Lew), ratio DW/CS in early-wood (Rew), double wall thickness in transition-wood (DWtw), cell radial lumen in transition-wood (Ltw), ratio DW/CS in transition-wood (Rtw), double wall thickness in late-wood (DWlw), cell radial lumen in late-wood (Llw), ratio DW/CS in late-wood (Rlw), fiber length (FL), and micro-fibril angle (MFA).

Based on optimization process, which gives the maximum response in objective function based on a linear selection index under a certain selection intensity, genetic response ( after one generation of truncation selection ( $i=2$ ) was calculated based on multiple trait selection. Selection indices which maximize response in volume ( $I_{VOL}$ ), one that maximizes response in volume, and places restriction on change in relative density ( $I_{VOL\_RD}$ ), and one that maximizes response in dry-weight ( $I_{DWT}$ ) were used. It was shown that significant improvement can be achieved by selection for volume alone, using the index  $I_{VOL}$ . Constraining RD to zero, by the index  $I_{VOL\_RD}$ , leads to a significant reduction in volume improvement. The achievable change in RD is negligible relative to the achievable change in VOL, considering improvement of their joint function DWT.

Selection on both  $I_{VOL}$  and  $I_{DWT}$  resulted in a positive response in tensile strength of wet-webs  $T_{ww}$ , tensile strength of paper  $T_p$ , and tensile strength of mechanical pulp  $T_m$ , but a negative response in tear of weakly ( $TR_1$ ) and well bonded ( $TR_2$ ) paper.

Comparison of simultaneous response in different objective functions is obtained for different scenarios by using the NIMBUS multi-objective programming system. Based on the optimization of single and multiple objective functions, gain can be assessed and comparisons made for all other value functions or combinations of value functions of interest. Simultaneous improvement of volume growth and value of certain pulp and paper properties always would require a trade-off. In some cases, however, positive response in multiple value functions was possible and the trade-off was minor. More significant trade-offs would be faced if simultaneous improvement of three value functions VOL,  $T_{ww}$ , and  $TR_1$  is sought after within one breeding population. Although positive response was possible in all three functions at the same time, at the point where  $T_{ww}$  and  $TR_1$  intersected (mini-max solution), the VOL function was at less than a quarter of the total achievable improvement. Intersects of function VOL and the two functions related to pulp and paper properties are relatively close to zero improvement. Introducing relative density in the selection indices and constraining its change would increase the necessary trade-off in certain pulp and paper properties. For example, for VOL\_RD and  $T_{ww}$ , the space where trade-off exist would be extended and shifted towards negative values. The higher trade-off and loss in the other objective functions than when selecting for VOL without any restrictions.

GENETIC EFFECTS ON FIBER AND STRUCTURAL WOOD PROPERTIES  
IN WESTERN HEMLOCK

Mathew P. Koshy, John King, Charlie Cartwright and Gene Namkoong

The objectives of this project are to estimate genetic variance, heritability, and genetic correlations of fiber characters and structural properties of western hemlock (*Tsuga heterophylla* (Raf.) Sarg.), study the effect of silvicultural treatments on genetic effects in fiber and wood properties, screen a breeding population for fiber and wood properties, and derive economic weights for wood and fiber properties. Four sets of trials are being investigated under this project. The first study included 30 open-pollinated families from the Carmanah site. Ring measurements, morphometric measurements on four rings from bark, fiber length, and fibril angle measurements were completed on this material during the past year. The second trial included a silviculture (thinning)-genetics interaction study at Bonanza. Samples from 70 open-pollinated families were collected before thinning from this site. Ring and morphometric trait measurements were completed and data analyzed. Fiber length and fibril angle measurements in these families were also completed. Core samples were collected from these trials, where different thinning regimes were carried out to study the interaction of genetic and silvicultural treatments on wood properties. Study of wood properties in these cored samples is in progress. The third study looks into fertilizer treatment-genetic interaction on wood properties. A trial at Sombrio is used for this purpose. Fertilizer treatment was carried out in this trial during 1999. Wood samples will be collected from these trials during July-August, 2000 to study the interaction of genetic and fertilizer effects. A fourth study includes 59 families of US origin included in the BC breeding program. Morphometric traits outlined in the spruce study are evaluated in all these materials.

DECISION-MAKING STRATEGIES FOR CONSERVATION AND USE OF  
FOREST GENETIC RESOURCES

Mathew P. Koshy, Gene Namkoong, Paulo Kageyama and Andre Stella

A framework for prioritizing species, populations, and conservation management interventions integrating genetic diversity, threat, and management data is critical in making forest gene resource management decisions. This includes factors of the estimated state of genetic variation, threats, and opportunities for recovery and sustainability of the resource for production and conservation. Two distinct but not independent factors, value and risk, affect rankings, both of which are complex and both are usually estimated with uncertainty. The framework uses Bayesian estimators to optimize decisions on rankings. The value of management then depends on the value of making the right decisions and the costs of making the wrong ones, as well as on the probabilities of errors in judgement.

Usually, judgements are made on the basis of some information, even if the information is intuitive. A decision tree is constructed based on estimates of the conditional probabilities. The relative values of designating the classes are estimated and a sensitivity analysis performed to estimate what a "best" decision is. An estimate of the expected value of making any decision at that level of information is also made. The decision is then evaluated to see when additional information would be useful recognizing that additional information can often reduce the errors of mis-classifying conservation status but that it usually costs the manager in time and resources to obtain that information. To estimate whether obtaining additional information is expected to be worthwhile, a comparison of the expected values of decisions is made at increasing levels of information. This project has developed a framework for decision making and it is being tested in a field study in Brazil.

**FOREST GENETICS AT THE FACULTY OF FORESTRY, THE UNIVERSITY OF  
BRITISH COLUMBIA, 1998-2000**

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GENECOLOGY, GENE CONSERVATION AND ADAPTIVE TRAIT VARIATION  
S.N. Aitken

Genecological investigations are underway to better understand the distribution of variation for adaptive traits to both refine seed transfer guidelines and to address broader evolutionary questions. Using a combination of sequence tagged site (STS) markers and adaptive traits, PhD student S.Y. (Yaw) Bennuah is investigating the genetic structure of the introgression zone between Sitka spruce (*Picea sitchensis* (Bong.) Carriere) and white spruce (*P. glauca* (Moench) Voss) in the Nass/Skeena region of northwestern BC. Postdoctoral Fellow (PDF) Greg O'Neill is investigating genetic variation in induced wound responses related to resistance to *Pissodes strobi* in the same introgressed materials, and finding steep genetic clines in both constitutive and induced resin canal-related traits. Greg is also assessing breeding zone delineation for interior spruce (*Picea glauca x englemanni*) in Southeastern BC. PDF Isabelle Chuine has modelled growth and reproductive phenology relative to local climatic regimes for an adaptive generalist (*Pinus monticola* Dougl. ex D. Don) and an adaptive specialist (*Pinus contorta* Dougl. ex Loud.) in western North America.

The conifer at greatest risk of loss of genetic diversity in wild populations in BC is whitebark pine (*Pinus albicaulis* Engelm.). Jodie Krakowski (MSc student) is investigating genetic diversity in this species (with Y.A. El-Kassaby). Spatial population structure and efficient *ex situ* sampling designs for capturing rare alleles will be investigated by PhD student Washington Gapare. The effects of forest harvesting on mating system and genetic diversity of the understory species *Vaccinium alaskaense* are being investigated by MSc student Larisa Stankovich. Mutation rates are important for determining the effective population size needed to conserve genetic diversity under mutation-selection-drift balance, thus a study is underway to attempt to quantify the contribution of somatic mutations to genetic variation for quantitative traits in Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco), in collaboration with M. Lynch (U. of Oregon).

Correlated responses to selection for economic traits in adaptive traits including cold and drought hardiness, and implications for tree breeding programs, have been investigated in a number of species, including lodgepole pine (with Tongli Wang (Research Associate, UBC), Michael Carlson (BC Ministry of Forests), Philippe Rozenberg (INRA, France) and Kathleen Kavanagh (U. of Idaho) and western hemlock (*Tsuga heterophylla* (Raf.) Sarg.)(with Mats Hannerz (SkogForsk, Sweden). We are also investigating the physiological basis of norms of reaction to temperature and moisture resulting in genotype x environment interaction in coastal Douglas-fir (with Tongli Wang (UBC) and Jack Woods (BC Ministry of Forests). S. Aitken is collaborating with U.S. Forest Service scientists David Neale and Kathleen Jermstad (Institute of Forest Genetics, Davis, California) and others on a project mapping QTL for cold hardiness in coastal Douglas-fir. We are also investigating the long-term effects of low-level inbreeding on the growth and yield of forest plantations using the model TASS (Tree and Stand Simulator) with BC Ministry of Forests scientists Ken Mitchell, Ken Polsson and Jack Woods, and Steen Magnussen (Canadian Forest Service).

ALTERNATIVE SILVICULTURAL SYSTEMS, MINOR TREE SPECIES AND GENE CONSERVATION  
Y.A. El-Kassaby

The development of successful forest management strategies requires an understanding of a wide array of topics such as: the extent and diversity of forest ecosystems, the impact of forest management practices on biological diversity, and tactics and strategies for gene conservation. Such understanding will allow forest managers and gene conservationists to work together to combine utilization with conservation in the most efficient manner. Two forest management practices are being investigated. These are: 1) the Montane Alternative Silviculture Systems (MASS). A research partnership was formed in 1992 to test alternative silvicultural systems for BC coastal montane forests, document the costs and feasibility, and study their biological and silvicultural impacts. The experiment includes replicated treatments representing a range of overstory removal (shelterwood, patch clearcut, and green tree retention), adjacent old-growth and clearcut 'control' areas (Web site at [http://www.pfc.cfs.nrcan.gc.ca/www\\_user/lgalbraith/mass/mass.html](http://www.pfc.cfs.nrcan.gc.ca/www_user/lgalbraith/mass/mass.html)). A genetic study is underway to quantify the level of genetic diversity and inbreeding under these alternative silvicultural systems. Estimates of inbreeding levels under these various tree removal systems will provide an idea of the genetic quality of natural regeneration and will assist in determining if artificial regeneration is required to augment natural regeneration. Two species are being investigated (western hemlock and balsam fir (*Abies balsamea* (L.) Mill.)). Parent trees and natural regeneration seedlings as well as seed crops were sampled for this study. Preliminary results indicate the presence of a relationship between tree density and the level of correlated matings. And 2) with Andy Benowicz (Research Associate, UBC), the impact of commercial thinning on biodiversity is under investigation in two Douglas-fir plantations located on southern Vancouver Island, BC. Biodiversity was evaluated before and after commercial thinning with respect to tree species composition/abundance, tree species genetic diversity assessed by allozyme analysis and stand structural diversity represented by diameter class distribution. In addition, understory plant species diversity is under evaluation for a 5-year period following thinning.

A substantial amount of my research efforts is being dedicated to the study of minor tree species in B.C. The species targeted for this work are Garry oak (*Quercus garryana* Dougl.), red alder (*Alnus rubra* Bong.), Sitka alder (*Alnus viridis* ssp. *sinuata* (Regel) Å. Löve & D. Löve), paper birch (*Betula papyrifera* Marsh.), mountain hemlock (*Tsuga mertensiana* (Bong.) Carrière), ponderosa pine (*Pinus ponderosa* P.Laws. ex C. Laws.) and whitebark pine. Due to their limited commercial importance to B.C. forest economy, these species received little research attention. These studies have proven to be a good learning ground for graduate students and the information generated by these studies will be of great value to minor tree species utilization/conservation efforts.

Knowledge on the distribution of genetic variation within and among the white pine weevil, (= spruce weevil) *Pissodes strobi* (Peck), populations as well as understanding its reproductive biology are essential for the development of an effective Integrated Pest Management strategy for protecting Sitka spruce. A study is underway to: 1) measure the genetic variation present in the spruce weevil populations and 2) focus on investigating the insect breeding system. The second objective specifically aimed to find out if female spruce weevils produce offspring from more than one mate and if female spruce weevils produce viable offspring the year following a mating event with no subsequent mating the second year. Isozyme protein and DNA microsatellite genetic markers were used to investigate the genetic diversity and reproductive biology, respectively. With collaboration with Dr. R. Alfaro and Ms. K. Lewis of the Canadian Forest Service (CFS), the genetic structure of 41 Canadian weevil populations (27 populations from BC, two of which were from East of the Continental Divide and the remaining 14 representing localities West of the Continental Divide) was investigated. With Drs. C. Ritland and K. Ritland the possibilities of multiple paternity and sperm storage in weevil is being investigated using offspring collected from experimental matings between virgin females and males. Using unique microsatellite genetic markers, MSc student C. Liewlaksaneeyanawin is studying the weevil breeding system. His preliminary results indicate that female weevils mated with multiple mates and that sperm competition is common with some males effectively siring the majority of the offspring. This represents the first results of multiple paternity in weevil.

## POPULATION GENETICS AND GENOMICS OF B.C. CONIFERS

K. Ritland

Research conducted in my lab spans conservation genetics, population genetics, evolutionary genetics, and recently, genomics. Recent and current projects have involved cedar, spruce, hemlock, wheat grass, *Linanthus*, shrews and bears. We have an emphasis on the application of molecular markers in conjunction with novel statistical methods. Only the research of concern for tree breeding and seed production is highlighted here.

## Mating Systems and Inbreeding

Lisa O'Connell (PhD student) in collaboration with John Russell, (BC MoF) is examining the evolution of inbreeding in western redcedar (*Thuja plicata* Donn ex D. Don). The rates of selfing in natural stands and ecological correlates of selfing, have been estimated with isozymes (O'Connell *et al.*, submitted). We have developed 12 highly polymorphic microsatellite markers (O'Connell and C. Ritland, in prep.) and will be using these markers to evaluate the role of bottlenecks in the reduced genetic diversity of this species. Also, in collaboration with Michael Stoehr, BC Ministry of Forests (BCMoF) we have been examining selfing, paternity, and pollen contamination in interior B.C. spruce seed orchards.

## Population Structure

Steve Travis (PDF) and Dilara Ally (MSc student) have been examining the local population structure of four BC conifer species. Transects through old-growth and naturally regenerated populations reveal marked local family structure, as detected by assays of isozymes and microsatellites. This study is also designed to document local neighborhood structure in natural populations, to estimate heritability of breeding traits using naturally occurring relationships in wild collected material, and to assess the genetic consequences of natural regeneration. Also, Terry Pape (undergraduate NSERC scholar) has conducted the first isozyme study of the highly valued B.C. conifer species, yellow-cedar (*Chamaecyparis nootkatensis* (D. Don) Spach). Marked regional variation was found (C. Ritland *et al.* in prep).

## Genomics

I have finished a study of the molecular basis of genetic load in three BC spruce species (in collaboration with the BCMoF). About 6 000 selfed spruce seedlings were planted in spring 1997 and grown for two years, then harvested, scored for several traits, and assayed for 12 polymorphic isozyme loci. By analyzing deviations from 1:2:1 at marker gene loci heterozygous in the parent, the mode of selection (recessive, dominant, overdominant) will be inferred, and this may have implications for breeding strategies. Next, we plan to use AFLP markers to identify individual quantitative trait loci (QTLs) in families showing high levels of inbreeding depression (work of Charles Chen, PhD student). Finally, Vancouver has been chosen as one of five federally-funded genomics research centers, and a consensus has been reached here that there will be a strong forests genomics initiative coming out of this Vancouver Center.

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## BRITISH COLUMBIA MINISTRY OF FORESTS GENETICS PROGRAM

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The British Columbia Ministry of Forests (MoF) program in forest genetics research is one of the largest in Canada covering issues in tree breeding and forest genetic resource management. The program consists of a total of 35 research scientists, technical, and administrative staff located in Victoria and at two research stations.

Researchers are concentrating on producing seed transfer guidelines, studying geneecology of major and minor economic tree species, commercial breeding programs for ten major conifer species, as well as genetic management and gene conservation of important forest species. Coastal tree breeding focuses on Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco var. *menziesii*), western hemlock (*Tsuga heterophylla* (Raf.) Sarg.), red cedar (*Thuja plicata* Donn ex D.Don), yellow cedar (*Chamaecyparis nootkatensis* (D.Don) Spach), Sitka spruce (*Picea sitchensis* (Bong.) Carrière), and white pine (*Pinus monticola* Dougl. ex D. Don), while interior tree breeding concentrates on interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca* (Beissn.) Franco), western larch (*Larix occidentalis* Nutt.), lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm.), interior spruce and several hardwood species. Recent advances in some of our programs are given below.

### TREE BREEDING AND ASSOCIATED RESEARCH

#### Coastal Douglas-fir (Jack Woods)

The Douglas-fir breeding program represents the oldest conifer tree improvement program in British Columbia. It is now providing selected parents for 2<sup>nd</sup> generation seed orchards and second generation breeding and testing is continuing. A series of second generation progeny tests for Coastal Douglas-fir is being established on 6 test sites (5 on Vancouver Island and 1 near Powell River) to provide information on and material for third generation production and breeding population selections. Realized genetic gain trials have been established to provide a linkage between progeny tests and stand growth/timber supply modelling. Geneecology studies in the sub-maritime seed zone are ongoing to learn more about seed transfer limits in this complex environment. The inbreeding/co-ancestry study is now over 10 years old and will provide information to support decisions on seed orchard populations. Jack Woods has recently left the MoF tree breeding program and Dr. Michael Stoehr is taking over as the coastal Douglas-fir breeder.

#### Seed Transfer of Douglas-fir in the Sub-Maritime Seed Zone (Jack Woods)

This 4-year project with BC Research Inc. is evaluating the physiological response of 43 populations of Douglas-fir throughout the sub-maritime seed zone. It will evaluate frost hardiness and drought response of various populations in order to refine Douglas-fir seed transfer guidelines in the climatically diverse SM zone and to identify populations with the highest wood production potential. It will also evaluate the ecophysiology patterns of genetic variation for the primary site-limiting environmental conditions. Preliminary results indicate that populations from higher elevations exhibit a trend for higher freezing

tolerance. This trend appears consistent for all west to east transects.

#### White Pine Blister Rust Resistance - Screening and Breeding of Populations (John King)

White Pine Blister Rust (*Cronartium ribicola* J.C.Fisch) has devastated native five needle pines since its introduction at the turn of the 19<sup>th</sup> century. Genetic resistance has been indicated by the improvement of populations in Idaho and Oregon after phenotypic selection (often after choosing the few trees that survived intense attacks). A major gene resistance has been found both in sugar pine (*Pinus lambertiana* Dougl.) and in some Oregon populations of white pine (although rust races have evolved with a virulence response). In BC, there has been nearly 15 years of effort mainly conducted by the Canadian Forest Service (CFS). Populations have undergone early screening under artificial inoculation. This project integrates the effort that has been made in BC with the resistance found in the Oregon populations, particularly for coastal white pine improvement. It seeks to construct pedigreed breeding populations for long-term field screening. The feasibility of hybridizing Eurasian five needle pines as a way of infusing durable resistance is being investigated.

Material gathered from Doreena (the Doreena diallels made in the 1980's) along with some crosses made from the CFS material was sowed in 1999. Seed was sown for outplanting to trials and for artificial inoculation. CFS researchers provided a ranking of the best available material from their screening program for coastal parents and plans are made for a major scion collection program. In May of 2000 the F-1 breeding program will be continued. The Happy Camp trials in Northern California will be visited to assess how successful the deployment of MGR might be in coastal populations of white pine. Happy Camp has been used as a monitoring site looking at the spread of a virulent rust race to MGR. Evidence to date indicates virulence spreads very slowly, indicating MGR could be successfully deployed as a short term strategy.

#### Spruce - Weevil Resistance Improvement - Screening and Breeding of Populations (John King)

Genetic resistance to white pine weevil *Pissodes strobi* (Peck) damage in spruce has been noted now for several years. This resistance can be quite marked with resistant families having only 1/10th the level of attack, and indeed some Sitka spruce clones have shown themselves to be immune under natural conditions. Work has been carried out identifying putative mechanisms of this resistance. This project seeks to determine the inheritance behind these resistant mechanisms by continuing the screening of populations and accelerating the construction of pedigreed breeding populations.

Weevil infestations were made by the CFS at Camp 4 and Snowdon near Campbell River in 2000. These trials will complete the current round of family trials - and will now only await series 4 that was established in 1999. CFS assistance will switch over the next few years from the screening of trials to helping Moff understand the mechanisms of resistance. The weevil infestation data has culminated with the first two series of OP screenings and 3 series of clonal trials (EP 702.06). With this data, the establishment of breeding and seed orchards is planned. A major part of spring 2000's work will be scion collections for these establishments. Crossing will continue at the Saanich Forestry Centre and in the provenance trials (EP 702 trial at Sayward). The *Picea arborea* at Kalamalka and at Chilliwack will be visited to inventory the species, make notes of general species susceptibility, and make plans to augment these and replicate them at the Cowichan Lake Research Station. If the cone crop looks good in the fall we will also continue to fill in the holes in our collections from the dry Douglas-fir zone.

#### Genetic Improvement of Western Hemlock (Charlie Cartwright)

Hemlock tree improvement in British Columbia commenced with selection of parent trees and provenance testing (seed transfer trials) in the 1960's. This was followed by progeny testing to select best parents for growth traits to include in seed orchards which continued into the early 1990's. It became apparent that for

orchard seed to be used it had to offer sufficient gain to offset the cost advantages of natural regeneration. Considerable progress could be achieved with the 300 hemlock families then in test, but diversity requirements, selecting for traits other than growth (wood quality), and inbreeding concerns meant a broader genetic base was required. For this reason, MofF staff initiated the Hemlock Tree Improvement Co-op (HEMTIC), providing access to 1200 progeny-tested first generation parents from U.S. Pacific Northwest programs.

From starting materials provided by HEMTIC an advanced generation breeding plan was devised. A broader based trial series utilizing 30 parents from each of the 5 testing regions – BC, North Washington Coast (Forks), South Washington Coast (Gray's Harbour), North Oregon Coast (Willamette), and Mid Oregon Coast (Oregon Department of Forestry) was designed. This series, designated *F-1*, tests the level of adaptation of materials from across the co-op on member lands and provides materials for recurrent selection. A second set of trials, the "elite" tests, uses only the best 6 parents from each program to permit construction of a very high gain seed orchard in the near future. To date, there are 7 *F-1* tests and 4 elite tests out-planted in BC.

Elite trials, 2.9 ha (4 000 seedlings) in size, were established on 4 sites in 1999. Survival, map checks, and maintenance (conifer release) of the tests continued in 2000. Other activities include update measurements for realized-gain trials and first generation tests established in 1979 (20-year height, DBH) and 1989 (10-year height, DBH).

Progress in hemlock tree improvement may be summed by looking at current products. Several seedlots with gain in excess of 15% are listed at the provincial Seed Centre. Levels of improvement in growth traits are likely to increase as new data on the American families are obtained from measurement of *F-1* trials in 2001 and more reliable age 10 and 20 measurements are taken from earlier BC first generation series

#### Western Red Cedar Genetic Tests for Identifying Elite Populations (John Russell)

Twelve million western red cedar seedlings are planted annually in BC. Nine million of these are planted in the wet maritime under 600 metres, which is the target area for the coastal industrial seed orchards. These orchards provide up to 100% of the seed to meet the reforestation needs in this area. Currently, genetic gain in volume growth for these first generation orchards is estimated at 2%. The western red cedar breeding program involves progeny testing of 600 polycrossed parent trees. Selection of the top parents in existing orchards or development of new 1.5 generation orchards based on 5-year results of progeny tests will lead to a 1-year reduction in time to reach free-to-grow on productive red cedar sites and a 10% to 15% volume gain at rotation for western red cedar reforested sites by 2005.

The year 2000's project was the third of four annual series of western red cedar polycross progeny trials. All sites will be maintained to minimize competition and deer browsing. It is anticipated that 5-year growth data will be collected from each series and orchards upgraded based on calculated breeding values.

#### Screening Western Red Cedar for Natural Durability (John Russell)

Natural durability of future second growth cedar is of concern. Tropolones, in particular the thujaplicans, have been strongly correlated with decay resistance. Old-growth trees are considered, on average, more durable than second-growth because of higher concentrations of tropolones. However, the tropolone

content of both old and second-growth western red cedar shows considerable phenotypic variation from tree to tree, with some second growth trees showing as much as old-growth. There is the potential for selecting second growth trees with higher than average tropolone content, resulting in enhanced durability similar to average old-growth trees. These selections can be incorporated into breeding and seed production populations ensuring minimal failure in future durable red cedar products from second growth trees. To accomplish this, wood cores will be analysed for tropolones (in particular the thujaplicans) and

tested for rot resistance using wood blocks inoculated with fungi. Three hundred clones from 18-year parent trees will be screened for natural durability. Analyses of the data from these samples have yielded the following interesting observations: 1) there is significant phenotypic variability in individual extractives, 2) some second growth trees have extractive levels greater than some old-growth trees, 3) consistent rankings among trees across stem positions for extractive levels, 4) no correlation between growth rate (ring area) and extractive content, and 5) ten-year-old trees from progeny trials have heartwood with measurable amounts of extractives.

The results give us confidence in analysing durability extractives using increment cores taken from 20-year-old parent tree clones. Sampling is currently ongoing. It is anticipated that at the end of this project we will have clonal values for durability for 300 parent trees. These values can be incorporated into second generation orchard and breeding populations.

#### Yellow-cedar Genetic Tests for Identifying Elite Populations (John Russell)

Currently, up to 2 million yellow-cedar seedlings and rooted cuttings are planted annually in coastal BC. Seed for this valuable resource originates from wild-stand collections and from untested parent trees in MacMillan Bloedel and TimberWest's seed orchards. Cuttings originate from mostly untested cutting-donors in various government and industrial hedge orchards.

The objective of this project is to provide up to 100% of the yellow-cedar seed and cutting needs with genetically-improved material, which will deliver 10%-20% volume gain and reduced time until free-to-grow, by the Year 2007 through: 1) clonal progeny testing of parent-trees in existing seed orchards and gene archives, 2) roguing of existing, or developing new 2<sup>nd</sup> generation seed orchards, and 3) development of new seed and hedge orchards based on 7-year clonal values.

For each of three annual series of field trials, the procedure involved establishing yellow-cedar clones from pedigreed material. One-year-old seedlings grown from seed of six 8-clone partial diallels were used as donor-stock for producing 1+0 rooted cuttings. Included in the cloned progeny tests were: 1) 1 800 clones from 96 full-sib families for progeny and clonal testing and 2) one group of wild-stand seedlots (containing 3-4 seedlots) from representative biogeoclimatic subzones for checks across sites and series and comparisons to select clones and families. The rooted cuttings were established in randomized incomplete block field trials. The final series was planted in 2000. Sites from series 1 and 2 have very high survival and are growing well. Sites have been brushed for weed competition.

#### Interior Lodgepole Pine Realized Gain Trials (Mike Carlson)

A series of realized genetic gain trial sites is being established in two seed planning zones in central and southern interior BC. These trials will provide unit-area productivity gain estimates for lodgepole pine across a range of site productivities, genetic levels, and stocking densities. The trials will be used to generate accurate growth and yield information from genetically improved stock to calibrate growth models (TASS etc.), including interactions among genetic gain, site index, and stand density. Eighteen 144-tree plots were planted on each of 6 sites in the Thompson-Okanagan seed planning zone trial in 1999 and a comparable trial will be planted in the Prince George seed planning zone in 2000.

#### Interior Douglas-fir Genetic Tests (Barry Jaquish)

Brushing and site maintenance was completed on 11 sites. Ten- and 15-year tree height and condition were recorded for sites in the Quesnel Lake and Prince George seed planning zones, respectively. Data analyses are in progress. Results will be used to estimate new parental breeding values and to rogue seed orchards. Site maintenance was also completed and six-year tree height was recorded for three sites in the Interior Douglas-fir elevational transect study. This study explores growth and adaptational differences among populations separated by 50 m of elevation along three elevational transects in the

Nelson (formerly Shuswap Adams) seed planning zone. Data analyses are in progress. Results from the study will be used to refine Interior Douglas-fir seed transfer guidelines and seed planning zones.

#### Interior Spruce Genetic Improvement Activities, 1999 (Barry Jaquish)

Routine site maintenance was completed on 33 sites. Three- and 10-year tree height and condition were recorded for the Prince George/East Kootenay second-generation tests (3-year) and the Series 1 Thompson Okanagan polycross tests (10-year), respectively. Data analysis is complete for the Thompson Okanagan series and new parental breeding values have been estimated by Best Linear Prediction (BLP). The existing Thompson Okanagan seed orchard will be redesigned based on these results. Seven new test plantations were established for the Bulkley Valley (BV) and Peace River (PR) zones. Some Alberta test material was included in the Peace River open pollinated test as part of the Tree Improvement Research Memorandum of Understanding between B.C. and Alberta. Two of the new PR sites were also manually brushed in late summer to remove competing vegetation.

#### Interior Spruce Somatic Embryogenesis (SE) Clonal Field Tests (Barry Jaquish)

Since 1992, B.C. Research Inc., the B.C. MofF, B.C. forest companies, and Forest Renewal B.C. have co-operated in establishing a number of interior spruce somatic embryogenesis (SE) clonal field tests. The objectives of these tests are: 1) to study and demonstrate variation among clonal lines and 2) to identify clones with superior growth, tolerance to terminal weevil, and SE induction ability. These plantings have been classified as clonal candidacy tests (CT) and clonal block (CB) tests. The plan for the CT tests was to establish about 1 200 clones in field tests and monitor and assess their performance for 5-15 years before selecting clones for widespread deployment. Since 1994, over 1 600 clones have been planted on 33 sites. Many of these clones were derived from high breeding value parents, or parents with some degree of weevil resistance.

In 2000, 16 sites were inspected for brush competition, labeling and mapping, and damage. Tree height and condition were recorded for one 6-year-old site (Hungary Ck), three 4-year-old sites (Aleza Lk, Indian Point and Tumuch) and five 3-year-old sites (Aleza Lk, Arctic, Ft. St. James, Hungary Ck. and Quesnel). Most test sites remain in good shape and are beginning to yield good growth data. To date, very little weevil damage has been detected on any of the sites. Analyses of data collected in 2000 are in progress.

#### Planting, Brushing, Maintenance and Grafting at the Barnes Creek Clone Bank (Barry Jaquish)

The Barnes Creek Clone Bank was established by the MofF in 1977 to serve as a long-term gene archive for important tree breeding materials. The 35 ha reserve is located on Crown land east of Enderby. It contains grafted trees from most of the parents in the provincial interior spruce, interior Douglas-fir, and western larch tree breeding programs and several important tree improvement and growth and yield research installations. The reserve was established with three goals: 1) long-term preservation of important breeding material, 2) *ex situ* gene conservation and 3) a source of male and female flowers for advanced-generation breeding and scionwood to establish seed orchards. For many clones, Barnes

Creek represents the only site where they will be held in perpetuity. Recently, most activity on the site has been directed toward routine site maintenance and establishing a transplant bed for Douglas-fir and western larch grafting. Presently, the western larch clone bank is about 30 percent complete. About 100 Douglas-fir grafts were transplanted from the Kalamalka Forestry Centre and approximately 700 trees were recently grafted and maintained for the expanded Nelson low elevation seed orchard at PRT, Armstrong.

### Western Larch (Barry Jaquish)

The BC western larch breeding population consists of 608 parents selected in natural stands in two seed planning zones: the East Kootenay and Nelson. Grafts of each parent tree have been established in breeding orchards and holding beds. Four series of open pollinated field tests have been established since 1991 and results from these series will be used to estimate breeding values of all selected parents.

## SEED PRODUCTION RESEARCH

### Douglas-fir Micro Orchard Elite Seedlot Production (Joe Webber)

Three years have been completed on testing open-pollinated efficacy for the production of elite seed crops in a crown-pruned, clonal-row, Douglas-fir micro orchard. Using DNA fingerprint analyses, SMP efficacy for year one and two was 50 and 70%, respectively. This is substantially better than the current flat rate of 25% credited to orchard managers who use SMP for improving the genetic worth of production crops. These rates are encouraging but they were obtained under relatively light pollen load using branch samples of flowers. Since competing pollen cloud density is one of the most important factors affecting SMP efficacy, we needed to test our techniques under a heavier pollen load.

For this test, we included a more operational pollination device that applies greater volumes of pollen to a wider cluster of flowers. We also included two ambient pollen cloud exclusion treatments: overhead misting and whole tree bagging. The latter involved tenting the entire tree with a porous, white, agricultural cloth. We did not try to exclude pollen from sifting through the protection cloth but rather we tried to impede and trap it by misting the interior of the cloth. The cloth was relatively easy to erect (using the overhead wire already in place) and was not seriously damaged by wind. The protection cloth was only used during the receptive period of the tree (7-10 days).

Four pollination treatments were used. Open pollinated with no misting (O-D), cloth protected (tenting) with no misting (T-D), open pollinated with misting (O-W), and cloth protected (tenting) with misting (T-W). Unfortunately, the 1999 flowering crop was not heavy and abortion was high. Only five clones with a crop on each of the ramets were available. Table 1 summarizes the filled seed per cone (FSPC) for the few cones that survived. The misting lowered seed yields for both the open-pollinated and cloth protected treatments. The best yields were obtained on ramets open-pollinated and not misted. SMP efficacy was not affected by overhead misting suggesting competing pollen was not "washed out" of the pollen cloud. However, protecting the crop with the tents did improve SMP efficacy substantially. Whether misting was an added benefit for the tented trees cannot be concluded from this data because of the low cone survival and seed yields from the remaining few cones.

Table 1. Mean seed yields and percent SMP efficacy

Treatment	FSPC	% SMP
Open-Dry	25,8	62,4
Tented-Dry	8,8	80,6
Open-Wet	7,2	66,2
Tented-Wet	3,1	100

Contrary to expectation, the flowering crop and pollen cloud density (pollen load) was low. Very heavy abortion rates were also experienced that may have been partially caused by the misting treatment. Higher abortion rates were noted on cones pollinating during cool, wet conditions. Since so few cones matured on misted ramets, it cannot be concluded that misting significantly reduced yields but the trend is there.

#### Western Red Cedar Pollen Management (Joe Webber)

Pollen from most conifer species is collected under warm dry conditions and stored under relatively low moisture contents. Western red cedar (WRC) pollen, however, is best collected under cool, moist conditions and stored at relatively high moisture contents.

To collect WRC pollen buds, we first excised lateral branches taken from major whorl branches. Smaller branchlets were then excised and placed in a high humidity room or alternatively, in sealed paper bags (pollination bags work well) that maintained high humidity around the shedding branches. We collected the lateral branches from the tree when we could actually see separation between the microsporangia, the stage of pollen cone development where the microsporophylls elongate and expose the individual microsporangia. At this stage, pollen shedding was imminent.

We tested several atmospheric conditions: W/D-warm (25 C) and dry (20-30%RH); C/D-cool (10 C) and dry (20-30%RH); C/W-cool (10 C) and moist (60-70%RH); and W/W-warm (25 C) and moist (60-70%RH). No pollen was shed under the warm dry conditions and only small amounts of one lot were collected under the warm and wet conditions. The best conditions were cool and moist. These conditions yielded both the highest volumes and viability assay response. We do not have precise estimates of volume of pollen shed per volume of branchlets but yields were in the order of 20 ml pollen from about 5 L of branchlets. Volume also varies by the intensity of pollen cones per branchlet. We only picked from clones that had a minimum of 60-80% of their branchlet tips with pollen cone buds.

#### Pollen Storage (Joe Webber)

For WRC, we tested three moisture content ranges (8-10%, 15-20% and 25-30%); two storage temperatures (+5°C and -20°C); and two storage atmospheres (air and no air). The no-air treatment used a nitrogen wash to replace the air (oxygen) in the storage container. In total, we extracted 11 lots, four of which had collections made from two ramets of the same clone which we handled separately. Each lot was tested for viability and then processed to 3 moisture contents and 2 storage atmospheres and stored at each of two temperatures. These lots were tested for *in vitro* viability and are currently being field tested for fertility (seed set).



After one-year storage under these conditions, it is clear that -20°C is better than +5°C and that the mid range moisture contents stored better than either the de-hydrated (low range) or hydrated lots (high range). However, viability assay response was considerably lower than the fresh pollen results of one year earlier. These lots are currently being field-tested and the relationship between field fertility (seed set) and viability response will be determined this fall.

#### Lodgepole Pine Flower Induction

Seed production in lodgepole pine seed orchards in the southern interior of BC is traditionally low due to the low number of filled seed per cone. One way to offset these shortages in seed supply is to increase the number of seed and pollen cones per ramet. Stem injections of GA and stem girdling have been found to be especially effective to increase cone production. In August of 1998, a 2x3 factorial experiment was conducted with 2 levels of girdling (yes vs. no) and three levels of GA<sub>4/7</sub> (0, ½ and full dosage) applied over 6 clones. The trial was conducted at PRT Orchard #311 (Armstrong, BC). The GA was applied as stem injections, at a concentration of 25 mg/ml for a half dose and at 50 mg/ml for a full dose. The actual dosage injected was dependent on stem diameter measurements just below the lowest live branch. Girdling was done as a double overlapping girdle. The following traits were assessed in the spring of 1999: 1) new seed cones, 2) new pollen bud clusters, 3) foliar damage, and 4) the number of aborted 1998 cones. Analysis of variance for the number of 1999 seed cones revealed that significant effects were due to clone and treatment. The half and full dosage GA treatments gave best results, based on the number of seed cones initiated, the number of pollen clusters initiated and causing the largest increases in number of cones in comparison to previous year's crop. These two treatments plus a control were then applied to 40 clones in Orchard #311 in August 1999. Efficiency of these treatments will be evaluated in the summer of 2000.

#### Gamete Contribution

Female gamete contributions of individual clones to seed orchard seedlots are estimated in BC by the total volume of cones harvested per clone. To establish correlations between cone volume and the number of filled seed per cone, 30 cones per clone from 80 clones growing in two orchards in Vernon, BC were harvested. The total cone volume and weight of the harvested cones per clone were measured. Using cone analysis, total number and number of filled seed per cone were then determined. Correlation coefficients among the measured seed and cone traits and their descriptive statistics are shown below in Tables 2 and 3.

Table 2. Correlations between several cone traits

Trait	Cone Weight	# Seed per Cone	Filled Seed per cone
Cone Volume (ml)	0,87	0,49	0,46
Cone Weight (g)		0,26	0,28
# Seed/Cone			0,83

Table 3. Mean, coefficient of variation and standard deviation of several cone traits

	Cone Volume	Cone Weight	# Seed per Cone	Filled Seed/Cone
Mean	14,5	7	103,7	46,7
CV (%)	25,6	27,6	24	48,3
SD	3,7	1,9	24,8	22,5

#### Molecular Markers (Michael Stoehr)

Our work with chloroplast DNA markers in several of our commercial tree species is continuing. In cooperation with Craig Newton, BC Research Inc., we have now paternally inherited genetic markers for Douglas-fir, lodgepole pine, and interior spruce. These markers are useful in confirming the integrity of control crosses, evaluation of supplemental mass pollination efficacies, pollen contamination in seed orchards and mating dynamics in seed orchards. Work on developing cpDNA markers for western hemlock and western larch is continuing.

#### Seed Orchard After-effects (Michael Stoehr)

Based on the results of our first after-effects study in interior spruce (Stoehr *et al.* 1998), we have completed the field pollinations at both the Vernon and Prince George arboreta for a second study that expands the number of parents (20) and includes both male and female as factors. These lots are now being grown and will be outplanted and tested for adaptive traits in 2001/02.

We are also continuing our studies of a possible mechanism for after-effects. Progeny derived from identical crosses but reared under two different temperature regimes show significant differences in spring and fall frost hardiness. Progeny from the lower temperature treatments are more resistant to frost show. Height growth and bud flush traits between the two temperature treatments were not significantly different.

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## WESTERN WHITE PINE IMPROVEMENT IN BRITISH COLUMBIA

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**Keywords:** *Cronartium ribicola*, rust, MGR, *Pinus monticola*

Because blister rust, caused by *Cronartium ribicola* J.C. Fisch., is limiting to the growing of western white pine (*Pinus monticola* D. Don) in British Columbia (BC). Improvement has focussed on selecting for rust resistance. Selection of parent trees started in 1984 and inoculation of seedlings started in 1986 and was completed by 1995. Some inoculated seedlings are still being monitored for resistant reactions. Seedlings with slowly growing cankers or healed cankers have gone to seed orchards in two zones, coastal and interior. The objectives of future work are to develop a better understanding of this resistance, including its inheritance, and to develop strategies incorporating additional resistant genes into the seed orchards.

### SLOW-CANKER-GROWTH RESISTANCE

Different phenotypes (Hunt 1997) will be examined for cytological similarities and differences. To understand inheritance, crossing among parent trees and a few seedlings has commenced. Resulting seedlings will be out-planted in test plantations and others inoculated.

### REDUCED NEEDLE LESION FREQUENCY

Ranking families for mean number of infection spots from inoculations has not correlated to family infection ranks in test plantations (Hunt 1999). This resistance may be juvenile as current and older needles vary in susceptibility with tree age and perhaps other factors (Hunt & Jensen 2000). This resistance is not being used in BC.

### MAJOR GENE RESISTANCE

A dominant single gene for resistance exists in some United States (US) western white pine (Kinloch 1999). Two US families carrying dominant single gene resistance have remained resistant for over 5 years on repeated inoculation with BC isolates of the rust fungus. Additionally, offspring from US sources

established for 14 years in BC will be inoculated to determine genotype and stability of resistance. Additional US sources will be established in new test plantations. Demonstrating transfer to BC trees by crossing and inoculating offspring has been initiated.

#### SPOTS ONLY RESISTANCE

Preliminary results indicate that this resistance fails at the BC coast for unknown environmental factors, rather than different genotypes of the rust at the coast compared to the interior. Research is continuing.

#### MOLECULAR STUDIES

1) Two potentially useful genes for genetic improvement have been identified. The MGR gene is up-regulated when rust infects foliage of sugar pine. Its homologous gene in western white pine stays up-regulated in the bark of infected trees. A pathogen gene appears to trigger a defence response in resistant pine while disease is caused in susceptible pine. 2) Research into pyramiding the MGR gene from sugar pine with the one from western white pine has been initiated. 3) A single chain functional anti-pathogen antibody gene was constructed for incorporation of antibody mediated resistance into white pine.

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PROCEEDINGS  
OF THE  
TWENTY-SEVENTH MEETING  
OF THE  
**CANADIAN TREE IMPROVEMENT  
ASSOCIATION**

**PART 2**

**Symposium**

**GENETIC RESOURCE MANAGEMENT:  
BUILDING STRATEGIES  
FOR THE NEW MILLENNIUM**

Sault Ste. Marie, Ontario  
August 15-17, 2000

Editors  
D. Joyce and J.D. Simpson

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COMPTES RENDUS  
DU  
VINGT-SEPTIÈME CONGRÈS  
DE  
**L' ASSOCIATION CANADIENNE POUR  
L' AMÉLIORATION DES ARBRES**

**2<sup>e</sup> PARTIE**

**Colloque**

AMÉNAGEMENT DES RESSOURCES  
GÉNÉTIQUES: DÉVELOPPEMENT  
DE STRATÉGIES POUR LE  
PROCHAIN MILLÉNIUM

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# KEYNOTE ADDRESS

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## **MUTUAL TRUST AND MUTUAL GAINS: A RECENT CROWN LAND USE PLANNING EXERCISE IN ONTARIO<sup>1</sup>**

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### **ABSTRACT**

Negotiations between industry, environmental partnership and government were intense, demanding, and created a high degree of confidence, candour and openness among participants. Over a three-week period, a very high level of trust was developed as vested interests were left at the door. All parties were expected to, and did, operate in an honest and forthright fashion. At the end of the process, participants were able to deliver a document built on mutual gains. Each party could honestly say they had gained from the process and not merely acquiesced to a form of consensus. The "Ontario Forest Accord" is, by any measure, a tremendous step forward for industry, government and the environmental community.

### **INTRODUCTION**

The paths of individuals, who often seem miles apart, converged at a news conference on March 29, 1999 to announce a remarkable partnership based on mutual trust and mutual gains. Politicians, environmentalists, citizens and the forest industry came together on this day to announce a commitment to stewardship of resources and the implementation of a Living Legacy of parks and protected areas. In addressing the news conference, Ontario Premier Mike Harris said strong leadership produced results. "Through strong leadership, we have succeeded in creating an historic and lasting partnership," he said.

This leadership that Premier Harris referred to had its conception several months earlier during a lengthy and controversial land use planning exercise called "Lands for Life," a leadership that emerges from the challenges that every forest manager faces on a daily basis.

Like the premier, every forest manager finds himself or herself balancing the interests of a diverse group of stakeholders. For forest managers, the pressure to reduce costs, maintain jobs, optimize quality and volume has never been greater. All managers are expected to achieve favourable results, while faced with the reality of rising fuel costs, escalating machinery and equipment costs, increasing haul distances and a shrinking resource base.

The greatest of all these challenges, and the most pressing threat facing our industry today, is the shrinking land base. The industrial land base continues to shrink as other competing users and uses increase their demands on the forest upon which we depend.

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<sup>1</sup> Reprinted with permission from The Forestry Chronicle 76(3): 425-427

## SETTING THE STAGE FOR CHANGE

Like all provinces, Ontario is facing difficult land use issues and the conflicting demands of multiple stakeholders. Unlike many other provinces, Ontario's recent experience saw a resolution of difficult land use issues, while respecting industry's needs for cost and volume stability. It is not a perfect solution but it is an extremely useful template for other stakeholders in other provinces and it is an enabling process for seeking win-win opportunities while broadening our partnership base.

Former MacMillan Bloedel CEO Tom Stephens commented some time ago that it is no longer enough for forest companies to undertake forest management based on government-approved forest operating licenses, it is essential for companies to ensure that they have and maintain their "social license" to operate.

The resource industry can only continue to operate on publicly-owned lands with on-going public support. One need only look at BC and Ontario to see how public perception shapes public policy. If the prevailing perception is that forests are in crisis and that forest companies are doing a poor job managing, legislators will eventually react accordingly; despite the forest industry's assertion and factual evidence that we are managing in a responsible sustainable manner.

Across Canada and the US, this issue has resulted in a "war of the woods," often culminating in massive, unilateral withdrawals of acreage and fibre volumes by governments. In the US Pacific North West, a reduction of nine billion board feet in annual harvest volume has been implemented on National and State Forests. In Ontario, management issues around Temagami and Algonquin Parks have continued to cause problems for successive governments and industry. It is clear that we cannot face public debate and concern in a reactive mode. In forest issues, as in most issues, there must be a balance among different interests and differing opinions. The challenge for the forest industry is to avoid its traditional approach to reaching land use decisions. A proactive approach is the best way, and perhaps the only way, to succeed.

There has never been a better time for the industry to undertake this initiative. Government, environmentalists and the public are increasingly interested in achieving progress. Stakeholders want to see a balance among jobs, economic growth, recreation and preservation in the form of concrete initiatives.

## ON THE ROAD TO LANDS FOR LIFE

When elected in 1995, Premier Mike Harris made a commitment to resolve the conflicts around land use on Crown Land in Northern Ontario. The Lands for Life land use planning process encompassed 40 per cent of the province of Ontario, in excess of 45 million hectares. It was easily the most ambitious public involvement exercise ever undertaken by the Ministry of Natural Resources.

The objectives of Lands for Life were: to complete Ontario's system of parks and protected areas; recognize the land use planning needs of resource-based tourism; provide greater certainty for resource industry users; and explore enhanced opportunities for outdoor recreation, including hunting and fishing.

The Ontario forest industry has long supported the concept of an approved land use plan for the province. This support was predicated on a strong desire to overcome the uncertainty surrounding the use of forest lands. However, industry's support quickly turned to concern after reviewing the Lands for Life objectives and their apparent lack of concern for the needs of the industry in terms of continuity of access, volume of fibre supply and stability of costs.



## THE PROCESS, THE PEOPLE AND THE CHALLENGE

The Lands for Life process required substantial public involvement. This was organized by Round Tables, each made up of 15 residents of Northern Ontario. The Round Tables were reflective of the forest regions of the North, Boreal East, Boreal West and the Great Lakes St. Lawrence, and reached out to more than 65 000 participants through public meetings, community workshops, questionnaires, written submissions and e-mail.

The industry, in its traditional role, successfully argued that the Northern Ontario economy would be devastated if the environmentalist proposals were accepted. Likewise, the environmental groups, realizing that the battle was being fought in Northern Ontario but the war would be won in Queen's Park, began to organize a politically astute campaign fully aware of an impending provincial election call. The Ontario government was left in a difficult position with little room to manoeuvre an acceptable settlement.

When the draft report was released at the end of October 1998, the Round Table's recommendations called for: 64 new provincial parks, 157 new conservation reserves, 89 new stewardship reserves, 92 enhanced management areas, 4 new heritage waterways, and 2 heritage coastlines.

It was a huge gain yet still fell short of the Premier's goal of 12 per cent of the land base, an important consideration given his personal commitment to the issue.

## A TURNING POINT FOR ONTARIO'S FOREST INDUSTRY

This was a critical crossroads for the industry. After full participation in the initial process, forest companies were approached in November 1998 to consider entering discussions focused on achieving the 12 per cent target. At first glance this appeared to be a losing proposition, and historically I believe the industry would have certainly viewed it that way. However, it was clear to some that the government would deliver on its targets – with or without the industry's assistance. Which road should we choose: intransigence or involvement?

In our opinion, it was far better to be at the table and participate than to be delivered a *fait accompli*. The Domtar position had always been supportive of the completion of the parks and protected areas program on the proviso that the company not be hurt in the process.

We agreed to accept the Ministry of Natural Resources' invitation with one stipulation. We insisted that the government be an active participant in the discussions, not simply a facilitator. This was to ensure that the new discussions were based on a real process of negotiation with full government involvement, rather than simply a debate among diverse interest groups.

As in most negotiations, we felt it critical to proceed with a clear vision of the output we desired. We developed lists for both the Partnership for Public Lands and the Ministry of Natural Resources on the conditions required for industry involvement. These were tabled very early and formed the basis of discussion at our first negotiating session. Common to both lists was the requirement to commit to the overriding principles of no increase in delivered wood cost and no loss of harvest volume in both the short and long term as a result of these discussions.

## MUTUAL GAIN AND A COURSE FOR THE FUTURE

The resultant Forest Accord comprises 31 commitments made by the representatives of the three interests which, taken together, map out a new relationship for the future. The Accord sets out a mutually acceptable approach to establishing future parks and protected areas while addressing the needs of the forest industry. Commitments were made to protect areas resulting from the Lands for Life process through regulation, detailed mapping of the 12 per cent protected areas and the establishment of a

mechanism for expansion of the protected areas through mutual agreement and consultation. Commitments were also made to support the concept of long-term continuity and security of wood supply so that the forest industry could confidently make investments for the future.

All parties were winners in the process:

- 1) The Government of Ontario achieved resolution of parks and protected areas, demonstrated leadership, reinforced its image as an environmentally responsive government and, most importantly, met Premier Harris' commitment.
- 2) The environmental community achieved its 12 per cent target for parks and protected areas and developed a resolution model for other jurisdictions.
- 3) The forest industry achieved commitments which include: no long term reduction in volumes, no net increase in the cost of wood delivered to mills, improved security of fibre supply and the ability to redirect wood flows (i.e., best wood to best mill).

Collectively, we achieved a new working relationship and a template for future consultation, discussion and negotiation. The high level of trust developed during the process is a valuable asset. It is important to realize the tremendous long-term value of this relationship and the doors it opens for the industry in its objective to find enduring, stable mechanisms for sustaining its business over the next decades. It is our hope and our goal to extend this new, positive relationship throughout our respective organizations.

Among the many innovative elements of the agreement, three aspects contained in three separate clauses of the accord stand out.

First, the industry will support the objective of 12 per cent parks and protected areas and become a partner in achieving this objective.

Second, all parties to the accord now become partners in growth and economic well-being. This is no longer the sole domain of forest companies and government. The accord not only redistributes this responsibility, but it provides the glue that binds all partners together to ensure that we work collaboratively to find mechanisms which provide forest companies continuity of supply at stable costs. That will require all partners to work together to grow more timber on less land and to reassess traditional objections to more intensive forest management.

Third, there is a credible, hands-on follow-up mechanism in the form of the Ontario Forest Accord Advisory Board. The OFAAB is there to ensure that all commitments are met and provides the vehicle for allowing the participants to the forest accord to agree on methods, assess progress, and solve problems along the way.

The culmination of this process resulted in a major announcement on March 29, 1999 in Sudbury. The Premier of Ontario, along with representatives from environmental groups, resource industry leaders and senior cabinet Ministers, announced "Ontario's Living Legacy." It was there that Premier Mike Harris talked about leadership, results and partnerships. "We are protecting Ontario's Living Legacy for generations to come, while sustaining jobs and setting the stage for long-term economic growth in Northern Ontario," he said.

The action taken by some industry players in agreeing to sit down with the environmental groups and the government was not without controversy. However, there is a strong belief that the outcome has and will continue to be beneficial, provided that the industry can regroup, set aside its differences and focus on ensuring the delivery of commitments.

There will be some difficult choices to make as the Living Legacy strategy is implemented. However, the negotiations around the Ontario Forest Accord have allowed for the creation of a unique partnership based on mutual trust and mutual gains.

## A TEMPLATE FOR THE FUTURE

The results of the Ontario experience speak for themselves: a truly historic accord honouring industry's needs for certainty in cost quality and volume and achieving huge gains in parks and protected areas for present and future Ontarians.

The overall lesson in Ontario is one of opportunity, leadership and results. To strengthen and enhance the

future of our companies and the industry, we have to abandon the never-ending war of the woods. Instead, we have to seek out opportunities in other jurisdictions and, when conditions are right, be prepared to not only participate, but provide the leadership necessary for success.

These opportunities are not always evident and, at times, seem more like crises or threats or public relations nightmares. However, whether the opportunity takes the form of an invitation or an accusation, the industry must act decisively. It must grab the opportunity to participate in public debate and public policy. It must take the lead in proposing win-win ideas and proposals. It must build mutual trust and create mutual gains. It must have the courage to lead and the strategy to produce results.



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GENETIC RESOURCE MANAGEMENT  
IN THE 21<sup>st</sup> CENTURY

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## STRATEGIC DIRECTIONS IN UTILIZING GENETIC RESOURCES

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### ABSTRACT

With further increase in Earth's human population likely, it is also likely that more wood will be needed than can be supplied from today's forests. Forest genetics will contribute to management of both native forests and plantations. The progression from strategies to increase adaptation to later focus on biomass allocation and quality are discussed. As breeds, pedigreed families, and clones become available and then well understood, various deployment options become possible and useful, and biodiversity concerns can be better addressed. A case is made for increased rotation length. Finally, genetic responses to expected climate changes are suggested, noting that cooling will probably require much more attention than the current warming event.

### PROBLEM STATEMENT

In their book "GLOBAL FORESTS: Issues for Six Billion People" Laarman and Sedjo (1992) surveyed forest inventories and issues of a decade ago, and offered some projections of (generally) short-term future supply and need for wood and other important services provided by forests. When considering the inputs of genetics, one needs to think of more distant futures. Predicting the future, particularly decades or even centuries ahead, is hardly an exact science. Acknowledging in advance that all such predictions are likely to be wrong, and many badly so, I will use the creative thinking of Sutton (1999, 2000) to provide a qualitative framework for the future need for forestry to utilize genetic resources well.

#### Native Forests

Although we have domesticated many plants and animals, and get the majority of our food and cloth from these domesticates, we have generally satisfied our needs for wood in a hunting-and-gathering mode. The reasons for this are many and probably not fully understood. For most wild crops that have been domesticated, productivity per unit area generally is greatly increased by that process, often many fold. While forest genetics has an important role in the understanding and management of native forests, forest genetics and tree breeding both play crucial roles in the domestication of trees for use in plantations (Libby in press).

#### The Need for Forest Plantations

Sutton noted, perhaps optimistically, that Earth's human population may soon reach 10 billion people and stabilize at about that level. For his low estimate of future wood needs, he used recent average per-capita wood consumption, approximately 0.6 cubic meters of wood per year. That leads to an estimated demand of 6 billion m<sup>3</sup> per year for 10 billion people. Recent harvests have averaged about 3.5 billion m<sup>3</sup> per year, leaving a future deficit of 2.5 billion m<sup>3</sup> per year. With about 80% of that 1990s harvest coming from native forests, and given various increasing restrictions and other demands on native forests, Sutton estimated that wood harvest from them could not be increased by more than about 0.3 billion m<sup>3</sup> per year. An

additional 0.2 billion m<sup>3</sup> per year will probably come from new plantations now planted, but not yet of harvestable age and thus not contributing to annual-harvest statistics. That leaves 2 billion m<sup>3</sup> per year shortfall. He then calculated that, if average harvest productivity of new plantations could be 20 m<sup>3</sup> per ha per year, it would take an additional 100 million ha of plantations to meet expected demand.

Sutton also considered the likely possibility that energy will become relatively more expensive. Since wood is highly energy-efficient compared to such alternatives as bricks, cement, plastic, steel, and aluminum, he reasoned that per-capita use of wood might therefore increase from its recent 0.6 m<sup>3</sup> per year to and perhaps beyond the current U.S. average of about 2.3 m<sup>3</sup> per year. That would require about 1.4 billion ha of plantations, which would cover about 10% of Earth's land area, plus 2.6 billion ha in native forests, totaling 28% of Earth's land surface in forests. That total of something near 4 billion ha of native and planted forests should provide enough wood, wood products, and other forest services such as water, wildlife habitat, and recreation to allow future civilization to work well.

#### Factors Affecting Plantation Productivity

Sutton's estimates of needed plantation areas are based on volumes of wood, and they can be modified by increasing or decreasing the productivity of the plantations. However, the concept of "productivity" is more complicated than just the cubic meters of harvestable wood that can be grown per year on a forested site. The concept also covers the quality of that harvested wood for various purposes. Even more broadly, it includes the productivity of other goods and services a native forest or plantation can or could provide. In some cases, all of these elements of productivity are improved or harmed by a particular practice; in other cases, tradeoffs among them must be considered.

The many factors that affect plantation productivity include site selection, species choice, nursery practices, site preparation, spacing control, planting practices, post planting care, control of competition, fire, pest and pathogen protection, fertilization, thinning, pruning and several kinds of genetic input. Most of these many factors interact with each other, and their importance is often situation dependent. Getting it wrong in one factor can negate the good that excellent inputs in several other factors might have been expected to achieve (Libby in press). This paper will focus on genetic inputs.

### TREE-IMPROVEMENT PROGRAMS

"Tree improvement" is a broad term that can include such non-genetic things as form-pruning. Most of us at this meeting equate "tree improvement" with domestication, which implies genetic changes in populations to suit human needs or purposes. But domestication is more than that. I noted above that any factor affecting plantation productivity can limit the entire enterprise if it is not done well. But even beyond that, domesticated plants and animals rarely reach anywhere near their full potential productivity or performance without husbandry that has been specifically adapted to the domesticates. We are still in an early stage of domesticating forest-tree species. Silviculturists will need to modify all aspects of plantation husbandry, from site selection through to harvest schedules, to take advantage of the differences among the breeds and clones that will be deployed. Working with silviculturists to achieve this is an important strategic direction for tree improvement professionals to pursue.

#### Provenance Studies

A well accepted principle for plantation forestry is that, first, one should know or find out each species' pattern of provenance variation (Zobel and Talbert 1984). For native species, this focuses on the size and shape of the 'breeding zones' serving the plantations. For exotic species, one needs to test various potential source populations, including land races that are developing in other regions using the same exotic species. Continually refining such information, as provenance tests are increasing in age and scope, will remain an important strategic direction in the future. Such activity is likely to result in discontinuing deployment of general collections from populations found to be maladapted, as well as



adding other populations or landraces to those being deployed as their performance in tests warrants.

### Selecting Base Populations

At a meeting held in Vancouver in 1999, *Unifying Perspectives Of Evolution, Conservation And Breeding* honoring Gene Namkoong, S. Barker gave us much good advice based on his extensive animal breeding experience. Relevant to building base populations, he noted that selecting parents with desired production traits from populations or land races that are already well adapted to your deployment destinations is much easier and more effective than the reverse, namely accumulating parents with good production traits from untested or inappropriate populations, and then trying to adapt the breed to your conditions.

In the first one or two generations of most tree domestication programs, much attention is given to finding and breeding trees that have grown much faster and are individually much larger than average. Early height growth in progeny trials is a frequently used criterion for assessing both growth-vigor and adaptedness. Traits such as bole form and branch configuration, and relative freedom from serious damage from both biotic and abiotic agents, are also used to evaluate the founding members of breeding lines and their immediate offspring. These have seemed to be reasonable principles, and as new breeding programs are begun, they remain so.

### Arboreal Biomass Productivity

In the next few generations of most tree domestication programs, the focus usually shifts to finding and deploying families or clones that produce more wood per hectare. This continues the strategy of finding and breeding populations that are well adapted to the sites of their deployment. Although some people *believe* that most organisms are perfectly adapted to their native environments, that is rarely true. Most are imperfectly adapted to the recent environments in which their ancestors survived and reproduced. When tree breeders attempt to increase the arboreal biomass produced per hectare per year in plantations, they select trees: 1) that better and more-completely use those plantation environments, and/or 2) that function well with reduced rates of catabolic respiration, and/or 3) that lose less of their biomass to things that damage them or eat parts of them. Deploying control-pollinated out-crossed families and clones eliminates the loss of health and growth vigor associated with planting inbreds in most forest-tree species, and contributes substantially to this goal.

It seems reasonable to expect diminishing returns in later generations. However, environments can be expected to continue changing. The pursuit of adaptations to changing environments will continue, and humans can assist in it. Thus, continued attention will be given to adaptive traits, but the greatest gains in adaptation will probably be recorded in the first few generations of tree breeding.

### Harvest Index

A second strategy, widely used in agriculture, is to improve the so called harvest index. In this strategy, biomass is reallocated within crop plants such that the percentage and/or value of the harvested portion of the plant is increased within a fairly constant total biomass produced per hectare per year. For forests, the families and clones deployed to plantations in later generations will be selected from highly adapted breeding lines and they will have combinations of additional selected traits that confer much higher harvest indexes than are typical of their breeding lines as a whole.

Once we have such well adapted breeding lines, I question whether greater early height growth remains a useful trait and, if it is positively correlated with height at harvest, whether it might even become counterproductive (Libby 1987). V. Koski put this into perspective for me at a IUFRO meeting in Montreal a decade ago. He called it "rubber band breeding", in which the same amount of wood is simply stretched into a taller and skinnier tree. Breeding for shorter, fatter trees may be much better for harvest index than continuing to breed for ever taller (skinnier?) trees. But since short trees are usually killed by their taller

neighbors, that requires either monoclonal deployment, or deploying reliable mixtures of clones that all grow to be shorter and fatter.

Another option, which may become available as we learn to genetically engineer our trees, is to reallocate biomass from sexual parts in trees to bole wood. Of course, if trees have been engineered to have no sex, they may just fill their photosynthate sinks earlier in the day, and produce no more wood than do sexually-active trees. However, experiments should soon be available comparing miniclones of the same macroclone, one miniclone competent to have sex, the other miniclone of that macroclone engineered to not have sex. With several such macroclones containing sexless and sex-competent miniclones in a well designed experiment, the degree to which the sexless miniclones allocate photosynthate not needed for sex to bole wood should be quantifiable.

### Product Quality and Other Benefits

As well adapted breeding lines with improved harvest index become available, product quality takes on increasing importance. Wood traits such as dimensional stability, stiffness, frequency of internal checking, frequency of collapse, specific gravity, tracheid dimensions, color, and durability are all getting some attention for solid-wood uses, as are physical and chemical traits useful for pulp. One may clonally evaluate progeny of parents bred for other (usually adaptive) traits. One then finds a few clones that also have the desired quality traits. In early generations, this is probably more effective than adding these quality traits to selection indexes during breeding.

As genetic engineering comes on line, it is not too big a leap to consider that forest trees might be engineered for capacity to produce some pharmaceuticals, bear nutritious fruits, or enhance site-nutrition during their growth or at harvest, along with their production of excellent wood. Other targets for engineering these brave new trees include self-pruning and ability to survive over spraying of herbicides.

## DEPLOYMENT OPTIONS

While deployment configurations are not, strictly speaking, a part of genetics, knowledge of the characteristics and performances of breeds, families, and clones allows managers to deploy these units in various ways that serve their goals. In general, clones allow this to be done most effectively and the advantages gained go down with the amount of genetic variation within the units being deployed.

### Management Efficiency

A great increase in management efficiency is one of the strongest arguments for developing a clonal program. As confidence in the clones increases, planting density generally is reduced and then adjusted to each clone (or family or breed), and the timing and intensity of various silvicultural treatments can be prescribed for each. At harvest, wood can be sorted by clone and better assigned to its more valuable uses, or used more effectively in such processes as papermaking.

### Arboreal Genetic Diversity

Productivity, risk, aesthetics, and service as ecosystem keystones are four concepts generally considered when deciding on amount and configuration of genetic diversity in plantations.

In general, arboreal biomass productivity per unit area is greater when several clones are grown in intimate mixture, compared to the average of those same clones grown in monoclonal stands. However, productivity may be more effectively improved by such things as fertilizers, pesticide applications, etc. if the clones are in monoclonal stands, where each clone's particular requirements can be more precisely met. Harvest value may be substantially increased if the trees are deployed in monoclonal stands, as it will

be easier to identify the different clones and assign them to their most valuable uses.

Estimation of risk of damage or loss due to various biotic and abiotic agents is complicated, in part because some of the pests and pathogens are short-lived and capable of evolving to overcome defenses of the host trees (Libby 1982). Since trees are very large, it is sometimes argued that a single tree is already a large genetically uniform niche for such pests and pathogens, and that monoclonal stands don't make the risk problem much worse. Furthermore, we are beginning to understand that large trees may not be as uniform a host for a pest or pathogen as their DNA might indicate. This is because there are differences in maturation state within each tree, and also because the presence of endophytes may produce substantial operational diversity to organisms attacking even different parts of the same branch. It is also claimed that the ability to salvage or simply replant following damage or mortality of a small proportion of the clones deployed in a region or landscape is greater if they are deployed in monoclonal stands, compared to the same damage or mortality being dispersed within an intimate mixture of susceptible and resistant clones.

The differences between intimately mixed and monoclonal stands of a single species are usually not discernible to most observers. (The general observation that intimately mixed stands use the site more completely than do monoclonal stands, thus producing more wood, may mean that there is more "niche space" available for associated species in monoclonal stands, a point in favor of mosaics of monoclonal stands.) However, there is a big difference in aesthetic response by most people to single species and multi species plantations (and their aesthetic response is generally even more favorable if spacing is irregular, compared to rigid rows and columns). Where random trees of some different species may not grow effectively together in intimate plantation mixture, there may be some clones from each species that are able to successfully coexist. There is substantial interest and some promising successes in planting multi-species stands, and genetics may be able to help in selecting families or clones well adapted to grow together.

It seems likely that other ecosystem services besides aesthetics, such as provision of wildlife habitat, are better served by multi-species plantations than by single-species plantations. It is intuitively attractive that the configuration of genetic diversity in a single keystone species will affect at least some ecosystem components. If a large plantation has been planted to a single species, one wonders whether mosaics of monoclonal stands are substantially different in such ecosystem services from widespread intimate mixtures of the same clones. This is clearly an area for careful research attention in the near future, as there have been few studies on this question.

#### Compatible Genotypes

A future goal of some clonal forestry programs is to have a set of well understood clones that can be deployed in prescribed mixtures, such that they make complementary demands on the site. If that goal can be achieved, the performance of such plantations should substantially exceed that of monoclonal mosaics, or of mixtures of poorly known clones, or of the sets of new and unique genotypes that one gets with seedling deployment. In some cases, some of the clones in such a mixture might be included as slower growing trees whose task it is to control branch size on the lower logs of the crop clones, and then self-thin or be thinned for low-value products. But successfully mixing 5 (square spacing) or 7 (hexagonal spacing) clones that are all supposed to make it to harvest in similar frequencies and at the same time will require a high level of knowledge with respect to their growth rhythms and mutual competitive interactions. This latter strategic direction may turn out to require more time and testing than its added value merits, but it seems worthy of some attention in the near future.

### BIODIVERSITY CONSIDERATIONS

Forest managers are increasingly aware of public and regulatory concerns about biodiversity and are responding to them. While we have long been aware of the implications of genetic diversity of the tree component of forests relative to productivity, efficiency, and risks, we have more recently needed to

consider the effects of the trees on associated species in forest ecosystems. Biodiversity can be considered at the stand level, but it is important to also consider it at the landscape level.

#### Forest Plantations vs Native Forests vs Agricultural Substitutes

Forest plantations usually have less total biodiversity than do native forests and their associated biota are also usually different in composition from those of native forests in the same area. This is an argument in favor of native forests if viewed on a stand basis.

With respect to agricultural substitutes for trees, most forest plantations host much greater biodiversity than do most fields of agronomic crops. It is sometimes argued that crops such as kenaf can and should be substituted for trees as a source of fiber. This argument will usually fail, in part because of the differences in associated biodiversity, as well as the greater erosion, greater pesticide use, and greater fertilizer use that typify agriculture compared to plantation forestry operations. It also fails when the likely near future need for agricultural lands for growing food is considered. An important strategic initiative is to accumulate reliable data on the biodiversity maintained in these contrasting forest-plantation and agricultural systems.

Many in the environmental community, and some of the general public, have developed strong negative positions when they evaluated the associated ecosystems in dense natural reproduction, or in European style plantations with 2 000 or more trees planted per hectare. Such dense stands of trees have been characterized as “biological deserts”. The dense stands of young trees exclude almost all other vegetation and thus the many other organisms that would live in or on the associated flora are also absent. Thinning these dense stands and plantations will normally allow these associated understory plants and their associated fauna to resume their presence.

#### Effects of Deploying More Reliable Genetic Material

A major advantage of deploying reliable families or clones to plantations is that planting densities can be low. Instead of having to plant 2 000 or more variably reliable seedlings per hectare, 1 000 or fewer reliable propagules can be planted per hectare, to still achieve similar or even better final harvest stands. Lower planting density not only reduces planting and later thinning costs it also leaves much more open niche among the planted trees, where a rich associated biota develops soon after planting and persists through much or all of the rotation.

#### Landscape Biodiversity

If viewed on a landscape level, answers to the questions concerning biodiversity in native forests vs plantations can be changed. For example, one may consider a landscape with 100% native forest vs a landscape with 100% plantations vs some appropriate mosaic of the two systems. The answer is clear if one accepts the principle that the worst thing one can do to foster biodiversity is to do the same thing over large areas. Thus, imposing single-tree selection over a large area is as damaging to the level of biodiversity as clearcutting the entire area in the same year. If the rotation is 80 years, clearcutting and planting 1/8 of the area each decade clearly produces greater biodiversity than does uniform single-tree selection. If appropriate proportions of managed native forests, plus preserved old-growth native forests, are parts of the landscape, as they should be, then the different suites of biota sustained in the different age cohorts of plantations in that landscape add to, not detract from, regional biodiversity. This is a clear positive benefit of properly sited and managed plantations.

#### Contamination of Native Gene Pools

By this is meant the migration into native populations of genes from other populations that may reduce the

overall adaptedness and fitness of the native populations.

A few decades ago, our main concern was for incorrect provenances used in plantations within the native forests. This was heightened when it became known that a common response by a tree under stress is to reproduce earlier or at unusual intensity. Thus, a tree well-adapted to the plantation site would want to stay there and would set about to do so by growing fast and tall, to stay safely ahead of its neighbors. It would probably not allocate unusual proportions of its nutritional resources to reproductive activity. If it found itself somewhat maladapted, it might decide to try its DNA in various new combinations on nearby sites, best accomplished by heavy production and short-distance dispersal of seeds. If it found itself lethally maladapted,

it died, and that is no problem for the native populations. But if it found itself seriously but non-lethally maladapted, it would try to get its DNA well away from that unfriendly place, best accomplished by early and massive production of pollen. This latter may be the main threat to the surrounding native forest, which would be the recipient of most of that fleeing maladapted DNA. For genetic contamination to occur, females in the surrounding forest would have to be receptive at the time of this escape-by-pollen; if they are in receptive synchrony, that could be big trouble.

More recently, we have worried about other kinds of genetic contamination. Seedlings or clones from our tree-improvement programs have been genetically selected to better serve the breeders' goals, but those gene combinations are not necessarily best for the surrounding native forest. Hopefully, the tree breeders will be deploying well adapted genotypes, so the extent of seedling invasion and pollen contamination should not be as bad as when we used to get cheap seeds from distant provenances and use them for reforestation. Still, it was and is a worry.

Even more recently, we have worried about the biotechnologists and genetic engineers releasing Frankentrees into our innocent forests. The logical counter to that is to require that transgenic trees be sterile, which may have other benefits as well.

I am personally aware of several good research proposals to study the extent of gene migration from planted stands into nearby native stands or plantations. These proposals have been submitted over the past decade or more, and they have generally not been funded. I find this curious, as scientists, foresters, and environmentalists are all concerned about possible genetic contamination of native populations, yet we have little data on which to base those concerns and with which to plan remedial actions. Finding out more about this topic is an important strategic direction for genetic research in the near future.

## ROTATION LENGTH

In recent years, there has been a tendency for rotation length to be reduced, driven by both financial pressures to recover capital quickly and by needs for wood now. Sutton (2000) has made two interesting arguments that rotation length may increase in the third millennium. An anticipated increase in rotation length will affect which traits are selected and how they are ranked in breeding and selection programs.

### Effects of Energy Costs

The per-capita use of wood will likely increase as higher energy costs trigger its substitution for more energy demanding alternatives, such as bricks, concrete, steel, and aluminum. These substitutions will largely be for construction purposes, which generally require high quality solid wood. This higher quality solid wood is better produced on longer rotations. The recent increased use of reconstituted wood may reverse under higher energy costs because reconstituted wood requires much more energy in its production than does solid wood. In Sutton's scenario, most high quality wood will be used first as solid wood and then reclaimed for energy production in electricity generation plants, or used as feedstock in a lignochemical industry, replacing petrochemicals for many products such as plastics. The demand for low quality wood that is pulped or burned for cooking and shelter heating, will also probably hold up and intensify under higher worldwide energy costs. Such low quality wood will probably be acquired as

thinnings or from marginal (low productivity) native forests.

#### Effects of Carbon Credits

If indeed carbon credits become available, they will probably be largely provided for two major forest management options: 1) increasing rotation length in established plantations and native forests and 2) establishing new forests and plantations on land that is not now forested. The first option is of chief interest for this topic. By requiring increased rotation length, carbon credits will have some serendipitous salutary effects. One is a likely increase in plantation productivity, as the plantations will fully occupy the sites longer before harvest. A second is an increase in the quality and therefore value of the wood when harvested, from either plantations or native forests. (The second option, serving essentially to provide cash flow for new plantations, allows management to better afford some early and mid-rotation activities that will probably increase productivity.)

### CLIMATE AND OTHER ENVIRONMENTAL CHANGE

Many sorts of environmental changes can be large enough to require adaptation to them by native populations or in planting stock for replanting harvested sites. If the change is even larger, the populations may need to migrate or plantation siting may need to be changed. Environmental factors to consider can include such human-caused things as weed invasion, air-pollution, or an increase in average temperature. But we should not ignore changes in climate independent of human causation. I recently completed an assignment to help prepare an assessment of likely effects of climate change on California's native giant sequoia groves (Stephenson and Libby 2000). The findings of this exercise probably have implications for Canadian forests as well.

Until recently, most planners and the general public assumed or accepted that the present climate is stable and the future was planned for similar conditions. More recently, planners began to comprehend that increased levels of greenhouse gases will result in general global warming with uncertain but probably serious consequences for near sea level communities and for most or all ecosystems globally. Since we were dealing with a species whose individuals can live for 3 000 or more years, our attention was soon focused on likely climate changes over periods of centuries and even millennia. This resulted in something of an epiphany for me. Because our findings were surprising to us and the basis for them is currently little discussed, I present them in some detail, with three Figures in support.

Identifiable pollen recovered from seabed, lakebed, swamp, and meadow cores indicate the plants that were rare or common in the vicinity of the cores at different times in the past; these data combined with oxygen isotope ratios from ice deposits are good indicators of past regional and global temperatures. Recent work with these indicators has greatly increased our knowledge of past events, summarized for the Sierra Nevada forests in Millar and Woolfenden (1999). It is reasonably clear that, during the past 2.6 million years, Earth's climate has been cycling from glacial to interglacial periods and back again. Following an earlier period of relatively short cycles, there have been about 7 longer cycles during the past 650 000 years, with quite consistent periodicity and large differences in temperature between the warm interglacial and cold glacial periods (Figure 1). During these past 7 major cycles, about 90 000 to 115 000 years of a glacial period have alternated with about 10 000 years of an interglacial period. Each major period contains secondary and lower order events with warmer than recent average or colder than recent average temperatures, or *vice-versa*, each lasting from a few years to many centuries (not shown in Figure 1).

It is clear that the human species, having existed for over 200 000 years, has survived at least two such cycles (Figure 2), and that giant sequoia has survived all of them. But what did these records tell us about the ability of giant sequoia groves to survive expected climate changes in their present locations?

Warming from the most recent glacial period apparently began about 18 000 years ago (Figures 1 and 2),

and the current interglacial (the Holocene) is dated from about 11 000 years ago. Thus, it appears that Earth is about due for the next glacial period, and may have already started into it (Figure 3). Furthermore, studies of indicators of past events suggest that large changes in average temperature from warm to cold or cold to warm sometimes occurred in only a few decades, perhaps in as short a time span as 10 to 20 years. Such rapid transitions occurred at both the onset and termination of the Younger Dryas, a 1 300-year cold event between 13 000 and 11 000 years ago (visible in Figures 2 and 3).

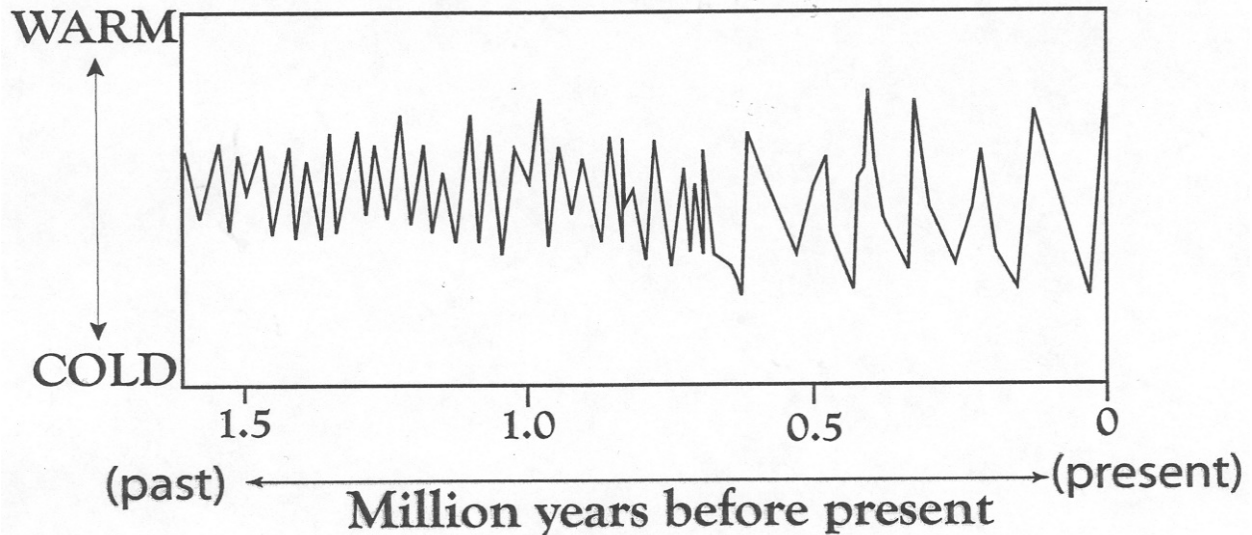


Figure 1. A smoothed curve of major glacial and interglacial periods, showing relatively short cycles until about 650,000 years ago, and then longer cycles with greater differences between the warm interglacials and the coldest parts of the glacial periods. Adapted from Figure 1A in Millar and Woolfenden (1999) with secondary events smoothed over.

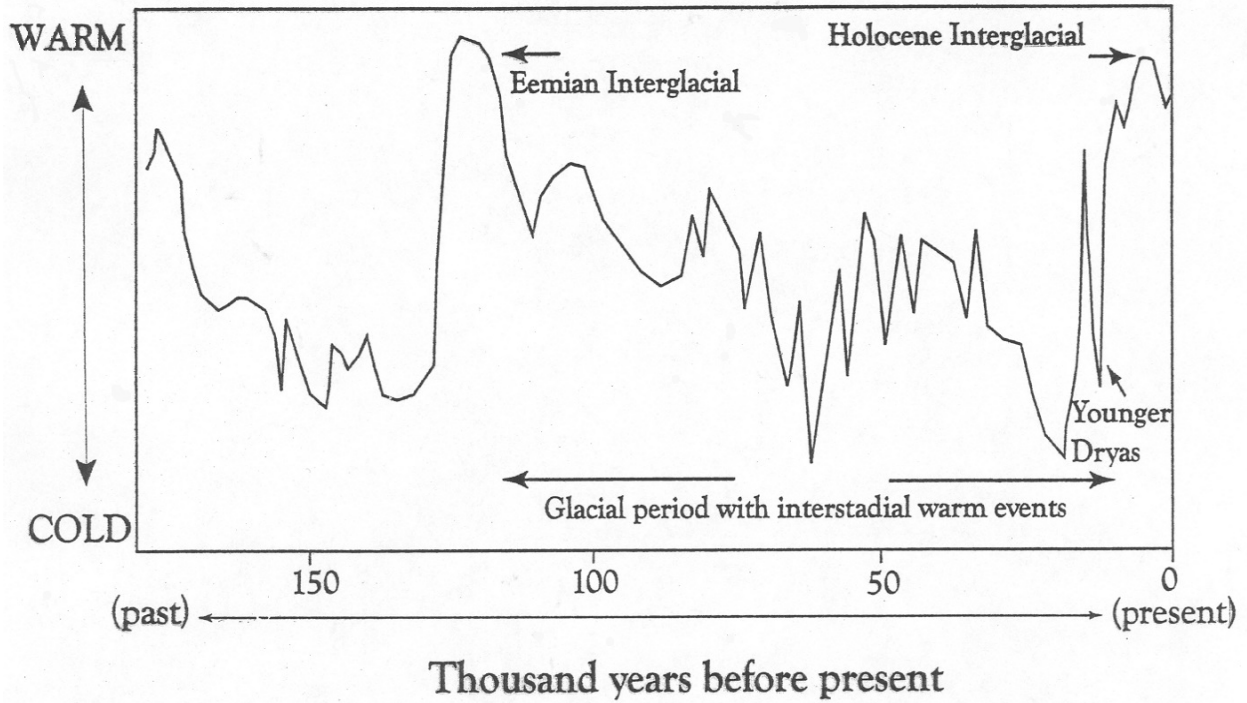


Figure 2. A smoothed curve of the past 180,000 years showing the two major glacial periods and the Eemian and Holocene Interglacials, with secondary events such as interstadial warm events and the Younger Dryas also shown. Adapted from Figure 1B (Millar and Woolfenden 1999) and Figure 2B (Millar 2000), with tertiary events and some secondary events smoothed over.



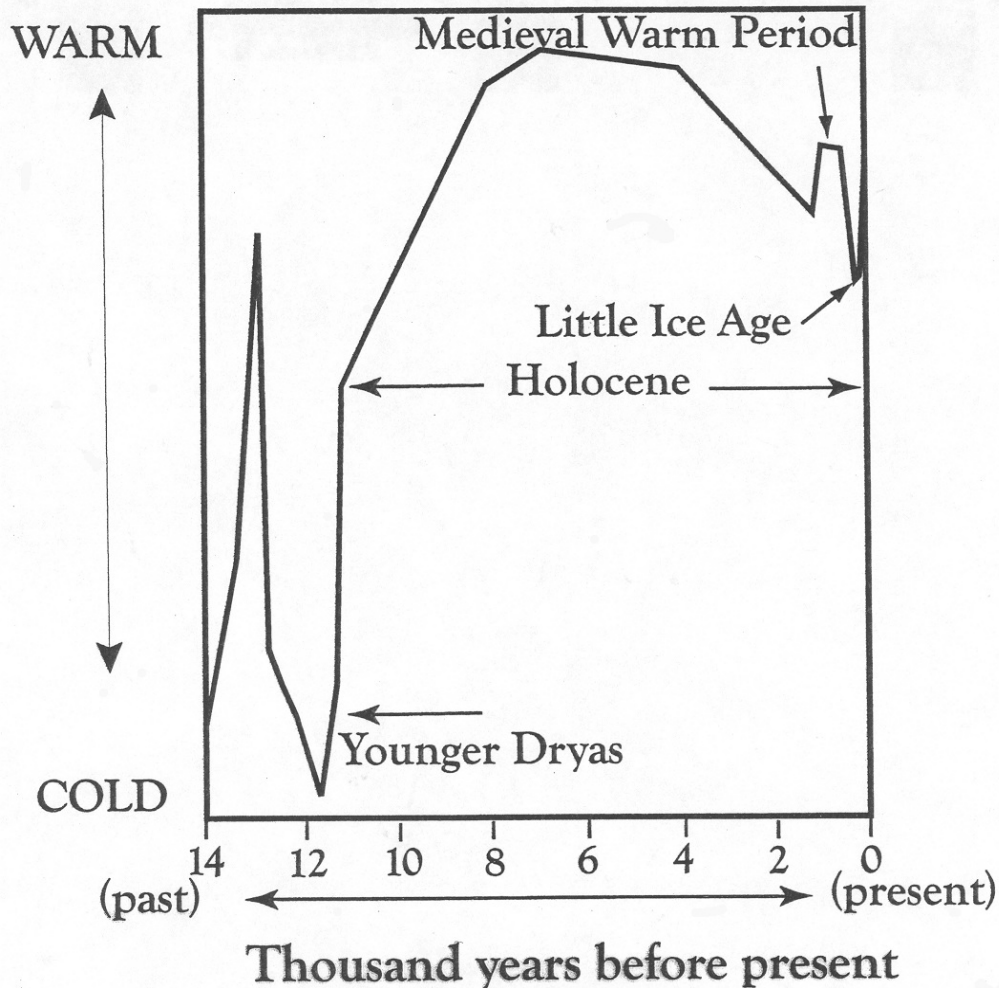


Figure 3. A smoothed curve of the past 14,000 years, beginning part way up the warming trend that began 18,000 years ago, showing the very rapid cooling and then warming of the Younger Dryas, the fairly rapid changes associated with the Medieval Warm Period and Little Ice Age, and the more gradual warming to and cooling from the warm Holocene episode between 8,000 and 6,000 years ago. Adapted from Figures 1B and 1C in Millar and Woolfenden (1999), with some secondary and all tertiary events smoothed over.

Average global temperatures increased about  $10^{\circ}\text{C}$  from the coldest parts of glacial periods to the warmest parts of interglacials, with regional differences smaller or greater, and some as great as  $20^{\circ}\text{C}$ . During the Holocene, global temperature peaked and reached a plateau between 8 000 and 4 000 years ago, with average temperatures about  $2^{\circ}\text{C}$  warmer than at present (Figure 3). Then, a period of fairly steady temperature decline commenced, reversing about 1 100 years ago (900 A.D.). This so-called Medieval Warm Period, recovering about 1 to  $1.5^{\circ}\text{C}$ , lasted until about 1350 A.D. Temperature and moisture differences varied in expression and intensity from region to region, with some areas being much warmer and drier than immediately before or since. Worldwide average temperatures then declined about another  $1.5$  to  $2^{\circ}\text{C}$  from about 1400 to 1900 A.D., a period known as the Little Ice Age. Temperatures then leveled and began to rise in the 20th Century, due to some combination of anthropogenic emissions of both cooling particulate matter and warming greenhouse gases, superimposed on an underlying periodicity that may be continuing the cooling trend into the next glacial period.

Based on pollen core and macrofossil evidence from the recent warmer period of the early Holocene and much colder periods of the Younger Dryas and before, migrations of the giant sequoia groves have been mostly up or down slope, generally over distances of less than 100 km (Millar and Woolfenden 1999, Stephenson and Libby 2000). Sequoia arrived and became abundant at its present Giant Forest site about 4 500 years ago. It is clear that any giant sequoias now over 1 200 years old had to have survived the Medieval Warm Period, with temperatures as much as 1.5°C warmer than at present, and the Little Ice Age, with temperatures less than 1°C colder than at present, in their present locations. (Their associated ecosystems may have changed substantially during these recent warming and cooling periods.)

Thus, when planning future strategies, we concluded that it is now appropriate to consider that meaningful climate change is likely, without being too certain about either the amount or even direction of average temperature change. Responses to the near certainty of substantial climate changes were suggested for the case where the magnitude of change allows the populations to remain on site and for the case when migration is necessary (Libby 2000).

#### Adaptation On-site

For some of our most treasured sequoia groves, such as the Mariposa Grove in Yosemite National Park, management might attempt on-site modification of the environment to adapt the local microclimate to the population. In the case of continued warming, management inputs might include such things as massive air coolers, irrigation within the groves, upslope charging of subsurface waterflow channels, etc. In the case of a return to the cooling trend of 1400 to 1900 A.D., management might employ space heaters within the groves, elevated clear plastic sheeting over regenerating areas to raise the microsite temperature and to dry the soil surface and seedling foliage, etc.

Adaptation of the local populations to the changing environment seems more likely to work than attempting to adapt the environment to the population, although one response does not rule out the other. Surprisingly, giant sequoia is presently substantially below the average for conifers in genetic diversity, both within groves and among groves (Fins and Libby 1982, Libby 2000). Whether that was the case throughout its recent history as it migrated from east of the Sierra Nevada to its present range, or is a very recent condition created by genetic bottlenecking due to few successful trans-Sierra colonists, is not known. It is known that relatively low levels of within-grove genetic diversity puts such populations at a disadvantage with respect to their ability to evolve and adapt in the face of change.

While among-grove genetic diversity is relatively low, it is non trivial and could be used to augment within-grove genetic diversity. Thus a strategy to keep some groves of giant sequoia in place, in the case of environmental change likely to be great enough to threaten the continued existence of the grove, would be to plant sequoia propagules from many different groves into some of the groves that are chosen to be kept in place. To be most effective, this would have to be done many many years in advance of the triggering environmental change, as sequoia is slow to reach sexual maturity and thus recombine in new more adapted genotypes. One could speed the process by one generation by overflying the target groves and massively releasing pollen from other groves during the adult trees' receptive period. Note that this is counter to general principles of *in-situ* genetic conservation, which needs to be a high priority in other groves. We would then not only have some groves designated as genetically conserved Genetic Resource Management Units (GRMUs), but also some groves managed as purposefully augmented GRMUs.

#### The Need to Migrate

As climate and other environmental variables continue to change, it is likely that giant sequoia will need to migrate from its current grove sites to more favorable sites under the new conditions. Some managers may choose to establish plantations with sequoia propagules from a single grove. It is hard to anticipate which grove-samples should be planted where in anticipation of the need for human assisted migration of the sequoias. One option is to "migrate" single grove populations to a variety of different sites, on the

logical assumption that at least some of the plantation sites will be much better when conditions change enough to force the migration. How many groves should be thus replicated on how many different sites is a matter for careful consideration.

A perhaps better suggestion for the continued human-assisted existence and evolution of giant sequoia groves is to plant 5 to 10 (or more) grove samples in intimately-mixed plantations. This is a much simpler approach and genetically more robust than that of guessing which groves will need to migrate where, or attempting to cover all possible change scenarios for each of many groves. If the migration forcing change happens soon after the plantation is established, the preadapted propagules in mixed plantings would better survive and grow. If the planted trees are on site long enough to intermate, then new genetic combinations would arise that might be better adapted than any of the trees sampled directly from existing groves. This is particularly attractive if the new environments are not simply faithfully translocated old environments.

Managers of timber plantations may wish to adopt this approach as well, intimately mixing propagules in their plantations from the best several groves. The best of these propagules will be their most valuable crop trees. If they attain sexual maturity before harvest, seeds from them could be the basis for a developing landrace of genetically more robust sequoias for future plantations. (It may be expected that some mixed-grove plantations established for timber production will later be redesignated as parks and reserves. These could then serve as long-term seed donors of the new landraces.)

#### Some Thoughts for Canada

It is clear that forest tree species native to northern North American forests have survived the repeated glacial cycles of the past 2.6 million years. So, there seem to be two important questions we can begin to consider: 1) Will human modifications of the landscape, such as cities, farms, and roads impede migration of forest populations enough to cause serious extirpations and even extinctions that would not have occurred in their absence? 2) Whether or not we ethically should mitigate anthropogenic impediments to natural migration, will forest migrations need to be faster, more massive, and more effective than would occur naturally, in order to continue to support a human population of 10 billion with wood and other forest products and services? If so, it is reasonable to begin planning how forest genetics might contribute to such human-assisted forest migrations. In considering options for northern North America, let us ignore the pea-shooter of global warming and concentrate on the cannon of a more or less rapid cooling trend into the next glacial period.

It might be possible to apply the option of modifying the climate in places like Toronto, or in especially valuable and cherished forest parks. But it seems unlikely that many large forest ecosystems could be artificially maintained within a general continental ice sheet for any substantial part of the next 90 millennia.

As with giant sequoia, some managers may prefer to migrate particular populations, or particular breeds or clonal mixtures, intact in advance of the expected climate change. The success of this will depend in large part on how well one can anticipate where to find near future climates similar to the ones where these populations, breeds, and clonal mixtures were successful.

Our final sequoia option seems attractive for eastern Canada as well as the mountains of British Columbia. While the distances populations will need to migrate from Ontario somewhere into the Ohio River Valley are much greater than the elevational migrations likely in California or British Columbia, most Ontario species have shorter life-cycles than do the western species. Thus, the times required for recombination among mixed-population plantations, and for subsequent natural selection to work on the recombinants, are substantially shorter. This could be a big advantage, particularly if the slide into the next glacial period is rapid.

The tools provided by genetic conservation and, more broadly, conservation biology, will be important as we develop strategies to either passively or actively respond to climate cycles and other major changes in

the environments of our plantations and native forests.

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## STRATEGIC DIRECTIONS IN CONSERVING GENETIC RESOURCES

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### ABSTRACT

The paper concentrates on forest genetic resources and, in particular, trees. Major influences for the directions of conservation strategies originate from the bio-geographical zone, the management system, and the species under consideration. There exist basic differences in the situation for boreal and temperate forests on the one hand and tropical forests on the other due to number of species, management history, and political and socio-economic conditions. In boreal and temperate forests, a combination of *in situ* (including all the associated species) and *ex situ* (only concentrating on the target species) measures is regularly possible. In tropical forests, *in situ* conservation is the only choice, in most cases, at the moment. However, even *in situ* conservation under these conditions is often difficult due to human population pressure, socio-economic situations, and administrative restrictions and weaknesses.

The management system determines whether *in situ* and *ex situ* measures can be combined or not. In plantation forestry with clear-cut, *ex situ* conservation is a necessity. Selective management systems with continuous forest cover allows an integration of *in situ* conservation. For temperate forests, the directions are discussed with the background of Central European experiences. Here, especially, recent changes due to the shift of forest management to more ecologically oriented systems are reflected.

Species contribute biological and management aspects. For species under management and included in tree breeding programs, more options are available than compared to species of only economic interest or to species of no economic interest. For species under management and included in tree breeding activities the specific necessities for integrating conservation considerations into tree breeding are discussed. Finally the vision of a regionally differentiated, gradually integrated network including both conservation and utilization is outlined.

### INTRODUCTION

Forests hold the vast majority of the world's terrestrial species and more than 40% of the world's economy is derived from biodiversity (Hamid 1999). Biodiversity seems also to be connected with cultural diversity. Out of the nine countries which together account for 60% of human languages, six of these centres of cultural diversity are also mega-diversity countries with exceptional numbers of plant and animal species (Posey 1999).

Trees are the characteristic species of forest communities and are the main economic interest in forests. They influence the microclimate and serve as a habitat for high numbers of associated species. Today, 1.75 million species of animals, plants, and micro-organisms are described, but these are only about 5 - 20% of all species existing. The majority is still unknown. The situation is better for vascular plants where about 80% of a total of 320 000 are known to exist (Barthloff *et al.* 1999). While discussing conservation of biodiversity we have to consider the associated species complexes as well.

Biodiversity is organized on different levels: 1) ecosystems, 2) species, 3) populations within species, 4) individuals within populations, and 5) genes within individuals. In the following I will concentrate on forest

tree species, their populations, individuals, and genes, but keeping in mind the diversity behind them.

Forest trees are with few exceptions among the most genetically variable of all living organisms studied to date. The demands on forests grow with the growth of the human population and the area of forest is diminished accordingly with all associated losses of biodiversity (Figure 1). In addition, there is increasing pressure on forests due to air pollution and climate change (Kleinschmit 1996). With an increasing standard of living, the consumption of wood per capita is increasing as well. FAO predicts an annual increase of wood consumption for paper of 3.1% between 1990 and 2010. There is no doubt that the increasing needs which have to be met from a smaller area can be met only by better utilization of the existing resources in a sustained way by management and tree breeding. Complete protection will be the exception in the long run. But how to conciliate this situation with the need for conservation of biological diversity?

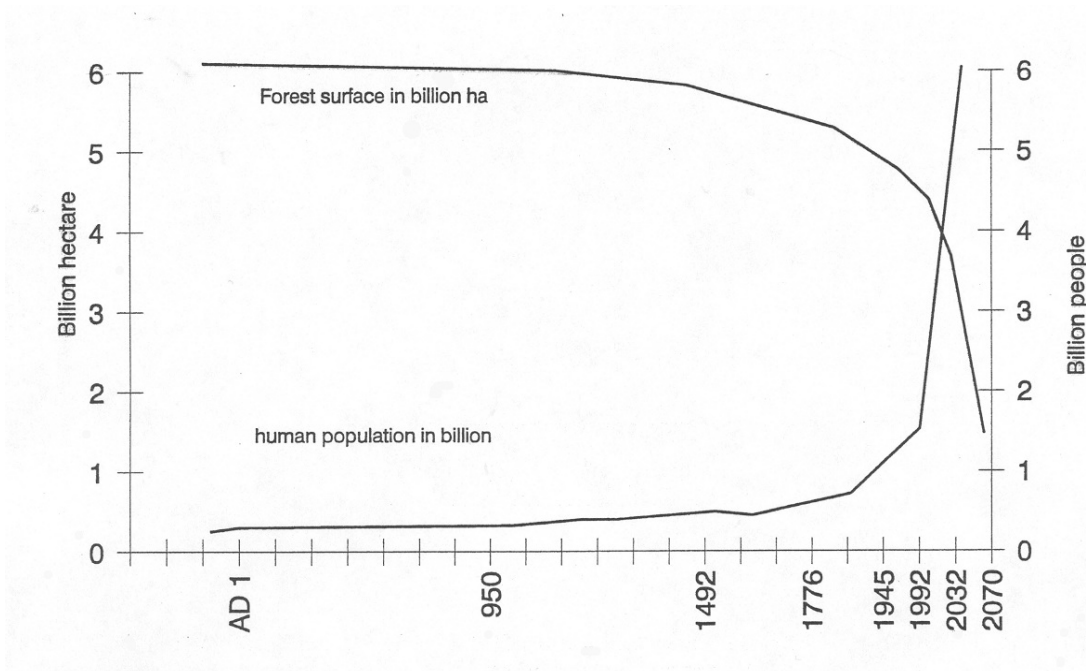


Figure 1. Global development of forest surface and human population.

Conservation of forest genetic resources is a subject of great concern today mainly due to habitat destruction and alteration, uncontrolled and undocumented movement of germplasm, and other problems of potential loss of genetic identity of diversified local populations (Palmberg-Lerche 1999). The Convention on Biodiversity was ratified by 172 countries. The principal objectives are the conservation, sustainable use, and equitable sharing of benefits of the use of genetic resources.

The definition of the amount and proportion of genetic variation which needs to be retained in the long-term, to ensure that species are able to adapt to future changes in environmental conditions is central to the question of conservation. What is the adequate size of populations, what number and location of conservation areas is necessary, how far can conservation be integrated into management, and how can biodiversity even be improved by management? Many questions are still open. Some losses in present day biodiversity over time are inevitable both due to natural and man-made causes. Diversity can be managed however through a wide range of human activities from establishment of nature reserves and managed resource areas, to the inclusion of conservation considerations in improvement and breeding strategies under intensive human use (Namkoong 1986).

*In situ* conservation implies “the continuing maintenance of a population within the community of which it forms a part, in the environment to which it is adapted” (Frankel 1976). This strategy includes the conservation of the associated species complexes. It is the major strategy if knowledge is scarce, regular management not existing, and the number of tree species in the ecosystem high. *Ex situ* measures include plantations, seed orchards, storage of seed, pollen, tissue or DNA sequences, and tree breeding activities. They will be mostly adopted if the species are under intensive management, especially if they are included into tree breeding programs.

## STRATEGIC DIRECTIONS

Major influences for the directions of conservation strategies originate from the bio-geographical zone, the species under consideration, and the management system.

### Bio-geographical zones

There exist fundamental differences between the different regions of the world. This concerns as well the natural situation of plant species as the utilization and transformation of vegetation by humans. The global biodiversity situation is reflected in Figure 2.

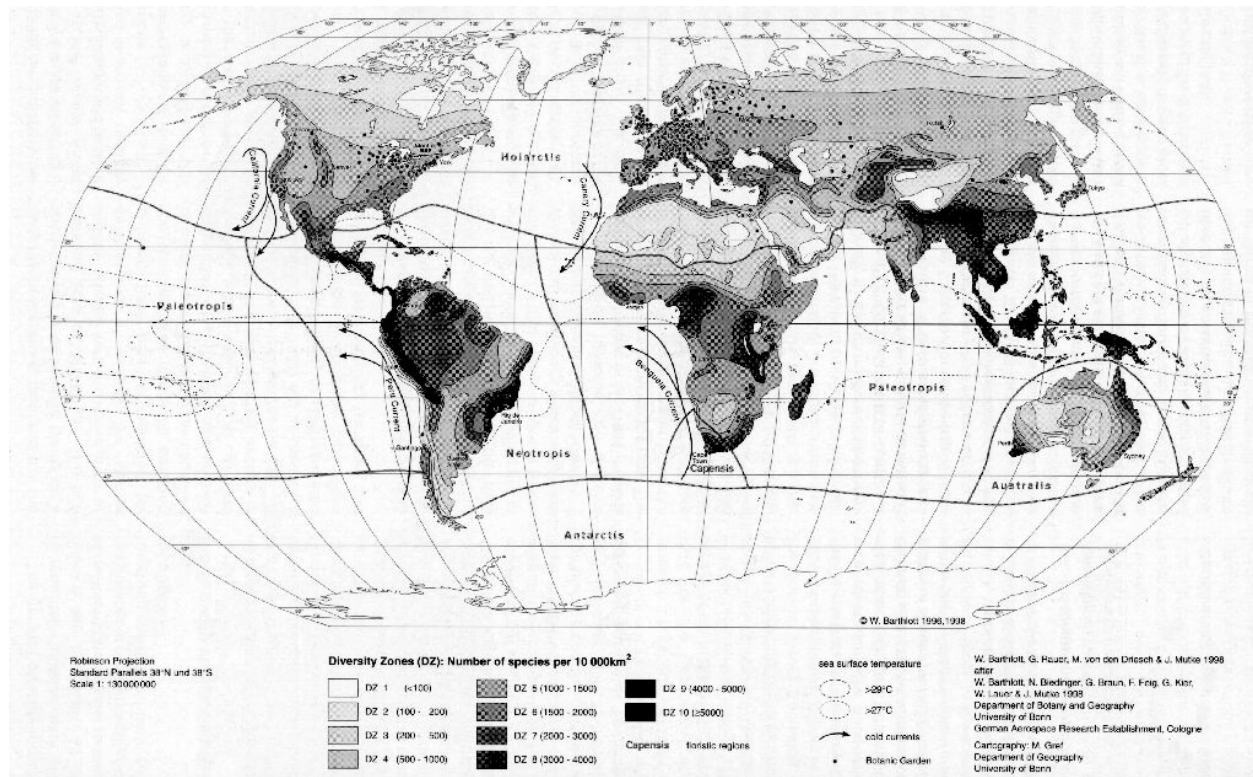


Figure 2. Global biodiversity.

In **boreal** zones, there exists only a small number of tree species. The human influence was historically comparatively restricted due to low population pressure and adverse climatic conditions. There still exist extended virgin forests and the managed forests have usually a similar species composition as the natural ones. They often originate from natural regeneration. Deforestation takes place in this region today, but by far not as dramatic as in the tropical countries. The development of a sound conservation strategy for this zone seems to be relatively easy.

In the **temperate** zone, the number of tree species is significantly higher (ranging from 45 in central Europe to 800 in Asia) and the human impact on the vegetation was particularly severe. In Europe and Asia there exist only a few relics of the original forest cover and intensive utilization for agriculture and settlement converted the majority of forests to other land uses. The remaining forests were over-utilized in the past and transformed to best serve human needs. This favoured different species in different historical times. Extensive transfer of species and provenances occurred in the past. It is difficult today to identify autochthonous material in many parts of the world. This is somewhat different for America, where intensive human utilization was comparatively short in time and population pressure less detrimental. On the other hand, efforts for the study of forest ecosystems and for reforestation are most developed in the temperate region of the world (Figure 2). By far the majority of research is concentrated in this zone. A considerable number of approaches to manage forests has been developed and tested in the past including more or less intensive forest tree breeding activities. Conservation activities in this zone have to be quite differentiated due to the different developmental situation and they have to include an important *ex situ* component to counterbalance the fragmentation and over-utilization especially of many of the minor species.

In the **tropical** region, the majority of biodiversity is concentrated. In tropical countries the human population growth is most rapidly associated with a dramatic loss of forest surface (Table 1). The transformation of forests to other land-uses is actively going on and the remaining forests are partly exploited and over-utilized. Forest management on a sustained base is only in an initial phase, often counterbalanced by human population pressure and mostly concentrated in plantations of fast growing exotics. The number of tree species by far exceeds those in the other regions of the world and most of the species occur in low frequency. The knowledge of the complex tropical forest ecosystems, especially of economically sound sustained management, is still scarce and the research activities, in spite of some international efforts, very restricted. The key problem in these countries, as for the world in total, is the human population growth. All conservation efforts have to take into account this fact and conservation activities are possible only in harmony with the local population.

## Species

Forest tree species are characterized by a long life span, they grow in a heterogeneous environment in space and time, they have a low specialization, a high degree of individual heterozygosity, and a high within- population variability. These characteristics support adaptability to an uncertain future.

Their present range is not necessarily an indication for their ecological potential but is influenced by competition of other tree species as well. Worldwide, there exist roughly 50 000 tree species, close to 90 % in the tropics, but only about 500 have been tested in plantations and only 60 are included into more intensive breeding programs (Kleinschmit 1996; Palmberg-Lerche 1999). Our genetic knowledge about trees is mainly derived from the 60 species included in breeding programs. That means, we extrapolate our knowledge from 0.12% of the species to the rest.

By far the best studied species originate from the temperate zone. These species are mostly monoecious, wind-pollinated, and they grow in pure or mixed stands. Some occur in very high frequencies others are more rare. Many of the tropical species are dioecious, insect-, bird- or bat-pollinated and they grow mostly in low frequencies in mixed stands. Within the temperate zone, the number of tree species existing on the continents very much depends on the glacial history. In Central Europe, only about 45 tree species exist as compared to similar climatic conditions in North America where more than 200 species and in Asia



where more than 800 species are described. The glacial, postglacial, and human influences on tree populations have, as a result of regional differentiation, not always optimally matched the genetic structure and the local environmental conditions. The pattern of variation can be more clinal in major species with a continuous range and regular gene exchange or ecotypic with minor species and a discontinuous range. Gene flow can occur by pollen and seed. Therefore, the vectors which transport these units very much influence the gene-flow. In rare species, the transport of seed by birds or other animals can obviously contribute to an efficient gene-flow.

Table 1. Present world forest inventory and related changes (from Dixon *et al.* 1994)

Geographic latitude		Area in millions of hectares			Annual changes in surface
		Total	Protected Forests	Plantation	
<b>Boreal</b>	Russia	884	178	43	- 0.2
	Canada	436	9	3	- 0.5
	Alaska	52	2	1	-
	TOTAL	1 372	189	47	- 0.7
<b>Temperate</b>	USA	241	14	2	- 0.1
	Europe	283	40	1	0.3
	China	118	-	31	0.6
	Australia	396	18	1	- 0.1
	TOTAL	1 038	72	35	0.7
<b>Tropical</b>	Asia	310	49	22	- 3.9
	Africa	527	113	2	- 4.1
	America	918	105	6	- 7.4
	TOTAL	1 755	267	30	- 15.4
<b>Overall Total</b>		4 165	528	112	- 15.4

In tropical countries *in situ* conservation is the only choice for major and rare species at the moment, since knowledge as well as economic means are lacking for more intensive measures. Due to population pressure, unstable political conditions, and local economic interest *in situ* conservation seems to be often more difficult in practice in these countries than theoretically thought (Boyle 1999). There is more and more evidence, that all these conservation efforts have to include the local population to be successful.

For major species of the boreal and temperate zone *in situ* conservation is usually possible and desirable, since the populations can adapt to changing the environment and carry along all the associated species complexes. This method can be integrated into forest management or in protected areas. Since these species are however of major economic interest, they will be usually included into tree breeding programs as well, which have to take into account the conservation of diversity too (Namkoong 1986; Namkoong and Koshy 1997; Eriksson *et al.* 1993). The conservation situation is different for rare species in these regions. Generally speaking, rare species with a narrow genetic base are more susceptible to inbreeding, genetic drift, and as a consequence, to a loss of adaptability. This is especially a problem with

fragmented populations due to human activities.

If we take the Noble hardwoods as an example for rare species in Europe, the main reasons for endangerment of the genetic integrity are small population size, hybridization with other species or with cultivars, and especially in the case of elms, diseases (Table 2). For these species, in spite of the rareness, *ex situ* measures in seed orchards are justified to reconstitute viable populations. The economic value of these species increases drastically (e.g. more than \$ 10 000 US per cubic meter in *Sorbus torminalis* as a maximum) partly due to the reduction of valuable tropical hardwoods on the market. Seed orchards are the most effective means to re-establish genetically diverse, adaptable populations and to add, at the same time,

a certain selection for genetic improvement. At the same time this development supports the planting of these species due to economic interest of the forest owners. The conservation is coordinated across Europe in an EUFORGEN (European Forest Genetic Resources) network within IPGRI in Rome (Turok 1999).

How intensive the introgression with cultivars may be, can be seen from the example of wild apple tree (*Malus sylvestris*) where the progenies of a single tree show all variability between wild and cultivars (Figure 3). Due to the low frequencies of *Malus sylvestris* as compared to cultivated forms, the main source of pollination since the younger stone ages (3 500 years) come from cultivars.

#### Management system

The management system, ranging from virgin forests without human intervention to mini-rotation forestry on agricultural land, decides the potential to include *in situ* conservation in management (Figure 4). If we look to within-tree species diversity, there may be an optimum not in virgin forests or nature reserves but in managed forests where the number of individuals of certain target species is much higher.

To maintain a high diversity of species in the forests we need a high diversity of silvicultural systems and management types (Scherzinger 1999). The knowledge of the influence of management on the diversity of tree species is poor however. Virgin forests are a good place to conduct conservation of biodiversity. However, as discussed earlier, they will be the exception in the future. At present, the protection of virgin forests or of natural reserves, which may be already altered by human intervention, is the major choice for the tropical zone. There they should be as large as possible and cover as many different habitat types as possible. There are strong efforts to create such protected units, however the long-term success was mostly disappointing (Boyle 1999). Parallel to this, single-tree selection systems in ecologically oriented managed forests have to be developed. Protection will be only possible, if at the same time sufficient wood is produced in plantations often with exotic species where knowledge of management is available.

In the temperate and boreal zone, protected areas are established in most countries. For Europe, at the moment, slightly more than 5% of the forest is under protection and the predictions are 10% due to political pressure (Bücking *et al.* 2000). However, most of the conservation must take place in managed areas since these are dominating (Joyce *et al.* 1999). Management interventions have to be adjusted, so that both forest management and genetic conservation aspects are considered in a balanced manner. This has to be monitored. Genetic diversity must be considered throughout all steps of tree domestication: selection, seed handling, nursery operations, planting, thinning, natural regeneration, and breeding (Teissier du Cros *et al.* 1999).

A good example for protected areas are the National Parks in U.S.A. and Canada. Their long-term maintenance however depends on the possibilities to efficiently produce the wood, necessary for human needs, in high yielding plantations as recently demonstrated by Li *et al.* (1999) for the Loblolly Pine Cooperative Breeding Program. Although only 15% of the commercial forests are currently in plantation (11 million ha), after 40 years of research almost 50% of the Southern U.S.A.'s timber supply will soon come from them. Bastien (1999) estimates that for France one third of the forest surface intensively managed with productive species and high yielding varieties would be sufficient to produce the wood for

industrial need and take pressure from the rest of the forests.

Table 2. Common Noble hardwood species in Germany

Species		Reason of endangering					
Native species	Importance	Seed legislation	Unregulated seed import	Hybridization with other species	Hybridization with cultivars	Small population size -> inbreeding, genetic drift	Diseases
<i>Acer pseudoplatanus</i>	****	*					
<i>Acer platanoides</i>	**		*			**	
<i>Acer campestre</i>	***		*				
<i>Alnus glutinosa</i>	****	*					
<i>Fraxinus excelsior</i>	*****	*					
<i>Ulmus glabra</i>	***		*	*		*	***
<i>Ulmus laevis</i>	**		*	*		*	***
<i>Ulmus minor</i>	**		*	*		*	****
<i>Tilia cordata</i>	***	*		*			
<i>Tilia platiphyllos</i>	**		*	*		*	
<i>Prunus avium</i>	****		*		*	*	*
<i>Sorbus torminalis</i>	**		*			*	
<i>Sorbus domestica</i>	*		*		*	**	
<i>Pyrus pyraster</i>	*		*		***	***	
<i>Malus sylvestris</i>	*		*		***	***	
Non-native species							
<i>Juglans regia</i>	*		*				
<i>Juglans nigra</i>	*		*				



Figure 3. Introgression in *Malus sylvestris*.

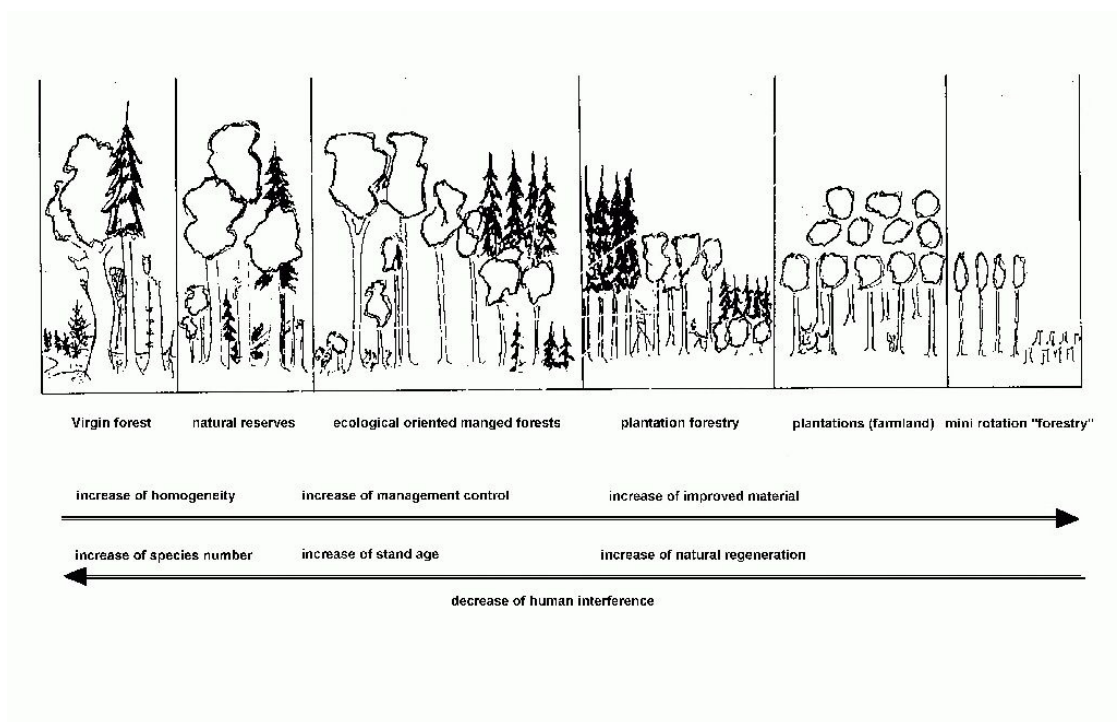


Figure 4. Potential for *in situ* conservation over a range of managed forest conditions.

The aspects of conservation of genetic diversity for the plantation species have to be an integrated part of the breeding programs for the target species as well. The number of associated species may, however, decrease drastically in these plantations. In Europe, there are strong efforts today to enter more and more of the forest surface into ecologically oriented managed forests which are characterized by the following principles:

- 1) soil protection and choice of site-adapted tree species,
- 2) increase of hardwoods and of mixed forests,
- 3) preference of natural regeneration,
- 4) improvement of forest structure,
- 5) utilization of single trees due to dimension,
- 6) conservation of old trees and rare plant and animal species,
- 7) integration of a network of protected areas,
- 8) guarantee of diverse forest functions,
- 9) ecological forest protection,
- 10) wildlife management in an ecologically sound way, and
- 11) use of technical equipment in an ecologically sound way (Niedersächsische Landesregierung 1991).

These efforts, supported by "Pro Silva Europe", by environmental groups, and by politicians lead to a significant change in forest management in some European countries. At this time, the majority of the forests are still mono-species age class forests but the conversion is proceeding. My prediction is, that these ideas will have increasing influence since they try to consolidate economics and nature protection. As far as the conservation of forest trees is concerned, this management system does not optimally guarantee the protection of genetic diversity, since the starting conditions are very much influenced by historical utilization and management. Also, extraction of big trees before regeneration may just take away the genetically most valuable parent trees. But this is different if regeneration is already established. Natural regeneration is not always the best option, neither for conservation nor for production. But planting of genetically valuable and diverse material is not excluded and in the transitional phase it is a necessity to reach the goals.

The integration of conservation, selection, and tree breeding into this system has still to be optimized. On the other hand, first studies show that biodiversity in such management systems can be even higher than in completely protected areas (Wehrmann 1999). Due to the higher rotation times, this management system has high standing volumes, binds more CO<sub>2</sub> than age class forests, and offers a mosaic mixture with protected areas for a continuous forest cover. The productivity and the economics of this system are astonishingly sound in those cases where it has been followed for a longer time.

### Tree breeding

Tree breeding of course, plays an important role in the conservation of forest genetic resources. Most of the early programs started with a comparatively narrow genetic base. To my knowledge, Gene Namkoong was one of the first forest geneticists who stressed the necessity of a balance between short-term gain and long-term improvement in 1969. The further developed multiple population breeding system (Namkoong *et al.* 1997; Eriksson *et al.* 1993, 1997) is a good example for incorporation of conservation aspects into breeding programs. It is obvious that genetic diversity can even be enhanced by well designed breeding programs. Most of the existing programs can serve as a base for *ex situ* conservation as well, and as mentioned earlier, our knowledge of the genetic structure of forest tree populations largely originates from breeding programs. This is especially true for adaptive characters. Biochemical-genetic studies supplied a lot of additional information, but often this information is not linked to the adaptive importance of the traits and conclusions drawn can be misleading if we discuss conservation of the last rare allele (Tigerstedt and Yao 1999; Hattemer and Ziehe 1997; Eriksson 1997). Testing of the adaptation potential of species, populations, and individuals assisted by gene markers, the study of phenotypic plasticity etc., are important fields of research in breeding and can help bridge the gap between markers and adaptive traits.

Without tree improvement and an accompanying management system, it is quite improbable that the future need for wood by the human population can be met. It is an important precondition to be able to set certain areas aside as protected areas for conservation. Therefore, it is astonishing to see the drop of appreciation and funding for these activities in many countries (Kleinschmit 2000; Teissier du Cros *et al.* 2000). Compared to the classical work, in the future more emphasis has to be put on adaptive traits and the increase of adaptability in view of the more rapidly changing environmental conditions.

#### Future trends and visions

International awareness of the conservation of biodiversity is growing rapidly. There is increasing pressure on wood exporting countries and on forest owners to meet minimum standards for sustainable management as the global certification discussion shows. Criteria and indicators of the genetic variation in forests become important for characterizing sustainable forest management (Turok 1999).

There exist severe restrictions in developing countries due to human population growth which will last at least for this century. Conservation is only possible in harmony with the local population (Souvannavong *et al.* 1994). We need a balance between human needs and nature protection and this means conservation and utilization or even conservation through utilization! Conservation can be only achieved in the long term if the resources have a value. Forest tree resources are renewable. If managed sustainably, they can be used without ever being used up (Ledig 1986)

There will be an increasingly critical view towards manipulation of the environment. Therefore, I am convinced that, generally, we will not move in forestry in a direction as in agriculture. There may be exceptions with mini-rotation forestry or highly intensive plantations on farmland.

In a long-term view, there must be a stabilization of the human population with a more or less permanent delineation of land use including some flexibility. Since large scale timber production from forests will continue in boreal, temperate, and tropical forests the means to improve conservation of biodiversity in production forests must be a priority (Hamid 1999). There must be a balance between conservation and utilization including all the options available, and if possible, in a mosaic mixture (Joyce *et al.* 1999). A monitoring system for genetic diversity has to be established and integrated into normal forest management practices. This needs studies of the effects of different kinds of interventions on the genetic diversity and adaptability in forest ecosystems and the inclusion of markers and adaptive traits in the study of geographic range, population size, mode of reproduction, breeding system, gene flow, and life cycle (Teissier du Cros *et al.* 1999).

An important point is the creation of awareness in all relevant groups including local people, politicians, seed merchants, nursery managers, forest owners, greens, etc. Country driven efforts should be supported by international activities. Regional and sub-regional workshops on the conservation, management, and sustainable utilization and enhancement of forest genetic resources are planned by FAO (Palmberg-Lerche 1999) including food security, poverty alleviation, environmental conservation, economic and social advancement, and the maintenance of cultural and spiritual values. Not an easy task! But also non-governmental organizations support this development like the Global 200 initiative (WWF 1999), a representation approach to conserving Earth's most biologically valuable eco-regions.

The production potential of intensively managed forests including selected material of fast growing species is by far higher than most of the present day forests show. This provides the opportunity to cover human needs on the one hand and to set aside completely protected areas on the other hand. There are many options for silvicultural systems and management interventions which will have a different weight in different regions of the world, in different ownerships of the forests, and under different local ecological conditions and which all have to include conservation and utilization. From a landscape and a biodiversity view it is desirable to have a mosaic mixture of the different systems. If a balanced situation is reached, fluctuations between deforestation and afforestation will be minor. The different developmental stages between temperate and tropical zones give an indication of how the directions may evolve.

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CONSERVATION OF  
GENETIC RESOURCES

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**GENETIC DIVERSITY WITHIN THE CONTEXT OF THE  
COARSE FILTER/FINE FILTER  
APPROACH TO CONSERVING BIODIVERSITY**

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I'm a conservation biologist. What does conservation biology have to do with tree improvement? Conservation biology can be defined as "science in the service of conservation". There are many things we might seek to conserve - scenic landscapes, clean air and water, rare species, genetic variation within species, and on and on. Modern conservation biology focuses quite broadly on maintaining and restoring biodiversity - the variety of life on Earth. Although the most commonly considered expression of biodiversity is species richness - the number of species in a site, habitat type, or clade - most biologists recognize biodiversity at multiple levels of organization, for example genes, populations, species, communities, and ecosystems. Furthermore, biodiversity includes not only entities at these various levels, but also ecological and evolutionary processes.

Whatever level of organization we select, biodiversity cannot be reduced to a single number. As information theorists demonstrated several decades ago, the richness and evenness of species or other entities can vary independently of one another. One site may have more species, but be strongly dominated by one or a few species. A second site may have fewer species, but greater evenness of abundance among species, such that the chance is lower that two randomly selected individuals will be of the same species. Which site is more diverse? The same reasoning can be applied to genotypes within species.

My main area of expertise is conservation planning. Hence, I am interested in highly practical questions about where we focus conservation efforts to achieve the most bang for the buck. This is, in part, is a question of geographic priorities, but it also must consider which elements of biodiversity we choose to measure and organize conservation projects around. Geographic priorities can change depending on which biodiversity surrogates we select.

One fundamental dichotomy - although it really shouldn't be - is species conservation vs. ecosystem conservation. Which should be the target of our conservation efforts - species or ecosystems? Species conservation is often interpreted to encompass conservation of genetic diversity within species. A current "best guess" is that somewhere around 14 million species exist worldwide, although some biologists believe the real numbers could be an order of magnitude larger. Populations of species, if defined on the basis of limited gene flow among them, will evolve more or less independently, with many becoming genetically distinct. An estimated 1.1 to 6.6 billion genetic populations exist worldwide.

Over the last 25 years The Nature Conservancy in the U.S. and Canada has developed and refined terminology and inventory methods to address species and ecosystem conservation. The "fine filter" approach focuses on species and populations. Individual occurrences of imperiled species (which may or may not correspond to populations) are located, mapped, and, if possible, protected. This approach works well for plants and small-bodied animals, not so well for large-bodied, wide ranging animals.

The "course-filter" approach seeks to protect high-quality examples of all natural communities or ecosystems in a region. If applied to small, localized occurrences of imperiled community types, as it often has been in practice, the coarse filter approach is really not much different from the fine filter approach.

However, if applied with the notion of representing all ecosystems in a region, across their natural range of variation, in protected areas, the coarse filter approach is an excellent complement to rare-species conservation. The Nature Conservancy has estimated, out of thin air but reasonably, that 85-90% of all species can be protected by the coarse filter. Species that fall through the pores of the coarse filter - such as narrow endemics - can be protected through a fine filter of species-level conservation. Conservation of large-bodied species, for example mammalian carnivores, is in practice a kind of coarse filter, as it generally requires protection of suitable habitat conditions over large areas.

I argue that both the fine-filter and coarse-filter approaches can serve the goal of maintaining genetic diversity. For example, the fine-filter focus on protecting distinct populations of imperiled species presumably will capture the genetic diversity associated with these species, both within and among populations. Nevertheless, little is known about distributions of many or most organisms in a typical region, much less about their genetic architecture. Many species remain to be discovered and described, even within well-surveyed groups. About 30 new species of North American plants are described each year. The coarse-filter strategy of protecting viable examples of all habitats and ecosystems in a region (i.e., complete environmental gradients) offers a way to protect the un-surveyed diversity of genes, populations, and species.

Let me offer an example of the need for increased use of coarse-filter approaches in conservation. The longleaf pine (*Pinus palustris* Mill.) - wiregrass (*Aristida* sp.) ecosystem was once the major terrestrial ecosystem of the southeastern coastal plain in North America. It now is one of the most endangered major vegetation types on the continent, having declined by around 98% since European settlement. As of 1993, 27 federally listed endangered and threatened species and 99 candidates for listing were associated with longleaf pine and/or wiregrass, the major ground cover. Botanist Joan Walker has documented 187 rare vascular plants associated with longleaf pine. Undoubtedly, many other species in less well-known taxa, such as invertebrates, bacteria, and fungi, associated with these ecosystems are imperiled - we just don't know much about them.

The conventional approach to this kind of problem has been to pursue conservation species-by-species, such as through listing under the Endangered Species Act and preparation of recovery plans. However, very few of the imperiled species of the longleaf pine ecosystem have recovery plans. The vast majority have not been studied well enough to prepare such a plan. We know virtually nothing about most of these species. Most of the attention has been devoted to the very few species that have been reasonably well-studied, especially the red-cockaded woodpecker. Unless this woodpecker is an ideal umbrella species, which is debatable, many other imperiled species may be falling through the cracks.

So, we might ask, wouldn't it make more sense to try to protect and restore the longleaf pine - wiregrass ecosystem as a whole, rather than taking decades and millions of dollars to figure out how to conserve each imperiled species individually? Better yet, perhaps we should try to conserve healthy ecosystems before they become endangered, and in the process save not only rare species but the larger pool of species that are not yet imperiled or about which we know virtually nothing. This is the compelling logic of the coarse filter.

The coarse filter is another name for the broader strategy of ecological representation, the history of which extends back more than a century. The first recorded mention of the need for representation was in F. von Mueller's 1890 address to the Australian Association for the Advancement of Science, wherein he suggested that "choice areas and not necessarily very extensive should be reserved in every great country for some maintenance of the original vegetation and therewith for the preservation of animal life concomitant to particular plants".

In North America, the history of representation parallels the career of a remarkable man, Victor Shelford, whom I consider the father of conservation biology but who has been all but forgotten by conservationists today. Shelford was instrumental in the founding of the Ecological Society of America in 1916 and The Nature Conservancy in 1950. Shelford was the first president of the Ecological Society of America. In 1917, at Shelford's urging, the National Research Council asked the Ecological Society to prepare a

"listing of all preserved and preservable areas in North America in which natural conditions persist" and "to urge the reservation of such areas as demanded immediate attention."

Shelford established a "preservation committee" to accomplish this task, the first major product of which was Shelford's *A Naturalist's Guide to the Americas*, published in 1926. By 1931 the work was being carried out by two sister committees: a fact-finding body, the Committee for the Study of Plant and Animal Communities, and an action body, the Committee on the Preservation of Natural Conditions. Their goal was "a natural sanctuary with its original wild animals for each biotic formation".

Shelford's committees were successful in providing arguments for the establishment of new parks and monuments in the U.S., such as Glacier Bay in Alaska. Ultimately, however, Shelford failed in his quest to get all American ecosystems represented in protected areas; or perhaps I should say he left that task for another generation. For example, as early as 1931, recognizing that grasslands are among the least well represented ecosystems in North America, Shelford campaigned for a 400 000 ha national park. We still don't have anything close to that; the largest tallgrass reserve is a 15 000 ha area managed by The Nature Conservancy, much of it in poor shape and undergoing restoration. Nor were Shelford and his committees successful in their pleas for enlargement of existing national parks and for surrounding parks with broad buffer zones to protect their sensitive species and other ecological values. Shelford was ahead of his time, as we have yet to see adequate buffer zones around our national parks. But, thanks to Shelford and his friends, the idea of buffer zones is well accepted among conservation biologists and practicing conservationists today.

So, there we have the origin and early development of the coarse filter idea. Now we should consider: What has the coarse filter taught us, and . . . has it worked? In 1988 David Crumpacker and coauthors published an analysis of the ownership status of 135 Kuchler potential natural vegetation types in the conterminous U.S. They found that 33 types (24%) were inadequately (< 53 000 ha) represented on federal or indian lands, with 9 types having no representation. Crumpacker did not discriminate among different management categories (e.g., wilderness areas versus forests managed for timber). However, National Park Service lands contain only 7 (5.2%) of the 135 vegetation types, and U.S. Fish and Wildlife Service holdings include only five (3.7%) of the 135 types.

The major national assessment of representation now in progress in the U.S. is the Gap Analysis Program of the U.S. Department of Interior (currently within the USGS). The GAP program assesses representation of vegetation types down to the Alliance level in lands assigned to 4 management status categories. An example from Idaho shows the kind of results you can get with GAP data. Altogether, in Idaho, 33 of 71 mapped vegetation types have < 10% of their current area in strictly or moderately protected areas.

Recent studies across the U.S. using GAP data have shown that 30-83% of mapped vegetation types have less than 10% of their area protected. Nationally, a preliminary assessment by Mike Scott and coauthors shows that about 60% of land cover types fail to meet the 10% standard. Moreover, most conservation biologists would agree that 10% is an arbitrary and probably grossly insufficient standard for representation.

Across regions, protected areas are found mostly in areas of high elevation and low soil productivity, whereas low-elevation cover types with high soil productivity are less than 5% represented in reserves. Those areas of low elevation and high soil productivity are overwhelmingly in private ownership. This biased distribution of protected areas is largely a consequence of the tendency of governments to select wilderness areas, national parks, and other major reserves for their scenic and recreational values rather than for biological reasons. It is no accident that those high-elevation areas are often the landscapes with lowest potential for resource production. Unfortunately, for many taxa, species richness tends to decline with elevation.

Hence, all available studies show that we have done a poor job applying the coarse filter in the United States. The same appears to be true for other nations. Let me turn now to some of the problems, challenges, and potential of various coarse-filter approaches. First, to what entities should we apply the

coarse filter: to vegetation or plant communities, to surrogate taxa, to physical habitats or features, or to some combination of these?

The GAP program in the U.S. assesses representation of vegetation types and of surrogate taxa, primarily terrestrial vertebrates, which are related to these vegetation types by simple habitat models. In Australia and Canada, on the other hand, more emphasis has been on representing what Americans call "environmental domains", and the Canadians call "enduring features", which in both cases are habitats defined by climate, substrates, topography, and other abiotic features. In much of Canada, the vegetation is still recovering from the glaciation, so it makes sense to focus on the much more stable, abiotic features of the environment. This approach is valuable under any scenario of climate change.

In addition to environmental domains, many Australian assessments of representation have focused on taxa that are reasonably well inventoried. Kirkpatrick and Brown, working in Tasmania, were apparently the first to combine abiotic and biotic features in a representation assessment. The biotic variables included vegetation and rare species whereas the environmental domains were based on climatic and geologic data. They found that either approach, by itself, missed important elements and that a combined approach provided much better representation of natural features.

My colleagues and I used a combined approach in a conservation assessment of the Klamath-Siskiyou ecoregion of northwestern California and southwestern Oregon, conducting gap analyses of both physical habitats and vegetation. Our classification of physical habitats was based on a cluster analysis of climate and soil variables. We hypothesized that the physical habitat gradients represent the range of biotic variation (or beta diversity) within GAP vegetation types, which were classified according to remotely-sensed overstory vegetation. A stratification of 26 vegetation types by 19 physical habitats yielded 215 combined habitat types. Approximately one-third of these habitats had less than 10% of their area currently represented in reserves. As found in other studies, the under-represented types were generally lowlands with the most fertile soils, whereas the best represented types were high-elevation habitats with poor soils. Hence, existing protected areas failed to include the landscapes that naturally would be the richest in biodiversity.

We are currently applying a similar methodology in a conservation assessment of the Greater Yellowstone Ecosystem and the Rocky Mountains of Wyoming and Utah. Again, we're finding great utility in a combined abiotic-biotic approach. The "oak" vegetation type (i.e., *Quercus gambelii*) is distributed across six physical habitat types. We can expect that the oak community will vary considerably across this environmental gradient. Furthermore, we hypothesize that oak genetics - and the genetics of associated species - will vary across this gradient. A number of studies have shown variation in heritable traits across environmental gradients. For example, a study of western white pine (*Pinus monticola* Dougl.) in southern Oregon by Campbell and Sugano showed that the geographic component of total genetic variation is highly correlated with the pronounced precipitation gradient in the region.

Among the remaining challenges in the representation assessments are the level of resolution of our classification (e.g., plant associations vs. alliances), the fact that our representation targets and standards are basically arbitrary, and that the required area and configuration of the habitat units to be represented is not at all obvious from the representation assessment itself.

Let's first consider the issue of level of resolution. The Nature Conservancy generally wishes to base its coarse filter on the U.S. National Vegetation Classification system (USNVC), ideally down to the level of associations. The finer the level of classification, however, the more unstable a unit is over space and time, although species fall into reasonably predictable communities from a spatiotemporally restricted vantage point. Over broader scales, most of them respond individually to their environment, as shown in the distribution of hardwoods along an elevation gradient in the Santa Catalina mountains of Arizona, as documented by Robert Whittaker, and as shown in the fossil pollen record since the Pleistocene, where plant species fall into different combinations at different points in time, depending on their adaptations to the environment and their rate of dispersal.

Furthermore, and this is no small matter, given existing technology, plant associations can't be mapped over broad scales. They're generally too small and the details of their species composition are too hidden to be picked up by remote sensing.

My recommended response to this challenge is: 1) to inventory and map the highly imperiled communities at the association level; these are the elements of diversity in their own right. As I noted earlier, this is essentially a fine-filter approach, as these are the mostly small-patch communities (at least today, although some, such as longleaf pine, were matrix communities in the past, and others are former large-patch communities). and 2) for the coarse filter, map higher-level entities (e.g., alliances) stratified by physical habitats or environmental domains. This approach has a higher probability of capturing the ever-shifting patterns of species distribution along environmental gradients as well as genetic diversity along these gradients.

Another challenge in representation assessments is the frequently asked question, How much is enough? That is, how do we determine when a community type or habitat is adequately represented? The usual approach has been to set arbitrary targets, for example, 10% of each community's total cover in protected areas within a region of concern, plus perhaps 100% of the viable occurrences of the most critically imperiled communities. I agree with the latter, but standards for the more common communities are more problematic.

Ecologically, what we might consider adequate representation will necessarily vary region to region and will depend on: 1) the abiotic and biotic heterogeneity of the region, with more heterogeneous regions requiring more protected area to capture all kinds of habitats, 2) the fineness or level of subdivision of the classification scheme, with more subdivided classifications requiring more area to achieve the representation target of each type, 3) the reservation threshold we subjectively set (i.e., the proportion of each community in the region protected), 4) the replication threshold (i.e., the number of occurrences protected), which is also set subjectively, and 5) the patch size threshold or reserve area that we think constitutes adequate protection. This will require consideration of the area requirements of the most space-demanding species, as well as the scale of natural processes, such as hydrologic and disturbance regimes.

Obviously, we're a long way from setting rigorous, quantitative, scientifically defensible standards for representation. That's ok. After all, the coarse filter is essentially a buffer for our ignorance. The coarse filter has its greatest potential value for protecting species that we know little about, taxa such as bacteria, fungi, and soil invertebrates, which have not been adequately inventoried, and the genetic diversity within these taxa.

At its core, the coarse filter hypothesis is inherently unfalsifiable - we will never have a sufficiently complete inventory of species or genetic variation in any sizable geographic area to put it to a rigorous test. Nevertheless, the challenge of conserving biodiversity at all levels of the biological organization is immense and simply cannot be met through the conventional approach of protecting small sites with known occurrences of rare species or communities. For conserving genetic diversity within and among populations of species, a combined coarse filter/fine filter approach seems to be the most intelligent strategy.

In addition, we cannot rely on reserves alone - however critical - to provide a sufficient fine filter or coarse filter. In most regions, reserves will never cover enough area to accomplish the task of conserving the full range of biodiversity. Increasingly, we must look to protected areas, multiple-use lands, and intensively managed lands (such as tree plantations) and ask: How can each individual area contribute most to meeting global conservation goals while also providing other values to society?

# FRAGMENTS, EXTINCTION AND RECOLONIZATION: THE GENETICS OF METAPOPOPULATIONS

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## ABSTRACT

The idea of a metapopulation - a group of local populations in a patchy habitat - recurs in both ecology and evolutionary biology. Although the metapopulation concept is at least 50-75 years old, it has recently resurged, as natural habitats become fragmented and are lost because of humans' use of resources. However, fragmentation is not the same as habitat loss per se, and patchy habitats do not necessarily make metapopulations. Some populations may behave naturally as metapopulations and are characterized by extinction of some local populations and recolonization of empty patches from the occupied patches. Alternatively, other populations may be forced into a metapopulation dynamic by human-caused habitat fragmentation or other introduced disturbances. The genetic effects of habitat fragmentation or introduced disturbance are subtle and depend on frequency of migration between patches, rates of recolonization of empty patches, and levels of genetic variation before fragmentation began. Other than generally reducing population sizes, the effects of metapopulations on breeding practices or adaptive evolution depend on the amount of genetic variation remaining within local populations, how genetically differentiated from each other local populations become as a result of local extinctions and recolonization, the strength of natural or artificial selection, and whether selection is locally strong enough to result in adaptation to local conditions. We offer limber pine (*Pinus flexilis* James) as an example of a forest tree species that experiences metapopulation dynamics.

## INTRODUCTION

While ecosystems may appear to the untrained eye as uniform mantles laid on the earth, the naturalists' view encompasses landscapes teeming with an exceptional variety of life, from tiny microbes to majestically giant trees. Both views have changed, however, as we continue to modify and develop our world. Perceptions of an altered world begin to converge and all are aware of the small fragments remaining from the unbroken vistas that used to be. As a result, our views of the populations inhabiting these fragmented landscapes also change. Rather than thinking of vast populations, we envision groups of survivors isolated in smaller and smaller pieces of suitable habitat. The worldwide loss of habitat and the prospect of declining species means that biologists must come to understand the dynamics of subdivided populations, and the conditions that permit species to persist as collections of smaller groups (Hanski and Simberloff 1997; Simberloff 2001). But further, habitat fragmentation will have long-term



effects, altering the genetics of populations and the potential for evolutionary change in the future (Barton and Whitlock 1997).

The purpose of this paper is to describe current approaches to the biology and genetics of subdivided populations. First we will define what is meant by metapopulation, the term most commonly associated with population subdivision. Second, we describe the genetic theory of subdivided populations and examples of population genetic studies. Third, we discuss how these concepts apply to forest species, using Limber pine (*Pinus flexilis* James) as an example.

## DEFINING METAPOPOPULATIONS

Research on the effects of patchy environments on populations has a long and storied history (Addicott *et al.* 1987; Wiens 1976; see Hanski and Gilpin 1997; Hanski 1999). On the one hand, arguments abounded over the role of patchiness in regulating population growth and whether spatial and temporal patchiness affects density-dependence (e.g. Andrewartha and Birch 1954). On the other hand, a tradition of examining genetics and evolution in patchy environments also developed, particularly in examining the relative influences of genetic drift, gene flow, and selection in a series of small populations (Wright 1978; Barton and Whitlock 1997). Similarly, the dynamic theory of island biogeography (MacArthur and Wilson 1967) created a conceptual framework for understanding the effects of patchiness on the composition of multi-species communities. It is from these traditions that the idea of a metapopulation arose (Levins 1969, 1970; den Boer 1968). After a quiescent period, interest in metapopulations recently resurged with the application of population biology to conservation of species in fragmented habitats (Hanski and Simberloff 1997).

A metapopulation comprises a group of local populations in a patchy habitat, linked by limited migration, where the number of occupied habitats is determined by extinction and recolonization of the local populations (Levins 1969, 1970; Hanski and Simberloff 1997; Harrison and Taylor 1997, Hanski 1999; Hastings and Harrison 1994). In this sense, a metapopulation is a "population of populations", with each local population having its own population growth or decline, while the entire constellation undergoes dynamic cycles of habitat patches being occupied, emptied by local extinction, and recolonized by dispersal from occupied patches (Figure 1). Classic metapopulations, as originally envisioned by Levins (1969), are difficult to distinguish from subdivided populations that do not undergo regular extinction and recolonization (Harrison and Taylor 1997; Hastings and Harrison 1994; McCullough 1996). Habitat patchiness itself does not define a metapopulation. If regular movement, either by individual animals or by pollen and seeds of plants, encompasses a number of patches, the amalgam of habitat will likely constitute a single breeding population (type B in Figure 1). At the opposite extreme, if a series of habitat patches are isolated enough to prevent successful dispersal or pollination, each patch comprises a single population (type C in Figure 1). Metapopulation stability and persistence is not possible if each habitat patch is so small that local extinction is likely but recolonization does not occur. Eventually, all local populations are expected to go extinct (Harrison and Taylor 1997; Thrall *et al.* 1998).

Classic metapopulations should also be distinguished from source-sink metapopulations or mainland-island metapopulations (type D, E in Figure 1). In these, one or a few populations are either large enough or have sufficient population growth that they never become extinct. Sinks or islands, however, never experience high enough population growth to ensure long-term viability and thus depend upon recolonization from the mainland or from other sources (Hanski and Simberloff 1997; Harrison and Taylor 1997). The critical difference between these models and classic metapopulations is that persistence of the whole is not affected by what happens to islands or sinks (Hanski and Simberloff 1997).

Thus, the long-term persistence of metapopulations seem precarious, depending on a balance between extinction and recolonization of local populations (Hanski 1999; McCullough 1996). Hanski *et al.* (1995) outlined four conditions needed for metapopulation persistence: 1) population structure, which is implied by patchy and fragmented habitats, 2) having no single population large enough to ensure long-term survival, 3) having no habitat patch so isolated that recolonization is impossible, and 4) asynchronous dynamics of local populations, so that simultaneous extinction of *all* local populations is unlikely. Before

conservationists took up metapopulation biology as a model for studying newly fragmented species, relatively few examples of natural metapopulations, based on long-term sampling, existed. Two exceptions were the American pika (*Ochotona princeps*) (Moilanen *et al.* 1998) and the Glanville fritillary (*Melitaea cinxia*) (Hanski 1999). Examples now abound (see Hanski and Gilpin 1997; Antonovics *et al.* 1994; Hanski 1999; Webster and Johnson 2000), although in many cases these are newly-minted and it remains to be seen if they will persist.

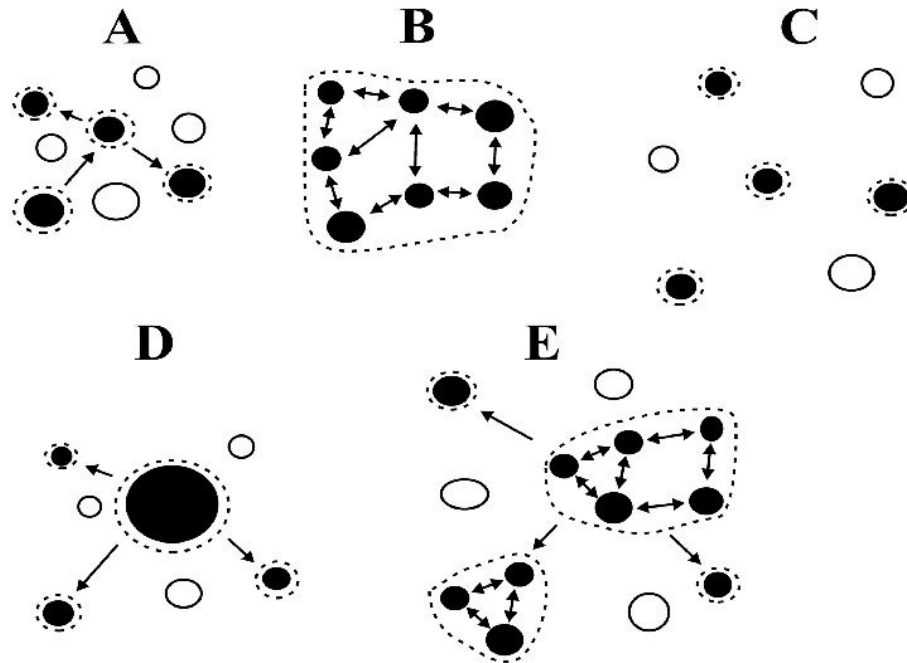


Figure 1. Types of structured populations. Filled circles represent occupied habitat patches; empty circles are vacant habitat patches; dotted lines show extent of local populations; arrows show dispersal. A. Classic metapopulation. B. Patchy environment with a single local population occupying all patches. C. patchy environment with no dispersal among habitat patches (non-equilibrium). D. Source-sink or mainland-island structure. E. Patchy habitat combining aspects of all other types. Redrawn after Harrison and Taylor (1997).

Finally, it should be pointed out that both patchy habitats and metapopulation dynamics may be transient. For instance, if empty habitats arise as a consequence of disturbance like fire, or if habitats become fragmented because of human resource use, the resulting patchy habitat may be conducive to metapopulation dynamics. However, natural regeneration through succession of species and ecological communities can be expected if the disturbance ceases. Thus, understanding whether a metapopulation is stable or whether habitat patches comprise a series of isolated population fragments awaiting species-wide extinction depends on larger-scale regional dynamics and the changing landscape where the metapopulations are embedded (Wiens 1997). For instance, the disappearance of an early-successional plant species from a group of clearings in a forest does not necessarily constitute extinction of a metapopulation.

## METAPOPULATION DYNAMICS

Metapopulations exist in a series of discontinuous habitats, linked by limited migration, where the proportion of occupied habitats is determined by extinction and recolonization of local populations (Levins 1969, 1970). The dynamics of a metapopulation can be written as a change in habitat patch occupancy as follows:

$$\frac{dP}{dt} = mP(1 - P) - eP$$

This simple model balances the loss of local populations by extinction ( $eP$ ) and the gain of local populations by recolonization of empty habitat patches ( $mP$ ), which occur in frequency  $1 - P$ .

This model, however, assumes the same migration rate and extinction rate affects all habitat patches and more realistic spatially explicit models have been developed (Hanski 1999). A highly successful model for analyzing metapopulation persistence is the incidence function model adopted by Hanski (1999) and colleagues at the University of Helsinki, Finland. Incidence refers to the probability of occupancy of each habitat patch at any given time and is influenced by the size of the patch and its isolation from other patches. The isolation of habitat patches depends on the size of surrounding patches, the distance from a habitat patch to surrounding patches, the relationship between patch distance, and the probability of migration, and whether surrounding patches are occupied. The model has been tested for two metapopulations, the American pika (Moilanen *et al.* 1998) and the Glanville fritillary (Hanski 1999). Both of these case studies entailed long-term population sampling, and in both the incidence model correctly predicted the turnover rate of local populations.

Finally, long-term persistence of metapopulations will be affected by the causes of extinctions of local populations (Hanski 1999). If extinctions occur randomly (stochastically), their causes can be classified into two broad categories: extinctions from demographic stochasticity and extinctions because of environmental stochasticity (Simberloff 1988). Demographic stochasticity increases probability of extinction because of slow population growth and the loss of small local populations. For example, a local population could become extinct if offspring of one sex only are produced for several generations. Environmental stochasticity, on the other hand, leads to extinction because of local disasters of one kind or another, which originate from outside the local populations and equally affect both large and small local populations. Good examples of environmental stochasticity are extensive forest fires or introduction of a highly virulent and highly infectious disease into a local population, quickly killing all individuals and causing a local extinction. In general, longer persistence of metapopulations is expected if extinctions result from demographic than from environmental stochasticity. Demographic stochasticity disproportionately affects small local populations, so that the overall rate of extinction from demographic stochasticity can be reduced by the "rescue effect" of migrating colonists from larger subpopulations (Hanski, 1999). Environmental stochasticity affects both large and small local populations, and makes long term persistence of the metapopulation more difficult.

## GENETICS OF METAPOPULATIONS

Three population genetics consequences, which overlap broadly, will arise when extinction and recolonization become a feature of subdivided populations. These are: 1) the effective size of the metapopulation, 2) the amount of genetic differentiation between local populations, and 3) the potential for evolutionary change in a metapopulation. Successfully predicting how fragmentation and local extinction will change large randomly mating populations depends on whether immigration into local populations continues after initial colonization, whether migrants are randomly drawn from the local populations, and the relative sizes of each of the local populations. Further, predicting the effects of fragmentation on

genetics and demography of a species depends on prior history of the spatial structure of a population before the fragmentation begins. For instance, a species that already experienced a history of inbreeding may not be dramatically affected by fragmentation and isolation because of habitat loss (Hedrick and Kalinowski 2000; Lande and Schamske 1985; Lande 1988; Thrall *et al.* 1998). We discuss each of the three genetic consequences in turn.

Habitat fragmentation can influence effective population size ( $N_e$ ), which measures a population in terms of how many individuals contribute to breeding and the amount of genetic variability that would be maintained by random mating in a population of size  $N_e$  (Barton and Whitlock 1997). In almost all cases, the effective population size is smaller than the actual numbers of individuals in the population. Effective population size is reduced by any factor that reduces the number of genotypes represented in the population. Typically, these include unequal reproductive success by males and females (i.e. harem breeding), differences in family size (some families are over represented), or recent population bottlenecks. Many formulations of effective population size have been developed, differing mainly by whether effective size is reduced by prior population bottlenecks and inbreeding, ongoing reproduction and genetic drift, or the overall loss of heterozygosity in populations (Crow and Denniston 1988; Pannell and Charlesworth 2000; Whitlock and Barton 1997). For our purposes, the reduction in effective population size because of genetic drift, called the variance effective size, provides an intuitive relationship between effective size ( $N_e$ ) and census number ( $N$ ):

$$N_e = \frac{4N}{V_k + 2}$$

Because  $V_k$ , the variance in reproductive success, is in the denominator, any increase in variance decreases  $N_e$ . Variance can be between sexes, between families, or in the case of metapopulations, between local populations. Considering that metapopulations are characterized by local extinction and recolonization, processes that inevitably generate variance in reproductive success among local populations, metapopulations will *always* have smaller effective size than unfragmented populations with the same number of individuals (Barton and Whitlock 1997; Chesson *et al.* 1993; Hedrick and Gilpin 1997; Whitlock and Barton 1997).

Another feature of metapopulations is the genetic subdivision between local populations, which comes almost by definition. Dispersal and gene flow among local populations counter local genetic differences arising from genetic drift or natural selection. Metapopulations are defined in terms of independent dynamics of local populations – with high dispersal and gene flow local populations will not behave independently. It is conceivable, however, that a series of local populations will become genetically differentiated from each other, while at the same time losing genetic variability within each local population. The question arises, then, how much more genetic subdivision will be found in metapopulations compared to fragmented populations that do not undergo episodes of extinction and recolonization? The answer depends upon the number of individuals that colonize and the source of the dispersers (Barton and Whitlock 1997; McCauley 1993; Wade and McCauley 1988). First, genetic variation among local populations will be increased when the number of colonizers is fewer than the number of subsequent dispersers. If initial colonists comprise a small fraction of the total immigration into a local population, the initial colonizers will represent a small fraction of the available genotypes from the occupied habitat patches. The result is genetic bottlenecks and founder effects in local populations. This is described by the formula:

$$k < \frac{2Nm}{1 - \phi} + 0.5$$

Here,  $k$  is the number of colonizers,  $N$  is the average size of the source populations,  $m$  is the migration rate after initial colonization, and  $\phi$  is the probability that colonizers carry genes that originate from the same source population. One prediction of this model is that recently colonized populations should be more genetically distinct than older populations, which has been seen in a number of genetic studies of metapopulations of both plants and animals (Giles and Goudet 1997; Hanski 1999; McCauley 1993; Roach *et al.* 2001).

This formula also shows the second important issue, which is the composition of the pool of migrants that move between populations. If migrants have a high positive genetic correlation,  $\phi$ , they are more related to each other than average, which creates founder effects among colonists and migrants and increases genetic differentiation among local populations. If  $\phi$  is zero, migrants are drawn at random from local populations and migration will tend to genetically homogenize local populations.

Finally, how will the evolutionary potential of a metapopulation change? This issue is particularly difficult to study, despite rigorous genetic theory and data that describe genetics of small populations (Falconer and Mackay 1996; Lynch and Walsh 1998). First, it is difficult to predict how genetic variation, measured by neutral molecular markers, will relate to fitness-related traits like reproductive success, seed size, pollen production, or dispersal (c.f. Lynch 1996). Fitness-related traits are ultimately of greatest importance to conservation and breeding efforts and will influence extinctions of local populations (Frankham 1996; Hedrick and Kalinowski 2000). Second, the effects of inbreeding on fitness are quirky. Isolated local populations are expected to become more inbred than those connected to others by dispersal, but whether inbreeding has a negative effect depends upon an element of chance. For instance, the severity of inbreeding depression in a population will be a function of genetic load (the overall number of deleterious mutations in a population), which in turn varies according to the history of past inbreeding (Hedrick and Kalinowski 2000; Lacy and Ballou 1998; Lande and Schemske 1985; Lynch and Walsh 1998; Templeton 1987). Third, the severity of inbreeding depends on environmental variability as well; a highly inbred population in a salubrious environment could prosper (Hedrick and Kalinowski 2000).

As in general models of evolution, adaptive evolution in metapopulations depends on the amount of genetic variation in the population as a whole. However, metapopulation dynamics mean that genetic variation within each local population is a balance between migration, genetic drift, and selection in each local population (Barton and Whitlock 1997; Lynch 1996). The problem arises because, like genetic drift, the strength of selection on a trait is a function of effective population size. Therefore, selection will be able to change allele frequencies in local populations only if  $N_e s > N_e m$ , where  $N_e$  is effective population size,  $s$  is the strength of selection, and  $m$  is the migration rate. Although natural selection in large populations can be a strong force, in small populations where  $N_e$  is small, drift will predominate unless selection is very strong. In other words, small local population size means that most genetic variation will be selectively neutral. This has two consequences for metapopulations. On the one hand, it will be more difficult for favorable alleles to increase in frequency. On the other hand, deleterious alleles will have an almost equal chance of becoming common in small populations, which will decrease overall productivity of the metapopulation and may increase the likelihood of extinction of local populations (Lynch 1996). Finally, when migration becomes severely restricted so that  $N_e s > N_e m$  and habitat patches have different environmental circumstances, local adaptations may evolve (Barton and Whitlock 1997).

#### A FOREST METAPOPOPULATION: LIMBER PINE

Limber pine represents a case of a species whose distribution has changed from continuous to patchy and currently displays metapopulation dynamics (Webster and Johnson 2000). At the last glacial maximum, 14 000 years ago, limber pine was widespread throughout the eastern side of the Rocky Mountains in Colorado and Wyoming, but currently is characterized by a patchy distribution, restricted to high stress habitats on a broad elevational gradient, from low hills in the short grass prairie (1 630 m) in the east to treeline (3 400 m) in the mountains (Schoettle and Rochelle 2000; Wells and Stewart 1987). Patches of limber pine can persist for decades, but occasionally go extinct from stochastic events like wildfires. Climax limber pine populations appear to persist because local extinctions caused by wildfires are rare. Seeds seldom survive longer than 2 years in soil and being wingless, they cannot disperse by

wind on their own. Nonetheless, burned sites are rapidly recolonized by seeds dispersed by birds, mainly Clark's nutcracker (Webster and Johnson 2000). While limber pine forms climax stands, in some environments it is also an early successional species. Therefore, disturbances in other forest types open habitat for limber pine, which gradually become smaller as succession proceeds. Consequently, limber pine populations are patchy and constantly undergo episodes of extinction and recolonization.

Despite this wide range and patchy distribution, limber pine shows little genetic or morphological differentiation related to elevational changes (Latta and Mitton 1997; Schoettle and Rochelle 2000; Schuster *et al.* 1989; Schuster and Mitton 1991, 2000). Genetic studies indicate, that within local populations, pollen is dispersed evenly among trees (Schuster and Mitton 2000) but that seed dispersal by birds results in local clusters of related individuals (Schuster and Mitton 1991). Differences in pollen phenology along elevational gradients could limit gene flow via pollen between local populations (Schuster *et al.* 1989), but low between-population differentiation suggests gene flow by stepping-stone pollination across intermediate populations. Dispersal of seeds, which can be carried up to 22 km from the parent tree by birds (Lanner and Vander Wall 1980), would result in gene flow across the elevational gradient. Genetic analysis of isolated populations on the short grass prairie in north-central Colorado demonstrated occasional long distance pollen flow and levels of genetic diversity similar to those in larger mountain populations (Schuster and Mitton 2000). The only large genetic differences in limber pine are on a regional geographic scale that may reflect isolation in Pleistocene refugia on the Great Plains east of the Rocky Mountains and in the Great Basin west of the Rocky Mountains (Lata and Mitton 1997; Mitton *et al.* 2000).

Limber pine represents an interesting counter-example. Despite living in metapopulations on a broad elevational gradient, limber pine shows remarkably low morphological and physiological variation (Schoettle and Rochelle 2000). Other species with long distance dispersal of seed by birds show similar genetic patterns (Bruederle *et al.* 1998). This is in contrast to wind-pollinated species that also depend on wind for their primary mechanism of seed dispersal. These species show not only local genetic differentiation, but also differentiation within local populations (e.g. Rehfeldt 1997). The capacity in limber pine for either physiological plasticity or broad physiological tolerances may be adaptive for a species that occupies an altitudinal gradient, but that has high levels of gene flow. In this case, the metapopulation structure of limber pine may have resulted in evolution for generalized physiology, where colonization of isolated habitat patches requires the ability to withstand a variety of environmental conditions. In terms of adaptation in metapopulations, limber pine represents a case of large effective population size because of gene flow, combined with strong selection for plasticity or tolerance because of colonization of new habitat patches. Limber pine may be a case where turnover of local populations, combined with high dispersal and gene flow, results in evolution of a generalist lifestyle capable of tolerating a wide variety of environmental circumstances.

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VOLUNTEER PAPER

ABSTRACTS

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## **NURSERY ORIGIN AFFECTS FIFTH YEAR HEIGHT OF SEED ORCHARD AND NATURAL STAND INTERIOR SPRUCE SEEDLOTS**

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An interior spruce (*Picea glauca* (Moench) Voss) X (*Picea engelmannii* Parry ex Engelm.) seed orchard and a natural stand seedlot from each of three seed planning zones (SPZ) was sown in 1994 at seven nurseries in British Columbia. Two crops were produced: one was summer planted at two sites in 1994 and the other was spring planted on the same sites in 1995. Second year analyses indicated the nursery where the seedlings were produced explained more of the observed variation in height than any other main-effect source in the model. Fifth year height and seedling vigor were obtained in the fall of 1999. The greatest difference in fifth year height was between the two sites and they were analyzed separately. After five years, the nursery where the seedling was grown still accounted for the most variation observed in height at Skimikin, while SPZ was the next most important source of variation. SPZ was the most important source of height variation at Prince George and nursery was the next most important source. Site, nursery, planting time, and SPZ affected seedling survival. The data suggest nursery culture can significantly (positively or negatively) impact the performance of both seed orchard and natural stand spruce seedlots for at least five years after planting.

**GENETIC VARIATION AND ADAPTATION: UNDERSTANDING THE MECHANISMS,  
CONSERVATION AND UTILIZATION OF DROUGHT ADAPTIVE TRAITS**

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Rapid climate change, resulting from natural and human activities, has become a pressing international environmental concern. Along with increasing temperatures, increase in drought frequency and intensity is predicted. Drought strongly limits productivity and alters species competitiveness. Drought resistance thus becomes a desired adaptive trait, but is it possible to have drought resistance and not compromise overall growth rates? Physiological adaptive mechanisms vary and are often unclear. Studies in physiological genetics have revealed the importance of genetic variation in drought resistance traits. Contributing to the drought resistance puzzle are issues such as “strategies” of drought avoidance (i.e. stomatal closure) and drought tolerance (i.e. maintaining photosynthesis), atmospheric drought, role of turgor, and the possible use of stable carbon isotope tools. In order to offset climate change effects, maintaining and utilizing existing forest genetic variation will be a key challenge.

## **EVALUATION OF CHLOROPHYLL FLUORESCENCE AND ELECTROLYTE LEAKAGE FOR ASSESSING COLD HARDINESS IN ASPEN PROVENANCES**

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As part of a project to assess adaptive variation in aspen (*Populus tremuloides* Michx.), the relative efficacy of chlorophyll A fluorescence and electrolyte leakage to measure frost hardiness was determined. Leaf and stem samples of twelve seedlots of aspen from northwestern Ontario were collected from two field trials and subjected to selected freezing temperatures in September and October 1999. Leaf and stem damage was assessed by chlorophyll fluorescence and electrolyte leakage respectively. The electrolyte leakage technique was expressed as relative conductivity (EC), index of injury (IT) and was quantified as the temperature needed to induce an EC of 50% (LT50%). Chlorophyll A fluorescence was expressed as  $F_0$ ,  $F_v/F_m$ , reduction percent in  $F_0$  and  $F_v/F_m$  after treatment, and  $F_v/F_m$  at LT50% (LT50% $F_v/F_m$ ). Chlorophyll A fluorescence data showed a very strong correlation with the assessments of injury by electrical conductivity indicating that the techniques can be used as a simple, non-destructive and objective measure to evaluate frost hardiness in aspen provenances. Significant levels of interprovenance variation were present for both chlorophyll fluorescence and electrolyte leakage variables. Multiple regression analysis between chlorophyll fluorescence and electrolyte leakage variables and climatic data showed that minimum temperature, precipitation, and heat sums were good predictors of the adaptive selection responses in cold hardiness to environmental factors.

**VARIATION IN ROOTING AND EARLY GROWTH  
OF GROUND HEMLOCK (*Taxus canadensis*)**

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Ground hemlock (*Taxus canadensis* Marsh.) is a woodland shrub which grows in eastern Canada and the U.S.A. It has recently been recognized for its potential as a source of secondary plant compounds called 'taxanes'. One of these taxanes, paclitaxel, is the active ingredient in Taxol® a widely used anti-cancer drug, and other associated compounds can be semi-synthesized into paclitaxel. Despite a rapidly increasing interest in ground hemlock as a source of biomass for paclitaxel and related compounds, little work has been done to either inventory wild populations in order to estimate sustainable harvest levels or to determine the levels of genetic variation in this species. Consequently, in 1997, CFS-Atlantic initiated a number of experiments to begin to quantify clonal variation in growth and taxane production within and among populations of ground hemlock. The main objectives of these trials are to identify clones that are both fast-growing and that produce high quantities of selected taxanes. These selected clones will provide the foundation of a tree improvement program for this species. A brief review of early results from rooting and growth studies is presented.



**THE EFFECT OF BUDBURST PHENOLOGY OF NORWAY SPRUCE (*Picea abies*)  
ON THE BIOLOGICAL PERFORMANCE  
OF THE WHITE PINE WEEVIL (*Pissodes strobi*)**

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The white pine weevil is an important pest for pine and spruce plantations in North America. The most damaged trees may suffer losses in height growth and develop stem deformities that inevitably reduce timber quality. The importance of the synchronicity between the insect and its host is well documented for spring defoliators. The objective of this experiment was to determine the influence of budburst phenology of Norway spruce on the biological performance of the white pine weevil. We hypothesised that trees having an early budbreak would reduce the weight and the survivorship of the insect. On the terminal leader we caged 3 males and 3 females on each tree of three budburst groups (early, medium and late) during the egg-laying period. After an oviposition period of 21 days and a sufficient period to allow complete larval development, the infested terminal leaders were collected and kept in a greenhouse. Emergence of the weevils was followed daily. It was found that the weight and the time of weevil development were not influenced by phenology. The number of eggs, emergence, and survival tended to be affected by phenology. Probably other factors play a more important role than phenology. Consequently, budburst phenology cannot be used as a selection tool by breeders to improve Norway spruce resistance to weevil.

## **COMPARISON OF MULTIVARIATE AND UNIVARIATE METHODS FOR THE ESTIMATION OF TYPE B GENETIC CORRELATIONS**

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Univariate and multivariate statistical methods for type B genetic correlation estimation are numerically compared based on simulated forest genetics experimental data. Results indicate that the multivariate method can effectively handle unbalanced data sets associated with heterogenous variances and yield empirically unbiased estimates of type B genetic correlations for various data structures. Constraining estimates of type B genetic correlations within theoretical parameter space when using multivariate methods helps improve estimation accuracy and narrow the confidence interval. While some univariate methods can produce equally unbiased estimates of type B genetic correlations for unbalanced data with heterogenous variances, multivariate methods are expected to be more efficient and flexible in accommodating various genetic relatedness structures as tree improvement programs move into advanced generations.

**HERITABILITY AND AGE-AGE CORRELATIONS OF *Pinus banksiana*  
IN SASKATCHEWAN**

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To estimate genetic patterns, phenotypic and genetic age-age correlations were calculated between height and diameter measurements of 89 *Pinus banksiana* Lamb. provenances from Saskatchewan and eastern Alberta. Height measurements were recorded at 5, 10, 15 and 22 years from planting and diameters at 10, 15, and 22 years in four field tests located in Saskatchewan. Phenotypic age-age correlations found height and diameter at 10 and 15 correlated highly to year 22. Genetic correlations were high between diameter measurements ( $r > 0.69$ ), but lower between height pairs and height to diameter pairs. Higher genetic correlations were observed between pairs of older measurements than between pairs of the youngest and older variables. Individual-tree heritability increased with age, with the family heritability approximately double the value of the individual-tree values. These genetic parameter values indicated that family selections for breeding at 10 years from planting would have resulted in a slight loss of genetic efficiency compared to selection based on the 15-year results.

## SCREENING FOR RESISTANCE TO WEEVIL ATTACK BY ARTIFICIAL WOUNDING OF SITKA X WHITE SPRUCE HYBRIDS FROM THE NORTH COAST OF BC

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Seedlings from 18 provenances along a coast-interior transect in the *Picea sitchensis* x *P. glauca* introgression zone in northwestern BC were artificially wounded at the beginning of their 3<sup>rd</sup> growing season to simulate natural attack by the white pine weevil (*Pissodes strobi*). Constitutive cortical and traumatic xylem resin canals of the wounded seedlings and non-wounded controls were examined four months after wounding terminal shoots. Traumatic resin canals were frequent in almost all wounded seedlings and absent in almost all non-wounded seedlings. Genetic differences among provenances were detected for number of traumatic and constitutive resin canals and for size of constitutive resin canals. Statistically significant multiple regression models related genetic variation in resin canal traits to geographic ( $r^2 = 0.66$ ) and climatic ( $r^2 = 0.57$ ) variables. Traumatic and constitutive resin canal number and constitutive resin canal size increased with latitude, elevation, and valley-bottom-distance to an inlet, and decreased with longitude. The similarity between these clines and those shown previously for white pine weevil resistance suggests that resin canal traits may provide a simple early selection trait for resistance to white pine weevil. Tests of weevil resistance in these materials are underway to confirm the potential for using resin canal traits in selection for weevil resistance.

**GENE CONSERVATION OF PACIFIC NORTHWEST CONIFERS:  
*IN SITU* AND *EX SITU* ANALYSES**

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The Pacific Northwest Forest Tree Gene Conservation Group is an ad hoc group of forest geneticists representing government, university, and private interests whose aim is to ensure that the evolutionary potential of important tree species in the region is maintained. As part of this effort, we are analyzing the spatial distribution of genetic resources conserved both *in situ* and *ex situ* for eight conifer species in western Oregon and Washington. We used a GIS-based “gap analysis” approach to determine the spatial distribution of *in situ* genetic resources. GIS coverages showing detailed distributions of tree species across the landscape were overlaid with coverages of reserves to determine the locations of protected populations. The populations were then stratified into presumably unique genetic units using a system of seed zones and ecoregions. For the analysis of *ex situ* genetic resources, we summarized all resources present in seed stores, provenance and progeny tests, seed orchards, and clone banks both in western Oregon and Washington and in other countries when the germplasm originated in western Oregon and Washington. These combined approaches provide more detailed information on the gene resource status of tree species than any other approach taken to date.

## **A METHODOLOGY TO DEVELOP BREEDING ZONES BASED ON SPATIAL DATA**

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Tree improvement programs for jack pine (*Pinus banksiana* Lamb.) and black spruce (*Picea mariana* (Mill) BSP) in northwestern Ontario are rapidly going into their second generation necessitating the verification of tentative breeding zones. A method was developed based on the digital Ontario Climate Model (OCM), several short-term provenance tests, and a further development of the Focal Point Seed Zone methodology (Differential Systematic Coefficient) to suggest both number and location of breeding zones for these two species. A principal components analysis (PCA) was run on seedling growth, phenological, and freezing variables obtained from the short-term trials. PCA summary scores were regressed against OCM variables. These regression models were converted to spatial data; weighted average Least Significant Difference values were geographically located; and, areas of rapid change in adaptive variation were identified by GIS. An example for black spruce from the western part of the Northwest Region is presented. The twelve breeding zones tentatively determined for this area were replaced with four new regions using the GIS approach.

## **GENETIC MODIFICATION OF WOOD PROPERTIES**

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Opportunities for modifying wood physical and chemical properties to enhance product qualities and yields have long been recognized. Exploitation has been hampered by high costs of trait measurement and lack of genetic information. Inexpensive measurement of small, nondestructively collected samples, however, is now possible. Lignin content, e.g., can be assessed in minutes on a gram or less of wood. Genetic control of most wood properties is moderate to strong. Sometimes negative correlations with growth may be overcome by increased selection intensities. Genotype X environment interactions typically are nonlimiting. Genetic markers are being used to manage breeding and production populations. Characterizing quantitative trait loci should help improve wood properties that are difficult or expensive to measure. Genetic transformation is being used to add genes from unrelated species, to alter activity of native genes, and to save time by avoiding the sexual cycle. Normally growing transgenic trees having reduced lignin and increased cellulose contents have been produced. Progress on all fronts has been considerable, and dividends from modifying important wood properties, whether for solid wood, paper, or energy products, are nearing realization.





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TREE SEED WORKING GROUP  
WORKSHOP ABSTRACTS

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## Workshop Theme

“The Role of Ex-Situ Germ Plasm Storage in Gene Conservation”

## THE ROLE OF THE NATIONAL TREE SEED CENTRE IN GENETIC CONSERVATION

**J. Dale Simpson**

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The National Tree Seed Centre was established in 1967 at the former Petawawa Forest Experiment Station and was transferred to Fredericton, NB in 1996. Its primary objective was to collect, store, and provide seed of known origin and quality for research. The Seed Centre began to establish an inventory by collecting and processing seed as well as acquiring seed from other agencies such as provincial governments and seed collectors. In addition, the Centre stored seed collected for use in provenance trials of various native species as well as facilitated the acquisition of seed from foreign countries.

A survey was sent to provincial governments in order to ascertain the extent to which genetic conservation via seed storage is conducted in Canada. A response was received from each province, Yukon and the Forest Gene Conservation Association in Ontario. Alberta and Prince Edward Island are the only provinces to store seed for conservation purposes although most provinces consider that their inventories of seed for reforestation and from plus tree selection could be considered for conservation. British Columbia and Alberta have intentionally stored samples from their reforestation collections. Total number of seedlots in storage is over 13 000 and these are all stored at provincial seed centres. Newfoundland, Ontario, and British Columbia indicated they plan to start a genetic conservation program. The government of BC will develop strategies for various species such as jack pine (*Pinus banksiana* Lamb.), noble fir (*Abies procera* Rehd.) and black spruce (*Picea mariana* [Mill.] B.S.P.) (rare species) and whitebark pine (*Pinus albicaulis* Engelm.) (threatened species) which, like Ontario, will include a combination of *in situ* and *ex situ* methods. Yukon may consider initiating a tree improvement program. The consensus was that it would be beneficial to have a nationally coordinated program.

In order for the National Tree Seed Centre to be truly "national" the long-term goal is to build an inventory of seedlots collected from natural populations from throughout the natural range of as many native tree and shrub species as possible. All provinces have operational tree improvement programs for commercial tree species. As seed requirements for reforestation are increasingly met by seed orchards, seed will not be collected from natural populations. With the exception of those provinces who have banked samples from operational collections the Seed Centre's inventory of seed from commercial species will become increasingly valuable as provincial governments and forestry companies make fewer collections from natural populations.

The National Tree Seed Centre should be considered as an additional site to store samples from seedlots. This is important for "insurance" purposes to protect against a catastrophic loss at the primary site. One way is for the Seed Centre to collaborate with the provinces and territories when conservation strategies are implemented. Species that are targeted to be conserved will be a provincial decision but more than likely populations of species whose natural range is limited and/or which are isolated or fragmented from the contiguous range will be targeted first. Seed should be collected from old-growth stands and unique populations too.

Conservation of genetic resources through seed storage is but one component of a conservation strategy. However, it may not be practicable for some species. For those species for which seed can be stored and maintain high viability for several decades the National Tree Seed Centre is ready and willing to participate and cooperate with the provinces and territories in any way that is feasible.

## THE ROLE OF PROVINCIAL TREE SEED CENTRES IN GENE CONSERVATION

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The primary role of a provincial tree seed centre is in the maintenance of an *ex situ* seed bank that represents the variation present on the landscape. Fortunately, north temperate conifers have orthodox seeds which can be dried to low moisture levels (<10%) and maintained under sub-freezing temperatures for years or decades. Deterioration is generally slow, but the following BC species deteriorate at elevated levels (presented as D germination capacity / year): *Thuja plicata* 1.44%; *Tsuga heterophylla* 1.22%; *Larix occidentalis* 1.06% and *Pinus monticola* 1.03%. Seed banks are a very efficient means of conserving {managing} and preserving {maintaining initial quality} genetic variability. A handful (100 grams) of white spruce seed can represent 50 000 genotypes.

A secondary role of a tree seed centre is to conduct operational trials to improve the germination or storability of species showing rapid deterioration. This may involve tree species that are not considered commercial, but are threatened by pests, destruction of habitat or lack a sufficient *ex situ* gene conservation effort. The tree seed centre should co-ordinate species and within-species representation with other agencies, within and outside the province, in a seed bank.

Seed banks do have limitations as seed deterioration will occur and there is the potential for selection to occur during storage reducing the total amount of variability present. If a population is required to be rejuvenated from seed there may also be selection on the seedlings. The selective forces acting on the rejuvenated material may be quite different from the original population resulting in a divergence of gene frequencies or loss of variability. The significance of this reduced variability has not been quantified with conifers. A seed bank should be considered as an insurance policy of genetic variability and should be complemented with a comprehensive *in situ* gene conservation scheme.

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# POSTER ABSTRACTS

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**GENETIC DIVERSITY OF CANADA YEW (*Taxus canadensis*)****Sauphie Senneville<sup>1,2</sup>, Jean Beaulieu<sup>1</sup>, Gaëtan Daoust<sup>1</sup>, Marie Deslauriers<sup>1</sup>  
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Canada yew (*Taxus canadensis* Marsh.) is a gymnosperm growing in the understory of mixed and deciduous forests of northeastern North America. This shrub had no economic importance until the discovery of paclitaxel, or Taxol<sup>®</sup>, which is a drug extracted from its foliage and used in cancer treatment. With the intensifying harvesting pressure on this species, the natural gene pool might be affected. The objective of the present study was to estimate the levels of genetic diversity and population structure in Canada yew before any sizeable effects resulting from harvesting appear. Six natural populations were sampled in Québec. Genetic diversity was estimated at 22 loci coding for 12 enzyme systems. At the population level, the number of alleles per locus was 1.32, the percentage of polymorphic loci was 26.5, and the observed heterozygosity was 0.102. Thus, these results show that Canada yew is genetically less diverse than other yew species and the great majority of gymnosperms. However, the amount of population differentiation was substantially higher ( $F_{ST} = 10.2\%$ ) than that for other conifer and tree species growing in the boreal-temperate zone. Hypotheses related to the biogeography of the species and a likely metapopulation structure are proposed to explain the observed trends.

## **GROUND HEMLOCK - A NON-TIMBER FOREST RESOURCE**

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Ground hemlock (*Taxus canadensis* Marsh.), also known as Canada yew or eastern yew, is a low growing spreading shrub. Not used for timber or pulp, but an important food source for wildlife, ground hemlock was considered rather insignificant until recently. After the discovery that the bark of the Pacific yew (*Taxus brevifolia* Nutt.), a west coast species, contained a natural substance which is very effective against breast and other cancers, interest in the east coast species increased. Ground hemlock has subsequently been shown to contain similar anti-cancer compounds. The high value of these chemicals has resulted in considerable harvesting of the plants in the wild. However, initial harvesting was not done using guidelines specifically developed for sustainable management. Natural Resources Canada – Canadian Forest Service in Fredericton has recently initiated a series of studies with three main objectives: 1) develop tools and strategies for the preservation/conservation of ground hemlock, 2) learn about the genetics and biology of ground hemlock, and 3) provide knowledge support for a domestication program. The information learned about the biology and ecology of ground hemlock is being used to develop and refine sustainable management guidelines as well as provide the research necessary to help ensure a viable long-term industry in the Atlantic Region.



**PRODUCING AN IMPROVED LARCH FOR REFORESTATION IN QUÉBEC –  
A MULTI-DISCIPLINARY APPROACH**

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Hybrid larches have shown great potential for intensive forestry. Exotic larches were first introduced in Québec in 1960 by the Canadian Forest Service. The genetic improvement program started in 1970. To date, 114 experimental plantations contain more than 130 seedlots from 4 species: tamarack (*Larix laricina* (Du Roi) K. Koch), European (*Larix decidua* Mill.), Japanese (*Larix kaempferi* (Lamb.) Carrière), and Siberian larch (*Larix sibirica* Ledeb.). Growth of hybrids vs parents is impressive; a 15% to 60% height advantage at 15 years.

Large-scale production of hybrid larch seeds difficult. There are many limiting factors such as phenology differences between species and low percentage of filled seeds. A new project began in 2000 for which the goals are a better understanding of floral biology and an improved production of hybrid seeds. A large-scale system is being developed for bulk propagation of elite families by cuttings under mist, with an objective of 1 million stecklings per year.

In the nursery, the objective is to determine the optimum environmental conditions and cultural protocols for growing stecklings and seedlings. Study factors include light level, air and substrate temperatures, air humidity, container types, nutrition, and irrigation regime. Survival, growth, and physiological performance of the stecklings and seedlings planted on different sites will be monitored throughout the growing season for 5 years.

## WHITE SPRUCE POPULATION RESPONSES TO POTENTIAL CLIMATE CHANGE IN QUÉBEC

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Forest tree species growing in eastern Canada are expected to be highly affected in the near future by climate change due to global warming. To mitigate negative impacts on forests, a better knowledge of responses to climate change must be acquired. In this study, we developed models to estimate such impacts on white spruce (*Picea glauca* (Moench) Voss) growing in Québec. Most often, predictive models have been obtained from an univariate perspective and generally for height growth only. The response of some important characters related to tree productivity such as wood traits is still poorly understood and needs to be examined closely. Moreover, in most studies, independent data sets are lacking, which makes it impossible to validate models. In this study, we used data collected in a provenance-progeny test including 41 provenances originating from the province of Québec and each represented by four open-pollinated families. The test was replicated on three different sites. Both wood and growth trait data were collected and analysed. Polynomial regressions were then developed to predict provenance performance, based on temperature differentials (and more generally on climatic differentials) between experimental site locations and provenance origins. These complex models were tested using data collected in a second provenance-progeny test series.

**AN EXAMINATION OF INTERIOR SPRUCE (*Picea glauca* X *P. engelmannii*) HEALTH  
AND VIGOUR MEASUREMENTS USING FACTOR ANALYSIS**

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Health or vigour of young trees can be an important indicator of performance in tree improvement research. Statistical analysis of tree health has not been feasible with the health coding system commonly used in our assessment programs. This study attempted to identify significant measures of health or vigour to develop a coding system conducive to statistical analysis. Tree health was examined using data from young improved hybrid spruce plantations in Prince George and Salmon Arm, British Columbia. Health of individual spruce trees was coded in the summer of 1999 using a list of 15 health concerns. Each code was then converted into binary format to allow for the analysis of multiple codes per tree. Factor analysis was used to determine which health codes were overall performance indicators. Latent constructs identified for the model were tree form and tree physiology. Preliminary results show that tree form is represented by non-flushing and multiple leaders while tree physiology is represented by general sickness, chlorosis, and height. These results can be used to develop a cumulative scoring system that integrates multiple health codes with tree height. This scoring system would allow for the evaluation of overall tree performance in any research program involving tree assessment.

**GENETIC DIFFERENCES AMONG INTERIOR SPRUCE FAMILIES PLANTED NEAR  
PRINCE GEORGE TO WHITE PINE WEEVIL, *Pissodes strobi* (PECK), ATTACK**

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Forty half-sib families of interior spruce (*Picea glauca* (Moench) Voss X *Picea engelmannii* Parry ex Engelm.) from Vernon Seed Orchard #214 were sown by the JD Little Forestry Centre in 1997 and planted in two trials near Prince George in 1998. Of these, several families have been identified and ranked according to white pine weevil, *Pissodes strobi* (Peck), tolerance. Five families, which originally ranked as high, intermediate, and low for weevil resistance were selected for further tests in the spring of 2000. These families were subjected to attack by the white pine weevil through weevil seeding trials under different light intensities in a 5 (family) x 3 (light level) x 2 (weevil density) factorial design replicated five times. From this study, tolerance or resistance to weevil attack was quantified according to family by the level of damage incurred in each family and by tree recovery after attack. Differences in weevil attack rate across treatments were shown based upon insect oviposition and larval development rates. Although insect resistance is a multi-component trait, the selection of trees showing such characteristics will aid reforestation programs in dealing with pests that invade young plantations.

## REDUCING THE IMPACT OF BLISTER RUST ON WHITE PINE IN MINNESOTA

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In 1997, the Minnesota State Legislature provided funding to reduce the impact of blister rust on eastern white pine (*Pinus strobus* L.) in Minnesota, USA through several research projects. Here we summarize the findings from the first two years. 1) A new, more detailed rust hazard map for northeastern Minnesota was created which delineates low, medium, and high rust hazard areas. 2) Research on flower induction was initiated to support shortened generation cycles (breeding-testing-selecting). A foliar-spray application of gibberellic acid during shoot elongation induced both male and female inflorescences, but not consistently across all genotypes. 3) A rapid and reliable method was created to screen seedlings for susceptibility to blister rust. Using this method resistant families can be identified within 1½ years. 4) Histological examinations of the early stages of infection of both resistant and susceptible white pine seedlings were conducted to understand potential defense mechanisms. 5) A breeding arboretum containing promising clones was expanded using selected material from an earlier progeny test. Refinements to the flower induction and early screening techniques are being developed during the next two-year period and preparations are being made for breeding work in the arboretum. Internal biological and chemical methods of blocking infection are also being explored.

**GENETIC STRUCTURE WITHIN NATURAL POPULATIONS  
OF *Pinus strobus***

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Understanding the genetic structure of white pine will help in predicting the effects of silvicultural treatments on genetic variation within populations and in designing management strategies for maintaining diversity of pollen and seed sources. Diversity, spatial structure, and population structure of two populations of eastern white pine (*Pinus strobus* L.) were determined by SSR marker analysis. An old growth and a second growth population were sampled, located within Hartwick Pines State Park, Grayling, Michigan. From each population, approximately 120 contiguous trees were genotyped at eight CA<sub>n</sub> loci, averaging 6.5 and 7 alleles per locus for old growth and second growth, respectively. Moran's I analysis suggests a randomly distributed second growth population versus weak positive spatial structure at short distances for the old growth population. We hypothesize that structure was removed during logging of the second growth site. In the old growth population, two of eight fixation indices show decreased heterozygosity below Hardy-Weinberg Equilibrium, possibly due to temporal Wahlund effects. There is little population divergence with significant differences in allele frequencies between populations for 62% of loci. These measures indicate diversity is structured within rather than between populations, emphasizing the potential influence of stand management on gene conservation.

## PHENOLIC COMPOSITION OF NEEDLES OF FOUR PINE SPECIES IN THE GREAT LAKES FOREST REGION OF CANADA

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Phenolic variation in needles of four pine species: jack pine (*Pinus banksiana* Lamb.), red pine (*P. resinosa* Ait.), Scots pine (*P. sylvestris* L.), and eastern white pine (*P. strobus* L.) which may affect feeding behaviour of the European gypsy moth (*Lymantria dispar* L., Lepidoptera, *Lymantriidae*) were investigated. HPLC analysis of the crude extracts shows that each of the four pine species has its own distinct profile in both the 280nm and 350nm scans. Although the traces of jack pine and Scots pine are very similar and show quercetin 3-O-rutinoside as the major flavonol in both, C-methylkaempferol 3-O-glucoside is prominent in jack pine whereas taxifolin characterizes Scots pine. The white pine and red pine traces are also nearly similar to one another and differ from jack pine and Scots pine in the prominence of the acylated flavonols. Despite this similarity, both quantitative and qualitative differences in the acylated flavonols serve to distinguish white pine from red pine.

## PHENOLIC COMPOSITION OF LEAVES OF SIX MAPLE SPECIES IN THE GREAT LAKES FOREST REGION OF CANADA

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Phenolic constituents of leaves of 6 *Acer* species, representing 5 sections of the genus, were investigated by HPLC. Red maple (*A. rubrum* L.) and silver maple (*A. saccharinum* L), both Section Rubra (Pax), extracts were very similar in content and dominated by gallates, especially ethyl digallate. Striped maple (*A. pensylvanicum* L.) Section Macrantha (Pax) had a myricetin glycoside as a major peak. Sugar maple (*A. saccharum* Marsh) Section Saccharina (Pax) extracts had many proanthocyanidins. Chlorogenic acid, ellagic acid, and quercetin 3 rhamnoside were also prominent. Manitoba maple (*A. negundo* L) Section Negundo (K. Koch) extracts similarly were dominated by proanthocyanidins. Mountain maple (*A. spicatum* Lamb.) Section Spicata (Pax), extracts differed from those of *A. negundo* mainly in having a higher amount of ellagic acid. Thus, both quantitative and qualitative differences in the HPLC chromatograms serve to identify each species.



**INDUSTRY-LED TREE IMPROVEMENT PROGRAMS IN WEST-CENTRAL ALBERTA****Diane Renaud<sup>1</sup>, Deb Weedon<sup>2</sup>, and Sally John<sup>3</sup>****<sup>1</sup>Weldwood of Canada Ltd.  
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West-central Alberta includes much of the province's most productive forest land. Industry involvement in tree improvement has increased rapidly over the past decade. Seven active cooperative programs in 4 species: lodgepole pine (*Pinus contorta* Dougl. Ex. Loud.), white spruce (*Picea glauca* (Moench) Voss), black spruce (*Picea mariana* (Mill.) BSP), and trembling aspen (*Populus tremuloides* Michx.) are currently under industry direction and two more are being developed.

All programs are managed to maintain high levels of genetic diversity in both breeding and production (orchard) populations. Six programs also have genetic gain as a primary objective, while three are primarily seed production programs for species and regions where crops are infrequent, sparse, and expensive to collect.

Advanced orchards and breeding populations are being developed for two programs using forward selections from 20+ year old progeny tests. Wild parent selections have recently been completed for several other programs; orchard establishment and progeny testing are planned or under way.

More than 2,500 parents have been selected to date.



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PARTICIPANTS OF THE  
27<sup>th</sup> CTIA/ACAA MEETING

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# PHOTOS

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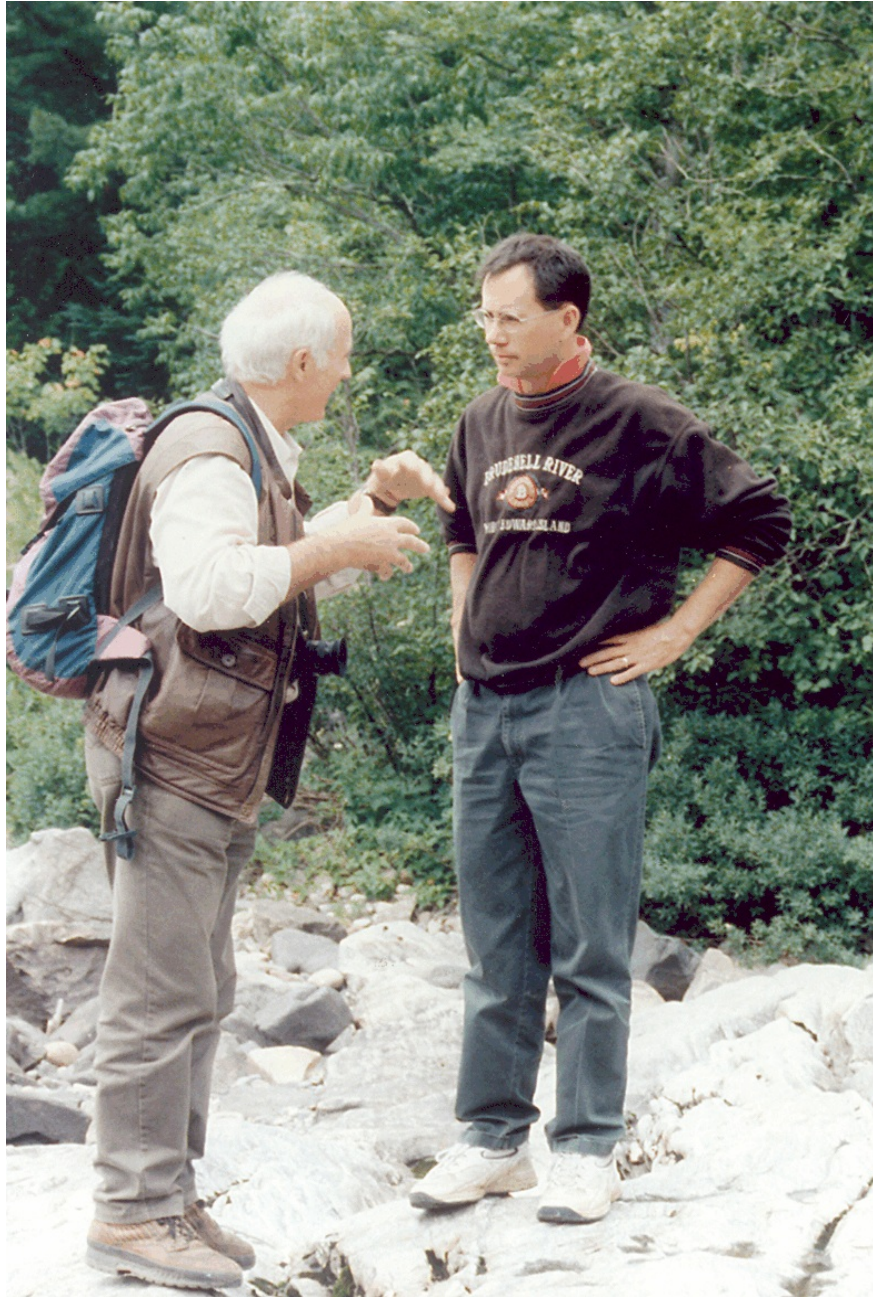
Bill Libby insists that it is the next ice age that will get us, not global warming!



Joachim Kleinschmit and Bill Libby putting on happy faces while Dennis Joyce is trying to decide which one he will give the picture to.



Jerry Klein laments, "All these dang spruce; not a jack pine in sight!!"



Joachim Kleinshcmit trying to convince Dan McKenney that the world is actually round.



"Albertans!" - Donna Palamarek and Bruce Dancik



"Hey, how about those shades?!" - Sally John, Donna Palamarek and Kathy Tosh.