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

PART 1 Minutes and Members’ Reports
PART 2 Symposium

Climate Change and Forest Genetics

Changements climatiques et génétiques

COMPTES RENDUS DU VINGT-NEUFIÈME CONGRÈS
DE
L’ASSOCIATION CANADIENNE POUR
L’AMÉLIORATION DES ARBRES

1^{ere} PARTIE Procès-verbaux et rapports des membres
2^{e} PARTIE Colloque

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Contents : Part 1. Minutes and Member's Reports. Part 2. Symposium.

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Conference Logo

The logo was commissioned by the conference organizing committee on behalf of the Canadian Tree Improvement Association. In commissioning this work of art, the Association recognizes the inter-dependence of natural systems and humanity's shared dependence on natural resources.

Michael Blackstock is a professional writer, visual artist, and forester. He is a Northwest coast native; a member of the Gitxsan house of Geel and carries the name *Ama Goodim Gyet*. Michael was born in 1961 and raised in small communities throughout British Columbia. His mother and father instilled the love of Mother Earth into Michael's upbringing. He now is, first and foremost, a naturalist.

The title of the logo is "Rain Raven." "First Nations believe water was a spirit; it is alive and biotic. Oral history of the Northwest Coast peoples talks about how Raven stole the sun from the Chief-of-the-Skies and brought it to the dark earth, then Raven stole fresh water and brought it to earth. This was a time of great climate change: sun and water were brought to earth. The Rain Raven image is meant to signify this story and respect for water. The Raven beak is in the form of the Gitxsan feast spoon (hoobix) and it holds the water that Raven stole from the Chief-of-the-Skies. The drops that fell from his beak formed rivers and lakes."

PROCEEDINGS

OF THE

TWENTY-NINTH MEETING

OF THE

CANADIAN TREE IMPROVEMENT ASSOCIATION

PART 1

Minutes and members' reports

Kelowna, British Columbia
July 26–29, 2004

Editor
J.D. Simpson

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COMPTES RENDUS

DU

VINGT-NEUFIÈME CONGRÈS

DE

L' ASSOCIATION CANADIENNE POUR L' AMÉLIORATION DES ARBRES

1re PARTIE

Procès-verbaux et rapports des membres

Kelowna, Colombie-Britannique
26–29 juillet 2004

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

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BUSINESS MEETING MINUTES

CTIA/ACAA 29th Business Meeting Minutes

Dave Kolotelo chaired the 29th Business Meeting of the CTIA/ACAA held at The Grand Okanagan, Kelowna, British Columbia on Thursday July 29, 2004. Seventeen members were present.

333 Minutes of the 28th Meeting

(as printed in the proceedings from the 28th meeting, Part I)

Motion: That the minutes of the 28th Business Meeting be approved as published.
Moved by: Kathy Tosh
Seconded by: Greg O'Neill
Carried.

334 Membership

334.1 Honorary Membership

The names of nominees were presented as follows:

Michael Meagher	Victoria, BC
Joe Webber	Salt Spring Island, BC
Cheng Ying	Victoria, BC

Motion: That the nominated Honorary Members be duly elected.
Moved by: Jack Woods
Seconded by: Jean Brouard
Carried.

334.2 Active Membership

The names of nominees were presented as follows:

Brian Barber	Ministry of Forests Victoria, BC
Michele Bettez	Min. des ressources naturelles Berthierville, QC
Kathleen Brosemar	Forest Genetics Ontario Sault Ste. Marie, ON
Paul Charrette	Lakehead University Thunder Bay, ON
Al Foley	Ministry of Natural Resources Angus, ON
Scott Green	University of Northern British Columbia Prince George, BC
Andreas Hamman	University of Alberta Edmonton, AB
Christine Hanson	Alberta Sustainable Resources Development Smoky Lake, AB
Marek Krasowski	University of New Brunswick Fredericton, NB

Donna Palamarek	Alberta Sustainable Resources Development Smoky Lake, AB
Dave Reid	Ministry of Forests Saanichton, BC
Deogratias Rweyongeza	University of Alberta Edmonton, AB
Annette van Niejenhuis	Western Forest Products Ltd. Saanichton, BC

Motion: That the nominated Active Members be duly elected.
Moved by: Bill Parker
Seconded by: Greg O'Neill
Carried.

334.3 Corresponding Membership

No nominations received.

335 Chair's Report

The 29th meeting of the Association was held in Kelowna, BC in conjunction with the following organizations:

Western Forest Genetics Association (WFGA)
Northwest Seed Orchard Managers Association (NWSOMA)
British Columbia Seed Orchard Association (BCSOA)
IUFRO Unit 7.01.04 Resistance Breeding Working Group.

There are large benefits to having joint meetings with other organizations in terms of helping with the meetings organization (not duplicating efforts) and in expanding the base of people interested in attending our meeting. Many organizations can only justify sending individuals to one meeting per year, so it makes educational and fiscal sense to co-ordinate larger joint meetings.

The organizing committee did a wonderful job that spanned 18 months and 15 conference calls. There are also many others involved in putting together this meeting and I have tried to include all the people who put in time for CTIA 2004. Those names underlined also served on the organization committee.

Chair	<u>Dave Kolotelo</u>, Tree Improvement Branch, BCMoF
Vice-chair: Finances, Facilities & Meals	<u>David Reid</u>, Tree Improvement Branch, BCMoF
Welcoming Address	Dale Draper, Tree Improvement Branch, BCMoF
Invited Speakers, Posters & Program	<u>Greg O'Neill</u>, Research Branch, BCMoF
Sponsors	<u>Tim Lee</u>, Vernon Seed Orchard Company <u>George Nicholson</u>, Riverside Forest Products
Sponsored Students and President of WFGA	<u>Michael Stoehr</u>, Research Branch, BCMoF
Registration & Logistics	<u>Diane Douglas</u>, Tree Improvement Branch, BCMoF
Rain Raven Print Design	Michael Blackstock, RSI, BCMoF

Field Tour and Gifts	Michael Carlson, Research Branch, BCMoF John Murphy, Research Branch, BCMoF Barry Jaquish, Research Branch, BCMoF
Accompanying Persons Program	Vicky Berger, Research Branch, BCMoF Hilary Graham, PRT Group
NWSOMA Meeting & Organizing Committee	Harv Koester, USDI, BLM
Organizing Committee	Randy Johnson, USDA Forest Service Alvin Yanchuk, Research Branch, BCMoF
IUFRO Resistance Breeding	Alvin Yanchuk, Research Branch, BCMoF John King, Research Branch, BCMoF
Tree Seed Working Group	Dave Kolotelo, Tree Improvement Branch, BCMoF
Gene Resources Management session	Don Lester, Genetic Resource Management Jack Woods, Forest Genetics Council of BC
Audio Visual Support and Management	Ron Planden, Tree Improvement Branch, BCMoF Don Summers, DW Summers and Company
Registration Logistics and Design	Cheri Tayler, Tree Improvement Branch, BCMoF Tania Johnson, Tree Improvement Branch, BCMoF
Registration and Logistics at Meeting	Debbie Poldrugovac, Tree Improvement Branch, BCMoF Giselle Phillips, Research Branch, BCMoF
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Web Design and Updating	Gary Carleton, Carleton Communications Group Ltd.

Several organizations provided financial support that allowed us to offer the meeting at a first-class resort, invite world-class speakers on the theme of “Climate Change and Forest Genetics”, and continue with our important Student Sponsorship program. We also decided to offer students a $100 discount off the registration fee. The following sponsors provided much appreciated financial support for the meeting:

BC Ministry of Forests, Tree Improvement Branch
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Natural Resources Canada
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Western Forest Products
Riverside Forest Products

In closing I'd like to offer some comments concerning CTIA 2004 and some food for thought.

The CTIA executive is primarily concerned with the organization of the subsequent meeting of the organization. This is important and the quality of meetings the CTIA has hosted is an incredible legacy for the organization. Discussion of issues relevant to the organization has been something I have tried to promote between meetings as chair. I think this is important and although time consuming I believe it allows contributions from those not able to attend from across the country. Attendance is often skewed towards the host province. I am hoping that the National survey of Management of Genetic Resources will push for the need for more discussions between meetings.

In my discussions with members there was great support for continuation or even expansion of student sponsorship at CTIA meetings. We even agreed on the addition of two permanent student awards at our business meeting!

The constitution has been discussed for several meetings as needing refinement or upgrading. This is not a pleasant task and a division among CTIA members in discussions of what our objectives are has scared anyone away from taking on this task. In addition to our constitution the functioning of the CTIA is directed by Policies that have been presented at Business Meetings. An example is the Policy of Support for Student attendance at CTIA Meetings that was passed at the business meeting of the 23rd CTIA meeting. These policies have not been assembled anywhere as a reference and again this task is not a pleasant one.

The issue of format of proceedings was also a key issue in planning the meeting finances. There was general support to go to electronic proceedings (with some copies for libraries) but some people did want to continue to receive hardcopy proceedings. This is a large cost (≈ $8 000) and perhaps there is a better use for this money by the Association.

In terms of venue, as of now we do not have a confirmed location for the next CTIA (2006) meeting, although Quebec City has graciously volunteered to host the 2008 meeting to coincide with their 400th Anniversary. Thank you. There are many provinces which have not hosted meetings, but they do not possess the infrastructure (tree improvement program with field trials or geneticists) to think they can host a CTIA meeting. I think there is value in hosting meetings at new venues and possibly expecting that some of these meetings will not profit as opposed to some of the larger meeting venues. I would also hope that members could help other provinces without resources in the organization of future CTIA biennial meetings.

Finally, I think the CTIA has to more closely look at its organization, financial resources, mandate, constitution, and form of communication between meetings. No one member has time for this and I suggest that the CTIA contract some of these duties to a retired CTIA member who is familiar enough with our organization, unbiased, and wishing to put in place the mandate of members at a reasonable cost. Contracts like this have been approved at business meetings in the past, so this is not a precedent setting activity.

The times certainly are changing in terms of communication. We strongly felt having an up-to-date web page greatly helped in promoting the meeting. An 'interesting' side-effect of advertising on the internet was the receipt of several inquiries that appeared similar to the standard "Nigerian gold scam" e-mails that many have probably received over the past two years. Some of the information regarding CTIA 2004 will continue to reside in the following link that I hope you find useful - http://www.for.gov.bc.ca/hti/CTIA/index.htm

Good luck to the next organizing committee and best wishes to all members of the CTIA.

Dave Kolotelo

336 Treasurer's Report

The financial statement for the period of July 2002 to June 2004 was presented by Treasurer Tannis Beardmore and tabled for information and acceptance by the membership (see Attachment #1). The statement shows a balance of $28,744.58 in the Association's account and GIC's totaling $8,000.00.

Motion:	That the financial statement be accepted as presented.
Moved by:	Paul Charrette
Seconded by:	Dave Reid

Carried.

337 Financial Contributions

BC Ministry of Forests
British Columbia Seed Orchard Association
British Columbia Tree Seed Dealers Association
Natural Resources Canada
Vernon Seed Orchard Company
Western Forest Products Ltd.

Motion:	That the CTIA/ACAA executive of the 29th meeting express our sincere appreciation to these contributors.
Moved by:	Dave Reid
Seconded by:	Brian Barber

Carried.

338 Editor’s Report

The proceedings were printed and distributed during August 2003 to all active members, honorary members, Canadian universities and libraries, registrants, and financial contributors of the 28th meeting. Two hundred and ninety-five proceedings were mailed.

A letter advising of the theme of the 28th biennial meeting, context of the proceedings, and a request for a $20 donation to obtain a copy was sent to all corresponding members, USA addresses, and International addresses. As a result, proceedings were mailed to 8 Canadian, 7 USA and 13 International addresses. Forty-five copies remain on inventory.

The mailing list contains 469 addresses comprised of: 15 Honorary, 78 Active, 110 Corresponding, 59 Canadian libraries, 81 USA, and 126 International.

Dale Simpson

339 Education Committee

As in the past, the organizing committee of the CTIA 2004 meeting decided to keep the tradition going and sponsor students from Canadian Universities with a forestry program. This sponsorship is highly encouraged by CTIA members and financial support (if needed) was offered by the CTIA Treasurer. Eight universities were contacted to nominate a student to sent to the meeting in Kelowna. With the exception of the University of Toronto, all others replied and the following students attended the meeting:

Adriana Almeida-Rodrigues	University of Alberta
Stephanie Beauseigle	Laval University
Jean-Francois Carle	University of Moncton
Jessica Courtier	University of Northern BC
Marianela Ramirez	University of New Brunswick
Claire Riddell	Lakehead University
Nicholas Ukrainets	University of British Columbia

Sponsorship included all costs of attendance, including return flights, accommodation, and meals as well as conference registration.

For the first time this year, CTIA gave out an award for best poster presented by a student. This award went to Cherdsak Liewlaksaneeyanawin from UBC for a poster entitled “Microsatellite analysis of genetic effects of domestication in lodgepole pine” co-authored by Y. El-Kassaby, C. Ritland and K. Ritland.

The prestigious Western Forest Genetics Association Critchfield Award, for best oral presentation by a student was won by Mark Lesser, Lakehead University, a student sponsored by CTIA for the Edmonton meeting in 2002.

Mark Lesser’s winning of this award is just one sign that the CTIA sponsorship of students is working to promote student’s interest in Tree Improvement and Forest Genetics. Furthermore, in Kelowna, there were at least nine participants attending the CTIA 2004 meeting that were previously sponsored by CTIA as far back as 1983.

Congratulations to all seven sponsored students and the two students winning presentation awards. Thanks to all CTIA members for actively supporting this worthwhile sponsorship program.

Michael Stoehr

340 Working Group Reports

340.1 Tree Seed Working Group

The Tree Seed working group published four editions (# 36 to 39) of the TSWG News Bulletin since our last report. Dale Simpson has done a great job of editing, assembling and distributing the News Bulletin. An electronic format was introduced with edition number 37 allowing us to reach many more people at a fraction of the cost. We are continuing with the idea of having themes for each edition of the News Bulletin. Here are the themes of the past four editions.

#36	Quality Assurance Monitoring
#37	Hardwood Seed
#38	Seed Orchard Practices
#39	Environmental Impacts on Seed Biology

For our 40th edition (December 2004) the theme is "What are your biggest problems or information needs with respect to tree seed?". We greatly appreciate the contributions that individuals make to our News Bulletin. As an incentive and 'award' we introduced a "News Bulletin Raffle" for everyone (except Dale and myself) who contributed articles to the News Bulletin since the last CTIA meeting. The names (article authors) were placed in a hat and the winner was - Michele Bettez and Fabienne Colas - congratulations. They received one matted and framed rain-raven print. Hopefully this precedent will continue.

The TSWG workshop theme for 2004 was "Quality Assurance in the Seed Handling System" and had the following presentations:

Introduction	Dave Kolotelo
Crop Maintenance and Collection in Seed Orchards	Chris Walsh
Quality Assurance in Cone and Seed Processing	Al Foley
Quality Assurance in Seed Testing	Dale Simpson
Quality Assurance in Seed Storage	Donna Palamarek
Quality Assurance in Seed Preparation	Dave Kolotelo
Quality Assurance in the Nursery	Susan Thorpe Fernando Rey

Volunteer Papers

Thermo-kinetics of water absorption, with special reference to Noble fir seeds	George Edwards
Effect of moisture content during pre-treatment or storage on the germination response of alder, birch, and oak seeds	Conor O'Reilly

I believe the workshop was quite successful and provided a good opportunity to discuss and debate a variety of topics related to tree seed. The only other outstanding issue is our TREESEED Listserver. With my CTIA executive duties virtually completed I will be trying to revise this method of communicating and exchanging information. Thank you to all the contributors and subscribers who have helped make the Tree Seed Working Group a vital and dynamic organization.

A note of sadness for the TSWG was the untimely death of Dr. David Gifford of the University of Alberta on August 15th, 2003. He has passed on, but his research findings and teachings will still be with us. Thank you for your contributions David Gifford.

Dave Kolotelo
Chair

340.2 Wood Quality Working Group

Due to Tony Zhang's schedule and Alvin Yanchuk's involvement in organizing the IUFRO Working Group 7.01.04 Resistance Breeding Workshop they were unable to organize a wood quality/technology workshop. An effort will be made to plan a workshop for the next CTIA meeting.

Alvin Yanchuk
Tony Zhang
Co-chairs

341 Business Arising from Previous Meetings

341.1 Bursary (previous meetings items 317, 305.2, and 328.1)

Michael Stoehr and Bruce Dancik agreed at the last meeting to form a standing committee to propose a terms of reference. Unfortunately, the committee was unable to meet and neither member was able to be present at the business meeting. Alvin Yanchuk passed along a suggestion from Bruce that an award should be named after Carl Heimburger.

Motion:	That the CTIA provide a $ 500 award to the student who presents the best paper at a CTIA meeting and the award be called the “Carl Heimburger Award”.
Moved by:	Alvin Yanchuk
Seconded by:	Greg O'Neill
Carried.	

Motion:	That the CTIA provide a $ 300 award to the student who presents the best poster at a CTIA meeting and the award be called the “Gene Namkoong Award”.
Moved by:	Alvin Yanchuk
Seconded by:	Al Gordon
Carried.	

341.2 Official Gavel (previous meetings item 318.1 and 328.2)

Dale reported that he had e-mailed Michel Villeneuve, who had agreed at the 2000 meeting to coordinate the crafting of a gavel using wood of improved species from each province. Michel is no longer involved with tree improvement but had passed along the “gavel file” to André Rainville before he left. Dale had e-mailed André prior to the CTIA meeting but had not received a reply. Dale said he would communicate with André to determine the fate of this project.

341.3 Constitution and Bylaws (previous meeting item 329.2)

Jerry Klein was approached to review and update the Constitution and Bylaws but he declined. Nobody at the meeting expressed an interest in conducting this work.

342 New Business

342.1 Survey of Forest Genetic Resources Management in Canada

A workshop was held Monday evening during which the results of the survey were presented. Discussion took place on possible approaches that could be taken to create a representative group to facilitate contact with the federal and provincial governments on policy issues. Jack Woods presented the following pre-amble.

All provinces and territories have an interest in the management of forest gene resources and five provinces (BC, AB, ON, NB, and NS) have forest genetic councils. Contact among provincial and territorial reps and provincial councils is minimal and informal. Formal contact among provincial and territorial reps and councils on policy and organizational matters may be beneficial to all provinces and territories. Federal policy initiatives would benefit from communication with a formal committee representing all provinces and territories.

Motion: That the CTIA endorse a committee of representatives from all provinces and territories, including reps from existing Councils, to be known as the Canadian Forest Genetics Councils Working Group of the CTIA and that this working group advocate and communicate, as needed, on matters related to federal-provincial/territorial policy interactions regarding the management of forest gene resources.

Moved by: Jack Woods
Seconded by: Sally John

Discussion followed on how such a group would function. The group could initially meet to discuss membership and identify topic areas to avoid any duplication with other groups. The spirit would be cooperation and information sharing. CTIA is a logical organization to form such a group. There is no national organization that speaks forcefully on tree improvement.

Carried

The following was presented to provide further guidance for the working group:

Purposes: 1) to facilitate communication among Forest Genetics Councils in Canada, and 2) to facilitate joint submissions from Forest Genetics Councils to policy makers on matters affecting forest gene management in Canada.

The Canadian Forest Genetics Councils Working Group (CFGCWG) will not take positions independent of the CTIA but will rather serve to facilitate positions to be endorsed by individual councils on a case-by-case basis. CTIA will serve to support the CFGCWG by providing opportunities to meet and other communication tools.

Membership on the CFGCWG shall be selected by: 1) for those provinces/territories with a Council, the Council will select the rep and 2) for those provinces/territories without a Council the active members from that province/territory will select a rep.

Motion: That the above guidelines serve as a starting point for the Canadian Forest Genetics Councils Working Group.
Moved by: Kathleen Brosemer
Seconded by: Jack Woods
Carried

Motion:	That Jack Woods and Kathy Tosh approach representatives of provincial Councils and seek volunteers from other provinces/territories to form the Canadian Forest Genetics Councils Working Group.
Moved by:	Brian Barber
Seconded by:	Paul Charrette
Carried	

343 Future Meetings

343.1 Location of 2006 Meeting

Following the 2002 meeting, Mike Butler agreed to host the meeting in Prince Edward Island with assistance from Kathy Tosh and Howard Frame. Due to the current provincial government program review, Mike was unable to confirm the commitment. Kathy Tosh indicated that New Brunswick may be able to host the meeting if PEI is unable to.

343.2 Location of the 2008 Meeting

Jean Beaulieu volunteered to host the meeting in Québec City to coincide with the 400th anniversary celebrations of the founding of Québec City.

343.3 Location of the 2010 Meeting

No bid was made at this time.

344 Election of New Executive

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

Chairperson:	Kathy Tosh NB Department of Natural Resources
Vice-Chairpersons: Symposium	Judy Loo and Yill Sung Park Canadian Forest Service
Vice-Chairperson: Local arrangements	Mike Butler PEI Department of Environment, Energy and Forestry
Treasurer:	Tannis Beardmore Canadian Forest Service
Editor:	Dale Simpson Canadian Forest Service
Executive Secretary:	Dale Simpson Canadian Forest Service

345 Adjournment

Motion:	That the 29th business meeting of the CTIA/ACAA be adjourned.
Moved by:	Alvin Yanchuk

Attachment # 1

CTIA/ACAA
Financil Statement
July 2002 – June 2004

Balance July 2002

Cash	$8,864.74
GIC	$16,000.00
GIC	$8,000.00
Total	$32,864.74

Credits

Interest (account)	$26.11
Interest (GICs)	$1,068.48
Purchase of proceedings	$329.54
GIC matured	$16,000.00
Reimbursement for CTIA 2002 meeting	$7,000.00
CFS contribution for printing of the proceedings	$2,500.00
Advance from the BC Ministry of Forests for CTIA 2004 meeting expenses	$10,000.00
Total	$36,924.13

Debits

Cost of printing the 28th proceedings	$6,830.80
Mailing envelopes etc. for proceedings	$180.49
Bank charges for the proceedings	$28.00
Expenses for CTIA 2004 meeting:	
Summerhill Pyramid Winery	$750.00
Grand Okanagan Resort	$4,005.00
Artwork	$400.00
Printing costs for artwork	$1,610.35
Dave Reid: for remainer of $10,000 advance	$3,239.65
Total	$17,044.29

Guaranteed Investment Certificates

GIC (matures Feb 05)	$8,000.00
Total	$8,000.00

Balance June 2004

Cash	$28,744.58
GIC	$8,000.00
Total	**$36,744.58**

ACTIVITY REPORTS
FROM ACTIVE MEMBERS

COOPERATIVE TREE BREEDING IN NOVA SCOTIA

Howard Frame and David Steeves

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E-mail: hmframe@gov.ns.ca

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., StoraEnso, 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, and coordination is provided by the Department of Natural Resources. Species of interest include black spruce (*Picea mariana* [Mill.] BSP), 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 21 million trees planted annually in Nova Scotia.

CHANGES IN WORKING GROUP'S STRUCTURE

Since 2000, the Province of Nova Scotia introduced Forest Sustainability Regulations which restructured the method used to fund private land silviculture. Companies acquiring privately owned wood for processing in Nova Scotia or for export are now obligated to either fund or carry out silviculture on privately owned land. The obligation to implement a silviculture program is based on the amount of wood harvested in any one particular year. With 70% of the land base in Nova Scotia privately owned, the demand for reforestation stock has dramatically increased in response to these regulations.

Accompanying silviculture funding restructuring, came a dramatic reduction in the Department of Natural Resources' tree improvement budget and subsequent reallocation of tree improvement staff. Our industrial cooperative members have had to take the lead role in the day-to-day tree breeding activities formerly carried out by the Department. With first-generation seed orchards able to supply the current seed demand for reforestation, the Department does not plan to move forward with second-generation orchard development. The industrial cooperators, however, are proceeding with second-generation breeding and orchard development. Kimberly Clark has leased the Department's Tree Breeding Centre and is using that facility for orchard propagation as well as housing their woodlands staff.

SEED ORCHARD PRODUCTION

First-generation white and red spruce clonal orchards have consistently produced excess seed to our needs. Rogued first generation black spruce seedling seed orchards are currently able to produce sufficient seed to meet the Province's reforestation requirements. The second-generation black spruce orchards have not produced any significant amounts of seed. Over the last 10 years, clonal Norway spruce orchards have produced fairly regular crops but trees were injected with $GA_{4/7}$ in 2003 to provide some assurance of a cone crop in 2004, which is already evident. All species are projected to have a moderate to heavy cone crop in 2004.

PROGRAMS

White Spruce

Breeding values (BV's) for 8-year height, derived from half-sib progeny performance, have been determined for 372 of 459 first-generation white spruce clones tested in 11 field test series established between 1991 and 1999. We anticipate completing measurements in 2006.

These BV's are being used to evaluate 454 random pair mates. As the information becomes available and the full-sib families reach measurement age, second-generation candidates are graded and selected. The goal, which is to select individuals from the 100 best crosses based on mid-parent value, is over 65% completed.

Red Spruce

Observation and analysis of 8-year heights in the first of our six, first generation red spruce test series indicated that this may be too early to obtain precise results. This and the temporary lack of an operating plan for this species following restructuring of the NSTIWG, has held up progress in this program.

To date, BV predictions have been made for only 129 of 519 tested clones. The first of the ten-year height measurements will, however, be made fall of 2004 and grading, selection, and propagation work is scheduled to proceed immediately following analysis of these data.

Black Spruce

Second-generation selections, that were made in several of our first-generation open pollinated family tests, have been and continue to be crossed with a standard 20-tree polymix. To date, two test series comprising 113 half-sib progeny are in the ground. An additional 88 crosses have been completed and are scheduled for planting over the next two years.

Norway Spruce

Due to poor seed production among untested Norway spruce clones over the past few years, the open-pollinated progeny testing program has ground to a halt. Because of the GA treatments applied in 2003, we hope to be able to establish another test series by 2006.

NEW BRUNSWICK TREE IMPROVEMENT COUNCIL UPDATE

Kathy Tosh and Yuhui Weng

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E3E 1G3
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Keywords: breeding, second generation, genetic gain, seed orchard, black spruce, jack pine, white spruce, red spruce, tamarack

The New Brunswick Tree Improvement Council (NBTIC) completed its 28th year of operation in 2004. 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 and breeding of second-generation white spruce clones. Testing of second-generation black spruce (*Picea mariana* [Mill.] BSP) and jack pine (*Pinus banksiana* Lamb.) is almost complete with one more series of tests to be planted. First-generation orchards are providing enough seed for all reforestation stock. Second-generation black spruce and jack pine orchards have started to produce substantial quantities of seed and several second-generation crops have been outplanted.

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 (DNR) which 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 second-generation white spruce orchards was started in 2000 and a total of 4.2 ha has been established with four agencies participating.

Seed production in 2002 and 2003 was moderate with a yield of 64 and 60 million seeds, respectively, from NBTIC agency seed orchards. In 2002, half of this seed was collected from first- and second-generation black spruce seed orchards. In 2003, over 39 million seeds were collected in black spruce orchards, of which 34 million seeds were from second-generation orchards. This is the largest collection to date from these second-generation orchards. Since 1994, a total of 113 kg of seed have been collected from second-generation clonal seed orchards.

DNR was the only agency that collected in second-generation jack pine orchards in 2002 and 2003, with a yield of 6.6 and 4.8 million seed, respectively. Other NBTIC agencies also had cones in second-generation orchards, but opted not to pick as they had sufficient seed in storage. A good white spruce cone crop was produced in 2002 with almost 12 000 L collected. Seed yield was 19 million in 2002 and 12.5 million in 2003. Many of these first-generation orchards have been rogued 40% or more.

BREEDING

The Council completed a complementary polycross breeding program which began in 1987 for white spruce and tamarack. The last series of white spruce tests was planted in 2001 and the last series of tamarack crosses was outplanted in 2002. Polycrossing of second-generation black spruce and jack pine has made tremendous progress with 87 and 90% of the breeding complete, respectively. This is partly due to polycrossing *in situ* on the 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. The breeding is 48% complete.

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 mating design. A total of 15 sub-lines have been established for black spruce and 16 for jack pine.

SELECTION PROGRESS

Second-generation selections in white spruce began in the fall of 1998. The white spruce strategy is slightly different in that the second-generation selections originate from selection plantations laid out in 48-tree plots. These selections are based on the results from 10-year progeny test measurements. A total of 175 of 400 trees has been selected to date for the second-generation population. A red spruce (*Picea rubens* Sarg.) tree improvement program was initiated in 2003 and plus tree selection started the winter of 2004.

TESTING AND DATA ANALYSIS

Testing continues to be an important component of the NBTIC program. Over the past 28 years, 314 tests were planted on over 359 ha. Over the past 14 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. In 2002, three series of progeny tests were planted including the eighth black spruce series, the seventh series of jack pine, and the last series of tamarack progeny tests. In addition, the third series of jack pine full-sib progeny tests was planted. In total, 183 seed lots, planted on 12 sites, was tested on 8.4 ha in 2002. In 2003, the third series of black spruce full-sib progeny tests was planted and the second black spruce realized gain test series was established. In the gain test, five seed lots were included: two orchard seed lots, two from natural stands, and one full-sib mix of second-generation material. The tests will be measured at 5, 10, 15, and 20 years, and the results will provide data for genetic gain estimates.

The data analyst position has continued to be funded by the NBTIC. Council members were saddened by the sudden passing of our data analyst, Bryce McInnis, in January of 2003. Bryce had worked for the Council for 6 years and his contribution and dedication to our program has been missed. The position was filled by Mr. Yuhui Weng in August of 2003. A total of ten NBTIC test series were analyzed in 2002 and 2003 which included 8 progeny tests, 1 family test, and 1 gain test.

PUBLICATIONS AND REFERENCES

McInnis, B.G.; Tosh, K.J. 2004. Genetic gains from 20 years of cooperative tree improvement in New Brunswick. For. Chron. 80(1):127–133.

Tosh, K.J. 2003. Nineteenth annual report of the New Brunswick Tree Improvement Council. NB Dept. Natural Resources & Energy, 20 p.

TREE IMPROVEMENT PROGRESS BY THE NEW BRUNSWICK DEPARTMENT OF NATURAL RESOURCES

K.J. Tosh and M.S. Fullarton

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Keywords: cross-pollinations, progeny tests, seed orchards, white spruce, black spruce, jack pine, tamarack, red spruce, balsam fir, Norway spruce

The tree improvement program conductd by the New Brunswick Department of Natural Resources (DNR) is celebrating its 30th 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 red spruce (*Picea rubens* Sarg.) and white pine (*Pinus strobus* L.) has substantially increased over the last couple of years and a tree improvement program for red spruce was initiated in 2004. Secondary species for tree improvement include balsam fir (*Abies balsamea* (L.) Mill.) for Christmas trees, Norway spruce (*Picea abies* (L.) Karst), and tamarack (*Larix laricina* [Mill.] Karst.).

TREE BREEDING AND TESTING

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

During the past two years, we have continued to plant black spruce and jack pine progeny tests. One more series of progeny tests should complete second-generation progeny testing in both species. There are now over 735 seed lots outplanted for these two species, meaning we are over 90% complete with progeny testing.

Since 2002, one series of full-sib jack pine tests and 1 series of full-sib black spruce tests were outplanted. These test series came from full-sib crossing done within sub-lines established for each species. These tests will be used for making third-generation selections in 5 to 8 years. A second black spruce gain test was planted in 2003.

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 in selection plantations. One hundred and seventy-five trees have been selected since 1998. This will continue until we have made about 420 selections.

In 2003, the first-generation white spruce clonal orchards were rogued again, leaving 50 out of 99 clones in the orchard. A total of 57% of the ramets remain. We have continued to stock existing orchards and establish new ones. The table below summarizes orchard establishment for DNR.

Table 1. Seed orchards established by DNR

Species	Generation	Type	Establishment Years	Area (ha)
White spruce	First	Clonal	1985-1987	9.0
	First	Seedling	1978-1982	8.6
	Second	Clonal	2000-2004	5.0
Black spruce	First	Seedling	1980-1987	32.0
	Second	Clonal	1989-1997	11.8
Jack pine	First	Seedling	1979-1986	25.0
	Second	Clonal	1992-1998	7.9
Tamarack	First	Clonal	1984-1986	8.0
Balsam fir	First	Clonal	1990-1992	2.7
Red spruce	One and one-half	Clonal	1999-2001	2.0
Norway spruce	First	Clonal	1999-2001	2.0
		Seed Production Area	1998	2.0

CONE COLLECTION

The second-generation orchards are producing increasing quantities of cones. Table 2 shows cone and seed production from first- and second-generation orchards during the past two years.

Table 2. Cone collection and seed yield from orchards in 2002 and 2003

Species	Orchard	2002		2003	
		Cones (L)	Seeds (Kg)	Cones (L)	Seeds (Kg)
Jack pine	Second-generation clonal	3 022	27.4	2 633	20.1
Black spruce	First-generation seedling	4 592	33.7	-	-
	Second-generation clonal	2 280	6.9	5 012	25.4
Balsam fir	First -generation clonal	2 544	61.9	-	-

RESEARCH ON GROUND HEMLOCK, REPRODUCTIVE BIOLOGY AND MULTI-VARIETAL FORESTRY STRATEGIES AT CANADIAN FOREST SERVICE – ATLANTIC

S.I. Cameron, M. Duffy, D. Fleming, J. Letourneau, I. MacEacheron, F. McBain-Hogg, Y.S. Park, J. Phillips, S. Pond, R.F. Smith, P. Stewart-Leblanc, J. Wang and L.D. Yeates

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GENETICS OF GROUND HEMLOCK (*Taxus canadensis*)

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P. Stewart-Leblanc, J. Wang and L.D. Yeates

The genetics program for Canada Yew (*Taxus canadensis*) was initiated in 1997. The two main areas of research are: 1) developing ecologically sustainable harvesting protocols in natural stands, and 2) developing a domestication (tree improvement) program to identify and select elite cultivars of the wild species and develop them into a commercially reared crop.

Sustainable Harvest Research Trials

Commercial harvesting of ground hemlock biomass for taxanes in eastern Canada has increased rapidly during the past few years. In each of 2002 and 2003, approximately one million kg was harvested, whereas in 2004, the figure is close to 4 million kg. Several harvest trials have been established in eastern Canada to quantitatively determine the response of ground hemlock to different harvesting intensities. In 2002, and after consultation with various partners in the Eastern Canadian Ground Hemlock Working Group, the Canadian Forest Service - Atlantic Forestry Centre designed and established a major research study to examine the effects of four harvesting levels on subsequent re-growth of ground hemlock and replicated it on five sites; one in each of the three Maritime Provinces (NB, NS, and PEI) and two in Québec. Although the first full measurement of the trial is not scheduled until the fall of 2005, one site was assessed in the fall of 2004. Two years following pruning treatments, the amount of regrowth on severely pruned plants (7 years of growth removed) was approximately one-tenth of that observed from any of the other three pruning treatments (3 years of growth but following different criteria for selecting the branches to be pruned). These results were consistent regardless of the time of year that the plants were pruned.

Tree Improvement Research

Cultivar Selection A total of over 4 000 plants, representing over 500 of the 1 300 genotypes in the range-wide provenance trials, were harvested in 2003 and 2004. The first 'final' harvest of four-year-old plants was conducted in the fall of 2004. These plants are now being measured and processed after which taxane levels will be determined. There has been significant variation in both growth and in taxane levels among clones, indicating a significant potential for selecting fast-growing, high taxane producing genotypes.

Nursery Propagation Using Rooted Cuttings If a domestication program is to be successful, the time must be minimized between the identification of elite plant materials and when large-scale production is realized. Until such time that tissue culture is sufficiently developed, large-scale rooted cuttings programs will continue to be required. A masters student at the University of New Brunswick, Laurie Webster, started her program which is focused on improving the rooting of recalcitrant genotypes and in reducing the costs of producing rooted cuttings. A technical note (Yeates et al. 2005) on rooting cuttings of ground hemlock was prepared.

Nursery Culture One of the objectives of our research is to determine how *T. canadensis* responds to intensive nursery culture. In 2004, four major semi-commercial outplanting trials (10 000 plants at each location) were established in Sault Ste Marie, ON, Gaspé, QC, Grand Lake, NB, and Charlottetown, PEI. An additional cooperative trial using chitosan as both an aid to early establishment and eventually as an elicitor of taxanes, was established with the Institut Agroalimentaire in La Pocatière, Québec.

Tissue Culture The most significant advance in the tissue culture research component of the project was the successful production of emblings from bud tissue. The first step in the process to initiate a patent for the SE of Taxus buds, the form for disclosure of IP, was completed.

A graduate from the CESAB (Centre d'excellence en sciences agricoles et biotechnologiques, Grand Falls, NB) biotechnology program, Melissa McGraw, was hired as a co-op student to fulfill the requirements of her course and to begin preliminary work on the bioreactor prototype. She gave her final presentation – a general description of SE in *Taxus* and its application – and graduated in August, 2004.

Methods to Increase Taxane Yields For *T. canadensis*, productivity is not limited to assessing the total amount of dry matter weight per unit area per unit time but also to maximize the amounts of taxanes produced. Greenhouse, nursery, and growth chamber studies have been initiated to develop method(s) to increase the taxane content of crop plants (or harvested plant tissues).

CONIFER REPRODUCTIVE BIOLOGY

R.F. Smith, and J. Letourneau

Research in the conifer reproductive biology project has been winding down. No additional cone induction trials were established. A significant effort was devoted to preparing and publishing a seed orchard management manual (Smith and Adam 2003).

Work on the molecular biology of reproductive development in black spruce was limited to completing sequencing of ESTs and SAGE tags, and preliminary data analyses. Approximately 50 000 and 22 000 SAGE tags from each of female and vegetative (post-dormancy) buds, respectively, were produced. Clones containing a further 30–40 000 SAGE tags for each of these two libraries are currently in frozen storage pending possible renewed funding for sequencing.

Work on conducting full-length sequencing of selected flowering genes is a long-term goal of this project. Efforts to date have been directed at trying to correlate the sequence information generated from ESTs and SAGE tags with similar genes from other species as identified in public databases. Depending on the level or redundancy observed, this may allow us to determine a first estimate of how many genes are being expressed in these tissues and an indication of the differential gene expression between vegetative and reproductive tissues.

DEVELOPMENT OF MULTI-VARIETAL FORESTRY STRATEGIES USING CONIFER SOMATIC EMBRYOGENESIS

Yill-Sung Park and Ian MacEacheron

Multi-varietal forestry (MVF) may be defined as the use of tested varieties in plantation forestry. The implementation of MVF offers many advantages, including: 1) obtaining much larger genetic gain than is possible from conventional seed orchard breeding, 2) flexibility to rapidly deploy suitable varieties with changing breeding goals and environments, and 3) ability to manage genetic gain and diversity in plantation forestry. Despite these advantages, MVF in conifers has rarely been practiced because of the general lack of an efficient vegetative propagation system that can consistently mass produce the same varieties over time. Recently, owing to the refinement in somatic embryogenesis (SE) technology, the implementation MVF with several conifer species has become an alternative to conventional plantation forestry. The implementation of MVF requires three critical phases: 1) development of efficient vegetative propagation and cryogenic storage techniques, 2) development of high-value varieties, and 3) prudent deployment of genetically tested varieties.

Conifer propagation by SE is the key technology for implementing MVF. Currently in eastern Canada, SE technology for spruce species and eastern white pine (*Pinus strobus*) is sufficiently refined for implementation. However, SE for jack pine (*Pinus banksiana*) remained difficult to obtain. During 2002–2003, our work concentrated on improving initiation of SE in jack pine through the manipulation of plant growth regulators and other tissue culture media elements. This work resulted in significant improvement in SE initiation from 0.2

to 3.7%, but it is still very low when compared to an average SE initiation percentage of 55% for eastern white pine. In 2003, we further studied the effects of 2,4-D and CPPU on SE initiation. The results indicated that, in eastern white pine, the 2,4-D containing media produced about 52% initiation but the CPPU containing media produced 36%. However, in jack pine, CPPU had a beneficial effect although it was small. The addition of nickel improved the initiation rate slightly.

Through the SE initiation experiment of summer 2003, with participation of J.D. Irving, Limited and University of Maine, about 2 600 clone lines of eastern white pine were developed. Of these, JD Irving propagated 180 lines for clonal field testing scheduled for summer 2004. Based on this collaboration, the University of Maine now has established a conifer tissue culture laboratory at Island Falls, Maine, USA and is propagating eastern white pine clone lines.

Experiments were also conducted to develop a ‘micro-plug’ system for the direct *in vitro* germination of somatic embryos and the subsequent mechanized transplanting of micro-plug germinated embyos into greenhouse containers. The micro-plug system consists of a preformed tray of cavities containing 1 cm (diameter) by 2.5 cm (long) plugs filled with rock-wool. The liquid germination media worked well however, we are in process of developing alternative germination media.

The development of high-value varietal lines involves genetic field testing of embryogenic clone lines. To develop an efficient testing strategy, a field test of SE-derived clone lines of eastern white pine was established at the Acadia Research Forest. This test contains 210 clone lines and is planted as two-tree plots with 6 replications. The test was established in 2002 as a mixed planting with tamarack.

Analysis of a clonally replicated test of white spruce was carried out. The preliminary results indicated that MVF with this species would result in much greater genetic gain than from conventional seed orchard breeding. For example, using the best 20 varietal lines (of 370) would result in a 30% increase in 10-year height. This is a huge genetic gain considering that seed orchard seeds would produce 6–7% genetic gain. Figure 1 also shows possible genetic gains through MVF when variable numbers of varietal lines are selected.

These results also illustrate flexibility in possible deployment strategies for MVF. Studies have shown that 10–30 varietal lines are sufficient for obtaining benefits of MVF while providing protection against potential risks due to diseases and insects. However, these results also show that much larger numbers of varietal lines can be included in the varietal mix while achieving a desired level of genetic gain. For example, a breeder may choose a 100-line varietal mix and obtain 15% genetic gain instead of obtaining 34% gain using 10 varietal lines.

We are also working on other MVF deployment strategies to balance genetic gain and diversity, including Mixture of Varieties and Seedlings (MOVAS) and linear deployment of varieties.

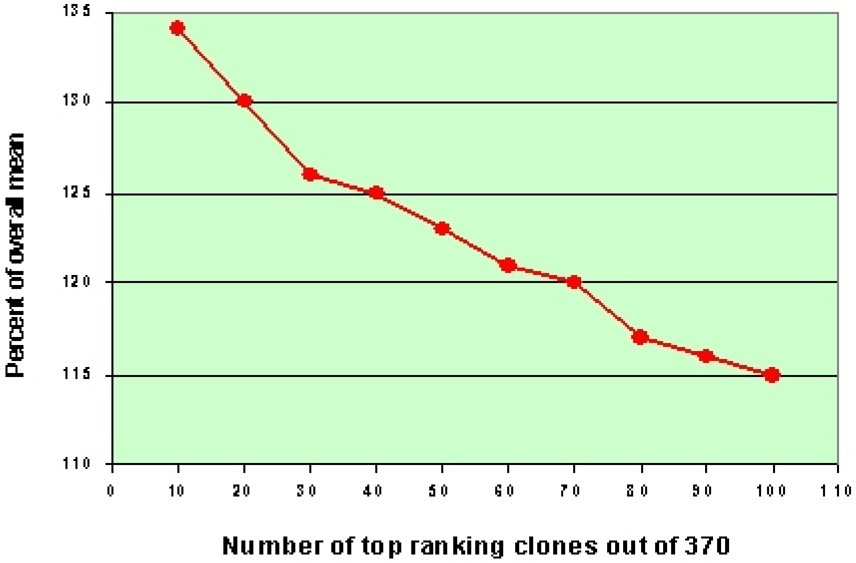

Figure 1. Change in genetic gain in relation to the number of varietal lines selected.

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GENETIC DIVERSITY RESEARCH AT CANADIAN FOREST SERVICE – ATLANTIC

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POPULATION VIABILITY ASSESSMENTS IN DECLINING TREES AND FOREST TYPES

Alex Mosseler and John E. Major

We continued with our efforts to develop and use various biological indicators to measure reproductive success, mating behavior, and genetic diversity to assess the viability of declining tree populations such as white pine (*Pinus strobus*), pitch pine (*Pinus rigida*), red spruce (*Picea rubens*), and Acadian late-successional, old-growth forest types. These studies are aimed at the potentially adverse impacts of certain forest management practices on the viability of populations and forest types at risk. Positive relationships between average stand age and size, and reproductive fitness and genetic diversity in red spruce, indicate that late-successional, old-growth forest types may represent important reservoirs of genetic diversity. Relationships between stand structural features such as stem density of reproductively mature trees show significant, positive relationships with reproductive success and genetic diversity. These findings have important implications for the management of residual populations following harvesting operations in species such as white pine and red spruce, which often occur in small, increasingly isolated, remnant stands. Maintaining a network of reproductively viable and genetically diverse stands may be especially important within an increasingly fragmented landscape where dispersal and gene flow among populations are necessary to minimize the effects of inbreeding and genetic drift and to maintain the reproductive health of natural populations and their ability to function as suitable and adequate seed sources for natural regeneration.

INTRODUCTION AND EVALUATION OF PITCH PINE IN ATLANTIC CANADA

Alex Mosseler and John E. Major

In 1994, seed was collected from across the Ontario range of pitch pine to assess the genetic and reproductive status of this rare and declining native species. Several genetic tests were established in Nova Scotia and New Brunswick. Based on the excellent growth performance observed in these Maritimes tests, further testing of pitch pine will be expanded to other locations across the Maritimes in order to assess the climatic limitations and general adaptability of pitch pine, and to compare its performance with native seed sources of jack pine (*Pinus banksiana*) and red pine (*Pinus resinosa*) which will be included in these tests. A series of these genetic and species tests was established in 2003 and 2004. The goal of the population genetics study of pitch pine is to conserve the gene pool of a rare and threatened native species, to assess its commercial and ecological potential across eastern Canada, and to understand the ecological and environmental limitations to the northward movement of southern components of Canada's flora as part of the forest sector strategy for adaptation to anticipated climate warming. One of the main impacts of this work will be to assess tree species alternatives for ecological restoration of habitats and difficult-to-manage sites, and as a potential alternative wood supply for forest industries in the event of species losses due to environmental changes or threats.

ADAPTIVE GENETIC VARIATION, MOLECULAR DIVERSITY AND RESPONSE TO CLIMATE CHANGE

John E. Major, Alex Mosseler and Om Rajora

Greenhouse gas levels are expected to double during this century and alter prevailing environmental conditions which alter physiological components of tree productivity. It was hypothesized that there would be significant species x genotype interaction with the projected climate change. A number of studies have been conducted to examine the potential importance of species and genetic x atmospheric CO_2 and genetic x soil drought interactions in black spruce (*Picea mariana*), 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_2 conditions and that red spruce seems particularly susceptible to damage. Also, red spruce allocates 40% more biomass to roots than black spruce.

We continue using molecular markers and genomic tools to understand genome organization, develop gene sequence data base and genetic maps, and identify, isolate, and map genes and genetic factors controlling traits related to productivity, adaptation to abiotic stresses, and particularly those relevant to global climate and environment change in red spruce, black spruce, and black x red hybrids. We have produced unique pedigrees of spruce ideal for genome mapping and QTL mapping of morphological and physiological traits related to abiotic stress adaptation. This will provide the foundation for future development of marker-assisted early selection for desirable traits.

ABOVE- AND BELOW-GROUND BIO-SEQUESTRATION OF A 30+ YEAR-OLD FOREST GENETIC STUDY

John E. Major and Kurt Johnsen

Below-ground forestry research is difficult, often neglected and sequestration information is severely lacking. We have been quantifying the above- and below-ground C inventory in a 35-year-old (F1) first generation cross black spruce experiment with distinct differences in above-ground volume growth. Second, in addition to providing a “snapshot” of carbon sequestration of these plots 30 years after planting, these data will be used to parameterize a process model (Johnsen et al. 2001b, Landsberg et al. 2001, Martin et al. 2001) that will permit the examination of black spruce responses beyond the spatial and temporal boundaries of this particular investigation. Along with soil coring, soil and stem respiration, and ground penetrating radar, the data will be used to estimate carbon fixation of a black spruce plantation and how much carbon is added to a system by planting black spruce.

ACADIAN ALTERNATIVE SILVICULTURE FOREST DIVERSITY PROJECT

John E. Major and Alex Mosseler

In 1999, a large 60 ha silvicultural impact test was established at the Acadia Research Forest 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 in particular. We have established a red and black spruce provenance trial under different silvicultural systems. 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.

POPULATION GENETICS OF PRODUCTIVITY IN NATIVE WILLOWS

Alex Mosseler and John E. Major

In 2004, a project on the productivity of *Salix eriocephala* and *S. discolor* was initiated to assess population genetic variation in native *Salix* species in order to quantify biomass production and related adaptive traits across several sites in central and eastern Canada and to assemble a sample of the native gene pool for conservation/protection of genetic resources and commercial breeding efforts. A short-term (3–5 year) objective will be to select clones for site and habitat restoration (e.g., mines, oil sands, pits and quarries, etc.) and afforestation of difficult-to-manage sites (e.g., riparian zones, abandoned agricultural lands, other poorly drained sites) across Canada. The longer-term (5–10 years) impact of this work is aimed at emerging chemical and energy industries able to use woody biomass feedstocks and the need for dedicated short-rotation plantations to sequester carbon to meet Canada’s greenhouse gas emissions reduction commitments under the Kyoto Protocol.

GENETIC DIVERSITY AND GENE CONSERVATION

Kathleen Forbes, Judy Loo, Donnie McPhee, Carlos Ramirez,
Marianela Ramirez and Dale Simpson

Research on genetic diversity of natural populations of forest trees continued to focus on developing conservation strategies for native tree species. The Canadian Forest Service (CFS) genetic resources group maintains and facilitates the informal New Brunswick Gene Conservation Working Group and has developed gene conservation strategies for four New Brunswick tree species (Loo et al. 2003). The CFS group is also working to raise awareness of the need for conservation of forest genetic resources and to develop a gene conservation working group at the national level. A meeting was hosted by CFS at Montebello, Québec, in February 2004 to explore the need and potential for such a working group (Beardmore et al. 2004). A survey was conducted in 2003 to identify the tree and shrub species requiring conservation attention across the country and 72 tree species (and six varieties) and 142 shrub species (and eight varieties) were indicated to be either in need of conservation measures or more information before designation could be made, in at least one jurisdiction within the species range (Simpson et al. 2004).

Isozyme analyses were completed for a genetic diversity study of eastern hemlock (*Tsuga canadensis*), using foliage samples, to determine whether genetic diversity measures differ between mature and regenerating trees in 16 populations throughout the Maritime provinces. None of the enzyme loci, having clear results, exhibited any genetic diversity, either in mature trees or seedlings. It was difficult to achieve clear results, so seed was collected for further analysis using isozymes, as well as for conducting germination trials, and seed storage studies. Seed from 15 trees from each of five populations were analysed and results indicated very low genetic diversity, with only one locus showing some variability. Seed will be collected in Québec to determine whether the phenomenon of extremely low genetic diversity is limited to the Maritime provinces or is more widespread.

Research continued on American beech (*Fagus grandifolia*) resistance to beech bark disease and on developing vegetative propagation techniques for production of resistant genotypes, in collaboration with Marek Krasowski at the University of New Brunswick. The disease is caused by a combination of two causal agents: the felted beech scale (*Cryptococcus fagisuga*) and a fungus (*Nectria coccinea* var. *faginata*). Alone, neither the insect nor the fungus results in serious damage, but together they are devastating. Trees exhibiting resistance are actually resistant to the scale insect, rather than the fungus, but in the absence of the insect infestation, the fungus does not attack the trees. Putatively resistant trees are documented on an ongoing basis.

Graduate student, Marianela Ramirez studied the feasibility of producing beech plantlets using tissue culture protocols, following up on work initiated by a previous student. Each of the vegetative propagation methods attempted to date yielded only partial success (J. Simpson, Masters thesis; K. Ellis, unpublished report). Buds were collected from diseased and putatively resistant trees in February 2003 and 2004 for continuation of micropropagation studies. None of the trials were successful in producing surviving plantlets, although there was a fair degree of success with production of roots on plantlets.

In summer 2002, more than 1 000 seedlings were grown from disease-free trees to provide root-stock for a grafting experiment. Scions were collected and grafted in late February and early March 2003 from 25 disease-free and 5 diseased beech trees. Beech scale eggs were collected in July for inoculation of the grafts in late summer to test for genetic resistance to the scale. Grafts were examined in July, 2004 and all but two of the putatively resistant genotypes showed very low or no scale survival. The scale insect became established with high survival on all of the grafts from susceptible trees as well as grafts from two of the putatively resistant ones. Where scale eggs were placed on or below the graft union, as well as above it, the scale became established on and below the graft union, even on resistant trees where the scale did not survive above the union, indicating the presence of a component in the bark of the resistant trees that inhibits scale development. The experiment was repeated in 2004.

In spring, 2004, four putatively resistant and one susceptible, roadside beech trees at each of two locations, were control-pollinated with pollen collected from putatively resistant and susceptible trees. If successful, the crosses will provide material to screen for resistance to determine the inheritance of the trait.

Restoration using genetically diverse, local seed sources complements *in situ* and *ex situ* gene conservation efforts for species such as bur oak (*Quercus macrocarpa*), that have declined significantly in a portion of the natural species' range. Bur oak restoration trials, established in 1998 and 1999, to determine the feasibility of this approach for gene conservation, were evaluated in early summer 2003. Seven trials were established in 1998 on a variety of sites including a coal mine spoil, where 72.5 % of the trees were surviving in 2003, but growth is slow; two islands in the Saint John River where annual flooding occurs and cattle are pastured in the summer. In spite of efforts to restrict movement of the cattle, they caused heavy mortality and just 20% of the trees are still surviving. Survival and growth was best, at 98% survival and height ranging from 35 to 220 cm, at Cherry Hill, a planting carried out in collaboration with Greg Adams at J.D. Irving, Limited. The site is maintained as a conservation and seed production area with near ideal conditions. Four additional trials, established in 1999, were also assessed in 2003. Survival ranged from 65% on a wet black spruce cutover site, where deer and rodents had browsed about 50% of surviving trees, to 90% in an old field with heavy grass competition. A site with partial shade, where competition from grass, raspberry, goldenrod and alder is severe, exhibited 86% survival with 66% of the seedlings exceeding 50 cm in height.

Graduate student, Carlos Ramirez, continues genetic diversity and quantitative variation studies on weeping pinyon (*Pinus pinceana*), conducting isozyme analyses, germination trials, and evaluation of needle wax quantity, growth parameters, and drought tolerance with the purpose of developing a conservation strategy for the species (endemic to Mexico and endangered). This PhD study is one piece of a larger collaborative research project supported by the government of Mexico and overseen by a subgroup of the North American Forest Genetic Resources Working Group (FAO's North American Forestry Commission). The objective is to understand ecology, management, and genetic issues and to develop a conservation plan for the species, which has value to local economies because of the high nutritional quality of the seed (edible pine nuts). The species is considered to be a keystone species because it is often the only tree species occurring in semi-arid ecosystems, where associated species are spiny shrubs and cacti. The germination component of the study has been completed and results from a series of germination trials indicated that the seed coat forms a physical barrier that severely inhibits germination if the seed coat is not manually cracked. Initial results of genetic diversity studies indicate highly significant differences among the three regions in Mexico where weeping pinyon occurs.

A gene conservation project for white elm (*Ulmus americana*) was initiated in 2001. The elm population was devastated throughout the 1960s, 1970s, and 1980s by Dutch Elm Disease. Trees are still succumbing to the disease when they are attacked by elm bark beetles which carry the disease however, large living trees can be still found scattered around the countryside. Are these trees escapes from the disease or are they resistant to the disease? Over several years 25 trees were located in New Brunswick. Cuttings were collected and grafted with a grafting success rate of at least 80%. Open-pollinated seed was also collected from many of these trees. The grafts were established in a clone bank where they will be challenged with the fungus that causes Dutch Elm Disease when they have reached an appropriate size.

SEED RESEARCH

Tannis Beardmore, Kathleen Forbes, Garry Scheer and Dale Simpson

Research is ongoing in evaluating the use of cryopreservation (storage at -196°C using liquid nitrogen) for the long-term storage of germplasm (e.g., seed, embryonic axes, buds, and pollen). Cryopreservation is an option for the storage of seeds or seed parts and embryonic axes) which are intolerant of long-term storage using conventional means (4°C and -20°C). In particular, efforts are focusing on working with Canadian tree species of concern. For example, butternut (*Juglans cinerea*) is being killed throughout North America by butternut canker caused by the fungus *Sirococcus clavigignenti-juglandacearum*. To date, there is no control for this fungal disease and no natural resistance has been documented Research is focusing on identifying methods for preserving the existing genetic variation of butternut, specifically cryopreserving buds. Cells within the meristem will survive cryopreservation and callus growth can be initiated from these cells. However, limited success has been met with producing viable plantelets following cryopreservation. Methods have been developed for the cryopreservation of bur oak (*Quercus macrocarpa*) embryonic axes. This method involves gradually lowering the temperature the embryonic axes are exposed to (from 4°C to -20°C). Attempts have been made to cryopreserve Garry oak (Q. *garryana*) embryonic axes, however, these axes are intolerant of cryopreservation and none of the tissue was found to be viable following cryopreservation. Garry oak acorns most likely represent the most extreme recalcitrant-like seed phenotype that we have in trees native to Canada.

Research was also completed on a project examining the ability to induce recalcitrant silver maple (*Acer saccharinum*) seed to become orthodox. Mature silver maple embryonic axes were treated with abscisic acid (ABA) and/or tetcyclacis (TC) to examine the effect of these treatments on the axes' tolerance to desiccation. Axes were placed on nutrient media containing 0, 20, or 60 µM ABA and/or 10-6 M TC for 2 weeks, after which axes were removed from the media and desiccated to approximately 5% water content. After desiccation all ABA- and/or TC-treated axes exhibited root growth ranging between 12 and 97% when placed on growth media. Only 97, 63, and 22% of the desiccated 20 and 60 µM ABA/10-6 M TC- and 10-6 M TC-treated axes exhibited shoot growth, respectively. In addition, 55 and 12% of the desiccated 20 and 60 µM ABA/10-6 TC-treated axes, respectively, germinated after cryopreservation. The control axes (desiccated immediately after collection from the tree) did not tolerate desiccation or cryopreservation. ABA content was examined in the embryonic axes and it was found that only the 20 and 60 µM ABA/10-6 M TC-treated axes maintained a high ABA content (57 and 62 pmole ABA/embryo, respectively). The ABA content of all other treated axes declined to 31 pmole/embryo and lower. These results suggest that inhibiting ABA degradation may have a role in developing tolerance to desiccation in silver maple axes and that ABA/TC treatment of axes may be useful for the storage of axes. While this work provides information on the nature of recalcitrance it is too time consuming to apply as a treatment for inducing desiccation tolerance and subsequent long-term storage of seed.

A project was recently initiated examining the variation in seed dormancy and the orthodox/recalcitrant-like nature of red maple (*A. rubrum*) across its range in North America. In the more southernly regions of its range red maple exhibits a recalcitrant-like seed behavior, while in the more northern regions mature seed is orthodox and may be dormant.

NATIONAL FOREST GENETIC RESOURCES CENTRE

Dale Simpson and Bernard Daigle

The National Tree Seed Centre (NTSC) is a key activity under the National Forest Genetic Resources Centre. The NTSC's mandate is to provide seed of known origin and quality for research and to store germplasm for *ex situ* conservation. Staff have been busy over the past two years collecting and processing seed, conducting germination tests, setting up and evaluating research trials, and supervising students conducting research for their theses.

Seed collection continues to be a major activity in order to expand the Centre's inventory. Collecting focuses on natural populations of native tree and shrub species with emphasis on making single-tree collections. During 2002 and 2003 about 435 seedlots were collected and stored from 40 species as well as 120 seedlots from four species were donated from several agencies. Germination tests were conducted on over 1 700 seed lots and 157 requests for seed for research were processed to provide 1 900 seed lots. The web site, www.atl.cfs.nrcan.gc.ca/seedcentre/seed-center-e.htm , continued to receive a large number of visits and the number of seed requests continued to increase as a result.

Developmental research is conducted in order to determine appropriate pre-treatment and/or germination conditions for species for which there is little known or to optimize current protocols. International Seed Testing Association (ISTA) rules for sugar maple (*Acer saccharum*) seed prescribe 8 weeks of chilling prior to germination at 20°C. Testing trials at the Seed Centre using local seed indicated 12–15 weeks of chilling was required but less time was needed for an Ontario seed source. A trial was established using seed obtained from New Brunswick (NB), Québec (QC), and Ontario (ON) provenances in which 2 constant germination temperatures (15°C and 20°C), 3 seed soaking times (0, 72 hrs, and 14 days), and 3 moist chilling durations (8, 12, and 16 weeks) were evaluated. Seed from NB imbibed about 10% more water than seed from QC and ON. Eight weeks of moist chilling were adequate for the QC and ON seed lots but 12 weeks were required for the NB seed. Soaking seed for 72 hours was beneficial for the NB seed but soaking did not improve germination of QC and ON seed. Soaking seed for 14 days tended to cause increased mortality. Germination was slightly higher at 15°C than at 20°C. Sufficient seed was available to allow the remainder to be stored for one year at -20°C and repeat the experiment to evaluate any impact storage may have on germination for seed treated in the same manner as above. ISTA rules for testing eastern hemlock (*Tsuga canadensis*) seed prescribe 28 days of moist chilling followed by 28 days in a germinator at 15°C. This length of chilling time is inadequate to alleviate dormancy of NB seedlots therefore the procedure adopted was to moist chill seed for 24 weeks and germinate at diurnal temperatures of 20/30°C which provided satisfactory results. A trial, using local seed, was established where seed that had been moist chilled for 4 week increments was germinated at either 10/15°C, 15°C, or 15/25°C. Just over 10% of the seed chilled for 4 weeks germinated at 15°C where as 65% germinated at 15/25°C. After 16 weeks of chilling, germination at these two temperature regimes was about the same (90%). Therefore, the evidence indicates that 4 weeks (28 days) of moist chilling is inadequate to alleviate dormancy in local eastern hemlock seed but germination at 15°C is sufficient. Further testing should be conducted to determine if there is geographic variation in chilling requirements. Being able to store seed for many decades is important when conducting *ex situ* gene conservation activities. The Seed Centre has been germination testing and storing seed for over 25 years and has accumulated a sizeable database for many species with seed collected from many geographic locations and different years. Germination data were evaluated for five hardwood and ten softwood species. Generally, after 25 years of storage germination exceeded 60% for all species and for some was higher than 90% (Simpson et al. 2004).

The "OECD Scheme for the Control of Forest Reproductive Material Moving in International Trade" is applied to certify the origin of seed which is destined for the international market. The Scheme is a means to promote and facilitate international trade and movement of forest tree seed, plants, and vegetative propagules. Participation in the Scheme is voluntary. Certified seed carries with it a Certificate guaranteeing the provenance and implicit that all rules and regulations were followed in the collection and processing of the seed. Certification does not cover seed quality, i.e., germination. The Scheme, which was adopted in 1974, consists of four categories of reproductive material: Source Identified, Selected, Untested Seed Orchards, and Tested. Certification work has been conducted almost exclusively in British Columbia because of the demand for seed from tree species located there. Most all OECD certified seed shipped from Canada has been in the Source Identified category with small quantities in the Untested Seed Orchards category. Over the past two years, 500 kg of certified seed were exported.

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TREE IMPROVEMENT PROGRESS BY THE DIRECTION DE LA RECHERCHE FORESTIÈRE

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WHITE SPRUCE TREE IMPROVEMENT

André Rainville

In the past two years, four first-generation white spruce (*Picea glauca* [Moench] Voss) seed orchards (out of 18 established) were evaluated in order to maximize genetic gain by collecting cones only from the best clones. By collecting cones from the best ten clones, additional gains are expected to be 12% over the gain from a general collection from all of the orchard clones.

Measurements of two full-sib progeny tests at 8 years were used to recommand the best crosses to be performed in the future, thus fulfilling needs of reforestation by cuttings. Gains of 11–15% over the cross means can be achieved by reproducing the 10 best crosses and propagating them by cuttings. Control crosses to evaluate GCA of the remaining 140 trees of the base population were completed and seeds will be sown in the spring of 2004. A part of the crosses needed to evaluate SCA has been done and will also be completed in 2004.

On a more operational level, analysis performed on ecological data was used to refine the seed transfer model (Li et al. 1996) and redefine the utilization territory of all the first-generation white spruce seed orchards. On a request from the forest industry, improved material, identified from tests located in the southern part of Québec, has been established in 5 tests in the north, in the black spruce-sphagnum moss cover type. While waiting for the first results, 167 trees were also selected in natural stands in the same region to create a new seed source.

NORWAY SPRUCE TREE IMPROVEMENT

Marie-Josée Mottet

An exceptional flowering year in 2003 allowed us to almost complete our Norway spruce (*Picea abies* [L.] Karst.) polycross program, as well as to move forward with the specific crosses program, done with 19 genotypes that demonstrate increased resistance to the white pine weevil.

The best families and provenances were identified for the St. Lawrence River improvement zone (sugar maple-basswood domain) from mean heights at five years in three open-pollinated progeny tests. For 10% of the best families, genetic gain varied from 8 to 17%. For the Laurentian improvement zone (sugar maple-yellow birch domain), ten-year results will be available in 2004. All of the new data will permit us to validate the proposed improvement zones. Tree selections are planned in these tests in 2004 and 2005, mainly for Polish progeny recently introduced into Québec that show superior growth gains as well as increased tolerance to the white pine weevil.

In collaboration with the Canadian Forest Service (CFS), a study of the effect of the white pine weevil on the wood quality of Norway spruce was completed using data from two other plantations at Duchesnay, in addition to the one at Valcartier. The analysis of mechanical and wood density resistance criteria led to concluding that damage by the weevil, in general, has little effect on these variables and that Norway spruce possesses superior qualities to planted white spruce.

JACK PINE AND SCOTS PINE TREE IMPROVEMENT

Roger Beaudouin

In 2002, roguing of the twelfth and last first-generation jack pine (*Pinus banksiana* Lamb.) seed orchard was carried out. For the four orchards and the test located in improvement zone “A”, the genetic gain was calculated using dominant trees and by taking into account site index quality of the related family test. The gain in merchantable volume varies from 2.6 to 8.8 m^3/ha at 40 years, when seeds are harvested from the retained families.

In 2002–2003, selection of 300 jack pine elite trees in zone “A” for the second-generation was completed. Total height of the best families makes up the principal selection criterion. Seventy-two clones form the elite population, in which biparental controlled crosses will be done. These clones are part of a 109 clone seed orchard established to produce improved seed for reforestation in zone “A”. The 228 other clones make up the support population, in which polycross controlled crosses will be carried out.

A total of 1 603 grafts were done in March 2003 at the Duchesnay grafting centre near Québec, in order to establish half of the zone “A” support population. With all varibles blended, the rate of grafting success after one year of growth was 92%. Forty-five percent of the grafts were top grafted and 55% were side veneer grafts. The survival rate of the top grafts was equal to that of the side veneer grafts. On two-year-old root stock with a mean height of 35–40 cm, the growth in 2003 of top grafts is 33% better (13.3 cm) than the growth of side veneer grafts (10.0 cm).

A detailed description of eleven visual symptoms observed on the terminal shoot, the buds, and the needles of Scots pine (*Pinus sylvestris* L.), as well as their frequency and the period they appeared indicates that the main cause of the loss of apical dominance, the formation of mutliple leaders, forks and large branches, and the slowing of height growth is attributable to a soil deficiency of boron. Foliar analyses showed that the mean concentration of boron varied from one site to another, from 7.1 to 15.2 ppm. Soil analyses indicated that the boron concentration of each sample was very low, varying from less than 0.1 to 0.3 ppm. These values are inferior to those recommended for optimal growth. Microscopic examination of needles also showed that important structural changes are produced in needles following boron deficiency. A forest research bulletin on this subject was published in 2004.

In 2003, three Scots pine seed sources that were genetically improved for reforestation were tested (rogued provenance tests, the Cleveland Township clonal orchard, and the Groenendaal clonal orchard in Belgium). On the other hand, two comparative plantations, including control plots and fertilized plots were established in order to identify boron dosages on different sites to supply optimal growth conditions.

BLACK SPRUCE TREE IMPROVEMENT

Mireille Desponts

In 2003, the first phase of the black spruce (*Picea mariana* [Mill.] BSP) program was completed. The last prescription for roguing a seed orchard was prepared and selection of elite trees in first-generation progeny tests was completed in all of the tree improvement zones. Setting up new clonal seed orchards and establishing improved populations for the next generation will be completed in 2005. Four clonal tests, composed of cuttings, were established in 2003.

Analyses of progeny test data, paired with data from two juvenile nursery tests, will continue in 2004, when nine progeny tests, paired to three juvenile tests, will be measured. The juvenile nursery tests, maintained and systematically thinned, will serve several purposes especially for reproduction studies and carrying out F_2 controlled crosses or backcrossing for which the pedigree will be known for three generations.

LARCH TREE IMPROVEMENT

Martin Perron

During the past two years we have continued implementation of the improvement strategy for second-generation European larch (*Larix decidua* Mill.), Japanese larch (*L. kaempferi* [Lamb.] Carr.), and their hybrid (*L.* x *marschlinsii* Coaz). The reason for using the latter species is to increase wood quality and volume of hybrid larch.

To that end, parents of European and Japanese larch were selected in 2003 and 2004, especially with respect to growth and indirect characteristics that influence wood quality. To accomplish this, data from 39 experiments were re-analysed, but tree selection was carried out in only 13 of them. Moreover, the hybrid individuals were removed using molecular markers specific to the species. Selection was done especially with respect to height growth, then mass selection was done using trunk straightness, crown quality (branch size, angle, and number), and the absence of damage (diseases). Selected trees also had to have a height/diameter ratio of less than one.

The 80 Japanese larch that were selected to make up the breeding population for the second-generation represent 0.34% of candidate trees. They come from the 28 best sources (provenances and progeny) among the 137 evaluated (20.4%). The 80 European larch that were accepted represent 0.39% of the total and they originate from 45 sources out of 280, or 16%.

Furthermore, the genetic improvement strategy for exotic larches was amended and improved following reception of comments from geneticists who are members of the CAGAF (Comité d'amélioration des arbres forestiers [Québec]; Forest Tree Improvement Committee).

HYBRID POPLAR IMPROVEMENT PROGRAM

Pierre Périnet and Marie-Josée Mottet

The hybrid poplar improvement program, started in 1969 by Gilles Vallée, is still very active testing the populations obtained since the beginning of the project, producing new hybrid material, and maintaining collections of poplar species (*Populus maximowiczii*, *P. trichocarpa*, and *P. nigra*). In addition to selection of Septoria-resistant clones for the St. Lawrence River valley area in southern Québec, the program is mainly oriented towards the production of *P. maximowiczii* hybrids well-adapted to forest sites located in bioclimatic domains 3, 4, and 5 (sugar maple–yellow birch, balsam fir–yellow birch, and balsam fir–paper birch domains).

From 1999 to 2004, 19 clonal tests were established mainly in southern Québec (domains 1, 2, 3, and 4) from Témiscamingue to Témiscouata for clonal evaluation of a hybrid population obtained in 1993. In northern Québec, 8 clonal tests were established from 2000 to 2003 with *P. maximowiczii* hybrids, particularly with *P.* X *rollandii* X *P. maximowiczii* (DNxB)XM), from the 1985 to 1992 breeding programs.

In 2005, the first two clonal tests from the 1996 breeding program will be established. More than 800 clones were selected from three 5-year-old progeny tests planted in 1997 in the Saguenay-Lac-Saint-Jean area. More selection is planned in three other progeny tests planted in 2000 in the Bas-Saint-Laurent area with the hybrid population from the 1998 breeding program.

A new population was bred in 2004 for the Abitibi-Témiscamingue area, using parents from local and Alberta balsam poplar provenances, selected hybrid poplar clones, *P. maximowiczii*, and progenies of *P. deltoides* or *P.* X *canadensis* from northern locations. Up until now, successful results have been obtained from most of the crosses.

In 2001, Septoria cankers were found for the first time since 1970 on hybrid poplars in the Témiscamingue area. Infected trees, representing different hybrids of *P. maximowiczii*, *P. balsamifera*, and *P. trichocarpa*, and *P.* X *jackii* in tests planted from1985 to 1993, are located in Notre-Dame-du-Nord and Angliers. Adjacent hybrid poplars (*P.* X *jackii*) planted in 1970 in Notre-Dame-du-Nord (1 km apart), are still Septoria-free. We expect a spread of the disease, at least in parts of bioclimatic domains 3 and 4. We don't know to what extent these recent infections might be related to climate change.

Technology transfer is routinely achieved with forest industry partners for operational planting of hybrid poplar, with provincial nurseries for steckling production (1-0 rooted cuttings), and with scientists from the Réseau Ligniculture Québec. The provincial list of selected clones for planting is revised regularly, based on the results of clonal tests. The poplar research team contributes to different projects on Septoria canker, wood quality, and molecular genetics studies with scientists from Université Laval, University of Alberta, Forintek, and the CFS.

HARDWOOD TREE IMPROVEMENT

André Rainville

Over the last two years, most of the effort in hardwood tree improvement have been to establish white ash (*Fraxinus americana* L.) provenance-progeny tests. Fifty-nine progenies from 14 provenances were represented in ten tests and will be used to evaluate genetic variation in quality and growth characteristics of white ash across its distribution in Québec and to identify improved material for reforestation.

Five year results of inspections performed in butternut (*Juglans cinerea* L.) conservation plantations revealed no statistical difference among provenances and progenies for susceptibility to butternut canker but interesting observations were noted about the epidemiology of the disease. Eradication of infected trees or diseased parts of trees within the plantations has been a very effective control method.

REALIZED GENETIC GAIN TESTS

André Rainville, Mireille Desponts, Roger Beaudoin and Guy Prégent

This new project was initiated in 2002 with the objective of evaluating long-term gains in productivity (volume) and quality associated with planting improved seedlings from first-generation seed orchards. Results will be used to validate estimations of gains from progeny tests and for use in growth models being used to calculate annual allowable cut. In the first two years, seed from five black spruce seed orchards was sown and sites were prepared for the first plantings in 2005. In the spring of 2004, seed was sown from six black spruce and four jack pine seed orchards in seed zone “A” and tests will be established in 2006.

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RECENT RESULTS OF TREE REPRODUCTION IN QUÉBEC

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Keywords: seed orchard management, pollen, pollen conservation, mass pollination, seeds, germination, stratification, *Picea glauca*, *Picea mariana*, *Larix decidua*, *Larix kaempferi*, *Larix marschlinsii*

This report summarises the research carried out and the results obtained during the past two years on sexual reproduction of trees by the Direction de la recherche forestière.

SEED ORCHARD MANAGEMENT

Larches (*Larix decidua* Mill., *Larix kaempferi* [Lamb.] Carrière)

Research on larch seed orchard management is being carried out on grafts grown in 100 L pots in shelters. A bagging method was developed to harvest pollen from the entire tree, which facilitates the harvest of a large volume of optimal-quality pollen. The pollen can either be used directly to produce hybrid seeds or be cold-stored in a pollen bank for later use. Our results show that stored pollen can maintain its initial viability for at least four years.

We currently use an electrostatic pistol for mass pollination, which allows us to rapidly carry out a very large number of crosses with a small crew. We are making headway with a method to extract seeds from European larch (*Larix decidua*), which is normally difficult.

Black Spruce (*Picea mariana* [Mill.] BSP)

We have developed a pollination trailer that has platforms at different heights, to make it easier to pollinate trees up to 6 m in height. Using a series of windbreak screens on the sides of the trailer and directly around the tree crown, we are able to significantly improve mass pollination efficiency using the electrostatic pistol, demonstrated by the increased number of filled seeds per cone. A second experiment on black spruce will confirm the result; the same protocol will be repeated on white spruce (*Picea glauca* [Moench] Voss).

GERMINATION OF CONIFER SEEDS AND SEEDLING PRODUCTION

White spruce seeds are delivered, to the nursery, stratified with their moisture content reduced to 15%. We have demonstrated that during the germination process, stratified seeds have a significant advantage over untreated seeds or seeds that are simply primed. This advantage is even more obvious in extreme temperature conditions (10° and 30°C). Moreover, in case of frost, stratified seeds have better resistance than do untreated seeds. These two results clearly illustrate the advantage that nursery managers have in using stratified white spruce seeds for seedling production.

Next we will be working on methods to modify the seeding factor for nursery produced white spruce, black spruce, and jack pine (*Pinus banksiana* Lamb.) seedlings. We want to determine a seeding factor as a function of the percent germination for the seed lot. An initial trial was undertaken in a greenhouse. A second trial was started in 2004 at four provincial nurseries.

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RECENT ADVANCES IN TREE AND FOREST GENOMICS

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Keywords: comparative and functional genomics, ectomycorrhiza, genome mapping, marker-aided selection, mitochondrial DNA, molecular ecology, molecular population genetics, phylogenetics, phylogeography, poplars, spruces, tree improvement, wood formation, xylem.

INTRODUCTION

The last two years have seen many new developments. D. Khasa and J. Mackay have established their research groups at Laval University. J. Cooke, who was formerly at the University of Florida in Gainesville, has joined us. Collaborations have intensified with colleagues from the Canadian Forest Service (CFS), J. Beaulieu, N. Isabel, and A. Séguin, who have the rank of adjunct professors in our group. The synergetic effects have been tremendous. One good example is the *Arborea* project, which was launched in 2002 with the aim to better understand the functional genomics of wood formation and defence mechanisms in white spruce (*Picea glauca*) and poplars (*Populus* spp.). This initiative is a major undertaking which regroups all of us and is lead by J. Mackay. It is funded by Genome Québec and Genome Canada, and it also involves S. Reagan from Carleton University and E. Retzel from University of Minnesota.

During the last two years, the group has welcomed several postdoctoral researchers, including C. Bomal, A. Guérin, J.-L. Jany, N. Pavy, C. Guillet-Claude, F. Lafarguette, T. Laurentiu, and Q. Yu. Many graduate students were involved in various research projects, including at the MSc level S. Beauseigle, H. Bérubé, F. Boileau, E. Campagnac, C. Côté, A. Gagné, J. Godbout, M.C. Gros-Louis, A. Noël, and P. Pollefeys and at the PhD level, F. Bedon, G. Bois, M. Bouillé, I. Gamache, J.P. Jaramillo-Correa, S. Legay, B. Pelgas, F. Pitre, S. Plante, and R. Sibout. Many of these students were co-supervised by adjunct professors J. Beaulieu, N. Isabel, and A. Séguin.

PHYLOGEOGRAPHY

J. Bousquet

Over the past two years, we have pursued the study of the phylogeography of Canadian conifers. In collaboration with scientists from the CFS and Forêt Québec (J. Beaulieu, N. Isabel, and M. Perron) and funding from Natural Sciences and Engineering Research Council (NSERC) and CFS, PhD student J.P. Jaramillo-Correa (supervised by J. Bousquet and J. Beaulieu) developed and characterized a number of sequence-based mtDNA markers in conifers (Jaramillo-Correa et al. 2003). Because they are maternally-inherited, these markers are less affected by gene flow and their geographical patterns of variation are more likely to reflect history. PhD student I. Gamache (supervised by ecologist S. Payette and J. Bousquet) tested this hypothesis by investigating the population structure of *Picea mariana* at the tree limit in northern Québec. While there was essentially no difference in gene diversity between subarctic and boreal populations, there were large differences in mtDNA gene diversity among boreal populations and between boreal and subarctic populations implying limited gene flow in mtDNA ($Nm<1$ as opposed to $Nm>15$ for nuclear genes). Populations from the subarctic were monomorphic in their mtDNA suggesting a founder event during the colonization of the Holocene (Gamache et al. 2003). Another study lead by Jaramillo-Correa showed that *Picea rubens* was essentially monomorphic for mtDNA but for a different mitotype than subarctic populations of *P. mariana*. Overall, *P. mariana* was more diverse and contained the variation observed in *P. rubens* (Jaramillo-Correa and Bousquet 2003) which confirmed a similar trend of a progenitor-derivative species relationship at nuclear gene loci (Perron et al. 2000).

More recently, range-wide genetic variation of *P. mariana* was studied using these mtDNA markers (Jaramillo-Correa with J. Bousquet and J. Beaulieu). This study was funded by NSERC and CFS and it was made possible thanks to the collaboration of colleagues of the Canadian Tree Improvement Association who kindly participated in the sampling effort. Low levels of mtDNA diversity were detected within the 32 populations surveyed but 10 mitotypes were found across Canada. A highly significant subdivision of population genetic diversity was detected, which was associated with geography (G_{ST} = 0.671, N_{ST} = 0.726). The distribution of mitotypes revealed four partially overlapping areas presumably colonized from three southern and one northeastern glacial refugia (Jaramillo-Correa et al. 2004). A similar range-wide study was also initiated for *Pinus banksiana*. It is being carried out by MSc student J. Godbout (supervised by J. Bousquet and J. Beaulieu). A highly variable minisatellite locus was discovered in the mtDNA of this species and the pattern of intra- and interpopulation variation is under investigation. Again, a highly significant subdivision of population genetic diversity has been detected. Similar studies have also been initiated for *P. glauca* and other major transcontinental conifers for which informative mtDNA variation has been detected.

MOLECULAR ECOLOGY AND POPULATION GENETICS

D. Khasa

With funding from NSERC and Ligniculture Québec and collaboration with P. Périnet from Forêt Québec and Alpac Forest Industries in Alberta (B. Thomas), several poplar SSR markers have been optimized and used for parentage analysis of poplar clones (Khasa et al. 2004). Some of these microsatellite markers and other gene markers including SNPs (in collaboration with J. Bousquet and N. Isabel) have been shown to be species-specific to identify five commercially important poplars and their interspecific hybrids in North America (Khasa et al. 2004, in prep.). These diagnostic markers will be used to assess potential gene flow from plantations of exotic poplar species into coexisting stands of native species and between native species potentially hybridizing naturally (*Populus deltoides* and *P. balsamifera*). On another front and in collaboration with CFS, MSc student M.-C. Gros-Louis, supervised by J. Bousquet and N. Isabel, has been developing nuclear and organellar diagnostic markers for the recognition of larch species and their hybrids. These markers are being used to certify hybrid progenies (M. Perron et al., Forêt Québec) and to estimate the extent of gene flow between exotic plantations and natural populations of indigenous species. This work has been supported by the Canadian Biotechnology Strategy (CBS), Forêt Québec, and Ligniculture Québec. The comparative study of population genetic diversity and breeding systems in western and subalpine larches is also nearly completed (Nadeem et al. 2003, Khasa et al. 2004, in prep.).

The molecular ecology of mycorrhizal fungi is also an important aspect of our research program. Using both an enriched genomic library for single- or low-copy sequences and data mining strategies, we have been successful in developing single-locus codominant microsatellite markers for several ectomycorrhizal fungi including *Laccaria bicolor* (Jany et al. 2004) and *Hebeloma* species (Jany et al. 2003). These sets of hypervariable markers will be valuable in environmental genomics studies such as monitoring the persistence of introduced mycorrhizal strains into the environment and the potential introgression of alien genes into the gene pool of native ectomycorrhizal species, or the assessment of their population genetic structure and mating system. Other strategies relying on the sequence analysis of ITS-rDNA have also been used to study mycorrhizal and root endophytic fungi of containerized *P. glauca* seedlings in commercial forest nurseries in northern Alberta (Kernaghan et al. 2003). In collaboration with Syncrude Canada and NSERC, a two step approach aimed at selecting both plant and mycorrhizal genotypes has helped us determine potential mycorrhizal plant systems for use in saline-alkaline habitats (Kerngahan et al. 2002, Khasa et al. 2002).

FUNCTIONAL GENOMICS

J. Mackay

J. Mackay has established a functional genomics research program that will focus primarily on issues related to wood formation and properties. A large-scale initiative lead by J. Mackay, project *Arborea* (www.arborea.ca) funded by Genome Canada, is now underway with a major focus on putative regulatory genes of secondary xylem (wood) formation in both poplar and spruce and defence response in poplar (Mackay et al. 2003). Several genes have been isolated that are similar to sequences described in model angiosperm plants and have been implicated in the regulation of primary and secondary vascular development. Gain-of-function experiments were initiated for several of these genes through over-expression studies in spruce or poplar in collaboration with A. Séguin from CFS. Preliminary results from these studies provide early indications that several of these genes are involved in regulating plant growth and development and affect vascular development either directly or indirectly. An integrated RNA analysis laboratory has been established by J. Mackay and J. Cooke to support diverse studies of gene expression from high-resolution studies of individual genes to large-scale analyses of thousands of genes using macroarray and microarray technologies. They are now beginning to use RNA profiling methods to assess the molecular function of targeted regulatory genes and conduct a variety of gene expression studies related to wood formation in spruce and poplar.

Within *Arborea*, a large-scale EST sequencing effort has been completed in *P. glauca*. High quality sequences have been obtained for approximately 35 000 ESTs from 17 cDNA libraries created from diverse organs and tissues. Part of the new sequence information is now publicly available at http://web.ahc.umn.edu/biodata/spruce and the remaining sequences will be released in coming months. An analytical pipeline has been established by N. Pavy and collaborators for the comparative analysis of ESTs from large databases (Pavy et al. 2004). Using conifer *knox-1* genes, an analytical pipeline has also been established for studying the functional diversity of transcription factors. This study is lead by C. Guillet-Claude in collaboration with J. Bousquet and N. Isabel. The phylogeny of plant *knox-1* genes has been estimated and indicates that conifer *knox-1* genes have evolved independently from angiosperms. They could further be divided into four classes. Signs of functional evolution were numerous, with accelerated rates after duplications and significant rate shifts at many amino acid positions. The same sites and additional sites in introns and promoter regions are monitored at the intraspecific level from up to 120 haplotype sequences for each gene. Conifer *knox-1* genes were also mapped and accelerated molecular evolution correlated with major translocations (Guillet-Claude et al. 2004).

STRUCTURAL AND EVOLUNTIOARY GENOMICS

J. Bousquet

In collaboration with N. Isabel, linkage maps of *P. glauca* were published (Gosselin et al. 2002). Over the past two years, PhD student B. Pelgas and MSc student S. Beauseigle (supervised by J. Bousquet and N. Isabel) have focused their efforts to further map the genome of *P. glauca*, establish base maps for *P. mariana*, and develop a set of anchor markers for spruce and conifer mapping. These will be useful to construct composite maps from various pedigrees within species and estimate map synteny between divergent spruce species including *P. mariana*, *P. glauca*, and *P. abies* in collaboration with European partners from INRA. Two types of anchor markers have been developed with variable success: microsatellites and expressed sequence tag polymorphisms (ESTPs). To accelerate the developement of ESTPs, we relied on DNA pool sequencing (DPS) to sample polymorphism. We showed that DPS is a highly reliable strategy to increase marker recovery, whether from the detection of indels or SNPs (Pelgas et al. 2004). More than 100 codominant markers are now available for establishing consensus maps in *P. glauca* and *P. mariana* with amenable genotyping strategies such as AGE, DGGE, or CAPS (Pelgas et al. 2004). Composite maps are near completion in *P. mariana* and *P. glauca* and synteny is currently being estimated among major spruce species. This joint project with N. Isabel funded by a NSERC-genomic grant and the CBS.

Studies have also been pursued to characterize the patterns of DNA variation at the intraspecific and interspecific levels in the genus *Picea*. PhD student M. Bouillé (supervised by J. Bousquet) showed that transpecies shared polymorphisms at the DNA level are numerous among distantly related spruce species, indicating long allele coalescence time and large historical population sizes (Bouillé and Bousquet 2004). Thus, these studies suggest a unifying mechanism for the maintenance of the high levels of neutral genetic diversity observed in conifers and in trees characterized by outcrossing mating system and high gene flow. We are also in the process of completing the estimation of the phylogeny of the complete genus *Picea* using a half-dozen genes from the nuclear, chloroplast, and mitochondrial genomes. The results obtained indicate that none of the traditional morphological classifications is entirely right. At the same time, the comparison between mtDNA and cpDNA phylogenies suggests cases of ancient lateral gene transfer.

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ADVANCES IN FOREST GENETICS, GENOMICS AND BIODIVERSITY AT THE CANADIAN FOREST SERVICE – LAURENTIAN FORESTRY CENTRE

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This report summarizes the progress of the Canadian Forest Service - Laurentian Forestry Centre's research in forest genetics, genomics, molecular ecology and biodiversity for the period 2002–2004. Our activities have mainly focused on breeding work in three spruces, eastern white pine (*Pinus strobus*) and Canada yew (*Taxus canadensis*). We have also continued to spend time on population genetics studies of forest tree species and in structural genomics in collaboration with J. Bousquet from Laval University (LU) and as part of our participation in the activities of the Canada Research Chair in Forest and Environmental Genomics (Tier I). Research was also done in collaboration with our colleagues from Forintek Canada Corporation and Laval University on genetic variation and control of wood characteristics. Some of us have also joined the functional genomics research program Arborea (Mackay et al.), a major initiative, funded by Genome Canada for studying functional diversity of transcription factors. On another front, in collaboration with J. Bousquet and M. Perron et al. (Forêt Québec), nuclear and organellar diagnostic markers for the recognition of larch species and their hybrids has been developed.

Research accomplishments were made possible with the generous contributions of dedicated collaborators and staff who deserve our thanks. They are: René Pâquet, Daniel Plourde, Jean-Paul Bilodeau, Yves Dubuc, Manuel Lamothe, France Gagnon, Marie-Claude Gros-Louis, Esther Pouliot, Sylvain Boisclair, Michèle Bernier-Cardou, Pamela Cheers, and many summer students.

GENETICS OF INDIGENOUS SPRUCES

Jean Beaulieu

White Spruce

Over the last two years, we completed most of the study initiated in collaboration with Tony Zhang (Forintek Canada Corp.) and André Rainville (MRNFP) to estimate genetic parameters of white spruce (*Picea glauca*) wood traits in order to develop a breeding program for growth performance and quality end-products. A genecological test, including 40 open-pollinated families from the Great Lakes-St. Lawrence region and replicated on two sites, was thinned in 2001. Two 210 cm logs were taken from each of the 320 36-year-old trees sampled and transported to the Forintek Canada Corp. facilities in Sainte-Foy, Québec. Logs were then either processed into 2 x 4 studs or cut in sections for analysis of veneer properties and decay resistance. A first paper, (Yu et al. 2003), investigated genetic variation in decay resistance and its correlation to wood density and growth. We found that decay resistance was inversely related to growth rate of the fungi on heartwood blocks. Narrow-sense heritabilities to decay resistance to brown rot and white rot were 0.21 and 0.27, respectively. Phenotypic and genetic correlations between the growth rate of brown rot and wood density were positive, whereas it was negative but not significant for white rot. A second paper, (Zhang et al., in press), investigated genetic variation in veneer quality and its correlation to growth. The narrow-sense heritability for veneer density, veneer modulus of elasticity, and veneer roughness was 0.62, 0.13, and 0.14, respectively. The phenotypic and genetic correlations between ring width and veneer density or veneer modulus of elasticity were negative. This means that selection for tree volume growth would lead to a decrease in wood density and veneer stiffness. Study of the genetic variation of solid wood mechanical properties is presently under way. The white spruce reforestation program is one of the most important in Québec with close to 30 million seedlings planted annually. This indigenous species is valued for its high yield (over 420 m^3/ha were obtained at 38 years with a fast growing progeny test established at Valcartier, for instance) and its general tolerance to insects and disease.

A study to determine the extent of the differences in tracheid length among 30-year-old white spruce open-pollinated families was carried out. Narrow-sense heritability was estimated as well as its genetic correlation with growth traits and wood density. Heritabilities at both the individual and family levels were low. Tracheid length was negatively correlated to growth traits but appeared to be independent of wood density. Vegetative propagation of the trees with the longest tracheids would be the most promising avenue to increase the average tracheid length in white spruce.

The development of pedigree populations was continued. Single-pair matings were carried out in order to have access to a large number of unrelated families for the genomics studies. White spruce individuals belonging to F_1 families were bulked up using rooted cuttings. A partial diallel cross using trees from families with high, medium, and low breeding values for height growth was completed. Seeds were sown in 2004 and trees will be propagated in the future using cuttings and replicated tests will be set up for genomics studies.

Black Spruce

The study on patterns of adaptive genetic variation and seed source transfer in black spruce (*Picea mariana*), initiated during the previous period, was completed and results were published (Beaulieu et al. 2004).

The development of pedigree populations was continued. Backcross, F_2 (self), and F_2 (intercross) families were obtained using controlled crosses. Vegetative propagation of these families (between 600 and 1 200 individuals per family) began in 2001, thanks to the collaboration of Michel Rioux from the Saint-Modeste cutting centre. Six tests were established using backcross vegetative propagules. Other pedigree families were also propagated using cuttings and are presently grown in a nursery at the Valcartier Research Forest. The controlled crosses for the development of third-generation black spruce pedigree populations have also been completed during the period under review.

POPULATION GENETICS AND PHYLOGENETICS OF FOREST TREE SPECIES

Jean Beaulieu, Marie Deslauriers and Nathalie Isabel

After developing and publishing mitochondrial DNA (mtDNA) PCR-RFLP markers for spruces (Jaramillo-Correa et al. 2003), range-wide genetic variation of black spruce was studied using mtDNA PCR-RFLP markers in a study led by Juan Pablo Jaramillo-Correa, a PhD student supervised by Jean Bousquet and Jean Beaulieu (Jaramillo-Correa et al. 2004). This study was funded by grants from Natural Sciences and Engineering Research Council (NSERC) and Canadian Forest Service (CFS), and it was made possible thanks to the collaboration of colleagues of the Canadian Tree Improvement Association who kindly participated in the sampling effort. Thirty-two populations, each represented by 15 to 30 individuals, were analyzed. Low levels of mitochondrial diversity were detected within populations. A total of ten mitotypes was found across Canada. A highly significant subdivision of population genetic diversity was detected, which was associated with geography (G_{ST} = 0.671, N_{ST} = 0.726). The distribution of mitotypes revealed four partially overlapping areas presumably colonized from different glacial refugia. We inferred at least three southern and one northern glacial refugia for black spruce during the last glaciation.

A similar study was also initiated for jack pine (*Pinus banksiana*). It is being carried out by Julie Godbout, a M.Sc. student supervised by Jean Bousquet and Jean Beaulieu. Juan Pablo Jarmillo-Correa is also participating in the study. A highly variable minisatellite locus was discovered in the mitochondrial DNA of this species and the pattern of intra- and inter-population variation is presently under investigation. Again, a highly significant subdivision of population genetic diversity has been detected.

The level of genetic diversity of 16 white spruce populations, including six populations from old-growth forest and 10 populations from second-growth forest, was estimated using allelic variants at eight ESTP loci (Beaulieu et al. 2003). A total of 23 alleles was detected in the 16 populations. All alleles present in the second-growth forest populations were also present in the old-growth forest populations and one variant was present in the old-growth forests only. The proportion of rare alleles in the old-growth forest populations was more than twice that in second-growth populations. Moreover, the population structure of old-growth was remarkably different from that of the second-growth forest, which was confirmed by both F statistics and cluster analysis.

With funding from Canadian Regulatory System for Biotechnology, NSERC, Ligniculture Québec, and the collaboration of P. Périnet from Forêt Québec several gene markers (N. Isabel and J. Bousquet) and SSR markers (D. Khasa and J. Bousquet) have been shown to be species-specific to identify five commercially important *Populus* spp. and their interspecific hybrids in North America. These diagnostic markers will be used to assess potential gene flow from plantations of exotic poplar species into co-existing stands of native species and between two native species potentially hybridizing naturally, *P. deltoides* and *P. balsamifera*. In parallel, with collaboration from LU, MSc student M.-C. Gros-Louis supervised by J. Bousquet and N. Isabel has been developing nuclear and organellar diagnostic markers for the recognition of larch species and their hybrids (Gros-Louis et al., submitted). These markers are being used to certify hybrid progenies (M. Perron et al.) and to estimate the extent of gene flow between exotic plantations and natural populations of indigenous species. This work has been supported by the Canadian Biotechnology Strategy, Forêt Québec and Ligniculture Québec.

An international symposium on silviculture and the conservation of genetic resources was organized as a side event of the XIIth World Forestry Congress on September 21, 2003 in Québec City. Eleven papers were given at that symposium and the proceedings were published (Beaulieu, editor 2004).

GÉNÉTIQUE DE L'ÉPINETTE DE NORVÈGE, DU PIN BLANC ET DE L'IF DU CANADA

Gaëtan Daoust

Épinette de Norvège

Pour l'épinette de Norvège, les efforts concertés du Service canadien des forêts (SCF) et du Ministère des ressources naturelles, de la faune et des parcs du Québec (MRNFPQ) ont permis de poursuivre l'avancement du programme conjoint d'amélioration génétique. En 2002 et 2003, 200 croisements polycross de première génération ont été réalisés dans le parc d'hybridation de l'Arboretum Serge-Légaré à Valcartier. Ces lots de semences nous permettront d'initier en 2005 la deuxième série de tests polycross (E411-II). La première série (E411-I), comprenant 90 lots sera établie au printemps 2004 dans 5 régions écologiques différentes.

Au cours de la même période, plusieurs croisements bi-parentaux d'épinette de Norvège ont été réalisés et seront ensemencés au printemps 2004 à la pépinière de Berthierville (E408-II). Ce test complètera la première série établie en 2000 et comprenant près de 200 croisements bi-parentaux. Des croisements bi-parentaux ont également été réalisés par la Direction de la production des semences et des plants (DPSP) du MRNFPQ dans le parc d'hybridation afin d'alimenter en semences de grande qualité génétique le programme de bouturage. Pour ces croisements, nous avons recommandé des génotypes sélectionnés pour leur résistance au charançon du pin blanc.

Les résultats des tests de descendances de la Série E390 ont permis de formuler des recommandations précises à la DPSP pour la récolte de sources performantes provenant de plantations commerciales, de tests de provenances et du parc d'hybridation. En se basant sur nos tests de descendances provenant de pollinisation libre, les clones du parc d'hybridation ont pu être classés en 3 classes selon leur potentiel de gain de croissance. Ces semences seront utilisées dans le programme de reboisement du MRNFPQ. Plusieurs collaborations ont été entreprises au cours des dernières années avec des compagnies forestières ou des groupes de recherche tel que l'Université du Québec en Abitibi-Témiscamingue afin d'acquérir de l'information sur la croissance et la rusticité de l'épinette de Norvège dans des régions plus nordiques.

Une étude sur la variabilité génétique de l'épinette de Norvège en test clonal a été réalisée et les résultats ont permis la réalisation d'un mémoire de fin d'études (Page 2003). L'étude entreprise afin d'étudier l'impact du charançon sur la productivité et la qualité du bois a été complété. L'étude a permis de faire ressortir le potentiel de cette espèce lorsqu'on la compare à l'épinette blanche tant pour la productivité que pour les caractéristiques du bois. Le faible défilement des tiges d'épinette de Norvège représente un atout majeur pour cette espèce.

Pin Blanc et Pins Hybrides

Au cours de la dernière période, les divers tests décrits dans le compte-rendu précédent ont été établis. Plus précisément, 3 tests comprenant 130 descendances uni-parentales (E601-II); 3 tests comprenant 90 descendances bi-parentales (E602) et 3 tests comprenant 36 descendances bi-parentales (E603, dialèlle 6 x 6) ont été établis dans différentes régions écologiques. Les données prélevées durant leur développement en pépinière (3 ans) nous permettront de faire une première classification du potentiel des génotypes sélectionnés produisant des semences dans notre parc d'hybridation de Cap-Tourmente et dans certains vergers à graines du MRNFPQ. Deux autres séries de tests comprenant des hybrides produits dans nos collections (E605) ou des pins exotiques haploxylons (E604) ont également été établis.

Les 5 clones hybrides *griffithii* x *strobus* obtenus du programme ontarien dans les années 80 ont été affectés très sévèrement par les rigueurs climatiques survenues durant l'hiver 2002-2003 à la Station forestière de Valcartier. La majorité des plants, qui atteignaient plus de 4 m de hauteur en moyenne, n'ont pas survécu à cet hiver rigoureux. Toutefois les mêmes clones hybrides établis à Cap-Tourmente, en bordure du fleuve Saint-Laurent et protégés des vents dominants n'ont pas été affectés par le froid.

Un bilan des travaux de génétique et d'amélioration du pin blanc au Québec a été présenté lors du White Pine Blister Rust Workshop tenu en mars 2003 à Ottawa (Daoust et Beaulieu 2003). Dans le cadre d'un projet d'études en statistique forestière à l'Université Laval, les données d'une série de tests de descendances, douze ans après plantation, ont été analysés. Les résultats obtenus démontrent une forte corrélation entre les hauteurs à 6 ans et à 16 ans après plantation, des héritabilités familiales relativement élevées pour la hauteur et le volume et des différences, pour le site le plus nordique des trois testés, quant au choix des provenances et des descendances recommandées (Gagnon et al. 2004). Une étude sur la stabilité somatique au niveau de loci de microsatellite nucléaire et chloroplastiques a été réalisé chez le pin blanc. Aucune variation à l'intérieur des ramets de 12 clones n'a été détecté chez les 12 loci étudiés (Cloutier et al. 2003).

If du Canada

L'étude des 3 populations de Charlevoix s'est poursuivi par une deuxième échantillonnage en 2002 sur environ 30% des individus étudiées en 2001. Pour le contenu en taxanes, aucune différence entre les populations n'a été observé encore une fois. Les variations entre les individus demeurent importantes et les corrélations phénotypiques entre 2001 et 2002 pour le contenu en taxanes sont significatives. Ces résultats confirment le statut des individus sélectionnés en 2001 pour leur forte concentration de taxanes. Des tests clonaux comprenant 50 individus pour chacune des 3 populations ont été mis en place dans Charlevoix par le projet sous la responsabilité de la Société d'aide au développement de la collectivité de Charlevoix.

STRUCTURAL GENOMICS AND PHYLOGENOMICS

Nathalie Isabel

In collaboration with J. Bousquet, linkage maps of white spruce have been published (Gosselin et al. 2002). Over the past two years, PhD student B. Pelgas and MSc student S. Beauseigle, supervised by J. Bousquet and N. Isabel, have focused their efforts to further map the white spruce genome, establish base maps for black spruce, and develop a set of anchor markers for spruce and conifer mapping. These will be useful to construct composite maps from various within-species pedigrees and to estimate map synteny between divergent spruce species including black, white, and Norway spruce. Two types of anchor markers have been developed with variable success: microsatellites and expressed sequence tag polymorphisms (ESTPs). To accelerate the development of ESTPs, we relied on DNA pool sequencing to sample polymorphism. We showed that DPS is a reliable strategy to increase marker recovery, whether for the detection of indels or SNPs (Pelgas et al. 2004). More than 100 codominant markers are now available for establishing consensus maps in white and black spruce with amenable genotyping strategies such as AGE, DGGE or CAPS (Pelgas et al. 2004). Composite maps are near completion for black and white spruce and synteny is currently being estimated among major spruce species (Pelgas et al., in progress). This joint project with J. Bousquet was funded by a NSERC-genomic grant and the Canadian Biotechnology Strategy.

Within the context of the Arborea project, an analytical pipeline for studying the functional diversity of transcription factors was developed using conifer *knox-1* genes (candidate gene for somatic embryogenesis). This study is lead by C. Guillet-Claude in collaboration with J. Bousquet and N. Isabel.

The phylogeny of plant *knox-1* genes has been estimated and indicates that conifer *knox-1* genes have evolved independently from angiosperms. They could further be divided into four classes. Signs of functional evolution were numerous, with accelerated rates after duplications and significant rate shifts at many amino acid positions. The same sites and additional sites in introns and promoter regions are monitored at the intraspecific level from large sampling (up to 120 haplotype sequences for each gene). Conifer *knox-1* genes were also mapped and accelerated molecular evolution correlated with major translocations (Guillet-Claude et al., submitted).

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MODELLING AIRBORNE POLLEN DISPERSAL TO AID REDUCTION IN POLLEN CONTAMINATION

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Pollen contamination can significantly reduce the genetic quality of seed used for reforestation and, ultimately, reduce wood yield per unit land area. Significant resources have been directed to Ontario's tree breeding program in order to produce seed of high genetic quality in seed orchards. This report describes the development of a computer model of pollen contamination that could be used to manage pollen contamination in seed orchards.

BACKGROUND

This work originated in the early 1990's with a series of field studies and developmental computer modelling efforts. In 2000, work was re-initiated with funding from Forest Genetics Ontario and was aimed at model development and application for a particular seed orchard. Extensive further work was done on both the model and the processing of input data for the model as well as an assessment of the field measured values. Assumptions made during model development in the early 1990's were tested and required modifications. Re-development with more rigorous assumptions indicated that the model generally over-estimated measured values. Although conservative results are acceptable when attempting to model environmental phenomena, especially in the context of anti-contamination methods development, at that time we believed that results would be more acceptable to the tree seed community if the degree of model conservatism was minimized. An evaluation of all aspects of the work indicated that some further work was necessary in refining the model, and possibly comparing model predictions against a second independent data set of dispersal data and dispersal model.

RATIONALE FOR LATEST DEVELOPMENTS

Funding for this further work was obtained from the Canadian Food Inspection Agency (CFIA). CFIA regulates the introduction of plants with novel traits into Canada including trees. This also includes the introduction of genetically modified plants. The key element in the use of modelling is the ability to replicate multiple years of gene-flow data at one-site or at many sites, thus allowing the variability in out-crossing (OC) to be quantified. A quantification of variability in OC allows confidence intervals or containment success probabilities to be assigned to, for example, isolation zone widths or flowering desynchronization methods. Such a probabilistic or "risk-assessment" type of approach to OC is more realistic than guidance based on limited site- and time-specific experimental data given the inherent variability in OC. This is an approach recently developed and utilizes the power of dispersal modelling more fully. Such an approach has been recognized by CFIA as adding additional useful information to their regulatory risk assessment process.

MODEL COMPLETION AND TESTING

The dispersal code was updated with contemporary stochastic Lagrangian algorithms. The resultant Langevin equation model (LEM; codified as POLDISP v.2.0) has been proven to emulate scalar dispersal within vegetative canopies more accurately than other commonly used dispersal models. POLDISP compared favourably against an independent tracer data set and against an “off-the-shelf” air pollution dispersal model (US EPA’s ISCST3 regulatory air pollution model, Fig. 1).

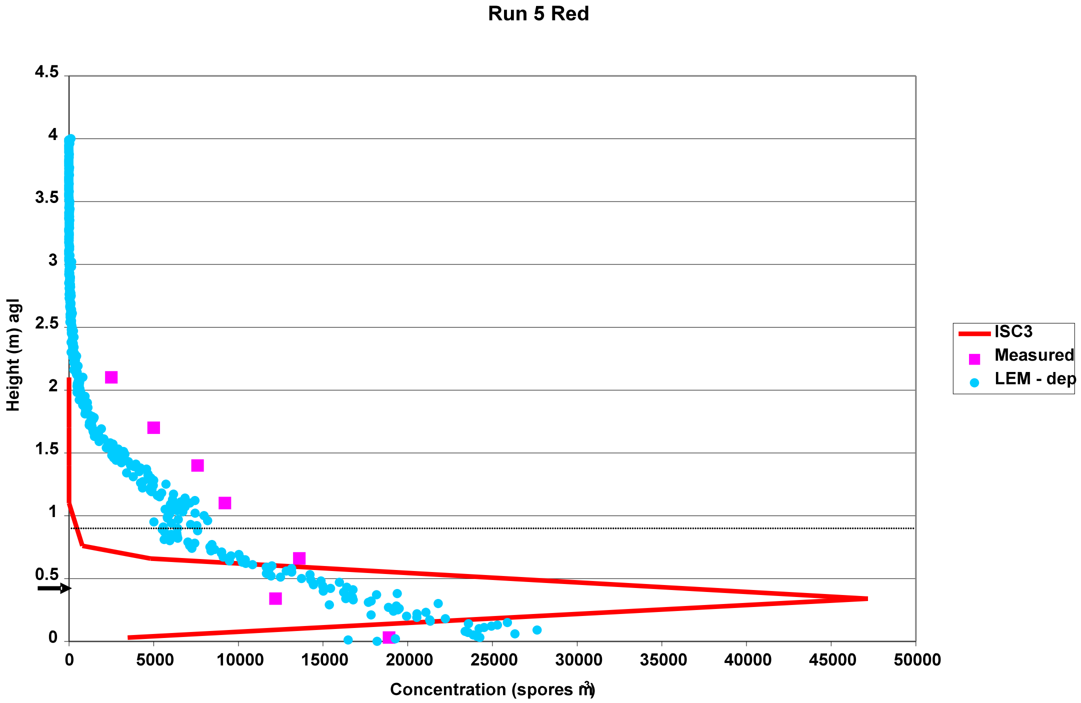

Figure 1. Observed (Aylor and Ferrandino 1989, Bound.-Layer Meteorol. 46: 251-) and modelled results of concentration profiles of marked Lycopodium spores at 2 m downwind from a release point at 0.4 m height under conditions u* = 0.38 m s^{-1} and L = -10,000 m. Results for the POLDISP model (=LEM) are shown where the deposition factor is fully applied (LEM – dep). Results are also shown for the ISCST3 model. The dotted, horizontal line indicates the approximate height of the canopy. Arrow on left-hand axis indicates the release height.

Presently available datasets for pollen dispersal and OC are lacking some of the information required to suitably test the model but those used thus far suggest the model is behaving well.

CFIA requested that this model be applied to wheat. There are many varieties of wheat, each with their own OC characteristics; i.e., pollen production/anther, anther extrusion, pollen viability, and settling velocity, etc. For generalized regulatory purposes a “worst-case” OC scenario was developed and OC at various distances from a source into a receptor field was simulated for nine locations across the major wheat growing regions of Canada and for 30 years at each location. At each location, OC at each distance downwind was combined for all 30 years to provide a mean and 95% CI. This was also repeated for all locations combined providing a “cross-Canada” result. OC data were then further processed to determine the probability of success of isolation by distance (isolation zones) for each of four threshold OC levels (0.1, 1.0, 5.0, and 10.0%) which, at this point, were chosen arbitrarily and for demonstration purposes only until CFIA decides on a “regulatory” threshold level, if one single level can be chosen.

The model is now ready to be used to optimize anti-contamination methods at orchards across Ontario and, if desired, further afield. Although further refinements are possible, we envisage a process of continual refinement through its practical application.

NORTHEAST SEED MANAGEMENT ASSOCIATION (NESMA)

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The past two years have been challenging and rewarding. Although the second-generation activities have demanded most of our attention, we have also made significant accomplishments in our first-generation programs. We continue to make progress toward accomplishing our goal to satisfy our partner's seed demand with improved seed from our first-generation orchards. NESMA has, to date, supplied over 130 million improved seed to its partners. An exhaustive second-generation tree breeding program, fueled by the Living Legacy Trust, has progressed considerably over the last two years. Successful breeding work has concluded in most of our breeding programs. A significant amount of effort and personnel were required to carry out the breeding work efficiently and in a cost effective manner. Improvements were made to overcome technical challenges, worker safety, and lower costs. Education and awareness of forestry, tree improvement, and our company continue to play a significant role.

FIRST GENERATION PROGRAMS

NESMA currently manages eight black spruce (*Picea mariana* [Mill.] BSP) and five jack pine (*Pinus banksiana* Lamb.) orchards located throughout northeastern Ontario.

Vegetation management, geared to competition reduction, is practiced at the orchards as required. Annual orchard fertilizing regimes are established based on the analysis of annual soil and foliage samples which are collected at all of the orchards in the fall of each year.

A combined Cone Crop Monitoring Study (CCMS) and a flower induction study were initiated at the Aidie Creek Jack Pine Seed Orchard in 2002. The study will provide flower counts on hormone treated trees in a managed jack pine orchard. It will also be used as a cone crop size predictive tool based on the monitoring of female flowers through their developmental stages and will provide insight as to the nature and impact of cone and seed predators.

To compare cone collection costs between orchard trees with and without crown management, a Crown Management Decision Support System (CMDSS) was developed and implemented at the Ramore Jack Pine Seed Orchard. Since 1994, crown management has afforded cone collection cost savings of 23%. Operational crown management, in conjunction with cone collection, is carried out annually at most of the orchards. In 2002, a total of 56.85 hL of cones were collected. A bumper cone crop in 2003 produced a total of 197.17 hL of cones from the orchards.

Roguing of the black spruce and jack pine orchards to approximately 20% of the original 400 families has been completed in all but two orchards (Lastheels and Curtis Black Spruce Seed Orchards).

Field colour-coding stratification of the final orchard population, according to family breeding values at the Island Lake Breeding Zone 1 and 4 Black Spruce Orchards, was completed in 2003. This allows for distinguishing between four classes of cones based on their "genetic worth".

At the Edward Bonner Orchard and at two genetic tests, two formulations of NEEM botanical insecticide were applied for the control of white pine weevil. This testing is being carried out to develop a reliable control method for the weevil and other insects which damage the leader of test trees.

An operational flower induction trial was also carried out at the Edward Bonner Black Spruce Seed Orchard. Three treatments were applied: 1) $GA_{4/7}$ hormone injections, 2) high-rate ammonium nitrate fertilizer, and 3) a combination of $GA_{4/7}$ and ammonium nitrate.

NESMA has developed a strategy to move the white pine (*Pinus strobus* L.) tree improvement program forward by developing three genetic tests, one of which may be converted to a seed orchard after testing has been completed. This strategy will capitalize on seed collection efforts undertaken by the Ministry of Natural Resources, Nipissing Forest Resource Management Inc., Ottawa Valley Forests, and Westwind Stewardship Inc. In 2002, three first-generation white pine genetic tests were established in Evanturel, Gratton, and Gurd Townships. Competing vegetation management, re-tagging, and re-planting of frost heaved seedlings were the focus during the 2003 season. Plus-tree cone collections for an additional three tests were made in 2003. Seeding will take place in early 2004.

SECOND GENERATION PROGRAMS

Tree breeding work was carried out in ten black spruce and jack pine programs involving 24 test sites distributed across northeastern Ontario. Rigorous analysis of the first-generation selections was made in order to strengthen the genetic gains and minimize possible inbreeding of the second-generation selections.

Access was created to and around all of the trees selected for breeding in order that the tree tops could be safely accessed with orchard ladders. An innovative tree bending technique was utilized on trees that were too tall for the modified 20 foot orchard ladders. The weather, staff procurement, training, and limited time proved to be challenges. In 2002 alone, over 100 people were recruited and trained in the art of tree breeding by experienced NESMA staff. An amalgamation of two jack pine programs (Durban Pj 25 and Aidie Creek Pj 4) to form the Durbie Creek Pj 4 program led to slightly reduced personnel requirements in 2003.

To date, all of the programs, with the exception of the Island Lake Pj 3, have produced sufficient seed to establish second-generation genetic tests. In addition to the regular breeding programs, special crosses with trees in the Edward Bonner black spruce program are expected to yield 25 – 30% gains. A vegetative propagation program is being developed.

Three Elite second-generation tests for the Island Lake, Breeding Zone 4 and the Edward Bonner, Breeding Zone 2 programs were established in the fall of 2003 with seeds collected from the elite controlled crosses made in 2001 and 2002. Seeds collected from open-pollinated trees in the infusion population were used to establish two infusion tests in each of the programs. Table 1 summarizes breeding activities conducted in 2002 and 2003.

Table 1. A summary of controlled crosses by program

	Breeding		Year	
Program	Zone	Species	2002	2003
Island Lake	1	Black spruce	32	39
E. Bonner	2	Black spruce	60	6
Ramore	3	Black spruce	41	43
Aidie Creek	5	Black spruce	47	40
Ramore	2	Jack pine	80	53
Island Lake	3	Jack pine	31	55
Aidie Creek	4	Jack pine	66	
Durbie Creek	4/25	Jack pine		78
Durban	25	Jack pine	72	
Hambleton	21	Jack pine	46	59
Total crosses			475	373

Pollen collected from across the northeast was sent to a processing facility near Englehart where they were dried, processed, and returned to the field in a timely fashion. In 2002, 686 pollen collections were handled while in 2003 the lab processed 454 collections. Some of the pollen was sent directly back to the field for breeding but much of it was vacuum freeze-dried and placed in storage.

Flower induction, to promote female flowering, was carried out at all of the test sites in the spring after rapid shoot elongation of black spruce and in mid-July during bud differentiation in jack pine.

Cones were collected from the Elite controlled crosses and from the infusion open-pollinated crosses in September of 2002 and 2003. The cones were sent to the Ontario Tree Seed Plant for processing. Further x-ray testing and "float" testing was done by NESMA to validate the viability of the seed prior to seeding. To date, over 4 million seeds have been collected from the tree breeding program.

Site acquisitions and field work (root-raking, brush pile burning, and cultivating) were made at five locations in preparation for future test sites.

Additional plus-tree selections, to fill in the "geographic holes" left by the first-generation selections, were made in the Island Lake Sb 1, Ramore Sb 3, Island Lake Sb 4, Ramore Pj 2 and Aidie Creek Sb 5 Breeding Zones.

NESMA will continue its efforts to establish second-generation genetic tests and manage first-generation orchards that will provide our partners with enhanced wood yields by using genetically improved seed. NESMA's future plans include breeding at the second-generation jack pine genetic test located near Chapleau, Ontario (established in 1987) and the development of a white spruce tree improvement program.

FOREST GENETICS RESEARCH AT THE ONTARIO FOREST RESEARCH INSTITUTE

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WHITE PINE GENECOLOGY STUDY

Pengxin Lu, Dennis Joyce and Bob Sinclair

Results from a short-term genecology study of eastern white pine (*Pinus strobus* L.) have been summarized. Seed movement guidelines were proposed based on revealed trends among provenances in growth potential, cold hardiness, and growth rhythm. A validation trial using 42 more evenly distributed provenances from eastern Ontario was established near Timmins in 2002. This trial will further test the adaptation and growth of southern provenances in a more northerly environment.

SCREENING EASTERN WHITE PINE FOR BLISTER RUST RESISTANCE

Pengxin Lu, Bob Sinclair and Tim Boult

In the past two years, a major effort was made to screen eastern white pine seedlings for blister rust resistance. Seeds were collected from putatively resistant trees of eastern white and interspecific hybrids from Ontario's white pine clone banks and field progeny trials. An artificial blister rust inoculation procedure was developed which, in conjunction with the modern growth facilities of Ontario Forest Research Institute (OFRI), enables blister rust to be inoculated on *Ribes* and white pine seedlings at about 100% infection rate and without the limitation of growing season. Four inoculation experiments have been carried out since, involving more than 12 000 6- to 18-month-old seedlings from > 250 open-pollinated families. Data collection was completed for the first 3 inoculations. The inherited disease resistance was evaluated based on seedling mortality. Preliminary results indicated that pure eastern white pine seedlings generally lacked genetic resistance to blister rust and suffered high mortality (> 97%) when heavily infected. Although the selected eastern white pine parent trees had been exposed to blister rust in previous tests, they did not transmit strong genetic resistance to their offspring. In contrast, some open-pollinated families of F_2 and F_3 eastern white pine backcross hybrids, especially those between eastern white pine and Himalaya blue pine (*Pinus wallichiana* A.B. Jacks.), have demonstrated stable inherited blister rust resistance, as shown by a significant improvement in seedling survival rates (> 50%) compared with those of pure *Pinus strobus* (< 3%) at the end the experiments. For some hybrid families, only about a 50% survival rate was expected because of the heteroallelic stages of hybrid female patents and little blister rust resistance expected from eastern white pine trees.

To retain more desirable characteristics of *Pinus strobus* in the hybrids and to improve their growth and adaptation in more northerly environments, an attempt was made to increase the genomic composition of *Pinus strobus* in the hybrids through back-crossing. Controlled-pollinations were conducted in 2003 and resulted in about 85 backcrosses. Seedlings from a few F_3 backcrosses were obtained, which have shown promise in blister rust resistance and adaptation.

In the near future, more eastern white pine and its interspecific hybrids are to be screened for blister rust resistance through artificial seedling inoculation. Segregation data on seedling mortality from open- and control-pollinated hybrid families will be used to infer gene-reaction modes. Vegetative propagation of selected seedlings is being conducted through rooted-cuttings for clonal testing both in blister rust resistance and field growth performance.

ROOTED-CUTTINGS OF JACK PINE

Pengxin Lu and Wayne Bell

In 2003, jack pine (*P. banksiana* Lamb.) was vegetatively propagated through rooted-cuttings at a relatively large scale. The method of Browne et al. (1997) was modified by eliminating the plant hormone treatment applied to cuttings and enhancing rooting environment control (i.e., relative humidity and temperature). A rooting rate of 70–80% was achieved using proliferated dwarf shoots taken from 2-year-old seedlings. The simplified rooting procedure markedly reduced operating time in cutting handling and, therefore, labor cost.

Using 2-year-old seedlings from 25 open-pollinated families as cutting donors, more than 7 500 rooted cuttings were produced with 4–5 ramets per seedling. Field trials are to be established in 2004 to compare growth performance between jack pine rooted-cuttings and seedlings.

WOOD DENSITY STUDY IN JACK PINE AND BLACK SPRUCE

Paul Charrette, Tony Zhang and Pengxin Lu

Collaboration among the Superior Woods Tree Improvement Association (SWTIA), Forintek Canada Corporation, and OFRI investigated genetic parameters between wood density and growth traits within breeding populations of jack pine and black spruce (*Picea mariana* [Mill.] BSP) in northwest Ontario. Increment cores were collected by SWTIA from two field progeny trials for each species and wood quality attributes including wood density were measured in Forintek's laboratory using an x-ray densitometer. Data analyses and interpretation were conducted at OFRI. Preliminary results indicated that wood density is under moderately strong genetic control, which is weakly and negatively correlated with growth traits, such as height, DBH, and volume in black spruce, but strongly negatively correlated with growth traits in jack pine. Implications of wood density to selections in tree improvement depend on the expected end products. If the breeding objective is to increase fibre production for pulp, the decrease in wood density due to selection for faster growth may well be compensated for by increased volume. Whereas, if the expected final product is solid lumber, wood density needs to be taken into consideration because selection criteria based on growth traits only (height and DBH) may result in economic loss due to deteriorating wood quality, especially in jack pine. Correlation breakers existed for both species, some of which are desirable candidates for increasing both growth and wood density.

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TREE SEED AND GENETICS RELATED ACTIVITIES AT THE PETAWAWA RESEARCH FOREST 2002–2004

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Keywords: seed dispersion, species introduction, moist chilling, repair mechanism, peak pollen release

Tree seed and genetics related activities have continued at the Petawawa Research Forest during the last two years. Cooperation with the Liaoning Provincial Academy of Forestry Science in the introduction of Canadian tree species to Northeast China resulted in a large-scale planting trial of jack pine and Petawawa helped with the procurement of 50 kg of seeds from Ontario latitude 46° N and vicinity for nursery sowing in 2003. The cooperation work is continuing and expanding to source trials of other tree species. On May 28, 2004, a delegation from the Liaoning Provincial Government headed by Mr. Xu Ming, Deputy Minister of Science and Technology, visited the Petawawa Research Forest and "An Offer of Cooperation Agreement between the Research Forest and the Liaoning Provincial Academy of Forestry Sciences" was signed. Results from more than 20 years of seed source trials of Canadian eastern white pine (*Pinus strobus*) provided sufficient confidence for the provincial forestry authority to initiate a large-scale operational planting trial. Petawawa was asked to procure a large quantity of eastern white pine seeds from latitude 46° N or proximity in Ontario if there are good seed crops in 2004. Details of the tree seed and genetics related activities are described below.

The collection of baseline data on natural seed dispersion in eastern white pine and red pine stands has yielded additional information. For assurance of genetic and physiological quality of seeds of local major tree species for research and operational purposes, seed collections have been initiated in good seed crop years with a view to establishing an in-house seed bank.

RESEARCH AND DEVELOPMENT

Repair Mechanism

It was found during an artificial aging study that moist chilling can induce natural repairing mechanisms in white spruce (*Picea glauca*) seeds as it was reported in black spruce (*Picea mariana*) seeds (Wang and Berjak 2000). This hypothesis was further proved by evidence from other germination data (Fig. 1 and Table 1).

Figure 1 demonstrates the natural repair mechanism induced by moist chilling in three white spruce seed lots from Nova Scotia. The cones were collected by one agency and each of the three cone collections was divided in half and processed by two different seed processing facilities. The germination tests of all seed lots were conducted at the National Tree Seed Centre located at the former Petawawa National Forestry Institute, Chalk River, Ontario. Seed dormancy was defined as the difference in germination percentage of non-chilled and 21-day moist chilled seeds. The degree of dormancy of seed processed at facility A varied from 13% in seed lot A, 15% in seed lot B to 31% in seed lot C. Germination test results of the non-chilled seeds processed by the two seed processing facilities (A and B) varied with 6% in lot A, 16 % in lot B and 13% in lot C. This difference in germination is most likely due to differences in handling and processing procedures used at the two facilities. However, when moist chilled, these differences in germination between the two facilities were essentially eliminated in lots A and B and reduced to 6% in lot C. Furthermore, the effect of moist chilling on seed germination consistently showed a 6–15% increase for the three seed lots that were processed by facility A than by B. If dormancy in seeds processed by facility A is considered true, then the 6-15% improvement in germination in the three lots can be attributed to the natural repair mechanism induced by moist chilling.

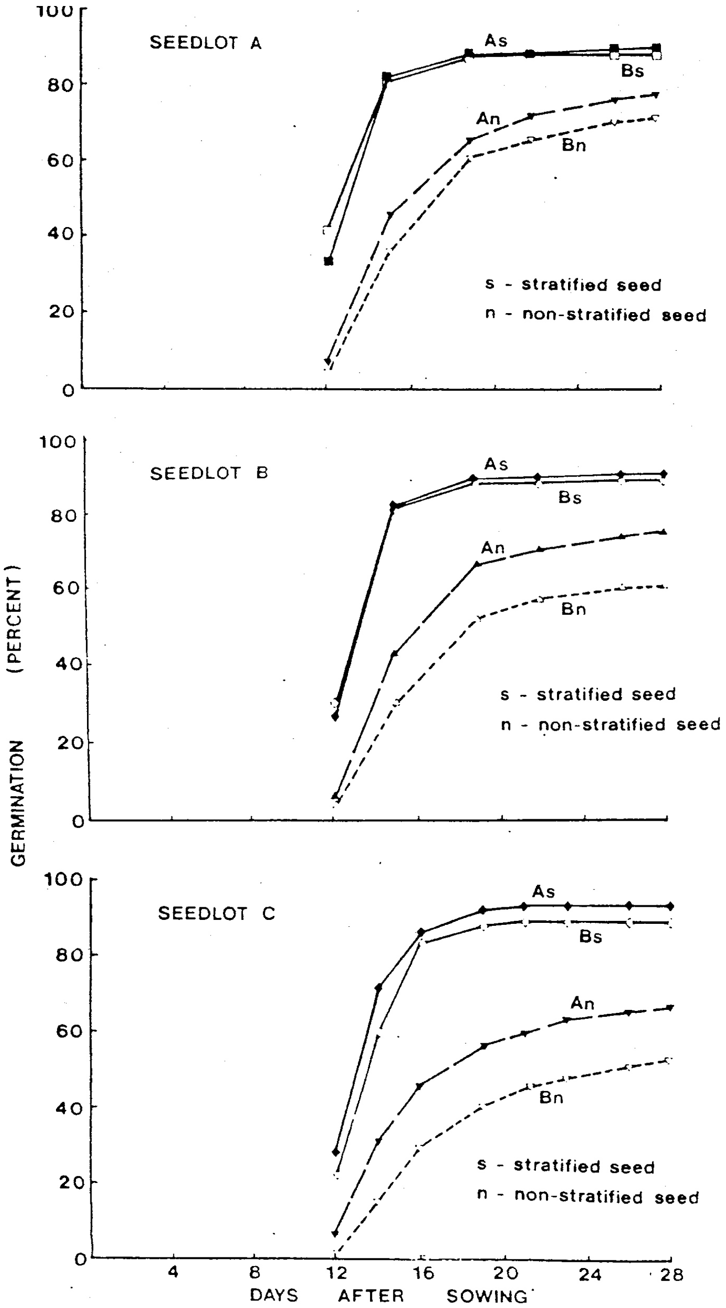

Figure 1. Effect of moist chilling on germination of three white spruce seed lots extracted from cones by two different processing facilities (A and B).

Table 1 shows that moist chilling induced natural repair mechanisms in white spruce seeds through comparison of seed germination results from cones picked in Alberta by hand and by a mechanized cone thrasher designed for lodgepole pine cone collection.

Table 1. Effect of moist chilling on germination of Alberta white spruce seeds extracted from cones collected by hand and by a mechanized cone thrasher

		% germination after 21 days at 20/30°C with 8 h light		
Seed lot	Collection method	21 day chill	No chill	Gain from chilling
A	Hand picked	90	73	17
	Mechanized	76	45	31
	Loss from cone damage	14	28	14
B	Hand picked	90	75	15
	Mechanized	75	51	24
	Loss from cone damage	15	24	9

It can be seen from Table 1 that germination increased 14% for lot A and 9% for lot B as a result of chilling seed collected using a mechanized cone thresher vs. hand collection. Damaged seeds repaired themselves during the 21 day moist chilling. Apparently, seeds were not injured severely enough to prevent them from repairing themselves. This natural repair mechanism, induced by moist chilling, has been previously demonstrated in black spruce (*Picea mariana*) by Wang and Berjak (2000). This is another important reason for nursery operators to use moist chilling as a pre-sowing treatment.

Peak Pollen Release

The Petawawa Research Forest has sporadically maintained a record, since 1950, of the date of pollen shedding for some of the major native tree species. Local origin trees are tracked for their pollen release in the spring and the ‘peak’ day recorded. Figure 2 shows the pattern of the peak pollen release of black spruce, white spruce, jack pine (*Pinus banksiana*), and red pine (*P. resinosa*). Other species monitored include tamarack (*Larix laricina*) and white pine along with some exotics.

The year to year variation for these species is as much as 31 days with an example of an early year being 1998 and a late year being 1997.

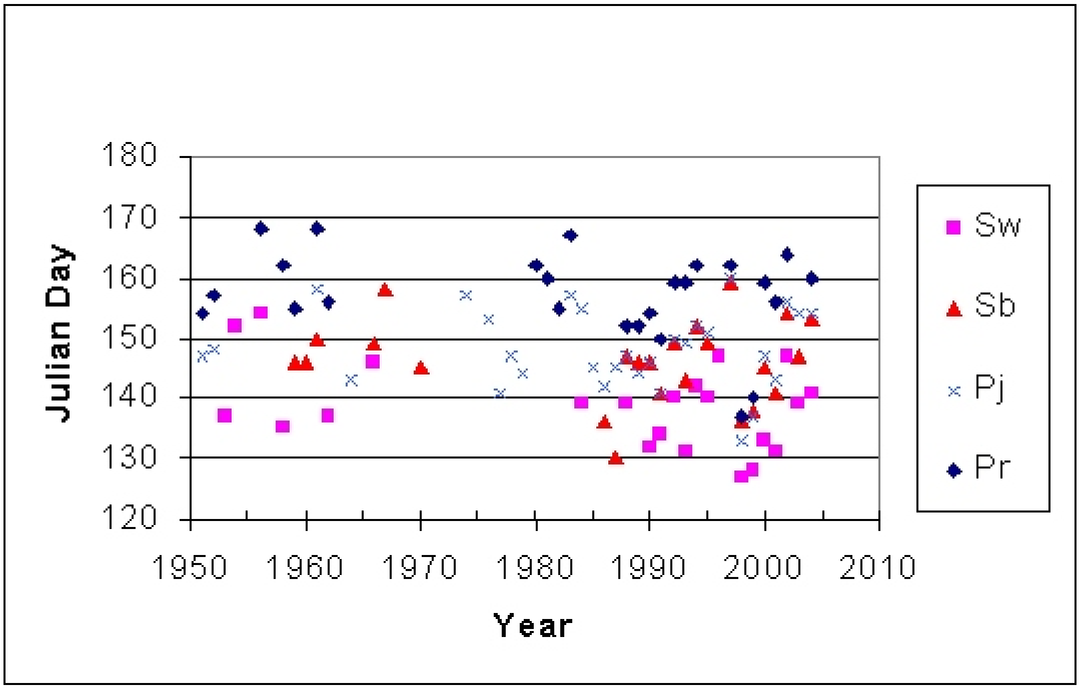

Figure 2. Peak pollen release at Petawawa by Julian day (Sw = white spruce, Sb = black spruce, Pj = jack pine, Pr = red pine).

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MANITOBA'S TREE IMPROVEMENT PROGRAM

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Keywords: jack pine, black spruce, white spruce, AAC determinations, GIS

Manitoba Conservation – Forestry has established tree improvement programs for the three main coniferous reforestation species in Manitoba: jack pine (*Pinus banksianna* Lamb.), white spruce (*Picea glauca* [Moench] Voss) and black spruce (*Picea mariana* [Mill.] BSP). Breeding zones for these three species are shown in Figs. 1 and 2. The three forest companies holding Forest Management Licences (FML's), Tolko Manitoba, Louisiana-Pacific Canada Ltd. (LP), and Tembec Forest Resources, cooperate in some of these programs within their FML's. A Tree Improvement Trust Account has been set up to allow cost sharing for work completed in these co-operative breeding zones. This report will highlight the major activities completed in the past 2 years.

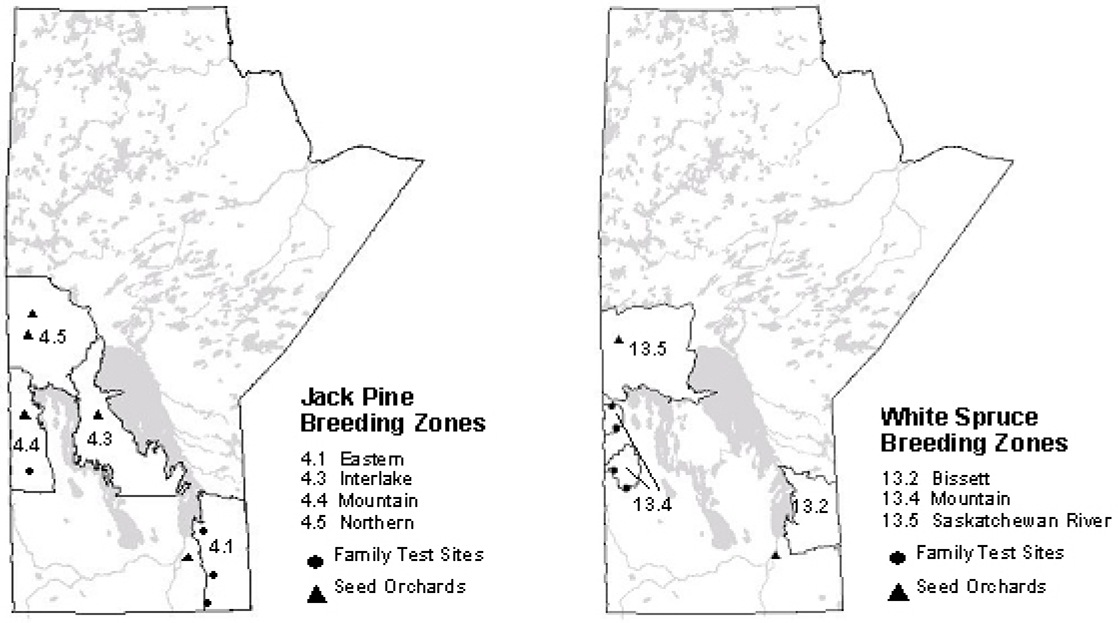

Figure 1. Location of jack pine and white spruce breeding zones within Manitoba.

TOLKO MANITOBA – MANITOBA CONSERVATION CO-OPERATIVE PROGRAMS

The first roguing of the Prospector black spruce seedling orchard in the Saskatchewan River Breeding Zone was completed in 2003. In 2003, 7.8 hL of cones were collected at the Prospector orchard in conjunction with crown management. The 10-year height measurements of the three black spruce family tests in the Nelson River Breeding Zone were completed in fall 2002 and spring 2003. Analysis of the height data has been completed and roguing of the Axis Lake seedling seed orchard will be completed in 2004. Maintenance continued on the three family tests and one seedling seed orchard established in the Highrock Breeding Zone in 1997/98.

There was a good white spruce cone crop in 2003 in the Saskatchewan River Breeding Zone with 12.1 hL of cones collected from the Reader Lake clonal orchard.

TEMBEC FOREST RESOURCES – MANITOBA CONSERVATION CO-OPERATIVE PROGRAM

The 15-year height, diameter, and form measurements were completed in 2003 on the three black spruce family tests in the Lake Winnipeg East Breeding Zone. The measurement data will be contracted for analysis in the fall of 2004 with the final roguing of the Brightstone seedling orchard to follow. In 2003, 7.0 hL of cones were collected in conjunction with crown management.

LP CANADA LTD. – MANITOBA CONSERVATION CO-OPERATIVE PROGRAMS

Maintenance continued on the black spruce family tests and seedling seed orchard that were established in the Mountain Breeding Zone in 2001.

Cone induction treatments using gibberellin injections were completed in the spring of 2002 and 2003 at the Birds Hill white spruce clonal orchard. Cones were collected from the orchard in the fall of 2002 (12.75 hL) and 2003 (8.0 hL). Two family tests were sprayed with Methoxychlor and/or pruned for weevil control in 2002 and 2003.

MANITOBA CONSERVATION PROGRAMS

The two black spruce mass selection seed orchards in the Interlake Breeding Zone were rogued for the second time based on data analysis of family performance as well as neighbourhood comparison, spacing, condition, and form.

Maintenance continued at the Northern and Interlake mass selection jack pine orchards as well as the jack pine clonal orchard in the Mountain Breeding Zone. The Southeast Breeding Zone pedigree jack pine orchard at Hillside suffered some minor damage due to a late spring snowfall in 2004 causing the breaking of crowns. Damage was especially evident in older, crown managed trees. A contractor collected cones in the Interlake (9.2 hL) and Hillside (4.7 hL) orchards in 2002.

A white spruce seed production area was established for the Southeast Breeding Zone in 2001–2002.

Over the past several years all tree improvement data have been supplemented with the inclusion of spatial information. All data for the provincial and industry co-operative programs have been entered using the ESRI Arc View Geographic Information System (GIS) program. This allows for such things as the mapping of plus tree locations for either top or bottom ranked families in a breeding zone, mapping and analysis of mortality or disease incidence in tests or orchards, and production of maps for the roguing of seed orchards.

In conjunction with the Manitoba Conservation Forest Inventory and Resource Analysis Section, trials are underway to determine size and frequency of plots to be established in plantations originating from improved seed to determine genetic gain. Plots will be established and measured over a number of years to determine an accurate genetic gain to be applied to wood supply analysis.

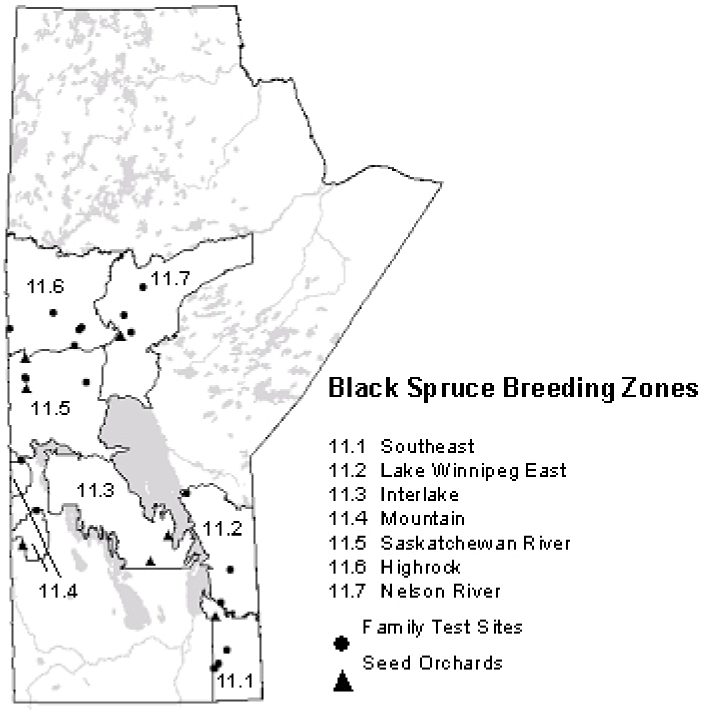

Figure 2. Location of Black Spruce Breeding Zones within Manitoba.

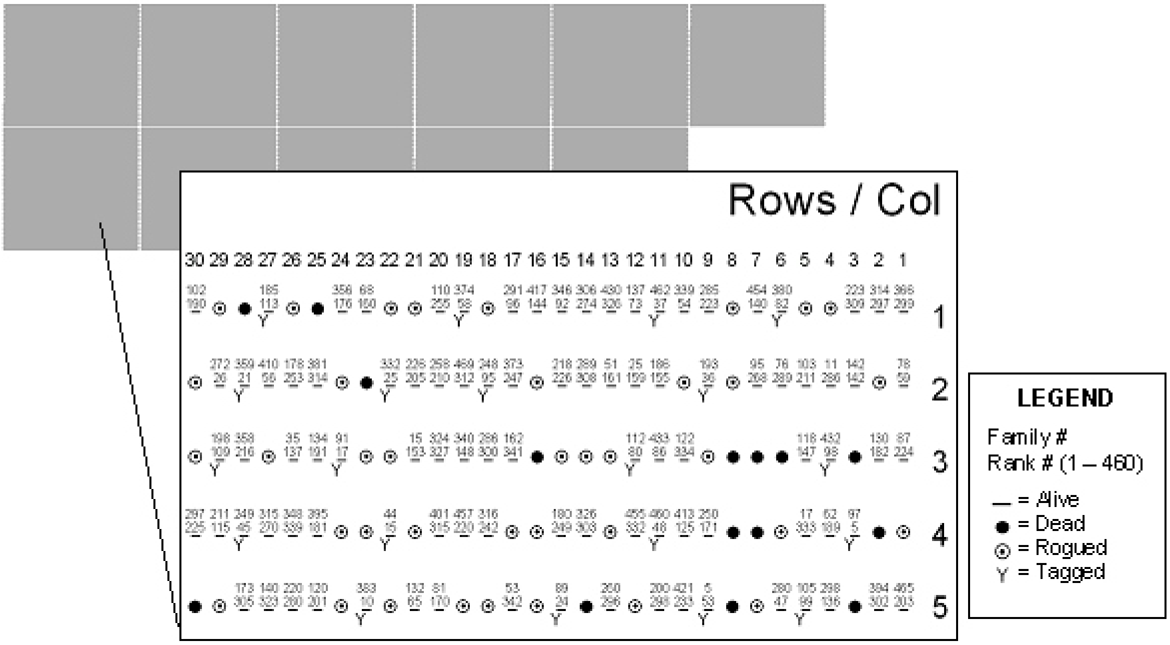

Figure 3. A segment of roguing replication data from Prospector Seed Orchard in Breeding Zone 11.5.

WEYERHAEUSER – TREE IMPROVEMENT IN SASKATCHEWAN

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Keywords: seed orchard, progeny tests, cross-pollinating, top grafting

Conifer tree improvement programs in Saskatchewan are managed and funded totally by Weyerhaeuser. The jack pine (*Pinus banksiana*) program was initiated in 1978 and was followed by white spruce (*Picea glauca)* in 1982.

JACK PINE PROGRAM

A grafted first generation orchard is exceeding all operational seed requirements. A small local market for improved jack pine seed has emerged over the last three years. Seed sales along with reduced cone collections have enabled us to improve management of our seed inventories.

Cross-pollination in ten of twelve breeding sub-lines is near completion. A protocol for “top-grafting” onto the crown of established orchard and breeding bank trees has been successfully developed and has allowed us to relocate a significant portion of our breeding work to the orchard property. Since 2001, a series of full-sib progeny tests has been established annually as seed becomes available from the sub-lines.

The final series of cross-pollinated progeny tests, sub-lines eleven and twelve from orchard trees, has been measured and the data were analyzed by Dr. Dudley Huber. Selections will be made in 2005 for inclusion into a second-generation seed orchard.

WHITE SPRUCE PROGRAM

A grafted first-generation orchard is now meeting all operational seed requirements with a generous surplus of seed which is available for sale. Crown management was undertaken by removing an additional whorl from the tops of the taller trees. The last top pruning was undertaken in 2001. At that time, the top two to three whorls were removed to control the height, leaving tree height at a mean of four m.

Data are currently being collected from open-pollinated progeny tests. Selections will be grafted for a second- generation seed orchard to be established starting in 2006.

The conservation of genetic diversity in public owned forests is a concern commonly addressed. Dr. Sally John compiled a report outlining a strategy for ensuring maintenance of adequate levels of genetic diversity in forest trees on Saskatchewan’s Prince Albert Forest Management Lease to include diversity maintenance in regenerated stands, seed orchard populations, breeding populations, and a plan for long-term conservation.

Weyerhaeuser Saskatchewan will ensure that diversity is maintained by: 1) setting standards for minimum diversity levels in wild seed collections and orchard seed lots, 2) instituting a monitoring program to quantify diversity levels of all future seed orchard crops, 3) increasing the size of the white spruce seed orchard population, and 4) working with the Saskatchewan government to develop an ecologically sound system of *in situ* conservation areas of special interest.

BLACK SPRUCE PROGRAM

There are no immediate plans for a black spruce tree improvement program. In the meantime, we will continue collecting black spruce seed from wild stands.

PUBLICATIONS AND REFERENCES

Corriveau, L.S. 2003. Annual tree improvement report. 8 p.

John, S.E.T. 2004. Maintaining genetic diversity on Weyerhaeuser's Prince Albert FMA. 2 p.

AAFC-PFRA SHELTERBELT CENTRE - TREE IMPROVEMENT SUMMARY

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Keywords: shelterbelt, agroforestry, tree improvement, *ex situ* conservation

The PFRA Shelterbelt Centre has, over the past 80 years, had an active program dedicated to improving tree species for the Canadian prairies. The objective of the program is to develop genetically diverse trees and shrubs that are functional agroforestry plantings. In addition, considerable effort is focussed on improved, clonally propagated *Populus* hybrids. The Centre also maintains germplasm collections of prairie woody plant genera. Improved trees and shrubs developed in the program are used for farm, field, and roadside shelterbelts, wildlife habitat planting, riparian buffers, phyto-remediation, and afforestation.

LARIX IMPROVEMENT

Seed representing four species *Larix sukaczewii* Dyl, *Larix sibirica* Ledeb., *Larix cajanderi* Mayr., and *Larix gmelinii* Rupr. was obtained from the Swedish University of Agriculture Sciences. This seed originated from collections of 1 005 individual *Larix* trees distributed over 16 regions and 45 stands in Russia. The seeds have been distributed to researchers in Russia, Scandinavia, Japan, and Canada. This collection represents a very wide genetic and geographic distribution of *Larix*. The Shelterbelt Centre was selected as the Canadian participant in the project. Seed from this project has been propagated and is planted in a block planting and riparian buffer strip. Seedlings have also been made available to the University of Saskatchewan for planting in an afforestation project. The objectives of this project are to evaluate the adaptability of exotic *Larix* populations to prairie growing conditions, to study genotype-environment interactions of the *Larix* species, and to provide genetic material for future selection and breeding.

POPULUS IMPROVEMENT

Populus improvement is a key activity at the Shelterbelt Centre. The program focuses on trait improvement related to biomass accumulation, cold hardiness, drought resistance, nutrient uptake, pest resistance, and wood quality. The Centre maintains an extensive clonal library, a breeding arboretum, and 40 clone tests situated across the prairie provinces. In 2003, a new clone, Katepwa, was released for agroforestry applications in the Canadian prairies.

Breeding Program

The current breeding program was initiated in 2001. The objectives are to develop hardy, fast growing, drought, and pest resistant hybrid poplar suitable for afforestation and agroforestry activities in the prairie provinces. The breeding project is conducted in partnership with Alberta Pacific Forest Industries. Controlled crosses were done to produce inter-specific hybrids of selected *Populus deltoides* Marsh. var *occidentalis* Rydb., *Populus balsamifera* L., *Populus maximowiczii* A. Henry, *Populus nigra* L., *Populus laurifolia* Ledeb., *Populus tristis* Fisch., and *P. x canadensis* Moench. Nursery evaluations and field testing will be conducted on control-pollinated (CP) seed lots to identify superior *Populus* genotypes. Since 2002, a total of 129 CP families have been produced in the program. The seedlings have been established in nursery trials at the Shelterbelt Centre. These plantings total over 15 000 individual genotypes. The plants (ortets) in the nursery trial will be used as a source of clonal copies (ramets) for field trials.

Clone Tests

One of the major areas of research being undertaken at the centre is testing of hybrid *Populus* clones. At this time, over 300 clones are being tested at 40 locations across the prairie provinces. All clone trials are planted in replicated trials. The objective of these tests is to evaluate performance and adaptation of *Populus* clones in afforestation and agroforestry applications. These tests have illustrated the variability in performance of clones and the importance of science based evaluation prior to large scale use of any particular clone.

Characterization of *Populus* Cold Hardiness

The ability of *Populus* to withstand winter damage depends mainly on how quickly they become cold hardy in the fall and how resistant they are to losing their hardiness in spring, rather than the ultimate level of cold hardiness attained in winter. We have examined patterns of low temperature acclimation in the fall and late winter or early spring de-acclimation in 21 clones of hybrid *Populus* commonly used or newly introduced to the prairies, using our newly established cold hardiness testing facility. All clones developed an extremely high degree of low temperature tolerance, but the dates of initiation, rates of development, and dates and patterns of de-acclimation differed strongly among the clones. Three general patterns of acclimation were observed in the fall: a very early initiation (without much exposure to low temperatures) accompanied by an extremely fast rate of acclimation, a later initiation (after exposure to low temperatures) but accompanied by a fast rate of acclimation, and a late initiation (after exposure to low temperatures) but with a slow rate of acclimation. De-acclimation patterns in spring could also be grouped into three general patterns: a very early group which were unable to re-acclimate after exposure to low temperatures, a very late group which de-acclimated only when risks of low temperatures were minimal, and an intermediate group which were able to re-acclimate quickly whenever low temperatures occurred. The patterns of acclimation in fall did not necessarily correspond to the patterns of de-acclimation in spring, e.g., hybrids that acclimated early in fall did not necessarily de-acclimate late in spring. These results indicate that both fall and spring hardiness patterns are important for successful planting of hybrid *Populus* clones.

ADAPTATION OF AGROFORESTRY SPECIES TO CLIMATE CHANGE

There is little information on the impacts of climate change on fragmented natural or created ecosystems, such as shelterbelts or other tree-based buffers that are integral components of the Canadian agro-ecosystem. Tree or shrub species and genotypes that currently exist in these environments will be impacted by climate change, yet we do not know how they will respond or whether there is sufficient genetic diversity within the populations to be able to adapt to the predicted changes. A number of studies are being conducted to address issues of climate change impact on agroforestry species across Canada. Techniques and technologies are being developed to help to rapidly screen populations or genotypes for adaptability to the different aspects of climate change. A detailed examination of species populations in the most vulnerable Canadian agro-ecosystem, the prairies, for their adaptability is focused on *Populus deltoides* Marsh. var *occidentalis* Rydb., *Fraxinus pennsylvanica* Marsh. var *subintegerrima* (Vahl.) Fern., *Quercus macrocarpa* Michx., and *Prunus virginiana* [A. Nels.] Sarg. The four year project addresses issues related to: vulnerability to winter damage, vulnerability to drought, and impacts on nutrition.

EX SITU CONSERVATION OF WOODY PLANTS

The Centre is involved in evaluation and conservation of woody genetic resources used in agroforestry. This includes sampling native woody plant populations and establishment of *ex situ* conservation nurseries. Collections have been completed for *P. virginiana*, *Cretaegus rotundifolia* Moench, *Shepherdia argentea* Nutt., *Symphoricarpos occidentalis* Hook., *Rosa woodsii* Lindl., *Q. macrocarpa*, *F. pennsylvanica*, *P. deltoides* var. *occidentalis*, *Prunus nigra* Ait., and *Prunus americana* Marsh. A new initiative to expand the collections outside the prairie region is being developed.

WESTERN BOREAL ASPEN CORPORATION

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Western Boreal Aspen Corporation (WBAC) began as an aspen tree improvement cooperative in 1992. Since then, the program has grown to include poplars and research and development of silviculture techniques for plantation establishment. The focus of our program is to ensure that future hardwood fibre needs can be met. Current members are: Ainsworth Lumber, Daishowa-Marubeni International, Footner Forest Products, and Weyerhaeuser Company. WBAC is a member of the Minnesota Aspen and Larch Genetics Co-operative and also works cooperatively with the Canadian Forest Service and former members. WBAC's mission statement is: to develop genetically improved aspen and to support research towards meeting companies' fibre needs. As a secondary focus, the corporation also supports poplar tree improvement.

WBAC has initiated a comprehensive genetics program for pure native aspen, including provenance trials, a grafted breeding orchard, clonal testing, and associated clonal archives. The group is also conducting a hybrid breeding program involving *Populus tremula* from Europe and *P. davidiana* from eastern Asia. WBAC members have begun testing hybrid poplars developed elsewhere and will initiate a balsam poplar testing and selection program. Tree improvement efforts focus on the testing and selection of superior clones for operational deployment. Initial candidate materials are collected from wild populations, but as progress is made with controlled breeding, candidates for clonal testing will be selected from progeny tests.

The group has initiated basic silviculture research involving density trials, site preparation, and planting stock production using seed, root suckers, greenwood cuttings, and tissue culture, as well as applied research associated with breeding (pollen handling, flowering induction, controlled crossing, seed processing, and seedling production). Establishment of aspen field trials began in 1995. Hardwood trial establishment and ongoing trial monitoring and maintenance are now a routine part of cooperators' in-kind contributions.

Notable achievements in the recent past: 1) development of an effective and economical method of mass vegetative propagation for operational deployment, 2) refinement of flower induction treatments in the potted orchard, 3) an early analysis of a 2001 clonal aspen trial, 4) a presentation titled "Aspen, adaptation, and climate change. Is Alberta aspen adapted to a fossil climate?" at the CIF/SAF October 2004 meeting, and 5) the hosting of a successful tree improvement industry meeting to discuss public education and awareness strategies about the industry in 2003.

Breeding and crossing efforts in 2001 and 2002 were very successful, following several years of difficulty. In 2003, WBAC successfully completed about half of its first series of controlled crosses in the native aspen breeding program. After completion of all the factorial crosses in 2004, seed was sown for progeny trials. One trial will be planted in 2005 and the remaining stock will be used for vegetative propagation to install several clonal-based progeny trials in 2006. Table 1 summarizes the various trials that have been established.

Table 1. Summary of various trials established by WBAC

Type	Number of trials	Number of Treatments	Type of treatments
Clonal tests	17	337	Clones
Exotic and hybrid aspens	25	165	Families
Provenance trial	5	43	Seed lots
Silviculture trials	8	Various	Browse, density, and fertilizer

GENETICS AND TREE IMPROVEMENT PROGRAM, 2002–2004 ALBERTA SUSTAINABLE RESOURCE DEVELOPMENT

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Keywords: tree breeding, provenance studies, species testing, seed orchards, clone banks, progeny testing, selection, climate change

This report summarizes the progress of the Public Lands and Forests Division (PLFD) genetics and tree improvement program for the period 2002–2004. A large part of the work was done in collaboration with forest industry, Alberta Agriculture and Rural Development, University of Alberta, North Peace Applied Research Association, Canadian Forest Service, U.S. Forest Service, and British Columbia Ministry of Forests.

PROGRAM DEVELOPMENT

The Standards for Tree Improvement in Alberta (STIA) were released in manual form for implementation in 2003. The manual provides a regulatory framework and standards which guide traditional reforestation activities, enables industry to plant genetically improved stock on Crown Land, and directs conservation efforts necessary to preserve the genetic diversity of Alberta's Crown forests. The Forest Genetics Alberta Association (FGAA) was formed with Alberta Sustainable Resource Development as one of the founding members. The objectives of the FGAA include cooperative project development and management for genetics and tree improvement work in Alberta involving the Alberta Tree Improvement and Seed Centre (ATISC) and industry. The Alberta Forest Genetic Resources Council (AFGRC) continued its work. Major initiatives of the council during the report period included review and endorsement of STIA, updating of the policy position on GMOs, technical review of reforestation with non-native species, and sponsorship of a Canada-wide survey of forest genetic resources management practices and policy in cooperation with Ontario and British Columbia.

GENETIC IMPROVEMENT

Assembly of Breeding Stock

Geographic and superior parent tree selections, made as part of Sustainable Resource Development (SRD)/Industry cooperative breeding projects, included 23 lodgepole pine (*Pinus contorta* var.*latifolia*) and 16 jack pine (*Pinus banksiana*). Companies participating in these projects include Manning Diversified Forest Products Ltd., Northland Forest Products Ltd., and Tolko Industries Ltd. (High Level Lumber Division).

Genetic Testing

Tests of white spruce (*Picea glauca*) and lodgepole pine open-pollinated families from Cypress Hills Provincial Park were established in 2003. The higher elevation portions of the park were untouched during the last glacial advance and it is presumed unique 'outlier' island populations of white spruce and lodgepole pine may have persisted. These populations show promise for selection and breeding for climate change adaptation in northern Alberta. Sixty-four white spruce and 20 lodgepole pine families were established in separate tests on four sites using an alpha design.

Eleven-year assessments of white spruce half-sib open-pollinated (OP) progeny trials for Breeding Region E (northeast boreal lowland) and Breeding Region H (northwest boreal lowland) were completed in 2002. Survival, tree condition, height, leader growth, and white pine weevil incidence were measured or assessed. The test results will form the basis for the first genetic roguings of the seed orchards associated with these breeding regions to be completed in the fall of 2004.

White spruce half-sib progeny trials for Breeding Region D1 (Slave Lake area boreal) were measured in 2003 at 21 years. Survival, tree condition, height, dbh, and incidence of white pine weevil were measured or assessed. A third genetic roguing will be undertaken in the Region D1 seed orchard based on the results.

Seed Orchards and Clone Banks

Seed Orchards In 2003, the most abundant cone crops to date were produced in the white spruce seed orchards located at the Alberta Tree Improvement and Seed Centre (ATISC). The Breeding Region D1 seedling orchard, comprised of 989 trees representing 89 families and established in 1982/83, produced 250 hl of cones yielding 315 kg of seed. The average number of cones per tree was about 4 600. The trees in the orchard averaged about 7 m in height and all were topped by approximately 2 m to facilitate cone collection. Until 2003, the 1999 crop was the largest. In that year, 142 hl of cones were collected yielding 213 kg of seed. The Breeding Region E white spruce clonal seed orchard, established in 1989, produced 78 hl of cones with a yield of 111 kg of seed in 2003. The orchard contains 1 161 trees representing 94 clones and, on average, each tree produced about 1 300 cones. Trees greater than 3 m in height (approximately 40% of orchard trees) were topped to assist with cone collection and to promote growth of a bushier crown. The most abundant crop in previous years was produced in 1999 when 14 hl of cones were collected yielding 16 kg of seed.

In 2003, the Breeding Region E1 (northeast boreal lowland) white spruce clonal orchard was expanded to accommodate the needs of the regional oil sands industry. The project is currently a cooperative venture between Northland Forest Products Ltd. and SRD. The size of the orchard was increased from 510 to 870 positions. To date, 487 ramets representing 59 parents are established in the orchard. Another 20 parent tree selections from the northern part of the breeding region are planned over the next five years to provide a better geographic balance to the breeding and orchard populations and to produce enough seed to meet oil sands industry requirements.

Forty percent of the trees in the Breeding Region H white spruce clonal orchard, established in 1989 at the Edwand site 15 km north of ATISC, were killed by wildfire in 2002. Complete loss of the orchard was avoided due to regular mowing of the site and pruning of lower branches on the grafts. This maintenance prevented the fire from spreading to the tree crowns. Re-grafting from the clone bank is underway and the orchard will be redesigned and replanted. A more substantial fireguard will be cleared and maintained around the site, located in an over-mature jack pine stand.

The interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) clonal orchard for Breeding Region F1 (southern montane), located at the Crop Diversification Centre at Brooks, was re-designed in 2003 to balance the number of ramets per clone. Eighteen grafts representing 11 clones were removed from the orchard and either discarded or re-established in the clone bank, also located at Brooks. Ten grafts representing 7 clones were removed from the clone bank and re-established in the orchard. Currently, the orchard is comprised of 138 ramets representing 45 clones.

Clone Banks Over the report period, 110 new clones were established in ATISC clone banks. The bulk of these represent white spruce and lodgepole pine but other species include black spruce (*Picea mariana*), jack pine, red pine (*Pinus resinosa*), limber pine (*Pinus flexilis*), Scots pine (*Pinus sylvestris*), and tamarack (*Larix laricina*). Two Douglas-fir clones and one western larch (*Larix occidentalis*) clone were established in the clone banks for these species located at the Crop Diversification Centre at Brooks.

GENETICS AND TREE IMPROVEMENT RESEARCH

Provenance Studies

Twenty-four- and 27-year assessments were completed on five and two trials, respectively, in the Alberta-wide white spruce provenance series. This series includes 13 trials established throughout Alberta. Twenty-seven seed sources were evaluated for survival, total height, and dbh.

Statistical and genetic analyses were carried out on 24-year measurements of white spruce provenance trials available from eight test sites. Large differences were found among provenances and test sites for growth traits. On an individual site basis, variation among provenances accounted for 6.3–9.45% of the total variance for height and 4.3–14.0% of the total variance for dbh. Variation among provenances across sites was moderate for height and low for dbh with both traits accounting for 5.5 and 3.5% of the total variance respectively. The provenance X site variance component was significant for both traits and amounted to 50.7 and 85.6% of the provenance variance for height and dbh respectively indicating the importance of the genotype X environment interaction. Height and dbh growth were related to latitude and elevation of seed origin. However, the strength of these relationships differed among test sites. No specific geographic pattern could be established for provenance survival.

Statistical and genetic analyses were also carried out on 15-year measurements of black spruce provenance trials established at seven test sites. For growth traits, differences among provenances were low and for test sites substantially large in comparison to white spruce. On an individual site basis, variation among provenances accounted for 0.9–7.2% of the total variance for height and 1.7–8.5% of the total variance for dbh. Variation among provenances across sites was also low and accounted for 0.9% of the total variance for both height and dbh, with 65.2 and 68.8% of the total variance for height and dbh respectively, being due to variation among test sites. The site X provenance variance component was 59.5 and 96.0% of the provenance variance component indicating the importance of the genotype X environment interaction. Geographic patterns for height were generally weaker than those of white spruce. No geographic patterns were observed for survival.

In 2002, three white spruce 'northern areas' provenance-progeny trials were assessed at 18 years from seed. The 125 families in the test series represent 23 provenances ranging in longitude from 111.28° (Fort McMurray) to 119.78° (Clear Prairie) and in latitude from 55.62° (Saddle Hills) to 58.62° (Assumption). Survival, height, dbh, and white pine weevil attack incidence were assessed. Overall survival for sites ranged from 79–89%. For the combined sites ANOVA, variation in height was significant for sites, provenances, and families but site by provenance and site by family interactions were not significant. Individual and family heritabilities were 0.15 and 0.47, respectively. Differences in survival were significant for sites only. White pine weevil incidence across sites ranged from 4–28%. For the site with the highest weevil incidence, individual and family heritabilities were 0.17 and 0.43, respectively. The quadratic regression of weevil incidence on longitude of seed source was significant (r^2=0.45) with incidence of attack increasing with longitude.

Climate Change and Genetic Variation of Forest Tree Species Populations

Based on 1961-1990 climate normals, a climate model for Alberta has been developed using the method of thin-plate splining. By this method, the data from fixed-point climate stations are transformed into continuous surfaces allowing the estimation of climatic variables at any point in Alberta. As a result, questions relating to climate-tree relationships at experimental sites and sources at considerable distances from climatic stations can be addressed.

An archive containing monthly mean daily temperature, monthly mean daily maximum temperature, monthly mean daily minimum temperature, and monthly mean precipitation data has been produced. Depending upon the variable, between 1 260 to 1 433 climatic stations are represented. The splining technique was applied to these primary variables. In addition, 13 variables considered important in the distribution and response of trees to climate were derived from the primary four. The derived variables include mean temperature of the coldest month, degree-days above 5°C, and annual moisture index.

Using the model to estimate the climate at provenance origins and at experimental sites, response and climate transfer functions are being developed with provenance trial data to evaluate growth and survival responses of species and seed sources to climate and climate transfer.

With the climate model as a base, future climate was estimated from global climate models (GCM). Estimates for changes in the four primary variables were obtained from the Canadian Climate Centre

Model 2 and the Hadley Centre Model 3. The changes estimated by these GCMs were added to the current values for Alberta to produce estimated values for the decades starting in 2030, 2060 and 2090. The thin-plate splining technique was applied to these data. Five derived variables were also calculated including: mean annual temperature, mean annual precipitation, mean temperature of the coldest month, number of degree-days > 5°C and annual moisture index. Provenance trial data is being used to explore the implications of predicted climate change on conifer species and populations.

TREE GENE RESOURCES CONSERVATION

Work continued on developing a forest tree gene conservation plan for Alberta in cooperation with Alberta Parks and Protected Areas. A list of tree species native to Alberta was finalised. It recognises 29 native tree species of which five species (western red cedar (*Thuja plicata*), western hemlock (*Tsuga heterophylla*), western larch (*Larix occidentalis*), western white pine (*Pinus monticlola*), and Pacific yew (*Taxus brevifolia*) are designated to be rare species. Two species, limber pine (*Pinus flexilis*) and white bark pine (*Pinus albicaulis*), have been recognised as "*watch list*" species because of special concern regarding declining populations due to an increasing threat from white pine blister rust. The plan would address conservation of representative wild populations of all native tree species in natural subregions and seed zones based on gap analysis and risk assessment. With the implementation of STIA, gene conservation has become an integral part of forest management planning. A procedural framework for implementing these in a forest management plan for southern Alberta was developed and is to be implemented as a pilot study.

Conservation activities consisted of special seed collections of limber pine from seven populations in cooperation with the Canadian Forest Service. Several ecologically significant populations of jack-lodgepole hybrid pine were collected in cooperation with Alberta Parks and Protected Areas.

PLANT PROPAGATION, WOOD, SEED AND POLLEN TECHNOLOGY

Plant Propagation

In 2003 and 2004, stock production at ATISC included approximately 89 700 seedlings. This includes 30 900 for establishment of genetic trials, the major project being the rearing of 28 000 Siberian stone pine (*Pinus sibirica*) seedlings for a research study with the BC Ministry of Forests (BCMoF) to test for species introduction, adaptability, and resistance to white pine blister rust (*Cronartium ribicola*) in Alberta and BC Under the conservation program, 51 800 seedlings and small potted stock were reared for projects including promotional trees for National Forestry Week, Arbour Day, and Junior Forest Wardens, white spruce and lodgepole pine reforestation and reclamation plantings in Cypress Hills Provincial Park, and establishment of wild fire resistant plantings of paper birch (*Betula papyrifera*) and tamarack for the community of Fort McMurray. Rootstock production for the grafting program was approximately 7 000 seedlings.

Graft production consisted of 2 673 grafts for establishment in seed orchards and clone banks. This included 1 290 white spruce, 932 lodgepole pine, 102 black spruce, 254 jack pine, 78 interior Douglas-fir, 2 western larch, and 15 red pine.

Wood Technology

Samples from a total of 115 parent trees were received for fibre length and wood density determination including: 30 jack pine, 83 lodgepole pine and 2 white spruce.

Seed Technology

Over the report period, 665 seed lots were added to the genetics seed bank. The bulk of these (316) were the Siberian stone pine seed lots provided by BCMoF. A total of 92 seed lots were gene conservation collections of limber pine (41), alpine larch (*Larix lyallii*) (25), Rocky Mountain alpine fir (*Abies bifolia*) (21), and white bark pine (5). The majority of the remaining seed lots were single-tree collections from selected parent trees included in the various SRD/industry tree improvement programs. The major species were lodgepole pine (92), jack pine (33), and white spruce (89). Other species seed lots added to the seed bank included Ponderosa pine (*Pinus ponderosa*) (18), Scots pine (11), black spruce (4), western larch

(4), Siberian larch *(Larix sibirica*) (2), tamarack (2), Colorado blue spruce (*Picea pungens*) (1), and Douglas-fir (1). To date, the seed bank contains 5 481 seed lots.

Reference seed lots, representing 2% of the seed bank entries, have been monitored for 23 years. Average germination of lodgepole pine seed lots has remained stable. Initial average germination for the species in 1981 was 88% and in 2003, germination was 87%. Germination of white spruce seed lots has declined slightly from an initial mean germination of 92% in 1981 to 86% in 2004. Mean germination of aspen (*Populus tremuloides*), balsam poplar (*Populus balsamifera*), and plains cottonwood (*Populus deltoides*) has declined from 34–50% after 12 years of testing.

Pollen Technology

Five clonal white spruce pollen collections were completed in the Breeding Region E orchard and viability tests (electrical conductivity and germination) were completed. These collections represent the top five families for 11-year height as assessed in 2002 in the half-sib OP progeny trials.

REFORESTATION SEED PROGRAM

The Reforestation Seed Program is responsible for the registration, storage, distribution, and tracking of tree seed used for public land reforestation. At the end of the reporting period, there were 18 tree species represented in seed storage by 1 690 individual lots for a total of 41 900 kilograms of seed. During the reporting period, 2 009 kg of seed were withdrawn for seedling production, direct seeding, research projects, and quality testing and 216 new seed lots were collected and registered for public land use. An emergency generator was added to the seed storage facility to further safeguard against temperature fluctuations due to power failure.

The Standards for Tree Improvement in Alberta, implemented on May 1, 2003, cover regulations that deal with the collection, processing, testing, registration, storage, withdrawal, transportation, and deployment of all tree seed for public land use. The seed movement guideline requiring that wild seed be deployed within 80 km and ±150 m of its origin has been replaced with a seed zone system. There are presently 84 seed zones based on geographic subdivisions of the Natural Regions and subregions of Alberta.

ISABELLA POINT FORESTRY LTD.: ACTIVITIES 2002–2004

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Keywords: breeding, seed orchard, progeny, provenance, experimental design

Isabella Point Forestry Ltd. is a small consulting firm providing technical expertise in forest genetics. During the period 2002–2004 we focused on a range of activities in Alberta, British Columbia (BC) and Saskatchewan. Activities included program planning, trial design and data analysis, and seed orchard research for tree breeding programs in Alberta and Saskatchewan, and investigation of the interaction of silviculture and disease with genetics in north-central BC.

ALBERTA AND SASKATCHEWAN

Program Planning and Implementation

Working with individual companies and industrial cooperatives, we provide technical direction for tree breeding programs in lodgepole pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm.), jack pine (*P. banksiansa* Lamb.), white spruce (*Picea glauca* [Moench] Voss), black spruce (*P. mariana* [Mill.] BSP), aspen (*Populus tremuloides* Michx.), and poplar (*Populus* spp.) hybrids. Our role includes preparation and updating of detailed breeding and work plans; parent selection; orchard design; test design, layout, and data analysis; and seed orchard operational research on topics such as flower stimulation, phenology, selfing, and crown management. In hardwoods, our work also focuses on reproductive biology, vegetative propagation, and silviculture. We focus particularly on sound and flexible strategy development, ensuring a broad and appropriate program genetic base, and error control through appropriate trial design and layout.

Sally John has represented a group of forest companies as councillor on the Alberta Forest Genetic Resources Council since its inception in April 2000.

BRITISH COLUMBIA

Cross-disciplinary Research

A small project, initiated by industry through the Babine Enhanced Forest Management Pilot Project (EFMPP), and continued with funding provided by the Morice and Lakes Innovative Forest Practices Agreement (IFPA), the Forest Investment Account (FIA), and Forestry Innovation Investment Ltd. (FII), considers some possible interactions of genetics with silviculture and disease.

Does Genotypic Rank Depend on Inter-tree Spacing? This component investigates the interaction between tree espacement and genotype as it affects growth performance. If ranking of genotypes in genetics trials was found to depend on inter-tree spacing, this could influence optimum trial design. A trial involving six families of contrasting crown architecture was established in 2001 near Burns Lake, BC, using a Marynen (or plaid) factorial design, with inter-tree spacing ranging from 0.6 to 2.4 m. Preliminary results are expected by 2006.

Does Resistance to Comandra Rust Have a Genetic Basis? Through earlier assessments of a 14–15-year-old lodgepole pine (*P. contorta* Dougl.) Ministry of Forests progeny test site for comandra rust (*Cronartium comandrae* Peck.) infection, we found that variation in susceptibility to this rust has a highly significant genetic basis, and that infection rates by family ranged from 0 to 69% in the study population. Latitude, longitude, and elevation did not explain variation in resistance. However, cluster analysis succeeded in partitioning the study population into nine geographical groups in such a way that 32% of the variation in infection is attributable to the grouping. Data and results from this study have been used by BC Ministry of Forests genetics staff to identify several provenances as resistant to comandra rust.

A series of trials established on five sites in the Bulkley Valley in spring 2004 is expected to provide precise estimates of rust resistance of families produced in the Bulkley Valley seed orchard. This is expected to facilitate targeted deployment of rust-resistant stock on high-risk sites.

FOREST GENETICS AT THE FACULTY OF FORESTRY, THE UNIVERSITY OF BRITISH COLUMBIA, 2002–2004

S.N. Aitken, Y.A. El-Kassaby and K. Ritland

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GENE CONSERVATION, ECOLOGICAL GENETICS AND CLIMATE CHANGE

S.N. Aitken

In the Centre for Forest Gene Conservation, we are developing *in situ* and *ex situ* gene conservation strategies, evaluating the degree of current protection, and characterizing the genetic structure and evolutionary ecology of forest trees. Funding for most of this research comes from the Forestry Investment Account of BC through the Forest Genetics Council. Research Associate Andreas Hamann has been analyzing the extent to which B.C.'s current protected areas sustain adequate populations to maintain natural genetic variation using Geographic Information Systems and spatial analysis. Washington Gapare completed his PhD research in 2003 characterizing micro- and macro-spatial patterns of variation from core and peripheral populations of Sitka spruce (*Picea sitchensis*). He genotyped large numbers of individuals from eight populations for eight expressed sequence tagged polymorphisms to determine optimum strategies for *ex situ* sampling. PhD student Andy Bower is investigating adaptive trait variation for the threatened species whitebark pine (*Pinus albicaulis*) in a range-wide common garden experiment. He is also assessing the relationship between inbreeding and infection by the introduced fungus causing white pine blister rust. The proposed theoretical tradeoff between gene flow and adaptation in peripheral populations is being explored empirically by PhD student Makiko Mimura, using Sitka spruce as a model species. She has conducted field and growth chamber common garden experiments to quantify adaptation to local climate and is estimating gene flow using microsatellite markers and two-generation analysis. Not all of the focus is on conifers. PhD student Mohammed Iddrisu (co-supervised by K. Ritland) is investigating the mating system and effect of habitat fragmentation on bigleaf maple (*Acer macrophyllum*). Summer student Karolyn Keir has been successfully adapting microsatellite primers developed for *Cornus florida* for use with Pacific dogwood (*C. nuttallii*). We plan on using these markers for a project on mating system and genetic structure.

A strategic grant was obtained (by S.N. Aitken and A.D. Yanchuk, BC Ministry of Forests [MoF]) in 2003, funded jointly by Natural Sciences and Engineering Research Council and the BIOCAP Canada Foundation, entitled "Adapting forest gene resource management to climate change". Research Associate Tongli Wang has been predicting future productivity of lodgepole pine (*Pinus contorta*) populations under global warming scenarios and predicting the optimal redeployment of orchard seed under these scenarios using data from lodgepole pine provenance trials established by Keith Illingworth. Postdoctoral Fellow Pia Smets is characterizing the norms of reaction of seedlings from a number of these provenances under different temperature and carbon dioxide regimes. In a related project, Andreas Hamann is predicting the future distribution of current "climatic envelopes" for tree species and ecological zones under different climate change scenarios.

A new area of research initiated in 2004 is a project on the ecological genomics of cold adaptation. This association study, to be undertaken partially by MSc student Jason Holliday, will investigate nucleotide sequence variation and expression in candidate genes for cold hardiness-related traits in populations of Sitka spruce.

APPLIED FOREST GENETICS AND BIOTECHNOLOGY

Y.A. El-Kassaby

During the past two years I have been involved in a wide array of research projects nationally and internationally. Nationally, the research topics focused on molecular analyses and modeling of various components of the forest tree domestication process, while others have highlighted forest gene resources management and conservation applications for commercially and ecologically important species, including the potential impacts of climate change. This work was conducted in collaboration with scientists from the

BC MoF and Canadian Forest Service. Two graduate students completed their M.Sc. thesis projects: “Genetic diversity and population structure of the potential biocontrol agent, *Valdensinia heterodoxa*, and its host *Gaultheria shallon* (salal)” (Jennifer Wilkin) and “Genetic structure and mating system in arbutus (*Arbutus menziesii* Pursh)” (Jaclyn Beland). As a part of the forest genetics team in the Faculty of Forestry, I participated in developing the “Forest Genetics” chapter to be published in the revised version of the Forestry Handbook, a widely-distributed resource published by the UBC Forestry Undergraduate Society. Internationally, as a member of the Panel of Experts on Forest Gene Resources of the Food and Agriculture Organization of the United Nation, I drafted a proposal regarding a global survey of the status of forest biotechnology and along with a group of international forest geneticists we completed a study on the “Criteria and indicators for sustainable forest management: assessment and monitoring of genetic variation”. Additionally, issues related to seed orchard genetics are being investigated with the Tree Breeding Division, Forest Genetic Resources Department, Korea Forest Research Institute.

POPULATION GENETICS AND GENOMICS OF BC CONIFERS

K. Ritland

My major activity has been a co-principle investigator (with three others at UBC) on the Genome British Columbia Forestry project, which spans four years (April 2001–March 2005). We are developing genomics tools (ESTs, microarrays) for spruce and poplar and applying these tools to understand the genomic basis of traits relating to forest health and wood quality. Several of my students have been involved in other forestry related projects, including Lisa O’Connell (PhD 2003, “Evolution of inbreeding in western redcedar”), Yanik Burube (MSc 2003, “Microsatellite genetic structure of yellow cedar”), Hugh Wellman (MSc 2004, “Molecular breeding in western hemlock”), Mohammad Iddrisu (PhD ongoing, “Mating system and genetic structure of bigleaf maple”), Cherdsiak Liewlaksaneeyanawin (PhD ongoing, “Evolutionary genomics of lodgepole pine”), and Dilara Ally (Ph.D. ongoing, “Evolution of clonality in aspen”). I also participated in developing the “Forest Genetics” chapter of the revised Forestry Handbook (see El-Kassaby’s section).

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TREE SEED ACTIVITIES AT THE BCMOF TREE SEED CENTRE

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Keywords: cone and seed processing, stratification, gene conservation, seed testing, extension

A primary focus of my work over the past two years has been in the publication entitled “Seed Handling Guidebook” which emphasizes the Seed Handling System as a chain of events (custody) from cone collection to the sowing of seed in the nursery. The guidebook is included under references and copies are available free of charge from myself. I served as co-chair of the Canadian Tree Improvement Association (CTIA) meeting in Kelowna and have served on a variety of advisory committees. Extension efforts have focused on strengthening the Tree Seed Working Group News Bulletin and performing extension to various groups within the seed handling system. Research has focused primarily on improving the quality of our products through operational Quality Assurance (QA) monitoring.

The advancement of the concept of the Seed Handling System has been my primary focus for the past two years. This has been done by extending the concept at a variety of meetings and continuing to quantify our operational experiences with British Columbia (BC) species. Seed has been the focus, but understanding the interactions with insects and fungi are very important to increasing overall seed efficiency (from production to sowing). We continue to perform fungal assays on high priority species and continue to co-operate with the Pest Management group within Tree Improvement Branch.

SEED PRODUCTION

Priorities for operational improvement have focused on western white pine (*Pinus monticola*) due to significant differences between germination test results on lab samples and operational quantities of seed. Results are quite promising and result from the following changes: extending cold stratification to 17 weeks, targeting moisture content to 37% (34 to 40 % acceptable operational range), reducing maximum stratification unit to 750 g (vs. 3 000 g for other species), using larger bags to improve aeration, and monitoring and mixing seed within a bag on Monday, Wednesday, and Friday. The target moisture content concept (non-destructive) has been extended to our QA monitoring of all species at time of shipping and to the dryback procedure in use for Amabilis fir (*Abies amabilis*), subalpine fir (*A. lasiocarpa*), and Noble fir (*A. procera*) seed lots.

Our QA program continues to perform germination tests at time of shipping (approximately 200 requests). Requests are made to nurseries for germination and comparisons made between germination at the nursery, operational seed preparation at shipping, and laboratory testing. This program helps to identify priority areas in need of further investigation. An interesting observation was a comparison in stratification moisture content between wild and seed orchard produced crops, specifically in spruce. For both Sitka (*Picea sitchensis*) and interior spruce (*P. engelmannii* x *glauca*), a lower stratification moisture content of approximately 5% was noted for seed orchard produced crops. Fortunately no decrease in germination was noted, but I think it is important to track the differences we see in seeds obtained from these two sources. Monitoring will continue.

TESTING

During this time period a new Retest schedule was introduced. This was based on an analysis of species deterioration rates (obtained by averaging individual seed lot deterioration rates [(Current Germination Capacity – Initial Germination Capacity) / time interval]. Other factors including sample size, degree of change in estimate since 1997, number of seed lots per species, and age of seed lots also played a role in the retest frequency entered into our local database program (CONSEP). The intent is to update these estimates at 5-year intervals and future emphasis will be moving from the species level to identification of seed lots showing greater than average deterioration.

The Tree Seed Centre has been very active during this period with large improvements to the process control of many testing functions. I take very little credit for this, but it is noteworthy.

GENERAL

I have been involved in a review of QA practices at the Tree Seed Centre. It is intended to review current practices, identify excesses and gaps in our efforts, and try to fill in gaps in our understanding of conifer tree seed as part of our stewardship mandate. Priority areas for Cone and Seed Processing (CSP) include improving the standardization of cone and seed evaluation methods (i.e., cutting tests) and quantifying variability in extraction efficiency by species. Inventory Management (IM) priorities are aimed at a continuation of existing sowing request QA activities including germination and pellet content assessment of western red cedar. An additional priority is the handling, testing, and re-distribution of returned seed not sown at nurseries. Emphasis for this program is on seed orchard seed lots and especially where deficits exist (i.e., lodgepole pine (*P. contorta*)). Testing (TST) priorities include the introduction of seed weight tolerances into our information system and no longer allowing germination test results to be based on three replicates (formerly accepted by the Association of Official Seed Analysts).

My commitment to various committees and organizations has been large during the past two years: 1) Co-Chair CTIA 2004 Meeting in Kelowna (and dealing with all CTIA specific issues), 2) Chair of CTIA Tree Seed Working Group involved co-ordinating of a workshop at 2004 CTIA and spearheading the News Bulletin with Dale Simpson, 3) various Forest Genetic Council Technical Advisory Committees: Coastal, Interior, Gene Conservation, Pest Management, proposal review committees, and various species committees, 4) technical review committee for new Chief Forester’s Standards for Seed Use, and 5) member of International Seed Testing Association’s Forest Tree Seed and Shrub Committee.

It has been an eventful and exciting two year period. I’m hoping I have more of a research component to report for the next proceedings.

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BRITISH COLUMBIA MINISTRY OF FORESTS FOREST GENETICS RESEARCH AND TREE BREEDING PROGRAM

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Keywords: tree breeding, insect resistance, disease resistance, adaptation, climate change, wood quality, genecology, somatic embryogenesis

The British Columbia Ministry of Forests' (MoF) forest genetics research program still maintains a strong focus on forest genetic resource management research, policy, and tree breeding. The significant downsizing in the MoF appears to be over and we have been able to maintain a relatively strong program comprised of 32 personnel (research scientists, technicians, station staff, and administrators) at headquarters in Victoria and at our two research stations, one coastal and the other in the interior. The breeding and research program is now largely funded through 'external' funds (i.e., non-MoF vote) and planned with the assistance of the Forest Genetics Council (FGC) through the FGC business planning process. Plans are now developed annually by the tree breeders in conjunction with industry clients and focus on 10 commercial species in British Columbia (BC) in over 40 separate research and development programs. Some of these programs now also include work on hardwoods and true fir species. Research is still being carried out in the areas of insect, disease, and deer resistance, climate change, and wood quality. Work on gene conservation is largely being undertaken with an FGC sub-program on gene conservation with the Centre for Forest Gene Conservation at The University of British Columbia.

Dr. Cheng C. Ying, our well-known provenance forester and senior scientist at Research Branch, retired in 2003. For more than 20 years Cheng oversaw the enormous provenance program. Over the last few years, he initiated the genecology study of hardwoods in coastal BC and created the basis for the genetic improvement of these species. Cheng still maintains activity in the Research Branch, under the Emeritus Scientist program.

Dr. Joe Webber, our flowering physiologist at the Glyn Road Research Laboratory, Research Branch, also retired after 30 years. Joe, as many of you know, worked on many aspects of seed orchard biology, flowering enhancement, and pollen and seed orchard management. Joe is now active as a consultant and living on Saltspring Island.

TREE BREEDING

Coastal Douglas-fir (*Pseudotsuga menziesii* [Mirb] Franco var. *menziesii*)

Low-elevation Coastal Douglas-fir Controlled pollinations for advanced-generation breeding for general combining ability (GCA) and full-sib testing progressed well, with over 200 crosses completed in 2004. Series 1 subline tests, planted in 1999 for third-generation seed orchard selections, were maintained and measured (height at 5 years). Series 2 subline tests (planted in 2003), also containing eight sublines, were weeded and fertilized. Realized gain trials, planted in 1996, were brushed.

High-elevation Douglas-fir The high-elevation Canfor Douglas-fir seed orchard (> 700 m), at Sechelt, is being progeny tested at two test sites on Northern Vancouver Island (Mt. Cain and Sutton Creek) and age 5 heights were used to rogue from below (20%). Breeding values, calculated based on year 7 heights measured in 2004, will also be used for additional roguing, with final selections to be made based on age 12 measurements. Breeding values, adjusted for selection at age 7 and forecast to rotation age 60 for the top 30 clones, range from 2 to 10, based on best linear projection (BLP) calculations. As the age-age correlation increases, these values will increase correspondingly.

Sub-Maritime (Transition Zone) Douglas-fir The newly established clonal seed orchard 181 at Puckle Road (Saanich) will be progeny tested using a polycross (GCA) test. For this purpose, all clones in the orchard were control-pollinated in the spring of 2003 using a polymix made of submaritime pollen (and some high-elevation coastal pollen). Of 94 parent trees in the orchard, seed was obtained from 91 and sowed for the production of test stock at Cowichan Lake Research Station. Progeny tests will be established in the spring of 2005 at three sites in the transition zone at elevations above 800 m.

Interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca [Beissn.] Franco*)

Controlled crossing in the Interior Douglas-fir program is focusing on the low-elevation Nelson seed-planning unit (SPU). This new zone is largely the result of merging the old Shuswap-Adams, Mica, and West Kootenay low-elevation zones. In 2003, a total of 171 crosses were completed in the Nelson zone and 188 were completed in lower priority zones. Approximately 200 pollen lots were collected, processed, and stored for future breeding.

Five, 15-year-old progeny test sites and two 20-year-old sites in the old Mica and Cariboo Transition zones, respectively, were maintained and measured. Data analyses for these sites are on-going. Determination of wood relative density was completed for the Mica Revelstoke Dam. Three, 10-year-old research sites from the Douglas-fir elevation transect study were maintained and measured.

The pilot *Armillaria* root disease resistance-screening project is now three years old and is near completion. This joint Canadian Forest Service (CFS)/MoF project uses artificial inoculation to screen 88 open-pollinated families of Interior Douglas-fir. To date, family mortality attributed to *Armillaria* ranges from 0 to 82%, so the results are extremely encouraging.

Interior Spruce (*Picea glauca x engelmannii*)

Interior spruce tree improvement began in the mid-1960s and has progressed to the point where much of the current spruce planting stock (over 75 million seedlings per year) originates from rogued first-generation seed orchards. Second-generation full-sib progeny tests are also in place for three seed planning units (SPUs). Over the years, refinement of interior spruce SPUs continued as relevant new information became available from genetic tests. Today, six large SPUs are in place, and selection, breeding, and testing activities are on-going in each unit.

Thirty-three (30 Thompson Okanagan and three Prince George) pollen lots were collected, processed, and stored for future crossing. Thirty-five crosses were completed in the new expanded Prince George (PG) zone. Controlled crossing for the PG zone is now 98% complete and we look to establish new second-generation progeny tests in 2006. Six, 20-year-old progeny test sites in the old Quesnel Lake, Finlay, and Bulkley Valley (BV) seed zones were maintained and measured, and four, five-year-old sites in the Fort Nelson zone were maintained. Eight, second-generation sites in the PG, BV, and East Kootenay SPUs were maintained.

The Shuswap Adams polycross test at the Skimikin Seed Orchard, which was augmented with cage-reared leader weevils in fall 2002, was evaluated for leader damage. When evaluation was completed, the site was clear-felled and wood disks were collected from each family to determine the relative density of the wood. In June 2003, spruce leaders containing weevil eggs were collected near Vernon and more than 10 000 weevils were reared in cages at CFS's Pacific Forestry Centre, Victoria. In early fall, adult weevils were released in the Thompson Okanagan Series I polycross test at Skimikin. Plantation damage assessment will commence in summer 2004.

Three spruce provenance tests (Quick, Verdun, and Bowes Ck.), that were established in the mid-1960s, were maintained, pruned, and relabelled. These tests represent the oldest interior spruce plantings with genetic structure in BC. Two, 10-year-old realized gain tests, in the old Hudson Hope zone, were maintained and measured. In these tests, the superior seed lots were 17% taller and had 15% greater survival than the composite wild stand seed lot. Six field plantings of somatic emblings were maintained and measured.

A new genecology study was established in the new PG SPU to: 1) further refine seed zone boundaries and seed transfer rules, 2) characterize growth and physiological differences between PG class A and wild stand seed lots, and 3) confirm weighting coefficients used for estimating breeding value. One raised bed site was established for intensive study at the Kalamalka Forestry Centre and three wild sites were established in the Prince George area.

Western Larch (*Larix occidentalis* Nutt)

This program was initiated in 1987 and has advanced very rapidly. To date, 609 parent trees have been selected and 607 wind-pollinated families have been established in progeny tests across 14 sites. The oldest of these progeny tests is 13 years old. Two grafted seed orchards were established in 1990 and are now in full production. Presently, over 70% of the 6.5 million western larch seedlings planted annually in BC originate from seed orchards. Second-generation controlled crossing is over 40% complete and three realized gain field tests will be planted in spring 2004. In 2003, 82 controlled crosses were completed and about 160 pollen lots were collected, processed, and stored for future crossing. One progeny test site (EK Semlin Ck.) was thinned and wood disks were collected for relative density determination.

Western Redcedar (*Thuja plicata* Donn ex. D. Don)

Breeding for first-generation polycross testing, involving just under 1 000 parents for the Maritime Low SPU, is complete. To date, six annual series of tests have been established totaling 39 sites. The last series will be established in spring 2005. Breeding values for volume at rotation are currently available for series 1 based on seven-year heights (150 parents), and series 2 and 3 based on five-year heights (248 parents). Approximately 50 parents from the first three series have been selected for advanced generation and established into breeding orchards. Information on the durability of the parents in the first three series is currently being developed. Sixty within-family selections for high needle monoterpene concentration/deer resistance were made at the Holt Creek (southern Vancouver Island) family/population study. These selections will be bred using a combination of selfing and outcrossing, and resultant progeny will be screened for monoterpene concentration and deer resistance. Both backward and forward selections can then be incorporated into a deer-resistant production population.

Yellow-cedar (*Chamaecyparis nootkatensis* [D. Don] Spach)

First-generation cloned progeny tests have been established and the focus is currently on maintenance and measurements. The first two series of trials were measured at five years in the field and clonal values from 3 000 clones were released. The third series will be measured in 2005. Advanced generation selections from the Western Forest Products clonal program and from MoF genetic trials have been established in three breeding orchards, including one high-elevation site. Maintenance continued in 2004 in these orchards, as well as monitoring of the performance and production of pollen for collection for advanced generation breeding.

Various technical support projects were maintained and measured. These include clonal maturation, clonal competition, pollen viability, and deer resistance studies. Provenance trials were also maintained. Analyses of 10-year data from interior population test sites revealed responses similar to those on coastal sites; significant population variation for growth with no discernible adaptive responses. Survival was high, with little evidence of cold-related damage for all populations except northern California. Breeding continued for a deer resistance heritability study.

Western Hemlock (*Tsuga heterophylla* [Raf.] Sarg.)

Low-Elevation Maritime The primary focus of the program at this point is advanced generation breeding. Data for height at age five have been collected from 11 trials and preliminary analysis has been performed. A full-scale formal report is awaiting further results, that are due in fall 2004, from nine trials established by American co-operators. Over 100 forward selections have been made and propagated but are being used for studies of methodologies for breeding juvenile material while confirmation from the later round of testing is awaited. Early results suggest that, to a large degree, our whole co-operative can be treated as one breeding zone with some Oregon parents performing well even on harsher test sites.

A secondary aspect of the hemlock forest genetics program involves provenance studies. Although tested parents from the breeding program are generally deployed in areas where they have been tested, smaller trials with a wider representation of plants from across the species' range are valuable for establishing the limits of safe transfer. As well, areas not warranting investment in a breeding program still need rules for transferring wild stand collected seed. Height at age five data were collected from three sites in the autumn of 2003 and a further five sites will be measured in 2004. As well, age ten results from eight tests were reported at a Western Forest Genetics Association meeting in Whistler, BC in July 2003.

At the same meeting, research was reported supporting hemlock's resistance to dwarf mistletoe. Trees from ten provenances were infected with the parasitic plant. No significant variation by provenance or family was noted, although one provenance clearly had half the rate of successful attack of the others.

Similarly, there was a wide range of response by family, but analysis suggests that these results might not be repeatable, probably because too few replications were used to detect the effect and so it could not be confirmed. The inoculations and scoring of the progress of infection was in the hands of forest health specialist Dr. Simon Shamoun of the CFS and two of his graduate students, Sue Askew and Lea Reitman.

High-Elevation Maritime Hemlock The high-elevation breeding program covers maritime hemlock regeneration from 600 m elevation to the transition to mountain hemlock. A last round of first-generation testing has just been sown which will bring the number of high-elevation selections tested to about 325. Ten-year-old data for height and diameters are expected for 91 parents with revised breeding values for these to follow by April 2004. Projected volume gains of selected available seed lots should rise from around 6% currently to over 10% with these results.

Second-Generation Family Testing of Lodgepole Pine (*Pinus contorta* Dougl. ex Loud. var. *latifolia* Engelm.)

The intercrossing of tested/selected first-generation lodgepole pine parent trees for second-generation family testing is complete for all five SPUs (low-elevations PG, BV, TO, NE, and CP). Factorial crossing sets comprise subpopulations bred for stem volume growth rate and wood relative density for each SPU (130 full-sib families per SPU). In 2002, the PG test series was planted. In 2004, the BV series will be planted, and the TO and NE series will be sown/grown for planting in 2005. The last test series, the CP, will be planted in 2006.

In addition to the BV SPU test series grown, lifted, and packaged in 2003, research trial planting stock for three trials was grown, lifted, and packaged for planting in 2004. These included the Comandra Rust Screening Trial for the Vernon Seed Orchard Company and two provenance screening trials, one each by Weyerhauser Co. and West Fraser Ltd. The fall 2003 lift and tagging for these four trials set a record for the pine team in that 83 000 test seedlings were lifted, of which 63 000 were individually tagged. A job well done by Future Forest Services Ltd. of Vernon.

Lodgepole Pine "Forward " Selections for Expanding Seed Orchard Production

The planting of lodgepole pine throughout the BC interior has greatly increased beginning in the early 1990s. Today, 90 million seedlings are planted annually. Our first-generation tested seed orchards were designed to meet earlier seedling needs. Regrafting to expand orchard seed production capacity began in 1996. Since then, more than 60 000 grafts have been made and several new orchards have been planted to meet approximately two-thirds of the total seed needs. The majority of parents grafted in this expansion effort have come from first-generation progeny test family arrays aged 15–18 years from seed, so called "forward " selections. These superior trees were identified using a two-step process. First, Dr. Chang-Yi Xie from the MoF Research Branch in Victoria took the ten-year measurement data sets and developed a selection index score for every tree in each particular test series (30 000 trees per test series). Each tree's final score or BV depends on the relative superiority of its family compared to other test families and its own superiority within the family (compared to its sibs). Site means, block means, and plot means are also estimated and are used to adjust individual tree scores (BVs). The analysis product is a listing of the top 500 BV-ranked trees across the sites in a particular test series. The second step was to visit one or more sites with the ranking list and examine trees in descending rank order. Tree height at age ten years is only one criterion used for tree selection. Height and diameter growth rates sometimes change with competitive interactions after age ten. Also, stem form and branching habits have significant impacts on log/wood values and can be assessed at ages 15–18 years. So, in addition to current tree height, stem diameter and form, branching characteristics including branch numbers, diameters, lengths, and stem growth cyclicity (monocyclic vs. polycyclic internodes) are all considered in selecting seed orchard parent trees. With this, the final year of forward selection, over 400 progeny test trees will have been selected and grafted (60–80 ramets each). Overall organization and direction of seed orchard expansion projects has been the responsibility of Select Seed Company (a corporation owned by the BC Forest Genetics Society, and reporting to the Forest Genetics Council).

Sitka Spruce (*Picea sitchensis* [Bong.] Carriere)

Activities in 2004 included establishment of the first phase of the F1 breeding program. Parents were designated by their resistance to the spruce weevil (*Pissodes strobi*) and their source (mainly Haney or Big Qualicum). Some susceptible parents were also used for inheritance studies. The trials have been established in the Adam's River drainage, North Vancouver Island and at Jordan River, South Vancouver Island. We have another site that we hope to establish on the Queen Charlotte Islands in spring 2005.

Breeding to establish future series is continuing. The F1s will replace the clones and families in our research efforts to understand the mechanisms behind resistance.

Parent trees have been screened for a more detailed investigation of resistance mechanisms. All of these have been field assessed for resistance to weevil attack after weevil augmentation, but a more detailed microscopic evaluation is being attempted in order to classify according to putative mechanism. This is particularly valuable for "constitutive" type of mechanisms such as sclereid cells or constitutive resin cells and we are working to extend these techniques to look at some of the "inducible" mechanisms, particularly traumatic resin cell production.

On-going trial assessments for weevil attack have continued. These have included some of the hazard assessment trials. The hazard assessments were a series of trials established to test resistance over a variety of ecological and potential weevil-hazard areas. The main objective is to aid in determining deployment guidelines. Some of these guidelines were assessed in previous years to investigate elevational and latitudinal transfer of weevil-resistant sources. To further this objective, we have sowed a small series of high-elevation selections in 2004, along with some resistant sib lots to be established in 2005.

Good progress has been made on the first draft of a report outlining the weevil resistance program. This report will present many of the details of the program, an outline of our scoring system for resistance, and a ranking of all our parents to date. The report will also present deployment guidelines for resistant material. In addition to last year's book chapters, we have published an article in the Journal of Forestry entitled: "Genetic resistance of Sitka spruce (*Picea sitchensis*) populations to the white pine weevil (*Pissodes strobi*): distribution of resistance."

Coastal White Pine (*Pinus monticola* Dougl. ex D.Don)

In 2004, we sowed and grew the first phase of the F1 breeding program. Parents for this effort came from the CFS screening program and were designated as either slow canker growth (SCG) or difficult to infect (DI). SCG or "slow-rusting" trees occur more frequently than DI. Also included as parents were some of the best of the Texada trees and some Idaho, Interior, and Dorena trees. We are identifying several sites to establish these trials and are looking at sites on Texada Island and near Sechelt.

We collected several more scions from the CFS screening list — two from Texada Island and a few from Vancouver Island, and several of the major gene resistance (MGR) trees. Much of this was to make up for the grafts made the previous year that did not survive. Grafting this year was done for us at Kalamalka Forestry Centre and grafts will be established in the North Arm clonal archive, Cowichan Lake seed orchards, and a newly established breeding orchard at Puckle Road (Saanich).

In September 2003, we toured the Interior provenance trials established by Rich Hunt (Root Rot Series) and Mike Meagher (Provenance Series) in the 1980's. We looked particularly at the Dorena MGR seed lots to see how well they held up in the Interior and, overall, they did not appear too bad. We are now in the process of measuring all these trials. These measurements will help us to evaluate the resistance of these sources and assess their transferability across the province. We are also currently doing a first assessment of the full-sib block trial initiated by Patti Brown, of Canadian Forest Products Ltd. This trial allows the comparison, in field conditions, of various CFS selections such as "low spotters", and "slow rusting" against Dorena and wild unselected lots. Although the data are still being gathered, some preliminary results are very encouraging. Some of the wild unselected blocks are 90%infected, whereas some of the Dorena x Dorena and Dorena X SCG are only 5%infected.

Our paper entitled “The five needle pines in British Columbia, Canada: Past, present and future ” by J. King and R. Hunt was published as a special USDA Forest Service Research Report, and a chapter for a special edition of the Journal of Forest Ecology and Management entitled “Genetic approaches to the management of blister rust in white pines” is well underway.

Queen Charlotte and Coast/Interior Transition Spruce

The Queen Charlotte program allows us to assess Sitka spruce growth free from weevil attack and supports the seed orchard program (SO 142 and its replacement). Our major difficulty has been in getting “free-to-grow” conditions, in this case not free from weevil or brush but from deer browse, and a good deal of our maintenance effort is on browse protection. In 2004, we spent a good deal of time cleaning up, tagging, and removing browse protection from the trials we established there. During fall of 2004, we hope to do a major measurement of our Queen Charlotte Islands sites. The transition program is designed mainly to test seed transferability in a very environmentally heterogeneous area with pressures from both frost and weevil. In the past year most of the activities for this program have concentrated on routine site maintenance, although a small weevil-resistance plot was established in the Bish River area near Kitimat. A series of measurements and assessments are planned for this summer.

FOREST GENETICS AND SEED TRANSFER RESEARCH

The Role of Site, Genotype and Seed Transfer on Branching and Wood Quality in Lodgepole Pine

Progeny test data from nine populations were used to examine the relationships of site climate, seed source climate, and transfer distance climate with branching and wood quality traits. A manuscript is in preparation.

Potential Genetic Gain Using Somatic Embryogenesis of Interior Spruce

Age 7 height of seedlings and 313 embling lines from 11 families was compared. Genetic gain was estimated for mass clonal selection and clone within-family selection, and compared with gain expected from seed orchards. A manuscript has been submitted for review.

Climate-Based Site-Specific Seed Transfer to Maximize Productivity

Age 20 lodgepole pine tree volume and survival data from 140 populations tested at 60 test sites were used to estimate the climate of the optimum and acceptable ranges of seed sources for regeneration. Presentations were made to compliance and enforcement officers in the MoF, for consideration of penalties to excessive seed transfer in BC. These data and supporting documents will be used to support the new Chief Forester Standards on Seed Use in BC.

Potential New Distributions of Lodgepole Pine Populations in BC

Ranges of climate variables of lodgepole pine populations were determined and mapped spatially. Layers of each variable were overlaid on each other to identify and map the location of climates of distinct individual populations (‘climatypes’). Data from global circulation models were used to map the shift in the location of those climates in BC in 2025, 2055, and 2085 to illustrate where climates of current lodgepole pine populations will be found in the future. At this point, these simulations are being used for internal discussion on what the next steps may be for seed transfer under various climate change scenarios.

Genecology of Interior Spruce

Interior spruce seedlings from 141 wild stands and 9 seed orchards were planted in spring 2003 at three field sites in central BC and one nursery bed in Vernon, BC, to examine the species’ geographic distribution of genetic variation. Results will be used to refine wild stand and seed orchard seed transfer for current and future climates and to help standardize breeding values of elite genotypes from disparate breeding programs.

Field Test Designs

As follow-up work on the use of incomplete block designs for genetic testing for parental selection (e.g., Fu, Y.B. et al. 2000. For. Gen. 7:287–293), we have also initiated a study to examine the most efficient field designs for forward selections. Complementary designs were not investigated as we are no longer considering them in most of our programs.

Population Structure With Negative Genetic Correlations

Dr. Leopoldo Sanchez, from INRA, Orleans, France spent two months with us in 2003 to further develop our breeding strategies in relation to population size and structure when there may be a negative genetic correlation. Collaborative work with Dr. Sanchez is continuing and we hope to further refine our breeding approaches with the use of his model and address some important questions with respect to optimum selection strategies currently being considered in animal breeding.

Forest Genetics and Biotechnology

We continue to be actively involved in various stakeholder group meetings, as well as in collaborative policy development programs related to the use of various biotechnologies in forestry. Alvin Yanchuk participated in the CFS workshop on Environmental Safety in Montebello, Québec, and spent six weeks at FAO, Rome to assist with various projects related to the status of biotechnology in forestry and additional writing projects on gene conservation.

Genetic Improvement of Hardwood Species in Coastal British Columbia

Utilization and management of hardwood resources in the coastal region of BC received considerable attention in the 1990s. This attention focussed on the management of three hardwood species with commercial potential, namely red alder (*Alnus rubra* Bong.), bigleaf maple (*Acer macrophyllum* Pursh), and black cottonwood (*Populus trichocarpa* Torr. & Gray). One consensus derived from problem analyses then was the major knowledge gap on the lack of genetic information on variation of adaptive and commercially important traits that would hinder the effective management of these species. Against this backdrop, genetic research was initiated in the mid-1990s.

Red alder and bigleaf maple, because of their high wood quality, have potential for value-added products such as furniture manufacture. One problem with these species is the difficulty in finding quality logs (large diameter with good stem form) in natural stands. Long-term provenance-progeny testing was initiated in 1995 for red alder and in 1997 for bigleaf maple with the objectives: 1) establishing seed transfer guidelines for selection of productive seed sources for planting and 2) evaluating the potential to grow better quality logs in plantation settings. A breeding strategy will be developed for red alder based on 10-year test results that will be assessed the fall of 2004 and selection will start spring 2005.

Black cottonwood is the only native poplar species with the potential of short-rotation (less than 10 years) fibre production through clonal forestry. The outstanding yield (mean annual increment > 30 m^3/ha/yr) of the selected black x eastern cottonwood (*P. deltoides*) hybrid clones in Oregon and Washington demonstrated this potential. However, most of these hybrid clones developed in the United States were not hardy when planted at sites on BC's mid- and north-coast. A short-term common garden study of black cottonwood with about 800 clones from 170 provenances has been completed. Three long-term provenance-clonal tests located in three geographic regions, namely south-coast, north-coast, and interior, will be established spring 2005.

MOLECULAR GENETICS PROJECTS

Determination of Selfing Rate in a Top-Pruned Interior Spruce Seed Orchard

In the past, seed orchards have routinely been top-pruned to facilitate easier and safer orchard management. This practice, however, brings male and female cones closer together, potentially increasing the chance of selfing, which in turn may reduce seed set and reduce progeny vigour. DNA markers are available to test for increased selfing in these top-pruned orchard ramets.

Before candidate clones are identified for study, orchard clones must be genotyped. For this purpose, total DNA was extracted from vegetative buds of each producing clone (78 clones in total) in interior spruce orchard 305. Several chloroplast DNA (cpDNA) markers were applied using the PCR technique to screen for unique clones, ones that are unambiguously identifiable among all orchard clones. These easy to score clones have been chosen for further study in 2004.

The results of the genotyping revealed that, with two primer pairs only, 12 out of the 78 trees in the orchard can be unambiguously identified (Table 1). Marker S2spF/R is, especially, extremely variable, yielding 14 alleles (different bands) alone. However, as some of the clones in orchard 305 are too small to conduct pollinations on or have been subsequently culled, genotyping was intensified using all 5 available polymorphic markers. The separation power increased so that 18 clones can be identified using 5 primer pairs (Table 2). This array of available clones will be used to make final selections for further study based on the expected cone crop of these clones in year 2004.

Table 1. Unique genotypes of interior spruce clones growing in Kalamalka Orchard # 305 identifiable using 2 genetic markers.

Primer S2spF/R	Pairs 89F/62R	No. Clones	Clone ID
A	b	1	575
B	b	1	3079
C	c	1	3180
E	d	1	1289
F	b	1	692
G	d	1	3243
H	d	1	3146
J	d	1	1299
K	a	1	3004
L	c	1	661
N	d	1	3254
O	d	1	2005

Table 2. Unique genotypes of interior spruce clones growing in Kalamalka Orchard # 305 identifiable using 5 genetic markers.

S2spF/R	89F/62R	84.1F/R	8F/8R3	7RR/7F3	No. Clones	Clone ID
a	b	d	b	b	1	575
b	b	d	d		1	3079
c	c	d	b		1	3180
d	c	d	bc	b	1	3173
e	c	d	b	a	1	3263
e	d	d	b	b	1	1289
f	b	d	b	b	1	692
g	d	d	b	b	1	3243
h	b	d	c	b	1	1364
h	b		b	b	1	2008
h	d		b		1	3146
j	c	d			1	2702
j	c	e	b	a	1	3324
j	d	d	b	c	1	1299
k	a	d	c		1	3004
l	c	c	c	a	1	661
n	d	d	b		1	3254
o	d		b		1	2005

Determination of Selfing in a Clonal-Row Spruce Orchard

In the past, seed orchards needed to be licensed to ensure that orchard management plans and orchard composition was up to standard. A seed orchard license was a pre-requisite for seed lot registration. This licensing requirement no longer exists and more emphasis is placed on the seed lot rating protocol. However, in an orchard with a new and innovative design, mating dynamics should be checked to ensure they conform to expectations. One type of orchard with a new and innovative design is a clonal-row orchard, where many ramets of the same clone are planted in a row at relatively close spacing. This type of orchard will make orchard management more efficient, as all ramets of a single clone are in close proximity for surveys, pollinations, cone harvesting, and other orchard management activities. However, this arrangement may also increase selfing levels as many “closest-neighbour” trees are genetically identical and will have very similar flowering phenologies, (receptivity and pollen shed). Clearly, before seed lots from this type of orchard are registered, it is prudent to evaluate selfing as increased levels of selfing in a seed lot large enough to raise 2.2 million seedlings per year may have serious implications. Not only will seed set be lowered, but also the vigour of the resulting seedlings is compromised.

Paternal analyses of seed from ten easily identifiable clones was conducted. For this purpose, all 30 clones of orchard 620 were genotyped using polymorphic chloroplast DNA (cpDNA) markers. Briefly, for genotyping, total DNA was extracted from all clones using vegetative buds. Potentially polymorphic sections of cpDNA were amplified using PCR and compared among the 30 clones. Ten clones with a unique multi-locus genotype pattern were chosen for further analysis. From the ten selected clones, a clonal bulk sample of seeds was collected and their embryos were analyzed individually to see if they have the same cpDNA pattern as their maternal parent (seed trees). The identical pattern in the embryo indicates a selfed seed, as cpDNA is carried by the male gamete only. A total of 50 seeds per clone were assayed for a total of 500 seeds.

Based on the 10 sample clones, there was no evidence that there is an overall increased level of selfing in this particular clonal-row orchard. Individual selfing on a clonal basis ranged from 0 to 14% with an average of 4.4%. Results for the sample clones are listed in Table 3. It is important to realize that these selfing levels are unambiguous as only unique orchard clones were selected for this study.

Table 3. Levels of natural selfing in 10 clones of a clonal-row spruce orchard # 620 at Kalamalka

Clone	Selfed seed	Total seed	Percent selfed seed
311	5	50	10
381	4	50	8
339	0	50	0
386	7	50	14
408	3	50	6
447	0	50	0
422	0	50	0
377	0	50	0
410	0	50	0
419	3	50	6
Average			4.4

PROCEEDINGS

OF THE

TWENTY-NINTH MEETING

OF THE

CANADIAN TREE IMPROVEMENT ASSOCIATION

PART 2

Symposium

CLIMATE CHANGE AND FOREST GENETICS

Kelowna, British Columbia
July 26–29, 2004

Editors
G.A. O'Neill and J.D. Simpson

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Kelowna, Colombie-Britannique
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Rédacteurs
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INVITED SYMPOSIA PAPERS

IMPACTS OF CLIMATE CHANGE ON POPULATIONS AND SPECIES DISTRIBUTIONS

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Concern about the current climate change is increasing. Ecological (Parmesan and Yohe 2003, Root et al. 2003, Walther et al. 2001) and socio-economic (Keeney and McDaniels 2001, Michaelis 1994, Yohe and Schlesinger 2002) impacts are more and more perceptible. Many studies have already shown that climate change is significantly affecting species development timing (Menzel and Fabian 1999, Parmesan and Yohe 2003, Walther et al. 2001), physiology (Cannell et al. 1998, Hughes 2000, Keeling et al. 1996, Myneni et al. 1997), competition (Hughes 2000), and geographical ranges (Parmesan et al. 1999, Parmesan and Yohe, 2003, Walther et al. 2002). These changes will have major consequences on biodiversity, silviculture, and agriculture (Jingyun et al. 2001, Nicholis 1997). It thus becomes urgent to develop predictive models to draw a picture of species distribution and ecosystem (managed or natural) functioning changes. Forestry should certainly be among the first human activity concerned with such changes, and there are going to be long-term consequences as well as short-term consequences of climate change on trees. The short-term consequences will mainly concern phenology and frost damage. Climate warming mainly advances leaf unfolding and flowering, such that they occur during a period when frost events are more likely (Hänninen 1991, Kramer 1994, Linkosalo et al. 2000). Another short-term consequence of phenology change will be an asynchrony between the phenology of trees and parasites (Bale et al. 2002, Dewar and Watt 1992, Fleming and Candau 1998, Fleming and Volney 1995, Hodar and Zamora 2004).

These short-term consequences will however probably be at low expense compared to the long-term ones, which will concern the distribution of the climatic niche of the species. If the changes observed during the 20th century continue and amplify we could see in a few decades the improvement of the regeneration of the northern range limit of some populations, but at the same time the loss of regeneration of the southern range of populations. How far north species distributions could move within this century is a question of major importance especially in North America where the exploitation of northern latitude timber could be valuable.

To investigate all these questions, we need species distribution models. There are two main kinds of models that are currently used to forecast species' distribution under climate change scenarios: process-based models and so-called niche-based models which are statistical models.

Process-based models simulate biological processes in response to environmental changes using mathematical equations. These equations are derived from experimental results that provide cues to understand how these processes are affected by the environment. Such models have a high predictive power and explanatory power and are particularly robust. The reason for this is that the model parameters are fitted on observations done in natural populations or during experiments of the processes described in the model. They are not fitted on the species present distribution. The main drawbacks of such models are that they require a long phase of development and lots of information on the response of adaptive traits to environment for each species.

Niche-based models either deal with the distribution of species or ecosystems and they statistically relate the presence or absence of the species to environmental variables. This is the principle of the climatic envelope. Such models can be quickly developed as they require the digitized distribution of a species and corresponding environmental information prevailing within and outside the distribution. They can thus be developed for any species providing its distribution is known. One of the main drawbacks of such models is that their robustness is difficult to assess because they use the species' present distribution to fit the parameters and cannot be tested in true external conditions. The use of half of the distribution chosen randomly to fit the model and the other half to validate it does not provide a robust validation as both datasets are highly auto-correlated. However, the use of one continuous part of the distribution to fit and the rest to validate does not provide an accurate model fit either. Validation is therefore an important problem for niche-based models, which is currently driving most attention (Thuiller 2003, 2004). Although niche-based models have good predictive power, they also provide very few insights to understand which key adaptive traits and environmental variables interplay to shape species distribution.

In this paper we use the predictions of temperate tree species' distribution change using a niche-based model, BIOMOD (Thuiller 2003, 2004), and a process-based model, PHENOFIT (Chuine and Beaubien 2001) to draw some conclusions on the impact of climate change.

The simulations of BIOMOD concern European timber trees and they do not take into account effective migration rate and survival rate of the species. They provide a predicted distribution of the climatic envelope of the species. The simulations use the Hadley Center climate model HadCM3 output and two IPCC scenarios, A1Fi which are consumerist individualist scenarios leading to a global mean increase in temperature of 4.5°C by 2100 in Europe and B2 which is a conservationist, communitarian scenario leading to a global mean increase of temperature of 2.5°C in Europe. The simulations of PHENOFIT concern North American timber trees and they do take the migration rate and survival rate of the species into account. The simulations also use the Hadley Center climate model HadCM3 output and two IPCC scenarios, A2 which is consumerist, individualist scenarios leading to a global mean temperature increase of 5.0°C by 2100 in North America and B2 which is a conservationist, communitarian scenario leading to a global mean increase of temperature of 2.2°C in North America.

The response of the species to climate change could be classified into three categories. The first category comprises species whose distribution will be relatively unaffected by climate change. Few of the species studied pertain to this category: common oak (*Quercus robur*) and sessile oak (*Quercus petraea*). Common oak is the least affected species overall. Its sister species, sessile oak, is a little bit more affected, especially in scenario A1Fi in which it disappears from an important part of its present distribution (Fig. 1).

The second category of species comprises species whose distribution will be significantly affected by climate change. This category principally concerns temperate and boreal trees, such as Scots pine (*Pinus sylvestris*) and Norway spruce (*Picea abies*) in Europe and lodgepole pine (*Pinus contorta*) and quaking aspen (*Populus tremuloides*) in North America. These species' distributions should contract substantially with climate change, especially in the A1Fi or A2 scenarios (Fig. 2), with migration northward being limited by the sea. The differences between the two scenarios were small.

The third category comprises species whose distribution will be very much affected by climate change and this is mainly Mediterranean and Temperate species such as European larch (*Larix decidua*) and silver fir (*Abies alba*), European black pine (*Pinus nigra*) and maritime pine (*Pinus pinaster*), sugar maple (*Acer saccharum*), and western white pine (*Pinus monticola*). These species should disappear from most of their present distributions (Fig. 3). In Europe, the new colonisable areas may be for some species disconnected from the present ones (*Pinus nigra*, *Pinus pinaster*) (Fig. 4).

These results are in agreement with those of Iverson and Prasad (1998). Using a niche-based model for United States to predict the distribution of 80 species using the Goddard Institute of Space Studies climate model for a doubled level of atmospheric CO_2, they show that species distributions will also shift northward substantially. In their study, *Populus tremuloides* and *Acer saccharum* are among the most affected species by climate change with *Populus grandidentata*, *Abies balsamea*, *Betula papyrifera*, *Pinus resinosa*, and *Thuja occidentalis* also severely impacted. One of the main conclusions of this presentation is that models, either niche-based or process-based, are in agreement. However, only process-based models provide insights to understand species distribution changes.

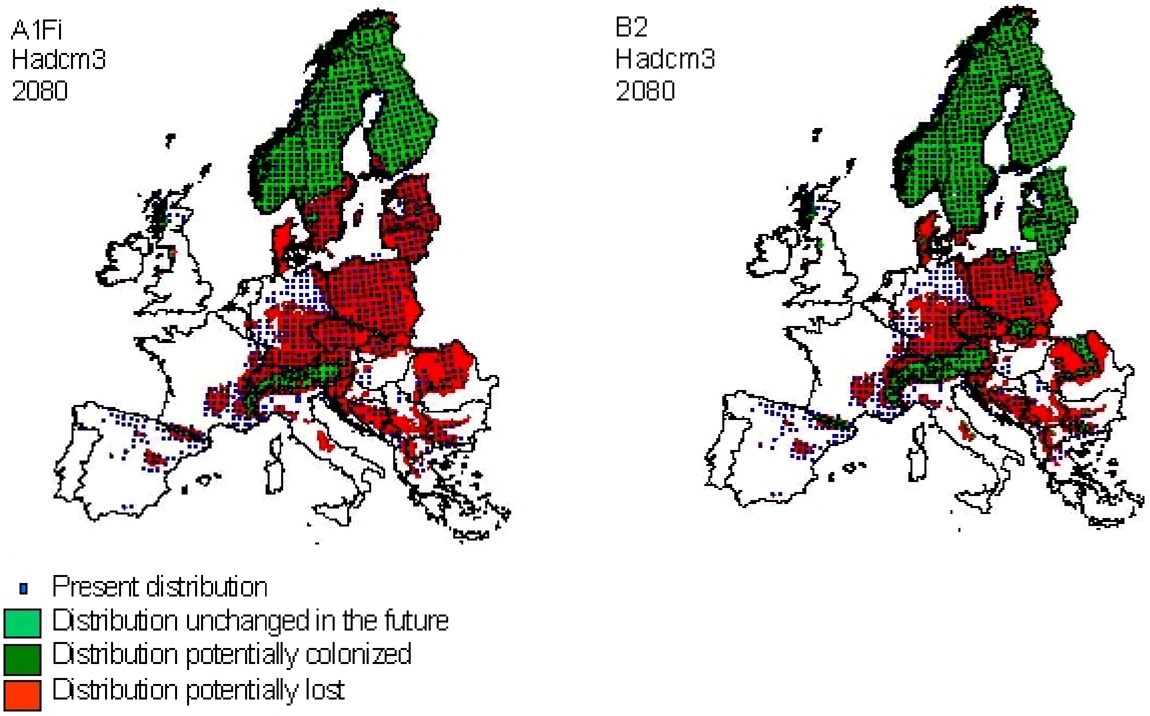

Figure 1. Predicted potential distribution of *Quercus robur*.

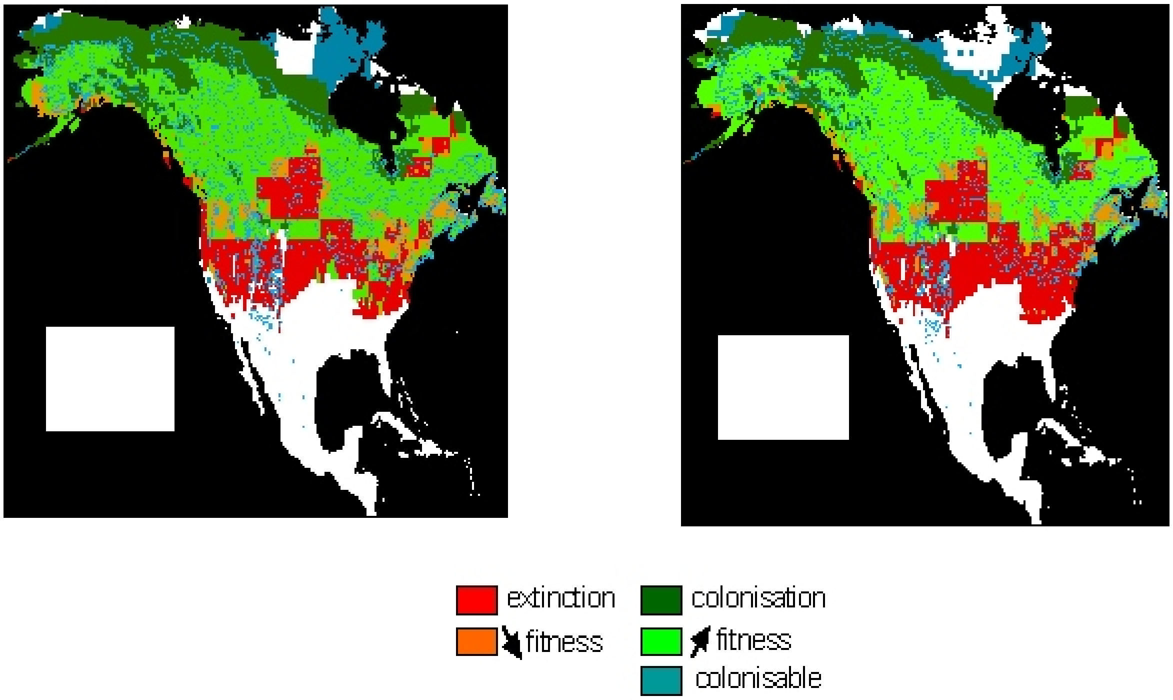

Figure 2. Predicted potential distribution of *Populus tremuloides*.

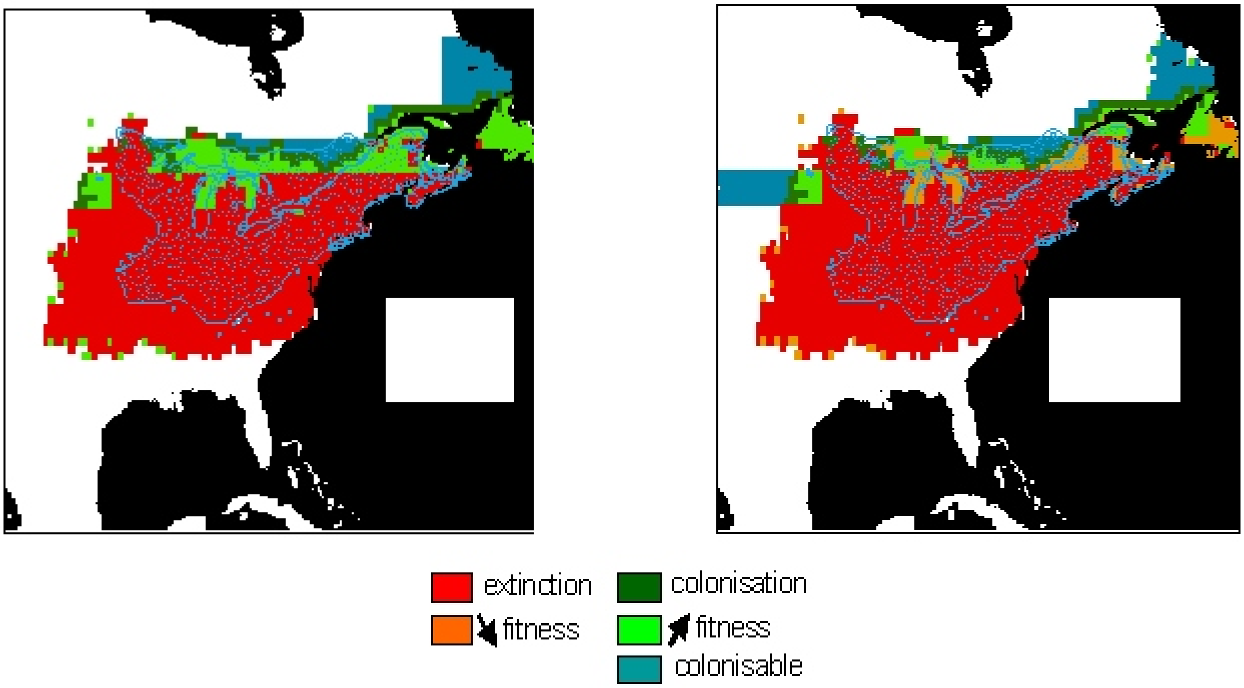

Figure 3. Predicted potential distribution of *Acer saccharum*.

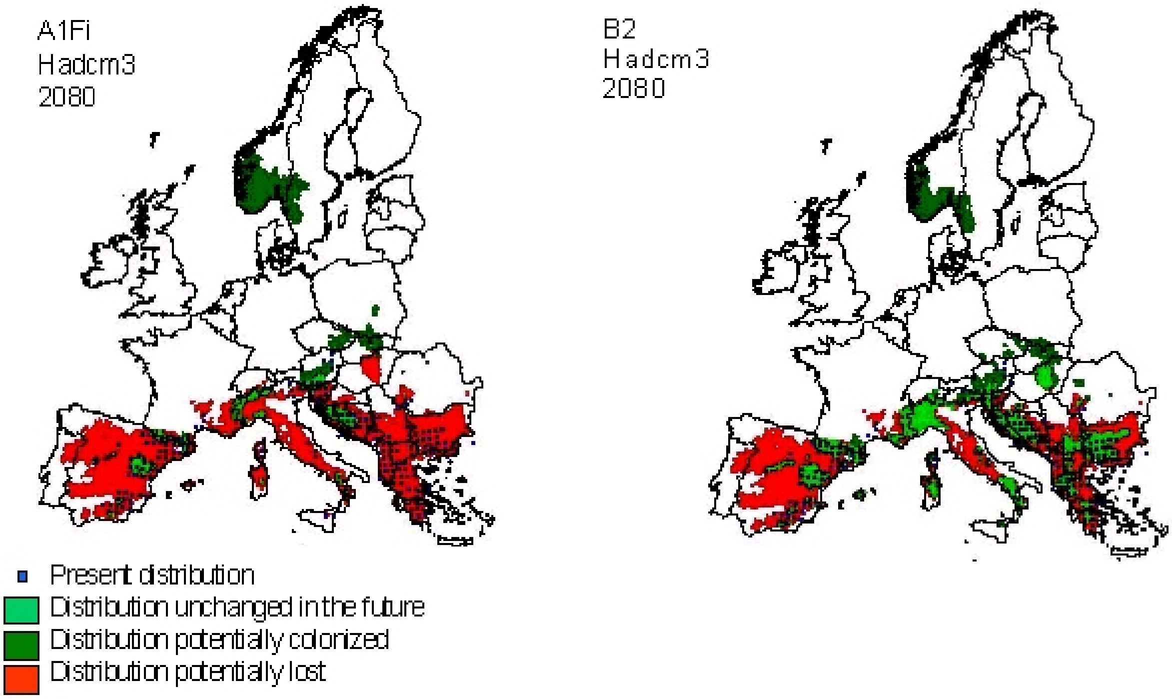

Figure 4. Predicted potential distribution of *Pinus nigra* sp.

During the last major climate change (i.e., from the glacial maximum around 18 000 BP to the climate optimum around 6 000 – 5 000 BP), vegetation showed a major global shift northward. From 10 000 BP to 3 000 BP species distributions shifted northward, at an average rate of 0.3° latitude per century to 1.35° latitude per century for the special case of Scots pine following the migration of their climatic niche. For the 21st century, the model predictions forecast that species' distributions will mostly contract in addition to a northward shift at a rate of 5° latitude per century for species from category one to 15 – 20° latitude per century for species from categories 2 and 3, i.e., 10 times faster than during the last climate change. The model predictions, either niche-based or process-based, are globally in agreement with each other. They show that the distribution of many temperate tree species will be affected, especially the Mediterranean/temperate species that will disappear from most of their current range. They also predict a northward migration and a regression of the southern part of the distribution, but more or less depending on the species. Process-based models show that some species may not be able to follow in real time the migration of their climatic niche.

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IMPACTS OF PAST CLIMATE CHANGE ON SPECIES' DISTRIBUTIONS OF WOODY PLANTS IN NORTH AMERICA

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The modern distributions and genetic structure of North American tree species represent, in part, legacies of climate changes of the past 25 000 years and more. Development of extensive networks of pollen and plant-macrofossil records from lakes, wetlands, and woodrat-middens across North America are revealing the magnitude and complexity of climate-change effects. Paleoecological and paleoenvironmental studies have advanced to the point where some generalizations can be made, which are summarized briefly in this paper.

Ecologically significant climatic change and variability occurs at all timescales, from interannual to tens of thousands of years (Swetnam and Betancourt 1998, Swetnam et al. 1999, Jackson and Overpeck 2000, Jackson 2004). Although trends and cycles can be identified, much of the variability is non-stationary across a range of timescales. The global climate system is continually evolving, and its regional and local manifestations are in continuous flux.

To date, substantial changes in distribution and abundance during the past 25 000 years have been documented for every species and genus of temperate and higher latitudes for which we have good paleoecological records (Huntley and Webb 1988, Betancourt et al. 1990, Jackson et al. 1997, Betancourt 2004, Webb et al. 2004). The extent and nature of the changes varies among species and regions, ranging from major habitat shifts (elevational, edaphic, aspect) to wholesale geographic displacement at scales of thousands of kilometres (Jackson and Overpeck 2000). Some species (e.g., *Pinus remota*) have undergone counterintuitive range shifts, contracting southward since the last glacial maximum (Jackson 2004). Some subalpine species (e.g., *Abies lasiocarpa* and *Picea engelmannii*) appear to have occurred at lower elevations in the southern parts of their ranges than to the north (Jackson et al. 2005). These unexpected patterns probably stem from spatial gradients of seasonal precipitation that differed radically from those prevailing today.

Many species that are geographically extensive and/or regionally dominant today (e.g., *Betula papyrifera*, *Pinus ponderosa*, *P. strobus*, *P. edulis,* and *Tsuga canadensis*) occurred as localized, dispersed populations during the last glacial maximum (Betancourt et al. 1990, Jackson et al. 2000, Betancourt 2004). Others (*Juniperus osteosperma*, *Pinus banksiana*, and *Picea glauca*) have been widespread and dominant since the last glacial period, but their ranges have shifted by 100s to 1000s of km while many of the extensive and dominant species of the last glacial period (e.g., *Pinus flexilis* and *P. remota*) are now localized and highly fragmented compared to the past. At least one species (*Picea critchfieldii*) that was dominant in the lower Mississippi Valley and extensive in the unglaciated Southeast during the last glacial maximum is now extinct (Jackson and Weng 1999).

Changes in distribution and abundance were widespread and rapid during the glacial-interglacial period, 15 000–10 000 years ago. Many species expanded rapidly into new territory during this period in both eastern and western North America (Webb 1988, Betancourt et al. 1990, Clark et al. 1998). Recent genetic evidence suggests that this rapid expansion may have been facilitated by existence of northern outlier populations during the last glacial maximum (McLachlan 2003, McLachlan and Clark 2004). The late-glacial period is characterized by extensive areas of vegetation with no modern counterpart, particularly in the mid-continent (central and western Great Lakes, Upper Mississippi Valley, Ohio Valley, and adjacent uplands) (Williams et al. 2001, Jackson and Williams 2004). This vegetation consisted of mixed forests of *Picea*, *Quercus*, *Fraxinus nigra*, and *Ostrya/Carpinus* (presumably *Ostrya*). This no-analog vegetation shows spatial patterns and temporal changes, but these are poorly resolved at present. Nevertheless, the records show unique plant communities and landscape patterns during this period, and populations of *Fraxinus nigra* and *Ostrya* were much larger over more extensive areas than today. When these species declined at the opening of the Holocene 10 000 years ago, they were replaced in the central-western Great Lakes region by *Ulmus* populations, again more abundant than anywhere today. Late-glacial vegetation in much of western Canada and adjacent Alaska also lacked modern analogs (Anderson et al. 1989, Williams et al. 2004).

The past 10 000 years – the Holocene – have seen continued movements of species and community reorganizations. However, aside from human activities, the magnitude of both environmental and biotic change has been generally lower than that of the glacial-to-interglacial transition. Tree species migrated over extensive areas of North America during the Holocene, expanding into new territory, abandoning old territory, shifting along edaphic and elevational gradients, and changing in abundance. These changes are recorded at innumerable local paleoecological sites distributed throughout the continent (Betancourt et al. 1990, Grimm et al. 2001, Shuman et al. 2004, Anderson et al. 2004, Grimm and Jacobson 2004), and are visible in mapped time-series of pollen abundances and macrofossil presence/absence (Webb 1988, Jackson et al. 1997, Gajewski et al. 2000, Williams et al. 2000, 2004). All of these ecological and biogeographic changes are related ultimately to climate change. However, the underlying climate change was not always gradual or monotonic. Recent intensive studies of late Holocene migrations, in both eastern and western North America, are revealing that decadal to millennial-scale climate variability have regulated species invasions, resulting in alternating periods of stasis and rapid expansion (Peñalba and Payette 1997, Jackson and Booth 2002, Shuman et al. 2002, Lyford et al. 2003, Booth et al. 2004).

Climate change and variability have emerged as the dominant drivers of changes in the distribution and abundance of tree species of the late Quaternary. Climate is multivariate, and important climate variables (e.g., seasonal temperature and precipitation) can change independently through time, resulting in continual recombinations of climate variables and reconfigurations of climate gradients across the continental landscape (Jackson and Overpeck 2000). Because different species respond in different ways to the array of climate variables, species have shifted their geographic ranges independently, often migrating in different directions and at different rates. Development of independent paleoclimate records are allowing delineation of the climate controls on these movements (e.g., Shuman et al. 2004).

Evidence for pre-Columbian human impacts on forest composition and geography is sparse. Impacts appear to have been local or occasionally regional in scope. Undoubtedly, the sophisticated agricultural civilizations of the mid-continent (Mississippian cultures) and the desert Southwest (Pueblo cultures) cleared extensive land areas, but evidence is largely lacking, in part owing to a dearth of suitable paleoecological sites that might have recorded such impacts. The Anasazi culture certainly had substantial effects, which are well-recorded at Chaco Canyon. There, local populations of piñon (*Pinus edulis*) were exterminated (Betancourt and Van Devender 1981), and *Abies* and *Picea* logs were transported some 75–100 km from adjacent mountains for use as timbers in pueblo construction (English et al. 2001). The best evidence for human impacts on vegetation in eastern North America come from pollen work at Crawford Lake, Ontario, where an Iroquoian village was established in the 14th Century and a few hectares of forest were cleared for cultivation for a few decades (McAndrews and Boyko-Diakonow 1989). However, such small-scale activities are difficult to detect in pollen records (Jackson 1997). Human impacts have accelerated in the past 300 years, and such events as agricultural land-clearance and the pathogen-induced declines of *Castanea dentata* and *Ulmus americana* are well-documented in pollen records.

Human-induced changes in tree species abundance and distribution will continue indefinitely, owing to continued land-use practices and to introduction of exotic invasive species and pathogens. In the next few decades, however, ecological impacts of human-induced climate change will become increasingly apparent, potentially overshadowing and certainly interacting with the effects of land-use, invasives, and diseases. The paleoecological record of the late Quaternary can provide important perspectives on these changes (National Research Council 2005). Populations, communities, and ecosystems have been exposed to both rapid changes (National Research Council 2002) and large-magnitude changes (Bartlein et al. 1998) in the past, but the combination of rapid and large-magnitude changes has been uncommon, particularly at broad spatial scales (Jackson and Overpeck 2000). One of the most potentially disruptive climate-change impacts, which has been inadequately studied, is rapid reconfiguration of climate gradients (Jackson and Williams 2004). Climate change will consist not only of changes in individual variables (e.g., annual or seasonal temperature and precipitation), but of fundamental recombinations of these variables. Climate realizations of the near-future may be as different from those of the 20th Century as those of the late-glacial period (see Fig. 10 in Jackson and Williams 2004), when forest composition over much of North America had no modern analogs (Williams et al. 2001). This presents a major challenge to our ability to predict biotic responses to climate changes of the coming decades and centuries. Paleoecological studies of ecological responses to past climatic changes may help identify the critical climatic controls of the distribution and abundance of individual species. Integrating paleoecological studies with the ecology and genetics of modern populations will provide benefits not only for science but society as we pass through a period of profound environmental change.

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GENETIC RESPONSES TO CLIMATE AND CLIMATE CHANGE IN CONIFERS OF THE TEMPERATE AND BOREAL FORESTS[1]

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ABSTRACT

The availability of climate data and sophisticated software for high speed computers has made it possible to assess the climatic factors underlying geographic patterns of genetic variation in forest trees. Analyses have demonstrated anew that the clines in genetic variation that typify most tree species indeed have been molded by and are perpetuated by the climate. Yet, distribution of genotypes across the landscape is controlled by an interaction between adaptation to climate and competition, the same factors governing the distribution of species. Genotypes occur where they can be competitively exclusive, but most, nonetheless, have been competitively excluded from their climatic optima. Most populations, therefore, exist in climates that are colder than the optimal for their growth, productivity, and survival, with the discrepancy between the inhabited and the optimal climate increasing with the severity of the climate.

Responses to climate change can be viewed 1) as short-term plastic responses that accrue in endemic populations as physiological systems adjust to change, and 2) as long-term evolutionary processes that realign genetic variability with environmental diversity. Immediate short-term responses to a warming climate are dependent on the discrepancy between the inhabited and optimal climates. Responses, therefore, should be highly negative in populations occupying the mildest climates but positive in the coldest. As a result, expected short-term responses in *Pinus sylvestris* and *Larix sibirica* of Siberia are strongly positive while those of *Picea engelmannii* of western United States are highly negative. Accommodating global warming in the long term will require a redistribution of genotypes within species to match genotypes with the climate for which they are best suited. The process undoubtedly will be driven by migration, gene flow, and selection. Natural processes, however, tend to occur at rates too slow to match the projected speed of global warming. Without the intervention of mankind in the evolutionary processes, accommodating the warming expected by 2100 may require many centuries.

INTRODUCTION

In the preface to his text on climate and plant distributions, Woodward (1987) notes that one of the central theses in plant ecology is that climate is the primary factor controlling the distribution of vegetation but that the relationship, nonetheless, is poorly understood. Forest trees provide a fine example. For at least three centuries, botanists have been aware that widespread tree species are composed of populations that are physiologically attuned to different climates (Morgenstern 1996). Forest managers, therefore, long have known that successful reforestation requires planting stock that is physiologically suited to the climate of the planting

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site. In an effort to provide guidelines to managers, common garden studies have been established for most of the world's widespread trees. By their very nature, common garden studies are controlled experiments in climate change; populations have been transferred from the climate of their provenance to that of the garden (Mátyás 1994).

Studies with forest trees have demonstrated, first with the results of Langlet (1936) and then subsequently in numerous works, that genetic variability among populations tends to be distributed along clines that can be described with models driven by geographic variables (Morgenstern 1996). These studies, therefore, have collectively demonstrated the principles of ecological genetics that are well known for plants in general (Brown and Gibson 1983): widespread species tend to be composed of populations that differ in innate growth potential and cold hardiness, the two of which are negatively correlated. Although involving a suite of traits, adaptation of populations can be viewed simplistically as a balance between selection for growth potential where the climate is mild and selection for cold tolerance where the climate is severe (Rehfeldt 1988, 1989, 1994).

While geographic patterns of genetic variation are invariably interpreted in terms of climate, attempts to substitute climate variables for their geographic surrogates have been hampered by an inability to estimate climate variables at the remote locations where forests typically grow. Recently, however, innovative steps have been taken by Booth (1990) and his colleagues (Booth et al. 1989a, 1989b) who used climate surfaces to guide the intra-specific transfer of seeds for reforestation and to pinpoint foreign climates suitable for the introduction of Australian species. Climate models of this type offer the potential of describing genetic variation with climatic predictors such that the impact of climate, fluctuating climates, and climate change on the distribution, growth, and productivity of forest trees can be assessed.

Advances are taking place on two fronts. One deals with a quantitative description of the clines that occur in response to climate and the second involves ecologic principles governing adaptation of populations. Both require site-specific estimates of climate variables.

CLIMATE ESTIMATES FOR REMOTE LOCATIONS

The historic approach to estimating climate for remote locations used data from the closest weather station to characterize provenance climate. This approach understandably has met with limited success except when applied in regions either covered by a fine network of weather stations or with little topographic relief. Of the exceptions, however, (Langlet 1959**)** demonstrated an R^2 of 0.89 between the 17-year height of 47 Swedish populations of *Pinus sylvestris* and the average Julian date when the mean temperature first reached 6°C.

Another approach (Rehfeldt 1995, Rehfeldt et al. 1999) uses polynomial regression models driven by geographic variables (latitude, longitude, elevation, and various transformations thereof) to interpolate the climate between weather stations. One such model, based on data from about 500 weather stations in western Canada, was found to be well suited to modeling temperature variables (e.g., R^2 for mean annual temperature of 0.90) but became more problematic for precipitation (e.g., R^2 for mean annual precipitation of 0.61) (Rehfeldt et al. 1999). The functions, therefore, seemed reasonably well suited for analyses confined to small geographic regions but were notably incapable of describing abrupt transitions in climate that occur, for example, across rain shadows. The approach, therefore, was less well suited to large regions of diverse topography where extrapolation would be necessary.

A third and more sophisticated approach uses the thin plate splines of Hutchinson (1991, 2000) to fit climate variables to geographic surfaces. The surfaces can be queried to obtain predictions of climate at point locations. While the suitability of the approach has been repeatedly demonstrated (e.g., Hutchinson and Bischof 1983, Booth et al. 1989a, 1989b, Booth 1990), applications aimed toward understanding the relationship between climate and vegetation (Rehfeldt 1994, McKenney et al. 2001, Tchebakova et al. 2003) are only recent. An example of a spline climate surface for degree-days > 5°C of western United States and southwestern Canada is presented in Fig. 1. To generate this figure, tri-variate splines using latitude, longitude, and elevation were fit to climate data from 3 006 weather stations. Predictions were made for each cell of a DEM (digital elevation model) matrix gridded at 0.0083 degrees (GLOBE Task Team 1999). The map is based on estimates for more than six million pixels; in the figure, degree-days are presented for ten classes that range from essentially zero (white) in the highest mountains to 6 700 in the deserts to the southwest (black).

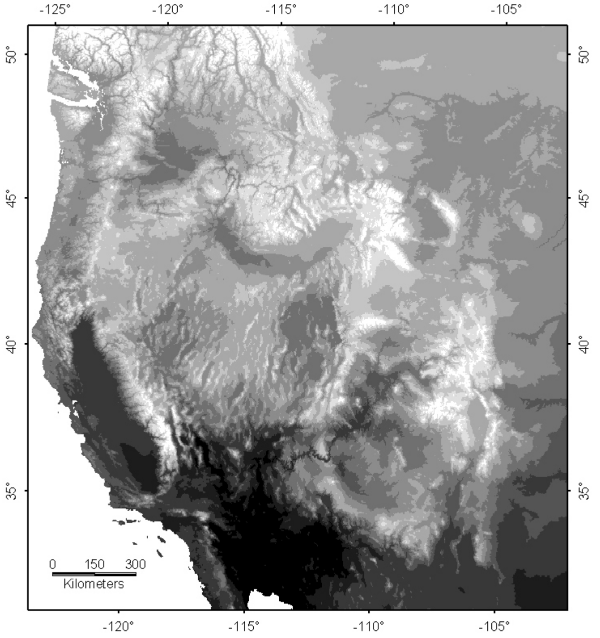

Figure 1. Map of degree-days > 5°C using shades of grey to code 10 classes ranging from zero (white) to 6700 (black) (from Rehfeldt, unpublished).

GEOGRAPHIC VERSUS CLIMATIC DESCRIPTORS OF CLINES

Recent analyses have allowed clines described with geographic variables to be compared with those driven by climate variables. One example involves the 2-year height of *P. sylvestris* populations tested in a common garden in Moscow, Idaho, USA. In Fig. 2, the relationship between genetic variation and the best fitting geographic variable, latitude, can be compared with that for the best fitting climate variable, degree-days > 5°C.The figure shows that clines described by either independent variable are steep, but that the relationship (R^2 = 0.80) between genetic variation and degree-days > 5°C of the provenance is the strongest. In this example, latitude makes a suitable surrogate for degree-days because summer temperatures are strongly correlated with latitude.

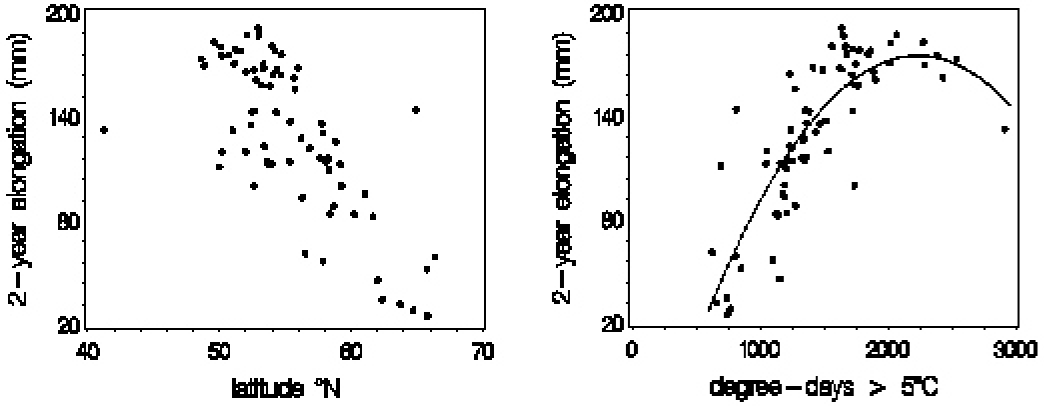

Figure 2. Mean 2-year shoot elongation of *Pinus sylvestris* populations measured in greenhouse-shadehouse studies plotted against the provenance latitude (left) and provenance degree-days > 5°C (right).

Another example (Fig. 3) deals with genetic variation among 215 populations of *Picea engelmannii* from western United States (Rehfeldt 1994). In this case, the best fitting geographic surrogate, provenance elevation, is a weak ($R^2 = 0.07$) but nonetheless statistically significant ($p < 0.05$) predictor of variation among populations. By contrast, the best fitting climate variable, degree-days < 0°C, is closely related ($R^2 = 0.62$) to genetic variation. In this example, geographic variables were poor surrogates for climate and led, therefore, to a fallacious view of the species' genetic structure.

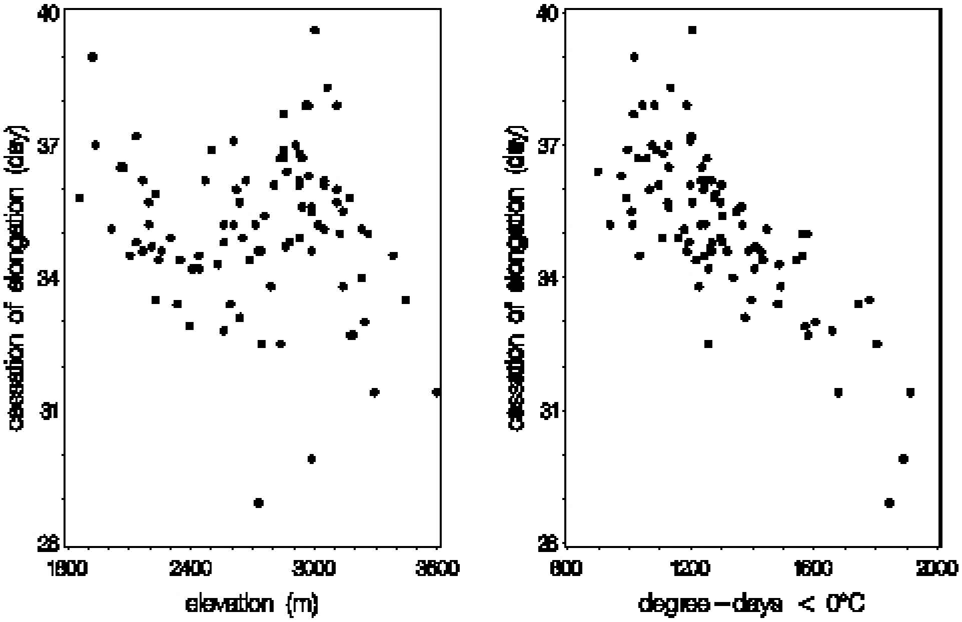

Figure 3. Mean date of the cessation of shoot elongation of 2-year *Picea engelmannii* populations measured in greenhouse-shadehouse studies plotted against the provenance elevation (left) (Rehfeldt 1994) and provenance degree-days < 0°C (right) (Rehfeldt 2004).

These results along with those for *Larix occidentalis* of western North America (Rehfeldt 1995) demonstrate that converting clines with geographic drivers to those with climatic drivers is not only feasible but also may lead to alternative interpretations. Among the climate variables tested to date, those closely linked to genetic differentiation of populations include summer temperatures (degree-days > 5°C and mean maximum temperatures of July), winter temperatures (degree-days < 0°C and mean minimum temperatures of January), and an annual moisture index (ratio of degree-days > 5°C to mean annual precipitation).

Many of the results presented herein involve measurements of juvenile trees made in common gardens far removed from native habitats. The results, nonetheless, are used to assess the adaptedness of natural populations growing in native environments throughout their long lives. To be sure, foresters tend to greet such extrapolations with considerable skepticism. Yet, 2-year shoot elongation measured in a greenhouse in Moscow, Idaho, USA accounts for 80% of the variance among *P. sylvestris* populations for 13-year heights attained in the most optimal of 46 test sites scattered across the former Soviet Union (Fig. 4). These results along with numerous reports of significant juvenile-mature correlations in forest trees support the veracity of short term testing programs for studying ecological genetics.

ECOLOGICAL INTERPRETATIONS OF CLINAL RESPONSES

From Langlet's (1936) demonstrations to the present, clines that parallel geographic gradients tend to be interpreted from the selectionist viewpoint: environmental selection alters gene frequencies to produce local populations physiologically attuned to their environment. Clines (e.g., Figs. 2 and 3), therefore, were thought to reflect optimization of adaptedness via natural selection. However, analyses of two long-term common garden studies of enormous scope have shown that this interpretation needs modification. The studies deal with *Pinus contorta* of western Canada and *P. sylvestris* of Russia. In each, numerous (> 100) populations were planted in designed experiments across a broad range of sites that numbered between 45 and 55. Because of the large number of test sites, data collected from these studies could be used to develop population-specific functions describing height and survival at age 20 for *P. contorta* and at 13 for *P. sylvestris* from climate variables (Rehfeldt et al. 1999, Rehfeldt et al. 2001, Rehfeldt et al. 2002).

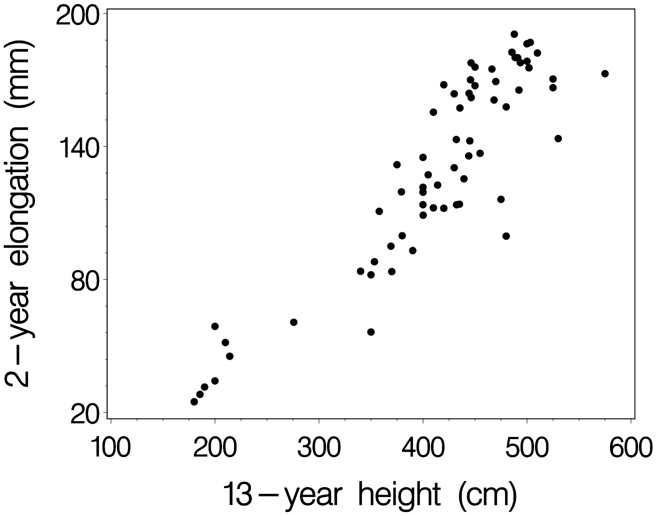

Figure 4. Mean 2-year shoot elongation of *Pinus sylvestris* populations measured in greenhouse-shadehouse studies conducted in Moscow, Idaho, USA plotted against 13-year height at the optimal of 46 test sites scattered across the Soviet Union.

Even though the two studies were planned and implemented independently, their results lead remarkably toward similar conclusions. These same conclusions, moreover, were reached earlier with a disparate series of analyses of populations of *Pinus banksiana* from eastern Canada (Mátyás and Yeatman 1992). In Fig. 5, for example, modeled responses of two populations of each species are compared in relation to the general temperature regime of the provenance. The pair of populations are from either warm or cold provenances. The mean annual temperature at McLeod Lake, for instance, averages 2.1°C while that at Atlin averages -1.5 °C; and degree-days > 5°C at Veshensk average 2 536 days while those at Surgut average 999 days. As one would expect, populations from the mildest climates exhibit a growth potential that is superior to those of populations from severe environments; and populations from cold climates achieve optimal growth in climates that are colder than those in which populations from warm climates attain their optimum.

These relationships are illustrated further in Fig. 6 for several *P. contorta* populations, the sample of which represents the range of responses among the 108 populations that were analyzed. The functions presented in these two figures thus demonstrate principles of ecological genetics that are well known for plants in general (e.g., Brown and Gibson 1983) and for forest trees in particular (e.g., Rehfeldt 1988, 1989, Morgenstern 1996): adaptation of populations appears as a balance between selection for growth potential in mild climates and selection for cold tolerance in severe climates.

If the responses of Figs. 5 and 6, however, develop from a selectionist strategy whereby adaptatedness is optimized, populations should occupy climates that approach their climatic optima. They do not. The Atlin and McLeod Lake populations of Fig. 5 occur in climates that are about 3°C colder than their optima, while the Veshensk and Surgut populations occupy climates that are cooler by about 400 degree-days > 5°C. An examination of all populations in both studies led to the unambiguous conclusion that most populations of these species occupy climates suboptimal for their growth and survival. In addition, disparity between the optimal and inhabited climate unquestionably increases as the climate becomes more severe (Fig. 7).

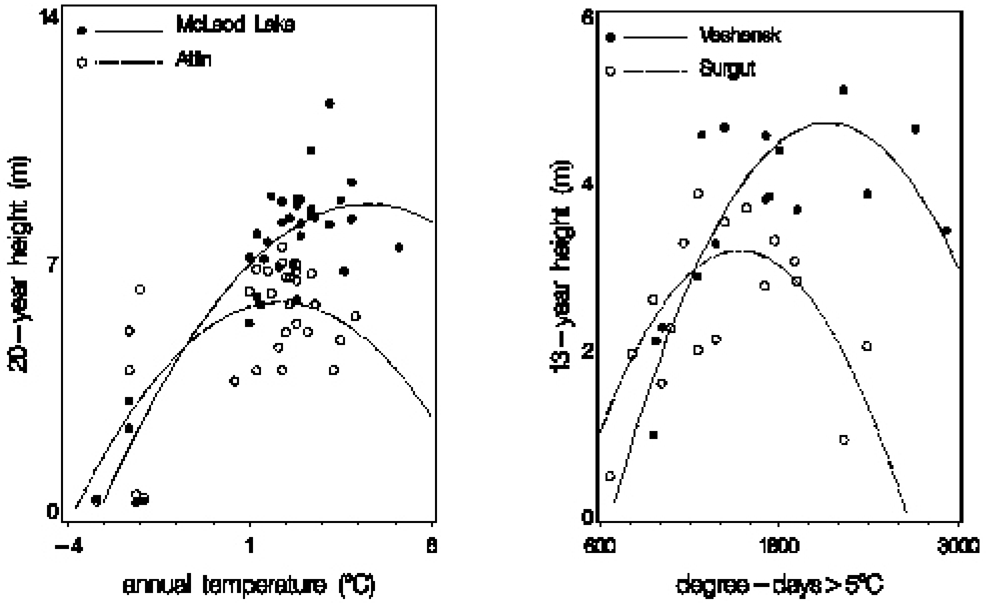

Figure 5. Population-specific response functions plotted in relation to the observed data for predicting the height of two provenances from the climate of the planting site for *Pinus contorta* (left) (Rehfeldt 1995) and *Pinus sylvestris* (right) (Tchebakova et al. 2003).

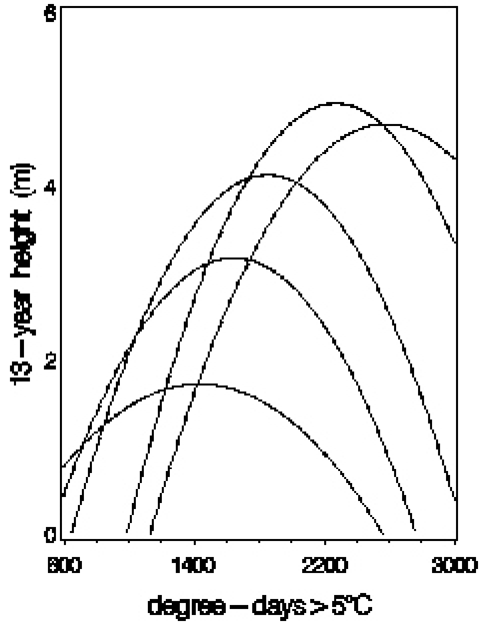

Figure 6. Response functions using degree-days > 5°C as a predictor of height for five populations of *Pinus sylvestris* that represent a variety of responses (Rehfeldt et al. 2001).

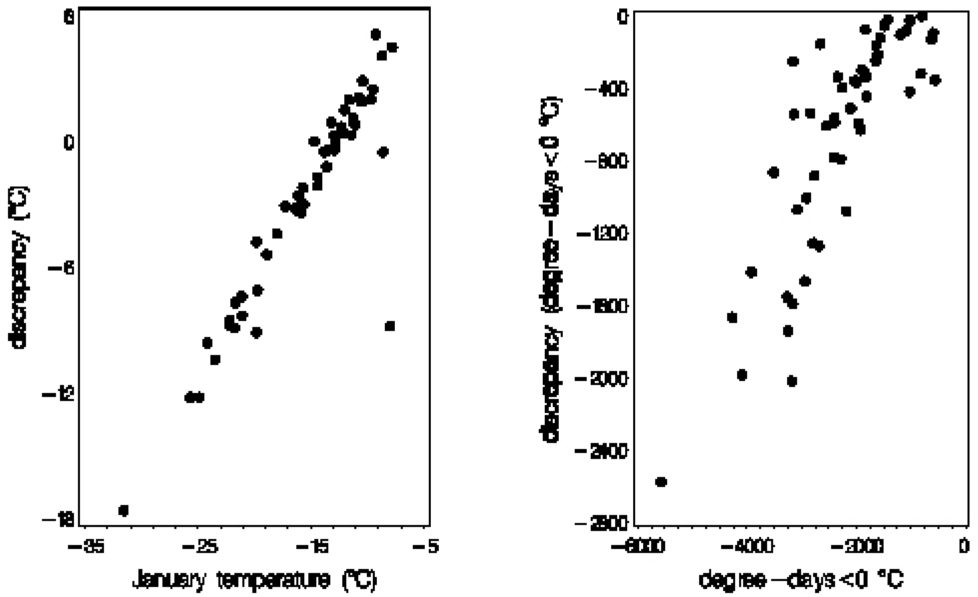

Figure 7. Discrepancy between the inhabited climate and the optimal climate plotted by provenance climate for *Pinus contorta* populations (left) (Rehfeldt 1995) and *Pinus sylvestris* populations (right) (Rehfeldt et al. 2001). Discrepancies are based on response functions that predict height from climate. Negative values occur when the inhabited climate is colder than the optimum.

Although evolutionary processes undoubtedly have produced the climatic clines that characterize the genetic systems of *P. contorta*, *P. sylvestris*, and *P. banksiana*, the results nonetheless lead toward the unambiguous conclusion that natural populations exist in climates that are suboptimal to their growth and survival (Arthur 1987, Mátyás and Yeatman 1992, Rehfeldt 1995, Rehfeldt et al. 2002). The only reasonable explanation for these seemingly antithetical results is for the distribution of genotypes to be determined as much or more by competition than by adaptation to the physical environment. Put simply, as stands of forest trees mature, self-thinning and density-dependent selection regulate densities to levels commensurate with the resources at the site. For these three species, over-reproduction is common and density-dependent selection can be intense. As a result, the distribution of genotypes within species is driven by adaptation to the physical environment (Figs. 2 and 3) and by density-dependent selection (Figs. 5 and 6).

According to this view, therefore, if seeds from Veshensk and Surgut were dispersed across a site with 1 500 degree-days > 5°C, seedlings from both undoubtedly could grow superbly (Fig. 5 right). Yet, genotypes from Veshensk would be 75 cm taller after 13 years than those from Surgut. In time, therefore, density-dependent selection would favor genotypes from Veshensk. Precisely the same argument can be made for *P. contorta* genotypes from Atlin and McLeod Lake (Fig. 5 left). Genotypes from Surgut and Atlin, therefore, would be competitively excluded from their climatic optima. Competitive exclusion would be initiated by the fastest growing genotypes which, by virtue of their high growth potential, would exclude genotypes of other populations from their optima (Figs. 5 and 6). Because genotypes occur where they are competitively exclusive, those populations with the highest growth potential initiate a cascading sequence of effects which ultimately relegate most populations to suboptimal climates (Fig. 6). While some populations are relegated to climates warmer than their optima (see Rehfeldt et al. 2003), most occur in climates that are colder than their optima.

It seems, therefore, that adaptation and competition, the processes controlling the distribution of species (Arthur 1987), also control the distribution of genotypes within species. To be sure, sexual reproduction in the face of the high levels of gene flow that typify many forest tree species disassembles in each generation those genotypes best suited for a given site. Consequently, the balance between high growth potential (competitive exclusiveness) and adaptation to the climate must be re-established each generation. Asymmetric gene flow along a climatic gradient from the center of distribution toward the periphery (Garcia-Ramos and Kirkpatrick 1997, Kirkpatrick and Barton 1997) couples with strong density-dependent selection to prevent populations from inhabiting their ecological optima (Rehfeldt 1995). Toward the periphery of the distribution, therefore, where the climate is most inhospitable, the discrepancy between the optimal and inhabited climates becomes the largest.

GENETIC DIFFERENTIATION ALONG CLIMATIC GRADIENTS

Genetic variation across geographic regions develops in response to multiple climatic gradients. Variation among populations, therefore, is continuous. However, as an aid to visualizing complex multivariate patterns across forested ecosystems and to provide tools to forest managers, continuous variation is frequently classified into climatypes, the climatic ecotypes of Turesson (1925). One means of classifying continuous variation is to equate the breadth of a climatype to the confidence interval surrounding a population mean (Rehfeldt 1988, 1989, 1994). With this approach, therefore, there is a reasonable probability that genotypes from disparate climatypes are genetically different.

This technique was used for mapping climatypes of *P. sylvestris* and *Larix sibirica* (see Fig. 4, left, Tchebakova et al., this proceedings) for the Sayan Mountains of Krasnoyarsk Krai in south-central Siberia (Tchebakova 2003). To produce this map, the climate transfer functions of Rehfeldt et al. (2002) were used to subdivide climate distributions into climatypes. These functions suggested that genetically different populations of *L. sibirica* tended to be separated by at least 650 degree-days > 5°C, 2 200 degree-days < 0°C, or 1.0 units of an annual moisture index (ratio of degree-days > 5°C to mean annual precipitation). Subdividing the climatic distribution of the entire species according to these limits produced three classes for degree-days > 5°C, two for degree-days < 0°C, and eight for the moisture index. In total, therefore, there were 48 possible climatypes for the species, 24 of which were projected for the Sayan Mountains. These 24 occupy 67% (318 586 km^2) of the region, leaving 32% beyond the climatic limits of the species for at least one of the three climate variables. Of the 24 climatypes, most are minor; five, in fact, account for 90% of the species' distribution. Of the five, two are mammoth, occupying about 55 000 km^2.

Note, however, that the map in Fig. 4 of Tchebakova et al. (this proceedings) reflects the potential distribution of climatypes. Although *L. sibirica* can flourish within these climatic zones, about 50% of this region is dominated by dark-needled conifers (e.g., *Pinus sibirica*) which tend to competitively exclude *L. sibirica*. The realized distribution, therefore, is much less than the potential. This discrepancy between potential and realized climatic distributions was addressed for *P. engelmannii* (Rehfeldt 2004). The approach involved mapping limits of distribution according to: 1) the species climatic envelope (Box et al. 1999), defined according to the absolute limits among 315 provenances for 17 climate variables, and 2) the limits determined by a canonical discriminant analysis using the same 17 climate variables from point-locations to separate 9 species. A visual comparison of two-dimensional range maps of Little (1971) with maps developed from these two approaches showed that both overestimated actual distributions but that together, the two methods provided a realistic estimate. A species' distribution prepared in this manner thus seems to provide a reasonable basis for portraying intraspecific variation (Fig. 8). For *P. engelmannii* of Fig. 8, climatypes are based on genetic variation in six variables described by clines driven by the winter temperature regime and summer maximum temperatures.

RESPONSES TO CLIMATE CHANGE

The response functions of Figs. 5 and 6 imply that a directional shift in climate will alter the productivity and adaptedness of individual populations and, therefore, of species as a whole. Because sessile forest trees are unable to track the climate in which they can be competitively exclusive (see Rehfeldt 1995, Rehfeldt et al. 2002), there will be both short- and long-term impacts of a changing climate in general and of global warming in particular. Short-term effects arise as plastic physiological systems respond to the change, while long-term effects encompass the redistribution of genotypes required to realign climatypes within the novel distribution of climates (Rehfeldt et al. 2001). Both effects are complex.

Short-term plastic effects depend on the relationship between the inhabited climate and the optimal climate (Rehfeldt et al. 2001). A warming climate will have a positive effect for populations occupying climates cooler than their optima, but a negative effect on those inhabiting their optima. The relationships in Fig. 6 suggest, therefore, a negative impact in the southern and low altitudinal portions of a species' distribution and a positive effect in the north and high altitudinal portions. Continual warming will push temperatures beyond the climatic optima of an increasing number of populations, with negative impacts accumulating sequentially across the landscape from warm provenances to cool. Extreme warming eventually will push temperatures beyond the ecological tolerances of the population and result, therefore, in extirpation.

Figures 5 and 6 suggest further that thresholds will be reached during warming when genotypes from distant populations become better suited to the new climate than endemic genotypes. At these thresholds, natural selection and migration will begin the long-term redistribution of genotypes required to balance adaptation to the physical environment with competitive exclusiveness (Rehfeldt 1995, Rehfeldt et al. 2002).

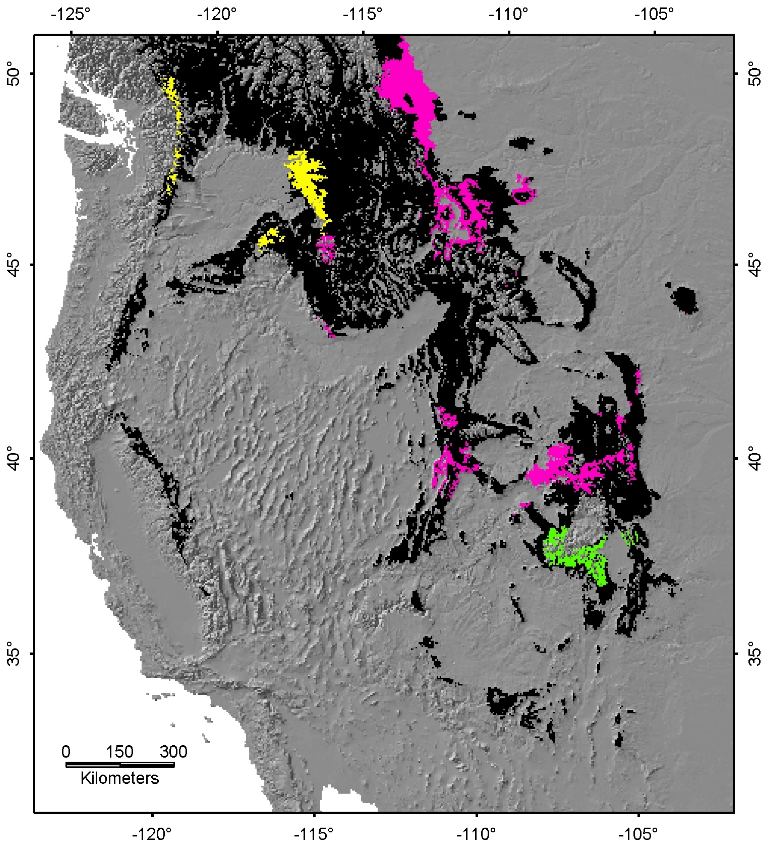

Figure 8. Three climatypes of *Picea engelmannii* superimposed on the species' climatic distribution in western United States and southwestern Canada (Rehfeldt 2004).

The extent of these long-term effects is illustrated in Fig. 3 of Tchebakova et al. (this proceedings) for *P. sylvestris* climatypes of the Sayan Mountains. In the contemporary climate of Siberia, these climatypes occupy climates much colder than their optima (Rehfeldt et al. 2003). It is not surprising, therefore, that Tchebakova et al. (2003) show that the climate of 2090 in the Sayan Mountains should be more amenable for *P. sylvestris* than at present. Indeed, the areal distribution of climates potentially suitable for the pine should increase from 71 to 91%. This increase is expected to accompany a warming of about 6 to 8°C according to the greenhouse gas scenario (1% increase per year in greenhouse gases) of the Hadley Centre (Gordon et al. 2000). As the acreage suitable for the pine increases, the number of climatypes suitable for the region should increase from 25 to 35. Of these, most are small: two, for example, account for about 50% of the area suitable for the species, while 12 account for less than 1%; in 2090, three should account for about 42%, while 17 would account for less than 1%. By 2090, however, the climate suitable for one of the two largest contemporary climatypes should disappear, while that suited for the second should become reduced by 38%. Of the three largest climatypes of the future, two are absent in the region today, while the third occupies only 3.3%. Twelve climatypes that occur in the region today are not expected to be present in the future and 23 expected in the future do not occur there today. Only 13 climatypes should be present throughout the century, but all are expected to be displaced altitudinally. This analysis shows clearly, as did similar analyses for *L. sibirica*, that the adjustment to global warming in species of the Sayan Mountains will require a complete redistribution of genotypes.

These long-term effects are illustrated further in Fig. 9 for climatypes of *P. sylvestris* currently inhabiting the Minusinsk Valley. As the climate warms, the climates sutiable for this climatype are displaced southward toward higher altitudes. While the contemporary altitudinal distribution of this climatype is from about 800 to 1 000 m, the altitudinal range of future climates for which this climatype is suited should be from 1 800 to 2 200 m.

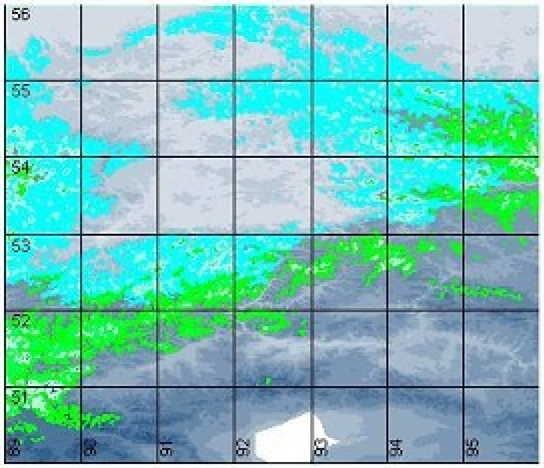

Figure 9. Climatype of the Minusinsk Valley in Siberia for the contemporary climate (blue) and the 2090 distribution of its climate (green) superimposed on altitude (white, < 200 m; black, 3 500–4 000 m) (Tchebakova et al. 2003).

The impact of global warming is expected to be much different for *P. engelmannii* of western North America than for species of the Sayan Mountains of Siberia. *Picea engelmannii* is a species of the subalpine forests that reaches the southern limits of its montane distribution in western USA. Many populations, therefore, occupy climates that approach their ecological optimum. Consequently, global warming of 2 to 3°C projected for this region (Gordon et al. 2000) should have a devastating impact on *P. engelmannii* on both the short- and long-term (Rehfeldt 2004). By 2090, the species' distribution is expected to shrink by 89% as distributions are forced upwards (Fig. 10) by as much as 1 000 m; climates suitable for the climatypes of Fig. 8 are expected to be lost by 2060; and the future number of climatypes that occur in the region should be approximately one-half of those that occur today and much reduced in size (Fig. 10).

These analyses indicate that the impact of global warming will be large and quite complex. While extirpation and immigration are expected at the margins of distributions (see Thompson et al. 2002, Davis and Shaw 2001) warn that the impact of a changing climate encompasses much more than shifts in the distribution of species. Indeed, intra-specific adjustments should produce a wholesale redistribution of genotypes across the landscape to realign climatypes with the distribution of new climates and thereby to maintain growth, productivity and survival (Rehfeldt 1995, Rehfeldt et al. 2002).

Nonetheless, there seems little doubt that natural processes are capable of accommodating global warming; adjustments during the Pleistocene glacial epic, for instance, accommodated temperature shifts of nearly 7°C in the western United States (Betancourt 1990). Migration and selection undoubtedly are the processes that will control the evolutionary adjustments (see Rehfeldt 1995). While seed-dispersed migration is the only feasible means by which genotypes can immigrate, natural selection coupled with gene flow undoubtedly will be the primarily processes acting to restore adaptedness. Yet, rates of migration tend to be slow (Davis 1989), and although responses to selection can be rapid, genetic gains per generation are limited by additive genetic variances, heretabilities, and selection differentials. Calculations for *P. contorta* (Rehfeldt 1995, Rehfeldt et al. 2001) and *P. sylvestris* (Rehfeldt et al. 2002) suggest that genetic responses to global warming may require as many as 10 generations. Analyses of migration rates (Davis 1989) coupleed with these estimates of genetic response suggest that in some regions, natural systems may require as many as 10 centuries to adjust to global warming.

Consequently, to biologists, the most daunting aspect of global warming is the projected speed rather than the absolute amount. Quite obviously, restoring and maintaining forest growth and productivity in the face of global warming will require the participation of mankind (Rehfeldt 1995, Rehfeldt et al. 2002, Rice and Emery 2003). Man's role will be to assist the natural processes using guidelines such as Fig. 10 as a blueprint.

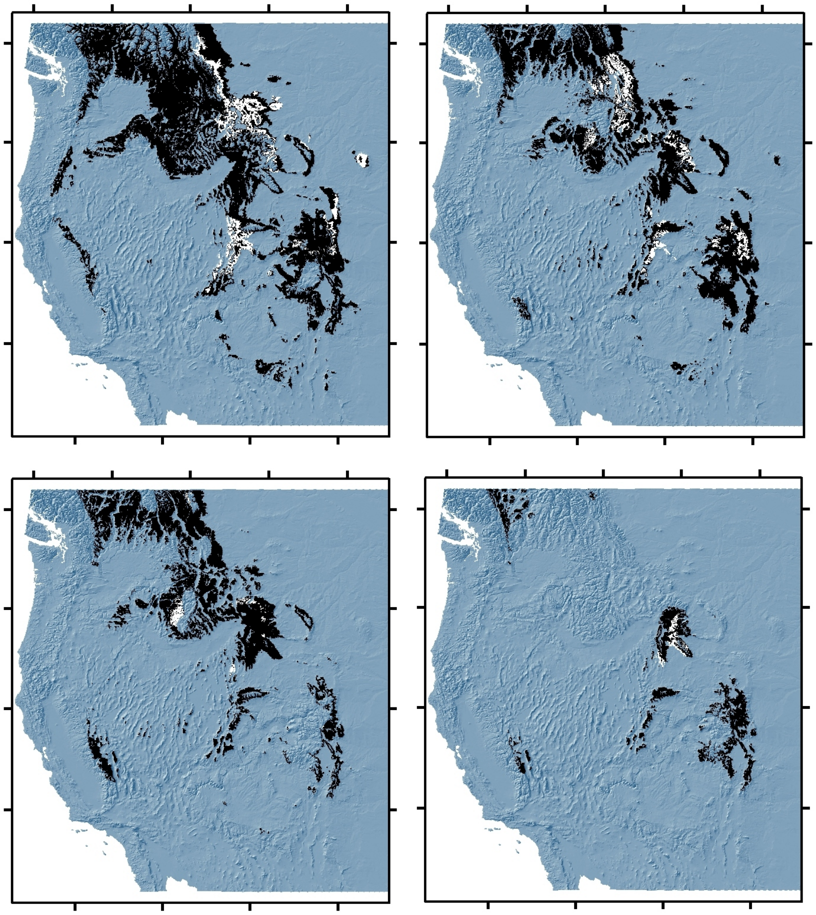

Figure 10. Distribution of a *Picea engelmannii* climatype superimposed on the climatic distribution of the species for the contemporary climate (upper left) and the distribution of future climates suitable for the climatypes in the decades beginning in 2030 (upper right, 2060 (lower left), and 2090 (lower right) (Turesson 1925). Future climates are based on a global warming scenario of the Hadley Centre of 1% (Gordon et al. 2000) increase in greenhouse gasses per year.

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REDISTRIBUTION OF VEGETATION ZONES AND POPULATIONS OF *Larix sibirica* Ledeb. AND *Pinus sylvestris* L. IN CENTRAL SIBERIA IN A WARMING CLIMATE[1]

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INTRODUCTION

Evidence for global warming over the past 200 years is overwhelming (Hulme et al. 1999), based on both direct weather observation and indirect physical and biological indicators such as retreating glaciers and snow/ice cover, increasing sea level, and longer growing seasons (IPCC 2001). Recent GCM projections of the Hadley Centre (Gordon et al. 2000) for Siberia show an increase in temperature of 4 to 6°C and an increase in precipitation of as much as 25% by 2100. These changes, moreover, could occur at a rate of 0.1 to 0.4°C per decade (Watson et al. 1996). The rapid rate of change coupled with the large absolute amount of change is expected to have profound effects on plants of the boreal forests at all hierarchial levels: from forest zones (Monserud et al. 1993), to ecosystems (Guisan et al. 1996), to species (Iverson and Prasad 1998, Box et al. 1999), to populations within species (Rehfeldt et al. 1999b, 2002).

Our goals are to estimate effects of a warming climate on Siberian vegetation, first, at the highest level of organization and second, at the lowest. The first considers the effects of global warming as zonal vegetation shifts across the plains and plateaus of central Siberia and the second considers intraspecific effects within the mountains of southern Siberia. For the second objective, we invoke Turesson's concept of climatypes, the climatic ecotypes that comprise species, and illustrate intraspecific effects for *Pinus sylvestris* and *Larix sibirica*.

METHODS

Study Area

Our studies of the effects of global warming on vegetation zones deal with the plains and tablelands of central Siberia, roughly 90–120°E longitude and 50–75°N latitude. Studies of the effects of global warming on climatypes deal with the southern mountains, the Sayan Mountains, bounded by 89–96°E longitude and 50–56°N latitude. Our base map for this region was a 1 km grid (GLOBE 1999) which contained 5 600 000 pixels for the plains and tablelands and 420 000 pixels for the southern mountains.

Mapping Current Climates

January and July temperatures, growing degree-days, base 5°C (GDD_5); negative degree-days, base 0°C (NDD_0); and an annual moisture index (AMI), the ratio of GDD_5 to mean annual precipitation were proven to

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be useful in previous analyses addressing plant responses to climate (Tchebakova et al. 1994; Rehfeldt et al. 1999a, 2002). We assembled these data normalized for the period 1900–1964 from 200 weather stations across Siberia, 60 of which were in the Sayan Mountains (Reference books, 1967–1970). We used Hutchinson's (2000) thin plate splines to produce climatic surfaces of these variables on our base map using the 1 km grid. Climatic and topographic images were visualized using IDRISI32 (Eastman 2000). The AMI surface was calculated by dividing the GDD_5 image by the annual precipitation image.

Mapping Future Climates

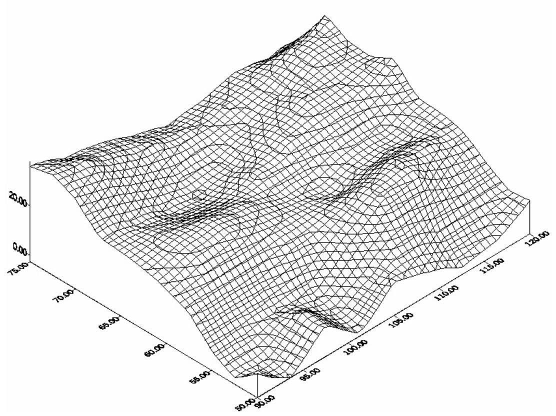
For predictions of global warming, we used the greenhouse gas scenario from the Hadley Centre, HadCM3GGa1 (Gordon et al. 2000) for the decade beginning in 2090. This scenario estimates winter temperature increases of 3 to 9°C, summer temperature increases of 4 to 6°C, and annual precipitation changes (in percentage) between -4 and +25% over the study area (Fig. 1). Future January and July temperatures and annual precipitation for each pixel were calculated from the change in monthly means for temperature and annual average for precipitation between the normalized period and the future decade (Fig. 1). Future values of GDD_5 and NDD_0 were calculated using the following linear regressions: GDD_5 was calculated from mean July temperature (R^2= 0.90), NDD_0 from January temperature (R^2=0.96). Future values of AMI were directly calculated dividing the future GDD_5 image by the future annual precipitation image.

Vegetation Zones

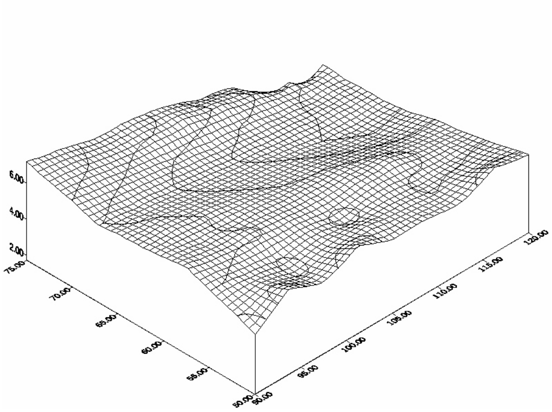
The Siberian bioclimatic model of Tchebakova et al. (1994) was modified to predict vegetation zones (types) from three bioclimatic parameters: GDD_5, NDD_0, and AMI. From the physiologic viewpoint, GDD_5 represents the plant's requirements for warmth; NDD_0 characterizes the plant's cold tolerance and AMI representing a ratio of GDD_5 to annual precipitation characterizes plants' drought tolerance (Rehfeldt et al. 2002).

Seven major vegetation types are recognized by geobotanists on the plains of central Siberia: 1) Tundra, 2) Forest-tundra and sparce forest, 3) Dark-needled (*Pinus sibirica, Picea obovata,* and *Abies sibirica*) taiga (northern, middle, southern) on elevated tablelands, 4) Light-needled (*L. sibirica* and *L. gmelinii,* and *P. sylvestris*) taiga (northern, middle, southern), 5) Birch (*Betula pendula* and *B. pubescens*) and light-needled (*L. sibirica* and *P. sylvestris*) subtaiga, 6) Birch (*B. pendula* and *B. pubescens*) and light-needled (*L. sibirica* and *P. sylvestris*) forest-steppe, and 7) Steppe (Shumilova 1964, Isachenko 1988).

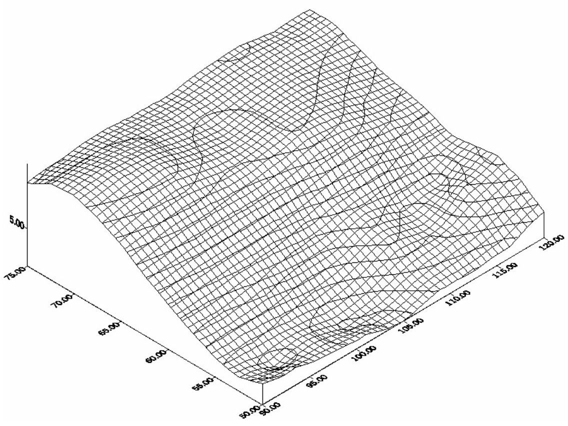
In our bioclimatic model, the annual moisture index separates vegetation into two large types**,** arboreal and non-arboreal (forests and steppes), and further subdivides the former type into dark-needled and light-needled forests. The cold parameter, NDD_0, also tends to separate dark-needled and light-needled tree species. In Siberia, permafrost prevents dark-needled species from spreading eastward across Asia (Shumilova 1964), although summers are sufficiently warm to allow them to survive as far east as Yakutia. The dark- and light-needled forest zones are further separated into latitudinal subzones (e.g., forest-tundra and sparse forests, northern, middle and southern taiga, forest-steppes) by GDD_5. Because southern taiga and subtaiga are not separated by GDD_5 these two types were combined into one zone. Although steppe, semidesert-desert, broadleaf forest, and temperate forest-steppe types are not found under current Siberian climate, these four classes are included into our model because of their potential importance under a warming climate. In total, therefore, our model considers 13 vegetation types, each of which can be defined climatically (Table 1).



a. Precipitation difference (%) between current and future climates in central Siberia



b. July temperature difference (°C) between current and future climates in central Siberia



c. January temperature difference (°C) between current and future climates in central Siberia

Figure 1. Climate differences by 2090 according to the Hadley climate change scenario (2001).

Table 1. Climatic limits for the modified Siberian model of Tchebakova et al. 1994

Vegetation type	GDD_5		AMI		NDDo	
	Lower limit	Upper limit	Lower limit	Upper limit	Lower limit	Upper limit
Tundra	None	< 300	None	None	None	None
Forest-tundra and sparse taiga	300	500	None	None	None	None
Northern dark-needled taiga	500	800	None	< 1.5	> -4500	None
Northern light-needled taiga	500	800	> 1.5	None	None	< -4500
Middle dark-needled taiga	800	1050	None	< 1.5	> -3500	None
Middle light-needled taiga	800	1050	> 1.5	None	None	< -3500
Southern dark-needled taiga and birch subtaiga	1050	1250	None	< 2.25	None	None
Southern light-needled taiga and subtaiga	1050	1250	> 2.25	None	None	None
Forest-steppe	1250	1650	None	< 3.25	None	None
Steppe	1250	1650	> 3.25	None	None	None
Semi desert/Desert	> 1650	None	None	None	None	None
Broadleaf forest	1250	1650	None	< 1.5	None	None
Temperate forest-steppe	> 1650	None	1.5	3.25	None	None

Climatypes

The distributions of *P. sylvestris* and *L. sibirica* were subdivided into climatypes using the results of Rehfeldt et al. (in press). These results were based on common garden studies that had been established across the former Soviet States. In such studies, seeds from numerous native populations were moved to and grown on an array of climatically disparate test sites. Because seeds are transferred along climatic gradients, such studies can also be viewed as climate change experiments. Differential performance of populations then reflects adaptive differences among populations that have accrued from natural selection in the climate of the provenance where the seeds originated. The results of such studies can be used to define a climatype as the climatic limits for a group of populations whose individuals are adapted to same or similar climate.

The analyses of Rehfeldt et al. (in press) used published data on the height and survival of 313 populations of *P. sylvestris* that had been planted on 36 sites and of 130 populations of larch (63 of *L. sibirica,* 42 of *L. gmelinii*, and 25 of *L. sukaczewii*) planted on 8 sites. These data were used to develop transfer functions that predicted 12-year height from the difference in climate between the provenance of a population and the planting site. The functions were based on a Weibull model which is Gaussian but can be asymmetric. For both height and survival, five transfer functions were developed, those driven by GDD_5, NDD_0, and AMI are used herein.

The transfer functions showed that height and survival decrease as transfer distance either increased or decreased from an optimum value which tended to be close to zero, the climate of the provenance. Confidence intervals about the vertex of the function were used to estimate (see Rehfeldt et al. 1999a) the climatic distance separating genetically different populations. For *P. sylvestris,* the limits were 240 GDD_5, ±575 NDD_0, and ±0.6 units of AMI and for *L. sibirica* ±325 GDD_5, ±1150 NDD_0, and ±0.5 units of AMI. Because these limits reflect the distance that seeds can be moved from their provenance before growth and survival begin declining, they also reflect the climatic breadth of a climatype.

Climatypes were defined by subdividing the climatic distribution of the species into classes bounded by these limits. Because the 313 pine provenances used in these tests ranged from 626 to 2 916 GDD_5, 5 classes, 480 degree-days in breadth were required to encompass the species distribution. Six classes were needed for both NDD_0 and AMI. All possible combinations of these classes produced an upper limit to the number of pine climatypes at 180. For the larch, there were 8 classes for moisture index, 3 for GDD_5, and 2 for NDD_0 which produced a maximum of 48 climatypes.

Climatypes defined in this manner must be considered as potential climatypes because many may not exist (e.g., high GDD_5 coupled with low NDD_0). Other combinations may exist, but the landscape may be occupied by species that have competitively excluded either *P. sylvestris* or *L. sibirica.* In the Sayan Mountains, for instance, the pine and larch rarely occur in climates inhabited by the dark-needled conifers even though they are capable of growing there (Ermolenko 2001). Nonetheless, for our analyses of intraspecific effects of a changing climate, we will assume that all climatypes exist.

Climatypes of both species were mapped for the Sayan Mountains using the climate maps of GDD_5,NDD_0,and AMI produced above. Mapping was done for the contemporary climate and for the climate expected by the Hadley GCM for the decade beginning in 2090.

RESULTS

Vegetation Zones

Estimates of the area occupied by zonal vegetation types in current and future climates of central Siberia are given in Table 2.

In the contemporary climate east of Yenisei River, light-needled taiga prevails, with *L. sibirica* and *L. gmelinii* being the domimant species. *Pinus sylvestris* can also dominate these forests in the warmer climates of the south or on sandy soils wherever they may occur. Dark-needled species appear in moist and warm climates, such as those along of the Yenisei Ridge at the mid-latitudes (60°E), in the Sayan Mountains in the south, and in the West Siberian Plain which is west of Yenisei River and south of 64°N. At the high latitudes of the Putoran Mountains (north of the the Arctic Circle), only larch taiga can withstand the cold climate and permafrost, although *P. obovata* and *Pinus sibirica* may be mixed with *Larix* in the large river valleys which tend to be warmer than the surrounding landscape. In the current climate, northern vegetation types like tundra, forest-tundra, and northern taiga cover about 60% of the landscape. About a quarter of the territory is under middle taiga, most of which is light-needled. Only 10% of the region is occupied by a southern taiga, in which dark and light taiga and subtaiga are equally represented. No grasslands are shown by our model north of 56°N (Fig. 2a).

Enormous changes in the vegetation cover of central Siberia are projected for a warmed climate (Table 2, Fig. 2b). Southern vegetation types such as southern taiga, subtaiga, and forest-steppe are expected to expand from about 10 to 70% coverage. This increase in coverage would be largely at the expense of northern and middle taiga each of which would then occupy less than 20%. Forest-tundra and sparse forests would nearly dissappear, while tundra and bare lands should disappear completely. These latter types would be replaced primarily by forest-tundra and dark-needled taiga in the Putaran Plateau and by dark-needled taiga in the Anabar Plateau. In a warmed climate, the forest-tundra which currently surrounds both of the northern plateaus should be replaced by light-needled taiga and even forest-steppe. Forest-steppe also is expected to reach the Putoran Plateau which is more than 1 000 km north of the contemporary distribution of this vegetation type.

Although forest-steppe, steppe, and semidesert do not exist in the current climate of central Siberia, these vegetation types are expected to occupy 50% of the study area in the climate of 2090. Large areas of steppe are projected for the central Yakutian Plain and the Tungus Plateau, while semi-desert should cover a significant area on the Angar Plain.

Table 2. Areas (10^4 km^2) of vegetation zones in Siberia in current and warmed climates

Vegetation zone	Current climate	Proportion (%)	Warmed climate	Proportion (%)
Bare land	3.6	1.3	-	-
Tundra	35.8	12.5	0.1	0.0
Forest-tundra and sparse taiga	54.3	19.0	1.6	0.6
Northern dark-needled taiga	22.5	7.9	17.8	6.2
Northern light-needled taiga	62.5	21.9	3.2	1.1
Middle dark-needled taiga	3.1	1.1	12.6	4.4
Middle light-needled taiga	75.3	26.4	17.0	6.0
Southern dark-needled taiga and birch subtaiga	13.1	4.6	9.2	3.2
Southern light-needled taiga and subtaiga	15.2	5.3	56.1	19.6
Forest-steppe	0.3	0.1	99.0	34.7
Steppe	-	-	22.6	7.9
Semi-desert/Desert	-	-	19.4	6.8
Temperate Broad-leaf forest	-	-	0.6	0.2
Temperate Forest-steppe	-	-	26.5	9.3
Total	285.7	100	285.7	100

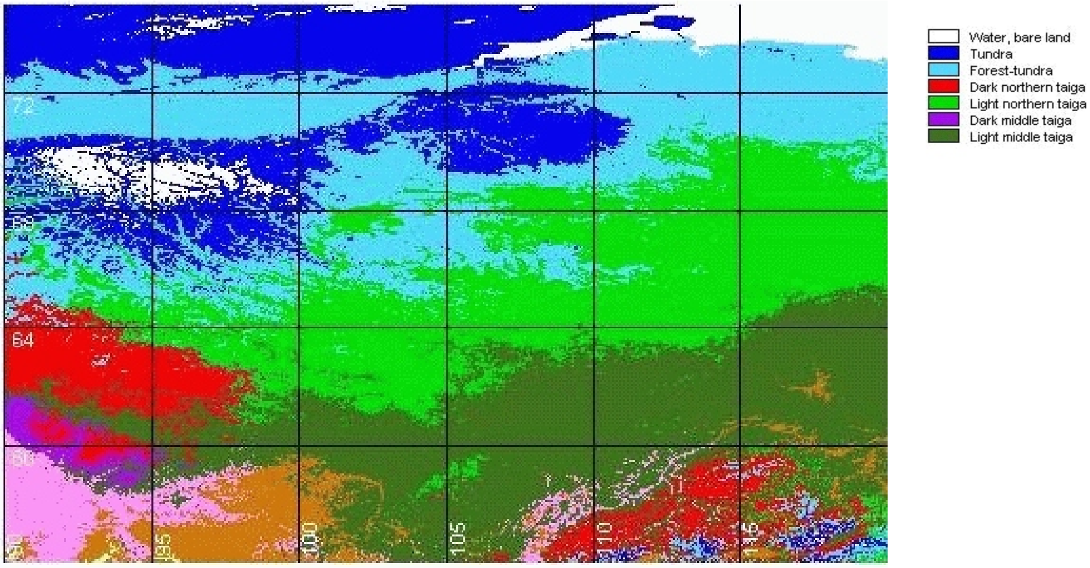


Figure 2a. Vegetation distribution in central Siberia in current climate.

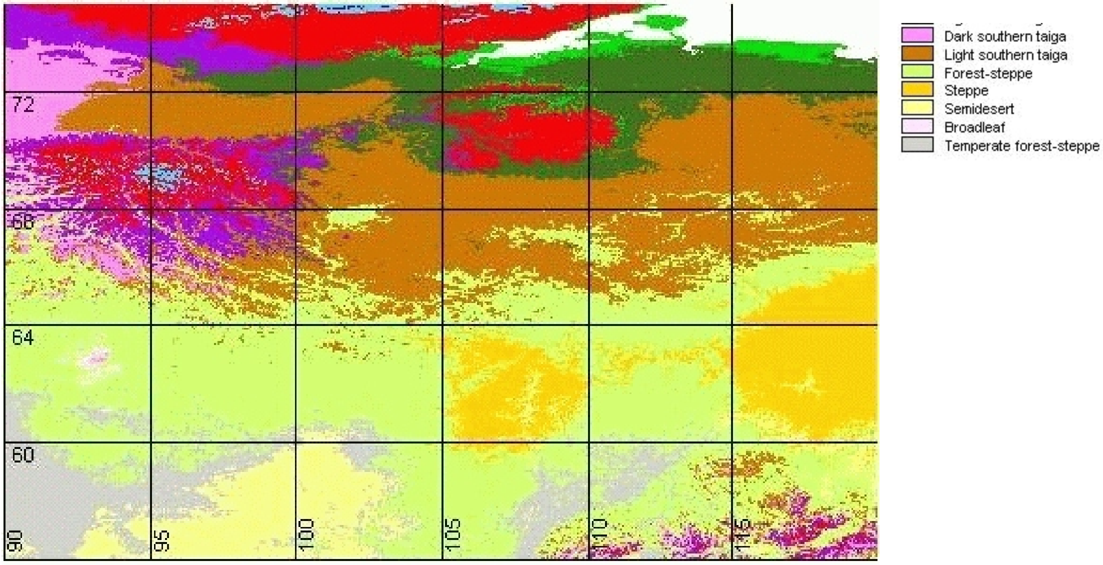


Figure 2b. Vegetation distribution in central Siberia by 2090 in a warmed climate.

Our model also shows that two additional vegetation types that currently do not exist in Siberia should occur there in a warmed climate. One is the temperate forest-steppe, found by analogy from our global vegetation model (Tchebakova et al. 1994). This type should cover a large area on the plains and tablelands where mainly dark-needled taiga occurs today (between latitudes 56°N and 60°N and longitudes 90°E and 100°E). The second novel type is the temperate broad-leaved forest which is expected to appear in the small valley of the Velmo River (about 93°E and 63°N). Because the climate change scenario we are using predicts a high degree of warming for Siberia, the concomitant invasion of broadleaved species into central Siberia seems reasonable. This is supported further by Khotinsky (1977) who reconstructed past vegetation from pollen depositions and concluded that birch and other broad-leaved forests once were distributed east of the Ural Mountains as far as 70°E and 57°N into the West Siberian Plain.

Climatypes

Pinus sylvestris Of the 180 possible climatypes (Table 3), 26 were found for the contemporary climate in the Sayan Mountains (Fig. 3a and b). These 26 occupy 71% of the region, leaving 29% (class # 0) beyond the climatic limits of distribution of the pine for at least one of our three climate variables. Note, however, that these results do not imply that pine occurs across 71% of the region; in fact, cover types show that the pine in reality occupies only about 10%, with much of the region inhabited by dark-needled species which competitively exclude the pine. Of the 26 climatypes of today, most are minor (Table 3); twelve, in fact, account for less than 0.5% of the total area (< 1 575 km^2). Only five climatypes cover more than 5% (15 750 km^2), and of these, # 4 and # 46, are mammoth, accounting for 16 and 20% of the total area, respectively (Table 4).

Figure 3b shows the distribution of climatypes expected in the Sayan Mountains for the projected climate of 2090 according to the Hadley GCM. This figure suggests that the future climate should become more amenable for the pine, with *P. sylvestris* climatypes then encompassing all but 9% of the region (Table 4, Fig. 3b). The increase amounts to 20% of the total land area (about 63 000 km^2) climatically suitable for the pine. Likewise, the number of climatypes suitable for the region should increase from 26 to 35 (Table 4), but again, many (18) of these should account for < 1% of the area. Of the 35, three (# 40, # 82, and # 88) are, accounting for 12 to 15% of the total area.

Table 3. 180 possible combinations of climatic indices (GDD_5, AMI, and NDD_o) for pine climatypes in Russia

Annual moisture index/Growing degree-days, 5°C	Negative degree-days, 0°C					
	-6000 – -4850	-4850 – -3700	-3700– -2550	-2550 – -1400	-1400 – -250	-250 – 0
0.6–1.8/ 600–1080	1	2	3	4	5	6
1.8–3.0/ 600–1080	7	8	9	10	11	12
3.0–4.2/ 600–1080	13	14	15	16	17	18
4.2–5.4/ 600–1080	19	20	21	22	23	24
5.4–6.6/ 600–1080	25	26	27	28	29	30
6.6–7.0/1080–1560	31	32	33	34	35	36
0.6–1.8/1080–1560	37	38	39	40	41	42
1.8–3.0/1080–1560	43	44	45	46	47	48
3.0–4.2/1080–1560	49	50	51	52	53	54
4.2–5.4/1080–1560	55	56	57	58	59	60
5.4–6.6/1080–1560	61	62	63	64	65	66
6.6–7.0/1080–1560	67	68	69	70	71	72
0.6–1.8/1560–2040	73	74	75	76	77	78
1.8–3.0/1560–2040	79	80	81	82	83	84
3.0–4.2/1560–2040	85	86	87	88	89	90
4.2–5.4/1560–2040	91	92	93	94	95	96
5.4–6.6/1560–2040	97	98	99	100	101	102
6.6–7.0/1560–2040	103	104	105	106	107	108
0.6–1.8/2040–2520	109	110	111	112	113	114
1.8–3.0/2040–2520	115	116	117	118	119	120
3.0–4.2/2040–2520	121	122	123	124	125	126
4.2–5.4/2040–2520	127	128	129	130	131	132
5.4–6.6/2040–2520	133	134	135	136	137	138
6.6–7.0/2040–2520	139	140	141	142	143	144
0.6–1.8/2520–3000	145	146	147	148	149	150
1.8–3.0/2520–3000	151	152	153	154	155	156
3.0–4.2/2520–3000	157	158	159	160	161	162
4.2–5.4/2520–3000	163	164	165	166	167	168
5.4–6.6/2520–3000	169	170	171	172	173	174
6.6–7.0/2520–3000	175	176	177	178	179	180

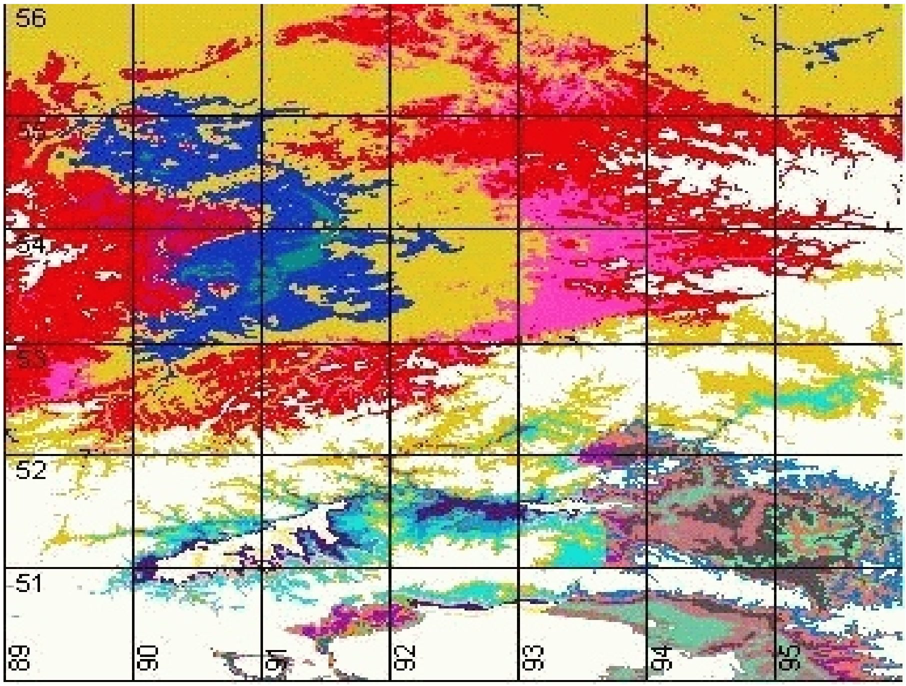


Figure 3a. Distribution of *Pinus sylvestris* climatypes in the Sayan Mountains in the current climate.

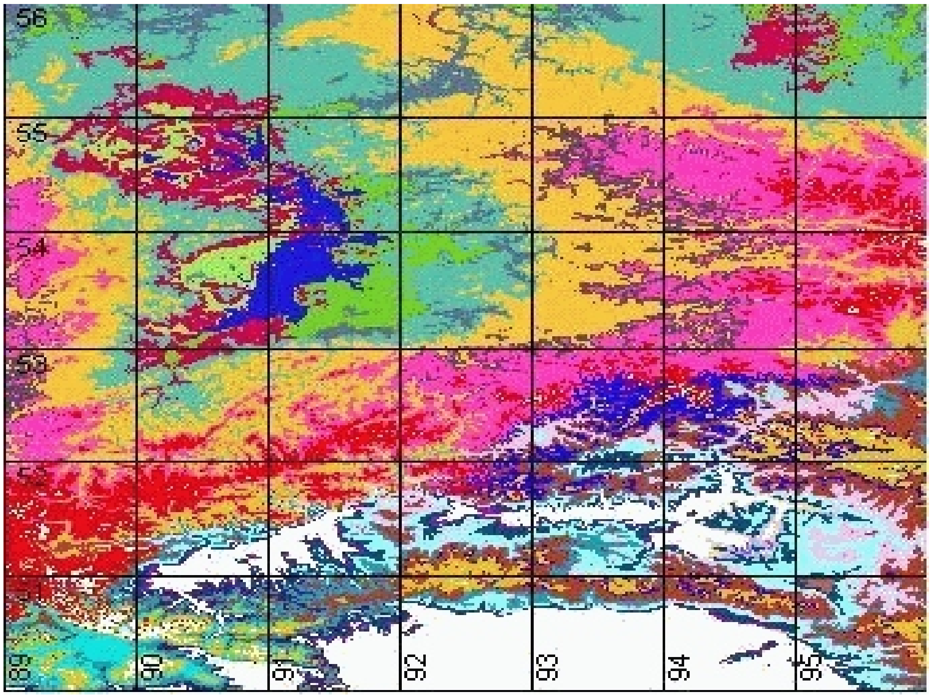


Figure 3b. Distribution of *Pinus sylvestris* climatypes in the Sayan Mountains in a warm climate. Different colors are 180 climatypes according to Table 3. Not all climatypes are realized in actual climatic space. White means that pine does not occur in a given climate.

Table 4. Areas (km^2) of seed zones for *Pinus sylvestris* in current and warmed climates in the Sayan Mts

Climatype number	Current climate	Proportion (%)	Warmed climate	Proportion (%)
0	93 383	29.16	29 282	8.90
2	5 565	1.72		
3	21 556	6.79	8 676	2.67
4	47 974	15.76	18 293	5.77
5			0.7	0.00
8	6 618	2.03		
9	7 985	2.47	4 331	1.31
10	6 004	1.99	67	0.02
14	1 743	0.53		
15	1 652	0.51	64	0.02
20	525	0.16		
21	253	0.08		
26	309	0.09		
32	70	0.02		
39	113		6 884	2.16
40	13 993	4.60	37 131	11.99
44	1 715	0.53		
45	798	0.25	19 729	6.11
46	59 278	19.87	12 181	
50	6 250	1.93		
51	2 406	0.74	8 779	2.69
52	16 900	5.55	46	0.01
56	4 592	1.41		
57	2 835	0.87	2 060	0.63
58	1 625	0.53		
62	4 020	1.22		
63	2 143	0.66	617	0.19
68	1 112	0.34		
69	495	0.15	86	0.03
76			9 033	2.94
81			1 201	0.38
82			44 558	14.70
87			8 522	2.64
88			43 240	14.46
92			5	0.00
93			9 929	3.06
94			12 455	4.14
98			315	0.10
99			7 367	2.27
100			3 511	1.16
104			34	0.01
105			1 610	0.49
106			72	0.02
118			35	0.01
124			8 003	2.70
130			7 914	2.62
134			24	0.01
135			453	0.14
136			4 876	1.60
140			51	0.20
141			465	0.14
142			20	0.01

A comparison of the current and future distribution of climatypes (Fig. 3) shows that by the end of this century, there should be a complete redistribution of climatypes across the entire region. Two of the three most important climatypes of the future, # 82 and # 88, do not exist in the region today (Table 3). The third, # 40, which is expected to cover 12% of the region in the future, currently occupies only 4.6%. The two huge contemporary climatypes, # 4 and # 46, should still be present in the future but are expected to occupy only about 5% of the total area. Twelve climatypes that occur in the region today are not expected to be present in the future, and 23 that should be present in the future do not occur in the region today. Even though contemporary and future climates are expected to have only 13 climatypes in common, their geographic locations should change greatly. Indeed, except for their physiognomic basis, Figs. 3a and b have very little in common.

Larix sibirica Of the 48 possible combinations of our climate classes (Table 5), 24 occur today within the Sayan Mountains (Table 6, Fig. 4a). These climatypes cover approximately 67% or the region, thus suggesting that 33 % lie outside the climatic limits of *L. sibirica*. Of the 24 climatypes, 11 cover < 1% or the area and only 5 cover more than 5%. Two of the climatypes, # 1 and # 3, are huge, covering 19 and 17 % of the total area, respectively. These two, therefore, account for almost one-half of the area that is climatically suitable for larch (Fig. 3a).

The climate in the decade beginning in 2090 is expected to become more amenable to larch, with about 92% of the land then lying within the species climatic limits (Fig. 4b, Table 6). This represents an increase of 24%, or about 75 500 km^2. This greater suitability for larch in the future climate is also reflected by the presence of 34 climatypes, an increase of 10. As a result, 71% of all of the potential larch climatypes should be found within the Sayan Mountains. As before, however, only six of the climatypes should occupy more than 5% of the region, and of these, only one, # 20, is huge.

Figure 4a and b, illustrates the change in the distribution of climatypes that would be expected for the decade beginning in 2090. While the present and future climates should have 20 climatypes in common, their relative importance (Table 6) and geographic positions (Fig. 3b) change greatly. Climatypes # 1 and # 3, which are huge in the contemporary climate, should occupy < 5% of the area in the future. Likewise, climatype # 20, which should dominate in the future climate, covers < 1% of the area today. In total, 7 climatypes that occur in the region today are not expected in the future and 14 that should be present in the future do not occur in the region today. As for *P. sylvestris*, the changing climate will have far reaching effects on the distribution of *L. sibirica* climatypes in the Sayan Mountains.

DISCUSSION

Climate change obviously will alter the adaptedness of forest tree species that are composed of climatypes. Genotypes of sessile forest trees simply cannot track their optimal climate as it changes. Our results join with those on *Pinus contorta* (Rehfeldt et al. 1999b, 2001) and *P. sylvestris* (Rehfeldt et al. 2002) to illustrate that intraspecific adjustment to change will not be trivial. Adjusting to global warming will require a wholesale redistribution of genotypes across the landscape to re-align climatypes in the novel climates and thereby maintain optimal forest growth and productivity (Rehfeldt et al. 2001). Response to climate change, therefore, is much more than a shifting of species' distributions (Davis and Shaw 2001). Indeed, effects of a changing climate reverberate throughout a species' distribution as genotypes become re-shuffled across the landscape (Rehfeldt et al. 1999b, 2002).

Our analyses suggest that by 2090, the climate of the Sayan Mountains should be more amenable for both *P. sylvestris* and *L. sibirica* than it is today. Nonetheless, the distribution of climatypes is expected to undergo a complete overhaul. The prominent climatypes of today should either be absent from or minor in the future forests. Likewise, the most prominent climatypes expected in the future are either absent or minor today. Even those climatypes that should remain in the landscape throughout the present century are expected to change in position and importance. To be sure, climate change as predicted by the Hadley GCM, should have widespread effects on the distribution of genotypes within these species.

Table 5. 48 possible combinations of climatic indices (GDD_5, AMI and $NDD_{o)}$) for *Larix sibirica* climatypes in Russia

Annual moisture index/Growing degree-days, 5°C	Negative degree-days (0°C)	
	-4500 – -2200	-2200 – -1200
0.8–1.8/ 650–1300	1	2
1.8–2.8/ 650–1300	3	4
2.8–3.8/ 650–1300	5	6
3.8–4.8/ 650–1300	7	8
4.8–5.8/ 650–1300	9	10
5.8–6.8/ 650–1300	11	12
6.8–7.8/ 650–1300	13	14
7.8–8.5/ 650–1300	15	16
0.8–1.8/ 1300–1950	17	18
1.8–2.8/ 1300–1950	19	20
2.8–3.8/ 1300–1950	21	22
3.8–4.8 / 1300–1950	23	24
4.8–5.8/ 1300–1950	25	26
5.8–6.8/ 1300–1950	27	28
6.8–7.8/ 1300–1950	29	30
7.8–8.5/ 1300–1950	31	32
0.8–1.8/ 1950–2350	33	34
1.8–2.8/ 1950–2350	35	36
2.8–3.8/ 1950–2350	37	38
3.8–4.8 / 1950–2350	39	40
4.8–5.8/ 1950–2350	41	42
5.8–6.8/ 1950–2350	43	44
6.8–7.8/ 1950–2350	45	46
7.8–8.5/ 1950–2350	47	48

Table 6. Areas (km^2) of seed zones for *Larix sibirica* in current and warmed climates in the Sayan Mts

Climatype number	Current climate	Proportion (%)	Warmed climate	Proportion (%)
0	103 636	32.53	26 043	7.96
1	58 330	18.84	26 741	8.33
2	14 945	4.95	19 482	6.27
3	50 777	16.68	12 845	3.94
4	15 064	5.03	142	0.04
5	20 351	6.52	2 325	0.70
6	2 501	0.83		
7	6 179	1.92	667	0.20
8	46	0.02		
9	2 753	0.84	154	0.05
11	1 355	0.41	3	0.00
13	552	0.17		
15	286	0.09		
17	261	0.08	5 532	1.76
18	93	0.03	24 060	7.85
19	4 276	1.40	14 863	4.65
20	2 376	0.78	39 466	12.97
21	4 855	1.60	14 191	4.40
22	4 009	1.29	22 296	7.41
23	5 923	1.89	10 619	3.27
24	1 117	0.36	7 489	2.48
25	3 420	1.05	7 789	2.39
26			1 583	0.52
27	3 755	1.15	4 397	1.35
28			264	0.09
29	3 264	0.99	2 657	0.81
30			3	0.00
31	175	0.54	1 167	0.36
36			3 127	1.02
38			20 078	6.76
39			0.8	0.00
40			23 130	7.77
41			1 020	0.31
42			8 339	2.75
43			2 207	0.68
44			4 484	1.47
45			2 700	0.83
46			4.4	0.00
47			2 053	0.63

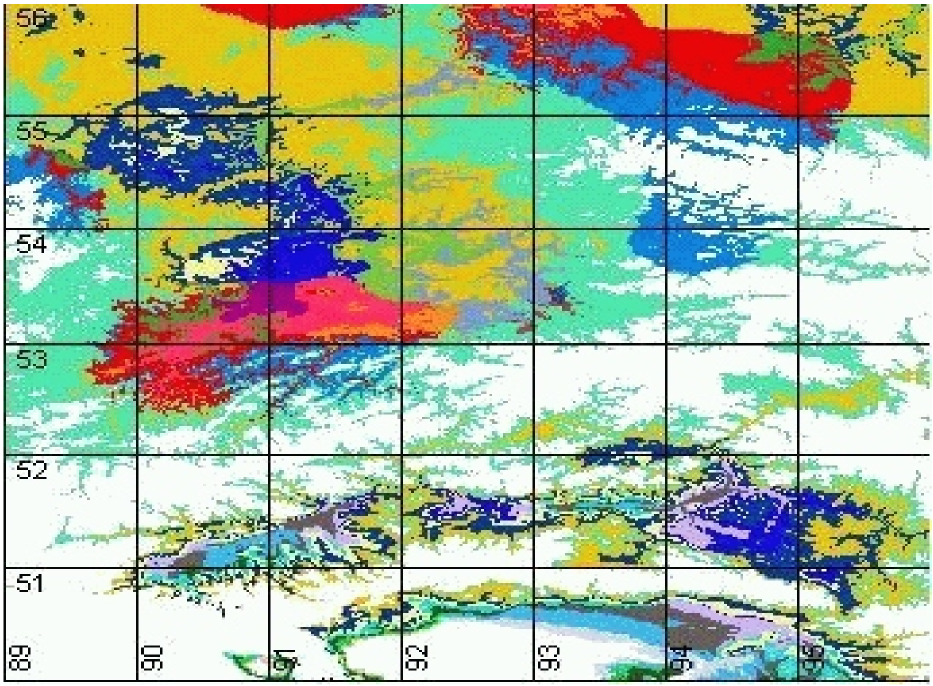


Figure 4a. Distribution of *Larix sibirica* climatypes in the Sayan Mountains in the current climate.

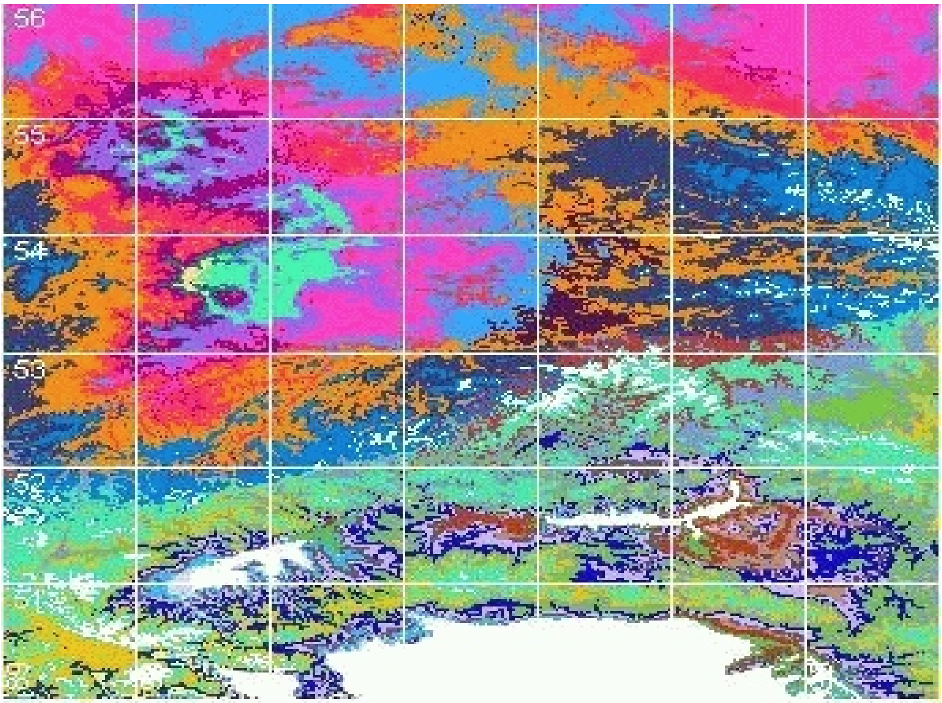


Figure 4b. Distribution of *Larix sibirica* climatypes in the Sayan Mountains in a future warm climate. Different colors are 48 climatypes according to Table 5. Not all climatypes are realized in actual climatic space. White means that larch does not occur in a given climate.

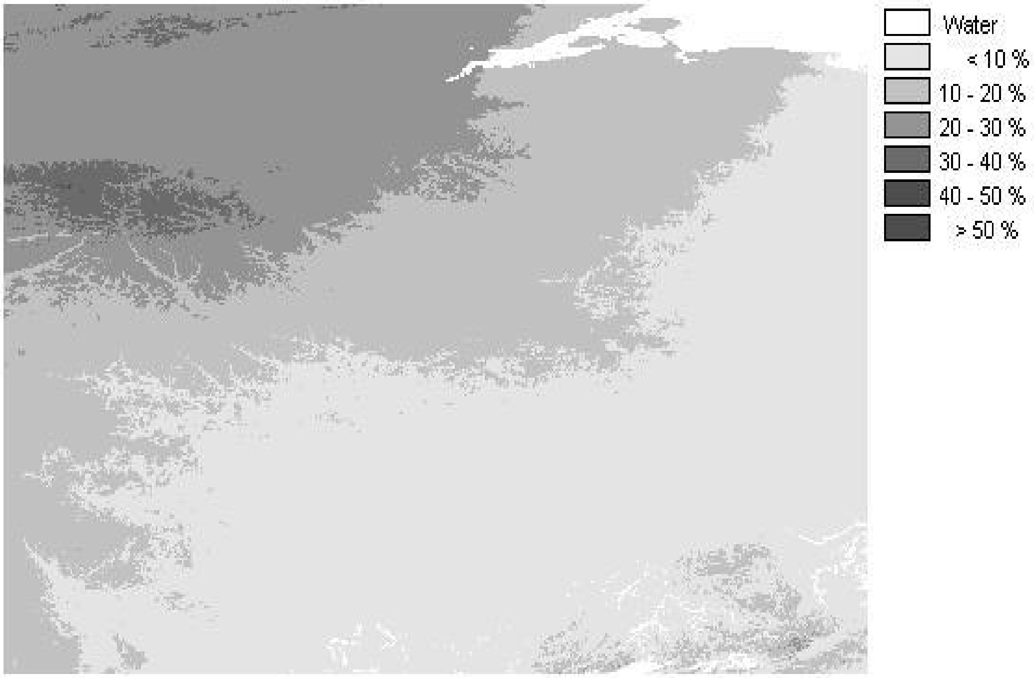


Figure 5a. Percentage of the freezing layer decrease by 2090 with respect to the current climate.

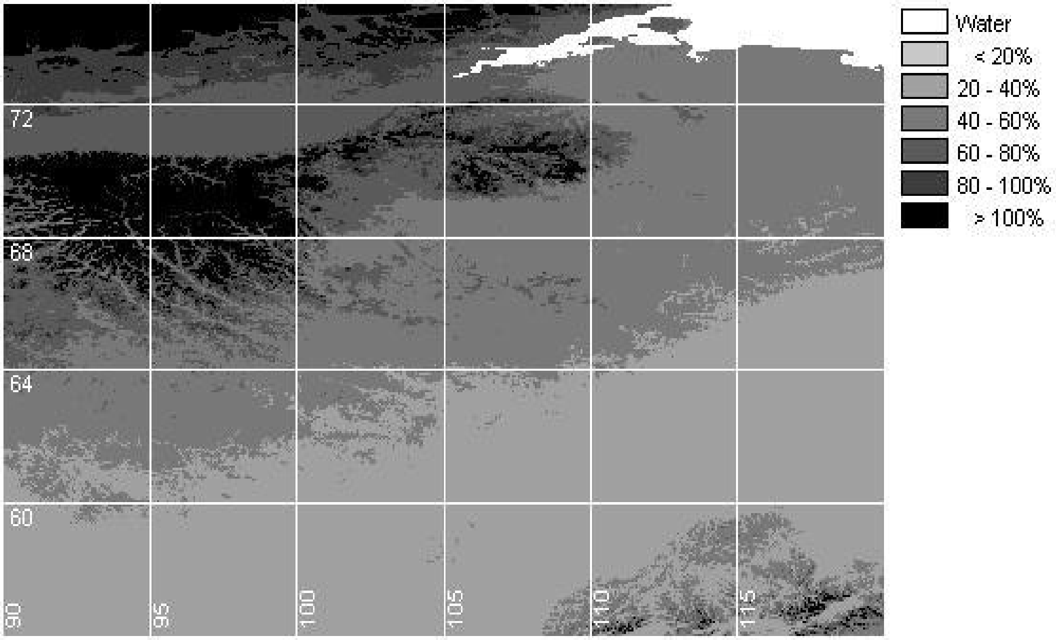


Figure 5b. Percentage of the thawing layer increase by 2090 with respect to the current climate.

As an indication of the scope of these intraspecific effects, it is instructive to assess the contemporary location of the climatypes expected to be of future importance in the Sayan Mountains. Of the three *P. sylvestris* climatypes expected to dominate future forests, one, # 40, is a minor component of the contemporary array. Nevertheless, this climatype is much more prevalent today toward the southwest in the foothills of the Altai Mountains, nearly 700 km away. Climatypes # 82 and # 88, which will be new to the Sayan Mountains, are currently present as isolated populations in Kazakhstan and Bashkiria, about 1 500 km and 20 degrees of longitude to the west. Climatype # 20, for *L. sibirica*, which is to be of future importance, also is present today in the Altai Republic. However, the climatic conditions with which this climatype is associated also can be found west of the Ural Mountains in European Russia. Because the dominant larch west of the Ural Mountains is *L. sukaczewii,* it is possible that the future climates of the Sayan Mountains may be suited to a mixture of larch species and their hybrids. Regardless, it is clear that the genotypes expected to be of importance to the future vegetation of the Sayan Mountains currently reside at long distances from their future habitat. These distances further illustrate the magnitude and complexity of the intraspecific adjustments necessary for the forest vegetation of the future to become physiologically attuned to the novel climate.

Migration and natural selection undoubtedly are the processes that will control the evolutionary adjustments necessary for plants to accommodate a changing climate. While migration is the only feasible means by which genotypes can invade and become established in climates beyond their contemporary distributions, natural selection is the process by which genotypes change when exposed to novel climates. Although rates of migration tend to be slow (Davis 1989), responses to selection can be rapid. Nonetheless, there is a limit to the amount that genetic systems can change in a single generation of selection. Estimates for *P. contorta* (Rehfeldt et al. 2001) and *P. sylvestris* (Rehfeldt et al. 2002) suggest that for Siberia, 5 to 10 generations may be required for the evolutionary process to adjust to global warming. This process, therefore, may take several centuries even where species' distributions are not changing.

Migration becomes even more problematic when dealing with the vegetation shifts illustrated in Fig. 2. Obviously, vegetation zones of either the plains or mountains will not shift as a unit. Individuals migrate, and, as a result, contemporary plant associations may or may not re-assemble in the novel climates. Nonetheless, the paleogeographic record demonstrates that the process by which migrants adjust to novel climates is complex and slow, requiring millenia. Because ongoing climate warming (3–6°C) is predicted to occur for 50–100 years, changes in vegetation due to migration should, first, lag far behind the climatic shifts (see Tchebakova et al. 1994) and, second, disrupt vegetation zones. Only seven species can withstand the severe contemporary climates of Siberia: five conifers (*P. sibirica*, *P. obovata, P. sylvestris, Larix* spp., and *A. sibirica*) and three broadleafs (*B. pendula*, *B. pubecens*, and *Populus tremulus*). Until natural selection adjusts the available genetic variability, it is concievable that none of the available genotypes of these species would be suited to the novel climate. If a species occurs under conditions beyond its climatic optimum it declines. For example, the southern tree border of species distributions are expected to shift northwards because moisture stresses will increase. A favorable climate, moreover, would promote competetive abilities of species inhabiting their climatic optima and these species may become dominating. For example, the growth of dark-needled species like *P. sibirica* and *A. sibirica* is expected to be enhanced in the middle taiga in a warmed climate. So, vegetation redistribution would depend on the joint actions of seed dispersal and environmental selection, with the latter determining which genotypes of which species become, first, established and, second, competitively exclusive. However, in the mountains vegetation redistribution due to tree migration seems feasible over short periods of 50–100 years. This is because migration of adapted genotypes across mountainous landscapes only needs to occur across a few hundred meters in order for genotypes to track the climate to which they are adapted optimally. For this reason, mountains readily serve as refuges during times of extripation.

Fire is another factor that is capable of influencing the speed by which vegetation adjusts to climate change. In the short term, fire will aid the redistribution of vegetation by opening sites for colonization that were previously occupied. In fact, forest fire succession is predicted to dominate central Siberia (Furyaev et al. 2001), and in doing so should increase the abundance of *Betula* spp. in warm zones and *Larix* spp. in cold zones.

In accounting for the effects of climate change on the vegetation, permafrost cannot be ignored. To be sure, permafrost is the principal factor controlling the distribution of vegetation in central Siberia and Yakutia. First, it allows forests to develop in areas where otherwise semi deserts would occur (Shumilova 1964). Second, it limits the eastward spread of dark-needled species (*P. sibirica*, *P. obovata*, and *A. sibirica*) in Siberia. Inside the permafrost zone, these dark-needled species can reach high latitudes only on sandy soils along river valleys and benches where permafrost may thaw as deep as 1–1.5 m (Shumilova 1964). *Larix gmelini* and *L. cajanderi*, by contrast, may grow on soils which thaw only about 10–30 cm in summer (Abaimov et al. 1999). Under the climate change scenario we used in this study, the heat resources will be available for melting permafrost. From Stefan's formula (Dostavalov and Kudriavtsev 1967), we estimated the ratio of the depth of the freezing layer during contemporary winters and those expected under a changing climate (Fig.

5a) and the ratio of the depth of the thawing layer during contemporary summers and those expected under a changing climate (Fig. 5b). The depth of the freezing (or thawing) layer is proportional to the square root of the ratio NDD_0 (or GDD_5) in future to current climates. At the highest latitudes, much milder winters and warmer summers should promote a rapid demise of the permafrost, especially in mountains. As a result, dark-needled species would be expected to track the retreating permafrost and thereby invade the Taymyr Peninsula and the Putoran and Anabar Plateaus, which are currently dominated by tundra and forest-tundra. The presence of dark-needled species at these locations during warm epocs is supported by pollen spectra (Khotinsky, 1977) from the mid-Holocene. In the middle latitudes covering about 65% of our area, the depth of thawing should increase by 40–60%. This amount of thawing most likely is not sufficient for allowing dark-needled species to become established. As a result, light-needled taiga would dominate this area. In the south, the thawing layer is predicted to increase only 20–40%, an amount that should allow forest-steppes and steppes to develop.

A tremendous amount of water stored in the permafrost of the northern plains and mountains is expected to be released under rapid warming. The release of this water undoubtedly will have a large impact on the Siberian landscapes. A part of this water collected from the basins of two big rivers, Lena and Khatanga, will flow directly into the Arctic ocean and may flood the coastal area between Khatanga and Olenek Bays. Another part of the water collected from the basins of the other two big rivers, Nizhniaia Tunguska and Kureika, will flow into the Yenisei River near the Arctic Circle. Our rough estimates of the possible flooding of its lower left bank occurring in the West Siberian Plain show that it may cover at least 1–2 km.

All together, our analyses thus demonstrate the far-reaching effects of a changing climate on the ecologic distribution and genetic composition of future forests. Forest zones and species boundaries are expected to change at the same time that genotypes within species will be redistributed within species. Because analogs to the future forests of Siberia exist within the present-day distributions, there is no doubt that the vegetation is capable of adjusting to the predicted changes. Current estimates, however, suggest that redistribution of forest zones and climatypes will require long periods to adjust to the amount of change being predicted. From the ecological perspective, therefore, it is the speed of warming rather than the absolute amount of warming that is most foreboding. Indeed, the lag in vegetal response to rapid change suggests that if the climate does not stabilize, the vegetation may never be able to approach equilibrium. From the practical viewpoint, therefore, it seems obvious that maintaining optimal levels of productivity in Siberian forests will require the participation of mankind in the natural processes to assure that the appropriate species and genotypes appear in the appropriate climates in a timely manner.

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CLIMATE CHANGE: IMPACTS AND ADAPTATION IN FORESTRY

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ABSTRACT

Current changes in climate are already affecting forest species. Future climate change will bring greater changes in range of occurrence, forest disturbance, and growth rates. These changes in turn will affect society's ability to use forest resources. We already take account of climate in forest management; in the future we will have to apply these techniques with a greater intensity and in different areas. Climate change adaptation strategies for the forest management sector should be based on the application of vulnerability assessment or risk management concepts. An adaptation plan must address biophysical and socio-economic impacts and include policy and institutional considerations. We will need to evaluate current vulnerability, speed recovery after disturbance, and reduce vulnerability to further climate change. The adaptation plan should include monitoring the state of the forest to detect change to aid determining when to intervene. An example of using this framework to adapt to changing forest productivity is presented. Many forest ecosystems and species will have to adapt autonomously because management can only influence the timing and direction of forest adaptation at selected locations. In general, society will have to adjust to how forests adapt. Sustainable forest management already embodies many of the activities that will be required to respond to the effects of climate change on forests. Including adaptation to climate change, as part of forest planning, does not necessarily require a large financial investment now with an unknown future payback time.

INTRODUCTION

By the end of the 21st century, the mean annual temperature for western North America could be 2–5°C above the range of temperatures that have occurred over the last 1 000 years (Houghton et al. 2001). An increase in winter precipitation and a decrease in summer precipitation may also occur. These changes would significantly affect forest ecosystems and their utilization by society (McCarthy et al. 2001, Spittlehouse and Stewart 2003). Predicted changes include the movement of species ranges northward and up in elevation with new assemblages of species occurring in space and time (Hebda 1997, Kirschbaum 2000, Hansen et al. 2001). Forest management decisions are usually based on the assumption that the climate will remain relatively stable throughout a forest's life. This may have worked well in the past, but future climate change challenges this assumption. Canada's natural resources and associated industries and communities are vulnerable to climate change and there is a need for the forestry community to be proactive in adapting to climate change (Davidson et al. 2003, Standing Senate Committee on Agriculture and Forestry 2003, Spittlehouse and Stewart 2003).

Adaptation to climate change refers to adjustments in ecological, social, and economic systems in response to the effects of changes in climate (Smit et al. 2000, Smit and Pilifosova 2001, Davidson et al. 2003). The development of adaptation measures for some time in the future, under an uncertain climate, in an unknown socio-economic context is bound to be highly speculative (Burton et al. 2002). Some people may view responding as a greater risk than doing nothing, or that adaptation is not a feasible option. Although forest ecosystems will adapt autonomously, their importance to society means that we may wish to influence the direction and timing of this adaptation at some locations. In other cases, society will have to adjust to whatever change brings.

This paper is based on Spittlehouse and Stewart (2003). My objective is to encourage the forestry community to begin assessing its vulnerability to climate change and develop adaptation strategies. I will present a brief summary of current and possible future changes in the environment and forest ecosystems and then present a framework for determining options to adapt to climate change.

CURRENT AND FUTURE CHANGES IN BC

Globally, there has been an increase in mean annual air temperature of over 0.5°C in the last 100 years. British Columbia has seen similar or greater changes, particularly in winter minimum temperatures, and with the increase being greatest in northern regions (Anon. 2002). There has not been a consistent long-term change in precipitation. Possible responses to these changes in temperature include retreating of glaciers, shift in the annual hydrograph, permafrost melt and increase in landslides in the north, and changes in fire occurrence (Leith and Whitfield 1998, Anon. 2002, Clague 2003, Gillet et al. 2004). There are no long-term measurements to allow assessment of biological response in British Columbia (BC)'s forest ecosystems to these changes. However, world-wide there are reports of an earlier start to the growing season, earlier arrival of migratory birds, increase in boreal forest productivity, earlier breeding of animals and genetic adaptation in resident populations (Stewart et al. 1998, Climate Change Impacts and Adaptation Directorate 2002, Stenseth et al. 2002, Walther et al. 2002, Reale et al. 2003).

Possible future climates for BC are presented in Table 1. The range of values reflects the uncertainty in future greenhouse gas emissions and differences in how the various models simulate the climate. All projections show a warming that tends to be greater in northern areas and larger in winter and spring. Winter precipitation is expected to increase and summer precipitation may increase or decrease. A number of factors will control biological responses to these climate changes. They include the rate and magnitude of climate change, species and population sensitivity to climate, fecundity, life span, habitat requirements, current distribution, frequency, timing and size of disturbance (fire, disease, insects, harvest), competition, barriers to movement and human adaptive actions. Climate change impacts for BC include: species ranges moving northward and up in elevation (Hebda 1997), increase in the frequency, intensity, and timing of disturbances such as fire (Stocks et al.1998) and pests (Sieben et al. 1997, Carroll 2003), change in forest productivity (Spittlehouse 2003) and change in biome distribution (Scott et al. 2002). For example, by 2080 there could be a significant expansion of true grassland and the forest/grassland transition climates in southern BC (Hebda and Spittlehouse, unpublished data); though how rapidly such changes may translate into movement of species is uncertain (Loehle 2003). Species ranges may be reduced if the current warmer/drier end of a range becomes unsuitable and species are unable to move into areas where the climate is suitable because of slow migration rates, unsuitable growing substrate or lack of habitat (Stewart et al. 1998). Some species will adapt better than others. Harding and McCullum (1997) suggested that in BC and Yukon about 70% of the bird and ungulate species and 20% of fish species would have an increase in habitat under climate change, while the remainder would have a loss.

Table 1. Future climate scenarios for 2020 and 2080 for southern and northern British Columbia presented as changes from current conditions. Data encompass predictions from eight global climate models, though there are outliers outside the ranges presented. Data are available from the Canadian Institute for Climate Studies (http://www.cics.uvic.ca/scenaros/index.cgi?Scenarios).

	2020		2080	
	Temp. (°C)	Precipitation (%)	Temp. (°C)	Precipitation (%)
Southern				
Winter	0 to 2	-5 to 15	2 to 6	0 to 25
Spring	0.7 to 1.7	-3 to 10	2 to 6	-5 to 15
Summer	1 to 2	-25 to 5	3 to 7	-45 to 5
Fall	0.7 to 1.5	-5 to 5	2 to 6	-5 to 15
Northern				
Winter	0 to 2	0 to 15	3 to 10	5 to 45
Spring	0.5 to 2.5	2 to 20	2 to 8	5 to 50
Summer	0.5 to 1.5	-10 to 17	2 to 6	-10 to15
Fall	0.5 to 2	-5 to 10	2 to 6	10 to 25

Forest management activities will not be immune to the effects of climate change. We already take account of climate in forest management; in the future we will have to apply these techniques with a greater intensity and in different areas. Fire management is an obvious example and we may need to focus on the protection of areas with high economic or social value, while in other areas fire is allowed to run its course (Stocks et al. 1998, Parker et al. 2000). Increasing winter precipitation will affect water management in forests. An increased risk of sediment transport to streams threatens water quality and fish spawning habitat. Warmer winters will reduce the opportunities for winter logging in areas where the frozen surfaces of forest roads and ice bridges are essential for site access, and where a snow pack is necessary to protect the land during harvesting (Pollard 1991). Harvesting restrictions could increase due to the increased risk of landslides under heavy rainfall. There will be changes in wood quality and timber supply locally and globally, and market impacts will not be uniformly distributed (Perez-Garcia et al. 2002). A changing climate means that the geographic extent of seed transfer zones will change. Thus we need to determine the limits of transferability of species and genotypes and develop new regeneration strategies (Ledig and Kitzmiller 1992, Rehfeldt et al. 1999, Parker et al. 2000). We will need to re-evaluating conservation and recovery programs because rare and endangered plant species usually have specialized environmental requirements and low genetic diversity (Peters 1990, Hansen et al. 2001). Attributes that parks and wilderness areas were designed to protect may no longer exist within the protected area (Halpin 1997, Scott et al. 2002) and a ‘hands-off” approach to wilderness management may not be an appropriate response.

ADAPTATION TO CLIMATE CHANGE IN FORESTRY

Forecasting impacts is difficult because of our limited knowledge about the vulnerability of ecosystems and species, and the poor spatial and temporal resolution of the future climate. Although we do not have a clear view of the future climate and forest, it is critical to begin the process of developing adaptation strategies now. Adaptation to climate change in forest management requires a planned response well in advance of the impacts of climate change. Evaluating vulnerability is critical for developing adaptation strategies. Vulnerability is the degree to which a system (organism, ecosystem, company, or community) is susceptible to, or unable to cope with, adverse effects of climate change. It depends on the magnitude and rate of climate change, sensitivity to climate, and the system’s adaptive capacity. Adaptive actions reduce the risks (decrease vulnerability) by preparing for adverse effects and capitalizing on the benefits. However, intervention will be selective and there will be impacts that cannot be prepared for or anticipated. Spittlehouse and Stewart (2003) presented an extensive list of adaptive actions proposed in the literature for forest management.

Adaptation requires (Dale et al. 2001, Spittlehouse and Stewart 2003) that the forestry community:
1) Establish objectives for the future forest under climate change.
2) Increase awareness and education within the community about adaptation to climate change.
3) Determine the vulnerability of forest ecosystems, forest communities, and society.
4) Develop present and future cost-effective adaptive actions.
5) Manage the forest to reduce vulnerability and enhance recovery.
6) Monitor to determine the state of the forest and identify when critical thresholds are reached.
7) Manage to reduce the impact when it occurs, speed recovery, and reduce vulnerability to further climate change

I focus here on a framework for planning adaptive actions. It is a format for risk analysis of which there are many examples in the literature (Kelly and Alger 2000, Davidson et al. 2003, Spittlehouse and Stewart 2003, Turner et al. 2003). A plan for facilitating adaptation in forestry must address biophysical and socio-economic impacts and will include policy and institutional considerations. First we need to identify the issue of concern. Next comes the assessment of the vulnerability (sensitivity, adaptive capacity) of the forest, forest dependent communities, and society in general to climate change. This assessment facilitates the development of adaptive actions to be taken now and those required for the future as change occurs. Current activities include those that facilitate future responses to reduce vulnerability. Adaptation options must include the ability to incorporate new knowledge about the future climate and forest vulnerability as they are developed. Until climate change has had sufficient impact to warrant intervention it is likely that in many situations there is a not much that is to be done ‘on the ground, in the forest’ for a few decades. However, we need to have a suite of options ready to go when we do wish to intervene; thus there is work to do now.

The following is an example of using the framework noted above on the effect of climate change on a managed forest. Other examples can be found in Spittlehouse and Stewart (2003). This example is not in the detail required for a full analysis but is presented to show how the risk analysis might take place.

Issue: A managed forest under climate change.

Vulnerability: Lower summer precipitation and increased temperature – reduce growth rates, change wood quality, increase the risk of disturbance by fire, insects and disease, change in species suitability, change in wildlife habitat, loss of recreational opportunities.
Increased winter precipitation and temperature – increase risk of erosion, increase in streamflow, reduced winter logging opportunities

Options for the future: Adjust rotation ages, utilise small logs, increase salvage after disturbance by fire and insects, modify seed transfer zones, upgrade culverts.

Actions to do now: Replace geographically defined seed transfer zones with zones defined by climate, identify policy and knowledge barriers to implementation, develop harvesting and wood processing technology to meet the future fibre supply.

Climate change adaptation strategies can be viewed as the risk management component of sustainable forest management plans. Actions can be taken that are useful now, but would also reduce the risk of unacceptable losses in the future. As can be seen in the above example, many actions required in adapting to climate change benefit the present as well as the future. Spittlehouse and Stewart (2003) proposed a number of questions that need to be addressed to facilitate adaptation planning. These included: what are the research and educational needs; what are barriers to the implementation of adaptation in forest management; what forest policies need to be in place to facilitate adaptation; and are current monitoring systems adequate to spot problems induced by climate change soon enough to allow implementation of an acceptable response?

CONCLUSIONS

Current forest utilization and preservation is based on how forests developed under past climatic conditions. Policy-makers and forest managers must accept that climate change in the near term is probable and that forests and forest dependent communities face significant challenges. Planned adaptation will reduce the vulnerability of commercial tree species at selected sites. However, many forest species will have to adapt autonomously and society will have to adjust to the result. Until climate change has had sufficient impact to warrant intervention it is likely that in many situations there is not much that can be done in the forest at present. However, it is necessary to start assessing forest vulnerability to climate change and developing adaptation strategies. Sustainable forest management already embodies many of the activities that will be required to respond to the effects of climate change on forests. Including adaptation to climate change as part of forest planning does not necessarily require a large financial investment now with an unknown future payback time.

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VOLUNTEER PAPER ABSTRACTS

TOWARDS THE DEVELOPMENT OF A COMPOSITE GENETIC MAP IN WHITE SPRUCE

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Comparative mapping is an alternative method for non-model species to better understand their genome organization and highlight homeologous chromosomic segments involved in adaptative and economical traits. Recently, (Pelgas et al. 2004, Mol. Breed.), we developed over one hundred multiallelic ESTP anchor markers for comparative mapping between *Picea mariana* (Mill.) BSP and *P. glauca* (Moench) Voss, two evolutionarily distant species in the genus *Picea*. Among these, more than 50 ESTP markers were identified as potential candidate genes involved in abiotic stresses and/or wood formation, and polymorphisms (either SNPs or indels) were detected for all of them. All ESTP markers were used in combination with AFLPs and microsatellite markers to generate a composite map for *P. glauca*. Two crosses were selected with one parent in common to maximize the number of segregating ESTPs. Up to now, four individual linkage maps have been constructed from these crosses, with a length ranging from 2 045 cM to 2 801 cM and a marker density of about 8.4 cM. The use of two pedigrees in *P. glauca* resulted in 25% additional anchor markers useful for interspecific comparison with *P. mariana*.

ECOLOGICAL GENETICS OF WHITEBARK PINE

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Whitebark pine (*Pinus* albicaulis) is considered a keystone species in the subalpine ecosystems where it occurs. It has been severely impacted throughout its range by the introduced disease white pine blister rust (caused by the fungus *Cronartium ribicola*) and by successional replacement. There is much concern about local extirpation in some areas and restoration efforts may be needed to maintain this species in areas where it is most vulnerable. Marker studies have indicated that whitebark pine populations are not well differentiated, however the level of differentiation based on quantitative traits was previously unknown. Seed collected throughout the range of whitebark pine has been grown in a common garden test on the University of British Columbia campus, to study the level of genetic differentiation among seed sources in quantitative traits. Seed weight and germination, phenology, growth, and cold hardiness have been assessed for a total of 157 open-pollinated families from 18 populations across the range of whitebark pine. The influence of various climatic and geographic variables on these traits has been examined to determine the degree and pattern of genetic differentiation among seed sources. There appears to be clinal variation for the timing of needle flush and cold hardiness in fall, spring, summer, with temperature of the parent tree location having the greatest influence on these traits. The clinal pattern of variation in these adaptive traits suggests that populations are adapted to their local environment; in which case, movement of seed should be carefully considered in order to minimize maladaptation of planting stock. The potential affects of climate change on whitebark pine will also be discussed.

EFFECTS OF GENOTYPE AND SILVICULTURE ON WESTERN HEMLOCK DIAMETER GROWTH AND WOOD DENSITY

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Wood quality is clearly responsive to genetics, with most traits having high heritabilities relative to growth traits. It is also apparent that site has a strong influence. It follows from this that silvicultural treatments might have an effect, and it is possible that there could be interactions between genotypes and silvicultural treatments. Seventy open-pollinated hemlock families in a progeny trial were thinned to two densities and aspects of cell morphology measured for the growth ring of the year before treatment, the year of treatment, and the year after. Similarly, on a separate site in the same series, the families were fertilized with either 300 or 600 kg/ha. In both studies the treatments resulted in improved growth, yet wood density was not diminished as might be anticipated. Family by treatment interactions were statistically significant in both investigations, however this result is rendered difficult to interpret because the treatment by family by year (growth ring) effect was not significant. Several possible explanations and some details of the results are rendered.

CLIMATE-CHANGE RESPONSE STRATEGIES AMONG THREE CO-OCCURRING, ECOLOGICALLY DISTINCT NORTHERN CONIFEROUS TREE SPECIES

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There remains considerable uncertainty about predicting the responses of trees and forests to climate change in Northern and high-elevation regions, where we anticipate the greatest future climate fluctuations. No general theory describing climate-driven responses among disparate tree species currently exists, owing to the diversity of ecological niches and growth strategies found among co-occurring species. Comparing species-specific tradeoffs in competition-survival traits across climate gradients (e.g., latitude, elevation) offers a systematic basis to characterize the response capacities of ecologically distinct tree species.

Inherent clinal responses for four quantitative traits thought to be adaptive in cold-limited environments were characterized in a controlled greenhouse study for three ecologically distinct and co-occurring Northern tree species: lodgepole pine (*Pinus contorta* Dougl. ex. Loud. var. *latifolia*, interior spruce *Picea glauca* (Moench) Voss x *Picea engelmannii* Parry ex Engelm., and subalpine fir *Abies lasiocarpa* (Hook.) Nutt.). For each species, clinal trends were quantified among populations adapted to increasingly cold-limited climates across a severe elevational gradient approaching the treeline.

Tradeoffs between competitive capacity and survival capacity across the climate gradient differed markedly among these tree species. Strong clinal trends observed in subalpine fir for all the quantitative traits indicated a highly conservative approach to climate response. Phenotypic plasticity in traits may be low among subalpine fir populations in severe climates and we might anticipate a limited capacity to express competitive responses to improving growing conditions under a warming climate. Trends in lodgepole pine and interior spruce suggested a more plastic strategy, favoring competitive traits across a wide range of climate conditions. These species might exhibit pronounced competitive responses to warming conditions, particularly near the cold extreme in the species climate ranges where high growth potentials are muted. Study findings suggest that it may be useful to characterize general differences among ecologically distinct species, such as early- and late-successional positions, in predicting forest responses to climate change.

POTENTIAL IMPACT OF CLIMATE CHANGE ON ECOSYSTEMS, SPECIES DISTRIBUTIONS, AND GENETIC RESOURCE MANAGEMENT IN BRITISH COLUMBIA

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One way to investigate whether expected global warming is likely to threaten forest ecosystems, tree species, or their genetic resources is through bioclimate envelope studies. We use canonical discriminant analysis to determine current climatic envelopes and subsequently a mahalanobis-distance based matching procedure to predict future distributions of various spatial units (ecological zones, species ranges, seed zones).

Ecological zones that are partially or entirely in mountainous areas have their climate envelope shifting upward. Most vulnerable is the Mountain Hemlock and Montane Spruce zone. Other large impacts are the initial expansion of the climatic envelope for Interior Coastal Hemlock and the rapid reduction of the Alpine Tundra and Spruce Willow Birch climates by 2025. Subsequently, Interior Douglas-Fir and Ponderosa Pine climate regions expand throughout the interior plateau replacing current climate envelopes of sub-boreal and boreal ecosystems between 2055–2085.

Tree species that have their current northern range limit within BC gain large amounts of new potential habitat, and increase in frequency where they already occur (e.g., *Pseudotsuga menziesii*). Hardwoods that already occur throughout British Columbia appear to be unaffected by climate change in their overall frequency but could potentially occupy higher elevations (e.g., *Betula papyrifera*). Some of the most important conifer species in British Columbia are expected to significantly decrease in frequency and loose a large portion of their suitable habitat (e.g., *Abies lasiocarpa*, *Picea glauca*, P. *engelmanii*, *P. mariana*, and *Pinus contorta*).

In British Columbia, transfer of seed and the use of planting stock from seed orchards is designed to match planting stock with climatic conditions where genotypes perform best. Using the same bioclimate envelope approach, coastal Seed Planning Units (SPUs) are predicted to shift upward in elevation by approximately 50 m per decade. Interior SPUs also shift northward at a rate of approximately 50–100 km per decade. SPUs currently covering the south (particularly NE) may provide suitable planting material for an extended portion of BC in the future.

More information: http://genetics.forestry.ubc.ca/hamann/climate

MODELLING FROST RISK IN NORWAY SPRUCE

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Norway spruce is most susceptible to frost injury from the time of budburst till the end of shoot elongation. Accumulated temperature sum can be used to predict the time of budburst for a defined genetic origin with relatively high precision. Thus, it is also possible to predict frost risk during the critical period of budburst and shoot elongation.

The purpose was to model the risk of frost occurrence during the critical period for Norway spruce of different genetic origins, i.e., for different critical temperature sums for budburst, for a reforestation site with defined geographic coordinates adjusted for local-scale topography. Effects of silvicultural practices on microclimate and time of budburst were also included in the model, e.g., shelterwood of various density and height, site preparation, seedling age, and seedling type. Long-term temperature records from a network of 357 climate stations throughout Sweden were used. The model can be used for predicting the effects of genetic origin and silvicultural practices both in large-scale at the national level and as an evaluation of a specific reforestation site. As an example of a large-scale output of the model, we found that the frost risk shifted from 20–30% to less than 10% throughout most of southern Sweden, if seedlings of Belarusian late-flushing provenances were chosen instead of the local provenance.

INITIATION OF STEM INFECTION IN WESTERN WHITE PINE BY BLISTER RUST

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The majority of early produced needle infection spots caused by a September inoculation of *Cronartium ribicola* were small and sectioning showed that the fungus readily gained access to the vascular cylinder of *Pinus monticola* by penetrating the endodermis. By inoculating only a portion of the foliage of *Pinus monticola* in September with *C. ribicola* and removing it at monthly intervals, it was determined that stem infection was initiated a month, or more, earlier than if seedlings had been classified as “cankered” by observing discoloured stems. Consequently, the majority of the reported “needle shedding resistance responses” in *Pinus monticola* seedlings to *C. ribicola* would be ineffective because they occurred after stem infection had already been initiated. Placing potted *P. monticola* seedlings beneath *C. ribicola* infected *Ribes nigrum* plants for weekly intervals resulted in infection from June through October in the interior of British Columbia. Because natural infections can occur earlier than September, stem canker initiation and development would be more advanced under natural conditions, than that determined from only a September inoculation, thus a “needle shedding resistance response” would be even less effective as a resistance response. These data are consistent with the notion that *P. monticola* lacks a “needle shed resistance response”.

GENETIC VARIATION IN TOLERANCE TO SWISS NEEDLE CAST IN COASTAL DOUGLAS-FIR

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Swiss needle cast (SNC) is impacting Douglas-fir (*Pseudotsuga menziesii*) in coastal Oregon and Washington and is reaching epidemic proportions along the north coast of Oregon. The genetic variation in tolerance to this disease has been investigated over the past 7 years. Foliage color and retention traits exhibit low to moderate heritabilities and tend to be less than heritabilities for growth traits assessed in the same trials. Foliage traits are correlated with subsequent growth in SNC areas, but selection on diameter growth seems to be the best single selection trait to obtain tolerance. Early selection for foliage traits is possible, but the economic benefits of early selection are not clear. Because we did not find family differences in the amount of fungus in needles, we propose that Douglas-fir exhibits tolerance, the ability to continue growth in the presence of the disease, as opposed to resistance, i.e., actively resisting the fungus. The tolerance mechanism is not completely understood, but some aspect appears to be associated with the tree's ability to shed unproductive needles. Although provenance variation has been shown for SNC tolerance, there is very little association between the climate of a seed source location and its tolerance level when examined within a seed zone. Breeding programs are actively underway to develop SNC tolerance and seed resulting from our most recent orchards should be appropriate for use in areas with moderate SNC symptoms.

EFFECT OF THERMAL CLIMATIC CHANGES ON VOLUME GROWTH RESPONSE IN SITKA SPRUCE

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The potential impacts of anticipated temperature increases due to climate change within the next century were modelled on population-level Sitka spruce (*Picea sitchensis*) volume growth. Twenty-year growth data from the series of IUFRO provenance trials planted throughout British Columbia, comprising 43 provenances representing the entire range of the species and replicated over 12 sites, were analyzed and used to predict volume responses. Data were corrected to remove potentially confounding effects of photoperiod change caused by latitudinal seed transfer. Projected increases in yield, primarily due to the longer growing season, will only result where summer precipitation is > 500 mm. In the maritime seed planning zones (approximately congruent with the moist and wet maritime and the hypermaritime subzones of the Coastal Western Hemlock biogeoclimatic zone) where summer precipitation is > 700 mm, up to 20% volume gain was predicted using the model. Results indicate that Sitka spruce will respond with a linear, rapid volume gain to increased precipitation and is less sensitive to rapid warming. Volume response due to more rapid accumulation of heat sum (4.3%) was approximately double that due to fewer frost free days (2.3%), given a mean annual temperature increase of 5°C. The actual impacts will be tempered by moisture availability, which current models can predict with only low certainty. Summer drought will likely be more prevalent, resulting in lower gains than predicted based on temperature alone.

GLOBAL WARMING AND THE CHILLING REQUIREMENT OF SOME CONIFERS

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The existence of a chilling requirement of some perennial, woody temperate zone plants has been recognized for over a century and has limited the areas suitable for establishment of non-indigenous trees. More recently, with the possibility of a general global warming, it may result in dramatically reduced survival and growth of both native and introduced plants. The term chilling requirement refers to the requirement of vegetative buds of some trees to be exposed for a period of at least several weeks to temperatures of about 5°C to prepare them for resumed growth in the spring. It may be considered analogous to the stratification requirement of some seeds.

Populations of potted 2-1 Douglas-fir (*Pseudotsuga menziesii*) seedlings, all in a receptive physiological state, were exposed for periods up to fifteen weeks to one of the following temperatures: 5, 7, or 9°C with an 8-hour daily photoperiod. During the subsequent 9-week growth period (15°C, 12-hour daily photoperiod) the incidence of bud break and new growth was recorded. Seedlings which had been exposed to five-degree temperature for thirteen weeks produced significantly faster bud break, had greater numbers of active buds, and weight of new growth.

A second study of grafted 2-1 Douglas-fir seedlings planted south of San Francisco was exposed to mean winter temperatures of 9–12°C. All seedlings and grafts had anomalous break the year after planting and most died within two years.

A third study of Douglas-fir seedlings grown under natural conditions in the Corvallis area but with mean temperatures raised 3½°C demonstrated reduced bud break and poor growth.

Accordingly, if the mean temperature of elevations below 300 m in the Willamette–Puget Sound–Gulf of Georgia Trench were to rise about 4°C between November and February we could expect to lose Douglas-fir and its associates.

WHITE SPRUCE LIMESTONE ECOTYPES: DO THEY REALLY EXIST?

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Previous laboratory and field studies have presented evidence for the existence of limestone ecotypes in white spruce (*Picea glauca* [Moench] Voss) from southern Ontario. Remeasurements made in 2001 of the range-wide 410 series of provenance trials were used for further evaluation of the existence of these ecotypes. Height measurements from 23 provenances grown at four test sites in Ontario, all located south of 46°N were used for the analysis. Digital coverage of the 1993 Ontario Geological Survey data set was used to classify test sites and provenances as occurring on either limestone or non-limestone parent material. While analysis of variance revealed significant differences among test sites and provenances, no significant interactions consistent with the existence of limestone ecotypes were detected. This finding is in contrast to that of an earlier field study that detected a strong interaction between test site and provenance bedrock type ($P < 0.001$). Examination of the relative performance of individual provenances from limestone and non-limestone bedrock types, revealed differences in performance at the four different test sites but few instances supporting the existence of limestone ecotypes. Results found in this study generally support a pattern of between-stand variation in southern Ontario. Although these results offer no support for the existence of limestone ecotypes in Ontario, they do not disprove their existence owing to the limitations of the 410 Series test design and the possible misclassification of provenances according to bedrock type.

APPLICATIONS OF SEED TRANSFER EXPERT SYSTEMS IN REFORESTATION AND RESTORATION

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There is an evolution of developing seed transfer guidelines from a two-dimensional zone approach to more sophisticated applications modeling patterns of genetic variation for adaptive traits in three dimensions. These models of continuous variation can utilize elevation, latitude, and longitude as independent variables or more recently, can focus on climatic variables. A natural extension of well designed genecological research is seed transfer expert systems. Based on 30 years of research by Dr. Gerald Rehfeldt of the USDA Forest Service in the Inland West has expert systems for *Pinus ponderosa* var. *scopulorum*, *Picea engelmannii*, and in cooperation with the Inland Empire Tree Improvement Cooperative for *Pinus ponderosa* var. *ponderosa*, *Larix occidentalis*, and *Pseudotsuga menziesii*. An expert system for *Pinus contorta* is under development. Adaptive traits or dependent variables typically consist of phenology, cold hardiness, and disease tolerance data. The basic approach to each model is as follows: a series of equations for each user query are satisfied and evaluated against each species' distribution, where coefficients of prediction do not exceed a least significant difference of 20%. Output can either be viewed as to where a particular seed lot can be planted, or given a parcel of land, where suitable cone collections can be made or existing seed lots utilized. Seed transfer expert systems are showing great promise in finding adapted planting stock following catastrophic fires in Montana, Arizona, Colorado, and New Mexico and on a more routine level, managing seed bank inventories on a regional basis.

SELFING RESULTS IN INBREEDING DEPRESSION OF GROWTH BUT NOT OF GAS EXCHANGE

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In most tree species, inbreeding greatly reduces seed production, seed viability, survival, and growth. In a previous large-scale quantitative analysis of a black spruce (*Picea mariana* [Mill.] BSP) diallel experiment, selfing had large deleterious effects on growth but no impact on stable carbon (*C*) isotope discrimination (an indirect measure of the ratio of net photosynthesis (*A*) to stomatal conductance ($g_{wv)}$)). It was hypothesized that selfing did not impact carbon gain via leaf level gas exchange but it did impair subsequent utilization of *C*. Alternatively, both *A* and g_{wv} may each have been impacted by selfing to the same extent. However, no gas exchange data were ever collected to further test these hypotheses. Here we present photosynthetic gas exchange data collected from three selfed families and three out-crossed families (all the result of controlled pollination) from the same diallel experiment. Photosynthetic responses to intercellular CO_2 concentration (A/C_i curves) were generated from four replicates per family, one block per day, over a four-day period in July. Results indicate no differences between selfed and out-crossed families in maximum carboxylation rate, maximum electron transport, (*A*) and g_{wv} (both estimated at 370 ppm CO_2 concentration), or the ratio A:g_{wv}. Selfed trees had higher mortality during the experiment thus it is possible that there were potential negative impacts on gas exchange of previously living selfed progeny. However, we clearly show that inbreeding can result in trees that have low productivity despite retaining high levels of leaf level A. Results are consistent with the hypothesis that gas exchange was similar between selfed and outcrossed progeny trees, thus subsequent utilization of *C* in selfed progeny must have been modified.

SELECTION, GENE FLOW, AND ADAPTATION IN SITKA SPRUCE: LIFE ON THE EDGE

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Understanding evolutionary population dynamics is essential to predict population fates in changing environments. Long-term population dynamics depend on spatial and temporal distribution of species across environments, which are influenced by a balance among selection, gene flow, and genetic drift. Adaptation to local environments of populations at the edges of their range may be limited by gene flow from central populations which are adapted to different environmental conditions. More restricted gene flow could accelerate local adaptation at the periphery.

Adaptation of populations in similar climates was investigated, but with different levels of gene flow, to determine the degree to which gene flow limits adaptation, and thus species range expansion, using *Picea sitchensis* as a model. The objectives are: to estimate tradeoffs between gene flow and adaptation and to reconstruct range expansion and impacts on genetic relationships during the last deglaciation. Three environmentally controlled growth chambers were used to simulate various environments. Some fitness-related traits showed physiological adaptations to local environments. Peripheral, isolated populations appear better adapted to local environments than peripheral disjunct populations for some phenological and growth traits. Mother-offspring genotyping is proceeding with microsatellite markers to estimate relative gene flow levels for continuous and disjunct populations.

BRAVE NEW BREEDING ZONES

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As climate changes, seed from breeding programs will have to be deployed to new areas to ensure that it is adapted to the climate in which it is planted. To examine the direction and extent of these changes, lodgepole pine (*Pinus contorta*) provenance test data were used to develop genetic maps based on current climate. Eleven breeding zones were delineated from the genetic maps in a manner that is expected to minimize maladaptation. The 'climate envelop' of each current breeding zone was defined and used in conjunction with future climate maps to map the location of future breeding zones.

Comparisons of current and future locations of breeding zones indicate that some zones will shift substantially northward within 50 years. In addition, several zones will change significantly in spatial extent, with implications for future seed demand and conservation needs.

COMPARISON OF SEED TRANSFER FUNCTION AND FOCAL POINT SEED ZONE APPROACHES REGARDING PRESENT AND FUTURE CLIMATES

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The Cauchy function was used to model height growth of white spruce (*Picea glauca* [Moench] Voss) based on data from a 25-year-old range-wide provenance test series. Transfer functions were produced for 3 test site locations from eastern Ontario based on late summer temperatures and predicted height of all sources at each test site was mapped. Data from a recently established greenhouse and 5 common garden trials were used to generate focal point seed zones for the same locations. Results for present-day (1961–1990) climate normals were compared with those determined for a future climate scenario (GCM1 2040–2069). Seed transfers for best present-day growth based on the Cauchy models are differentially compatible with predicted climate change depending on latitude. The use of focal point seed zone models forecast into the future provides an additional and more robust means to evaluate the adaptive suitability of potential seed transfers.

TECHNIQUES AND PRELIMINARY RESULTS FROM FOUR GENERATIONS OF SELFING WESTERN REDCEDAR

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Western redcedar (*Thuja plicata* D.Don) has many of the biological attributes that make it an ideal model species for genetic selection experiments. These include early flowering, ability to self, low inbreeding depression, and ease of vegetative propagation. A study was initiated 10 years ago with the objective of studying response to selection and inbreeding depression in western redcedar. F1 seedlings derived from single-pair matings from a base of 30 wildstand parents (F>0), were grown under accelerated conditions. Two seedlings were selected from each full-sib family based on early height growth, as well as two random seedlings. From these 60 lines (F=0 at initiation), four generations of selfing have been accomplished in eight years (F=0.938 in absence of selection).

In this talk, we will describe the techniques employed that have enabled us to turn over five generations in 10 years, some preliminary results from selection, and finally, future direction.

SURVEY OF GENE CONSERVATION REQUIREMENTS FOR FOREST TREE AND SHRUB SPECIES IN CANADA

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Determining gene conservation needs across the country will provide important information to ascertain the role that the Canadian Forest Service can play. A survey was conducted to identify priority native tree and shrub species requiring gene conservation. The survey included shrubs greater than 1 m in height and those shorter than 1 m but belonging to a genus that includes trees. Species that may require gene conservation measures were identified on the basis of a set of criteria. If one or more of the criteria were judged to apply, the species was assigned a rating ranging from attention may be needed but current knowledge is inadequate, to specific gene conservation measures are required. The resulting lists were sent to people, known to have expertise, in each province and territory. The data from each province and territory were amalgamated into a single data set and sorted by genus. This allowed us to evaluate the frequency with which a given species was given a rating. Species were often assigned different ratings in different jurisdictions depending on their status for a particular province or territory. To simplify summarizing the survey, we only considered the highest rating value which is indicative of the worst case scenario for that species.

A total of 57 tree species (12 coniferous and 45 deciduous), including 2 varieties, and 107 shrub species (including 9 varieties) were identified as requiring some level (*in situ* and/or *ex situ*) of gene conservation in at least one province or territory. The large number of tree species is influenced in particular by the 25 or so of these species unique to the Carolinian forest of Ontario. *Salix* species were identified in each province and territory. Forty-two of the 56 *Salix* species and varieties require gene conservation measures. Twenty-six of the 29 species and varieties of *Crataegus* growing in Alberta and Ontario east to Newfoundland and Labrador require some form of gene conservation. Three dwarf species within the *Betula* genus were identified to be in need of conservation efforts in the Atlantic provinces as well as four *Betula* tree species in three provinces. *Ulmus* was another genus consistently identified throughout its range, in 7 provinces, as requiring specific gene conservation measures.

The results of the survey provide a basis for identifying gene conservation priorities for tree and shrub species in Canada but there are other considerations such as: 1) geographic distribution of species is important for setting priorities for conservation work and supporting research, 2) determining the need to work on species with populations threatened in part of its range but under no threat throughout the remainder of the range, 3) prioritizing efforts on threatened, outlying populations of species with known information on economic, ecological, and genetic parameters vs. those where these parameters are unknown, and 4) difficulties in taxonomic identification of some species and varieties.

CLIMATE MODELS AND GENETIC APPLICATIONS FOR LODGEPOLE PINE IN BRITISH COLUMBIA

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Maps of interpolated climate normals have recently become essential tools for many types of forestry research, such as studying genetic adaptation of trees to local environments, modeling species range shifts, or forest productivity under climate change scenarios. In this paper we evaluate two widely used climate models (i.e., polynomial functions of Rehfeldt and others (1999) and the PRISM climate model) for British Columbia, and improved the PRISM model through an elevation adjustment for temperature variables. Both models accurately predicted temperature variables; however, the PRISM model had a greater ability to predict local variation in precipitation.

We applied the improved climate model to develop climatic response functions of growth for lodgepole pine (*Pinus contorta*) provenances from each Seed Planning Unit (SPU) using new methodology. The climatic response functions were improved by using predicted anchor points of the quadratic curves. Productivity maps were produced for current and predicted future climatic regimes using Geographic Information Systems in British Columbia. We found that overall productivity of lodgepole pine will increase with increases in mean annual temperature (MAT) up to 2°C over current. Further warming will result in productivity declines and a northward shift in the productive range of the species. Some areas in southern BC will be beyond the species' climatic tolerance if MAT increases by 5°C. Optimization of seed source selection for reforestation will not only dramatically increase productivity if mild global warming continues, but facilitate increases in productivity with moderate warming (up to current MAT +3.5°C) and partially mitigate declines in productivity for warming beyond this level.

HOLOCENE CLIMATE CHANGE AND ITS IMPACT ON GENETIC STRUCTURES

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Widely used measures of population structure assume equilibrium conditions and most simulations of genetic structure are run over hundreds of generations and under constant background conditions. However, recent advances in climate science indicate that climatic variability since the late Glacial Maximum has been substantial. We first review climatic cycles from interannual to millennial periodicities, focusing here on those from centennial to millennial scales. We then review Holocene climatic periods in the Great Basin, USA and consequent vegetation changes, drawing on some of our own data from the Eastern Sierra Nevada. From data on fine-scale genetic structures in whitebark pine (*Pinus albicaulis*) and coast redwood (*Sequoia sempervirens*), we argue that these structures are the consequence of climatic changes over the past 600 years. Such structures are consistent with theoretical analyses of climate change and evolution (Pease et al. 1989, Garcîa-Ramos and Rodrîguez 2002). These studies also predict that evolution will lag climate change, empirically illustrated by data in Rehfeldt et al. (1999).

RECONSTRUCTING A PAST CLIMATE USING CURRENT MULTI-SPECIES' CLIMATE SPACES

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We present an analysis of a ghost forest on Whitewing Mountain at 3 000 m in the eastern Sierra Nevada, southeast of Yosemite National Park. Killed by a volcanic eruption about 650 years ago, the deadwood on Whitewing dates by standard tree-ring analysis to 800–1330 CE, a period known as the Medieval Warm Anomaly. Individual stems have been identified as *Pinus albicualis*, *P. monticola, P. jeffreyi*, *P. contorta*, *P. lambertiana*, and *Tsuga mertensiana*. With the exception of *P. albicualis*, which is currently in krummholz form at this elevation, the other species are 200 m or more lower in elevation. One, *P. lambertiana*, is west of the Sierran crest and 600 m lower in elevation. Assuming that climatic conditions on Whitewing during this period were mutually compatible with all species, we reconstructed this climate by the intersection of the current climatic spaces of these species. We did this by first generating individual species' ranges in the Sierran ecoregions through selecting vegetation GIS polygons from the California Gap Analysis database (UCSB) that contain the individual species. Climatic spaces for each species were generated by the GIS intersection of its polygons with 4 km gridded polygons from the PRISM climatic estimates (OSU); this was done for annual January and July maximum and minimum temperature and precipitation and merged together for each species. Climatic intersections of the species were generated from the misclassified polygons of a discriminant analysis of species by the climatic data. The average data from these misclassified polygons suggest that the climate on Whitewing during the existence of this forest community was 230 mm, 1°C, and 3°C greater than present in precipitation, and maximum and minimum temperature, respectively.

DOTHISTROMA NEEDLE BLIGHT OF LODGEPOLE PINE IN NORTHWEST BRITISH COLUMBIA

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Dothistroma needle blight caused by the fungus *Mycosphaerella pini* is causing severe damage to managed and natural stands of lodgepole pine in northwest BC. There appear to be two principle causes behind the damage occurring in this specific area, at this time. First, forest management policy and practice has lead to an unprecedented amount of young lodgepole pine hosts on the landscape. Second, the weather of the past decade appears to be changing resulting in more frequent events of consistent days of warm rain during summer months. The weather events coinciding with a previous outbreak of Dothistroma in the study area were investigated. The weather events that possibly lead to the decline in this previous Dothistroma outbreak, two consecutive years of dry conditions, have not reoccurred during the current epidemic.

GENETIC VARIATION IN BLACK COTTONWOOD, *Populus trichocarpa*

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A genecology study of black cottonwood was initiated in the mid-1990s. Cuttings were collected from over 1 000 trees throughout the major drainage along the coast of British Columbia, and Washington and Oregon, USA. Two common-garden tests were established in 1999 at two contrasting sites, Surrey Nursery (south coast) and Terrace (north coast). About 900 clones were tested. Stem elongation was measured every two weeks from April till elongation ceased. Bud flushing in 2001 and 2002 was assessed at weekly intervals from late February till leaflets were fully extended. The north coast test suffered extensive damage caused by moose. As a result, data were collected primarily from the south coast test. Data analyses focussed on parameter estimates from fitting growth curves and vegetative cycles, and their variation associated with drainage, stands (provenance) within drainage, and trees within stands. Preliminary results indicate an ecotypic pattern of geographic variation with a division along the Skeena and Nass Drainage. Substantial variation exists also among and within stands.

TREE SEED WORKING GROUP

WORKSHOP ABSTRACTS

QUALITY ASSURANCE IN THE SEED HANDLING SYSTEM

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INTRODUCTION

What is Quality Assurance? Why do I need it? There are at least as many answers to these questions as people in this room. It is a 'concept' that is linked to the **continuous improvement** of activities you are involved with. As a starting point, I'll define Quality Assurance [QA] for our purposes as "the evaluation, monitoring, and management of information and practices related to activities within the Seed Handling System". It is a wide definition, but several concepts are apparent:

1) There is a need or desire to **improve** or better understand (evaluate) our practices.
2) This is not a one-time event, but a '**continuous**' process.
3) Change, especially constant change, is not something everyone is comfortable with.

Quality assurance has evolved from the manufacturing sector with the goal of reducing or eliminating product variability. When we are dealing with tree seeds the variability present in a seedlot will serve to insure our future forests against insects, diseases and yes even climate change. There is an intrinsic value in the variation present in our tree seed to ensure the resulting forest can survive until rotation age (if applicable). The common concept of reducing 'product variability' may not always be applicable and I'd like to emphasize the reduction in process variability (=standardization) in the Seed Handling System instead. I'm not saying we should encourage variation in our products, but that we need to recognize and not select against the genetic variation present in our seedlots.

For those producing a product it is more efficient to have cones, seed or seedlings all the same size and/or shape. The variability around these products is the cost of maintaining genetic variation in our products. Our closest seed industries (agriculture, bedding plants) do not have these same costs as they produce short-term crops with a relatively narrow genetic base. We often look to these industries for advancements in seed science and rightly so, but we must appreciate that these technologies will work more efficiently under the background of relatively little genetic variation. In these industries variation is frowned upon (i.e., if you pay for deep purple double petunias, you should get 100% deep purple double petunias). These industries are closer to classical QA as they truly wish to reduce and even eliminate variation. The distinction between our closest industries is important and needs to be appreciated.

I am not an expert on Quality Assurance, but it is something I truly believe is required to be efficient in our operations. It isn't very sexy, doesn't attract funding, and probably hasn't been a buzzword for several decades. Out of the reading I've done I'd like to present 7 'truisms' for QA before specifically discussing this mornings session.

QUALITY ASSURANCE "TRUISMS"

1) Focus on customer satisfaction (*understanding what they need*).
2) Concentrate on reducing variability.
3) Decisions should be based on data.
4) Root causes for problems should be sought out by disciplined investigation.
5) Data recording must be performed consistently.
6) Barriers between departments need to be broken down.
7) QA needs to provide significant added value and it needs to demonstrate it effectively to management.

The workshop is intended to be an opportunity to hear various people speak about QA and how it may be implemented in the Seed Handling System. Different speakers will approach the topic differently and no one will entirely cover their topic of discussion. There is no QA system recipe and system development can vary greatly between similar facilities. In order to obtain more comprehensive information I'm going to try and invoke some audience participation following each of our talks this morning. You participation will determine how successful this session is – please participate and speak your mind.

The Seed handling System can be broken down into discrete components, but it is a continuous chain of activities from reproductive bud development to the production of seedlings for reforestation. Following each of our talks I'd like to spend approximately 10 minutes discussing QA at this stage of the Seed handling System. Please comment freely indicating other QA activities your facilities may implement (QA - things you do / things you monitor). To ensure some feedback I'm going to pose two discussion questions.

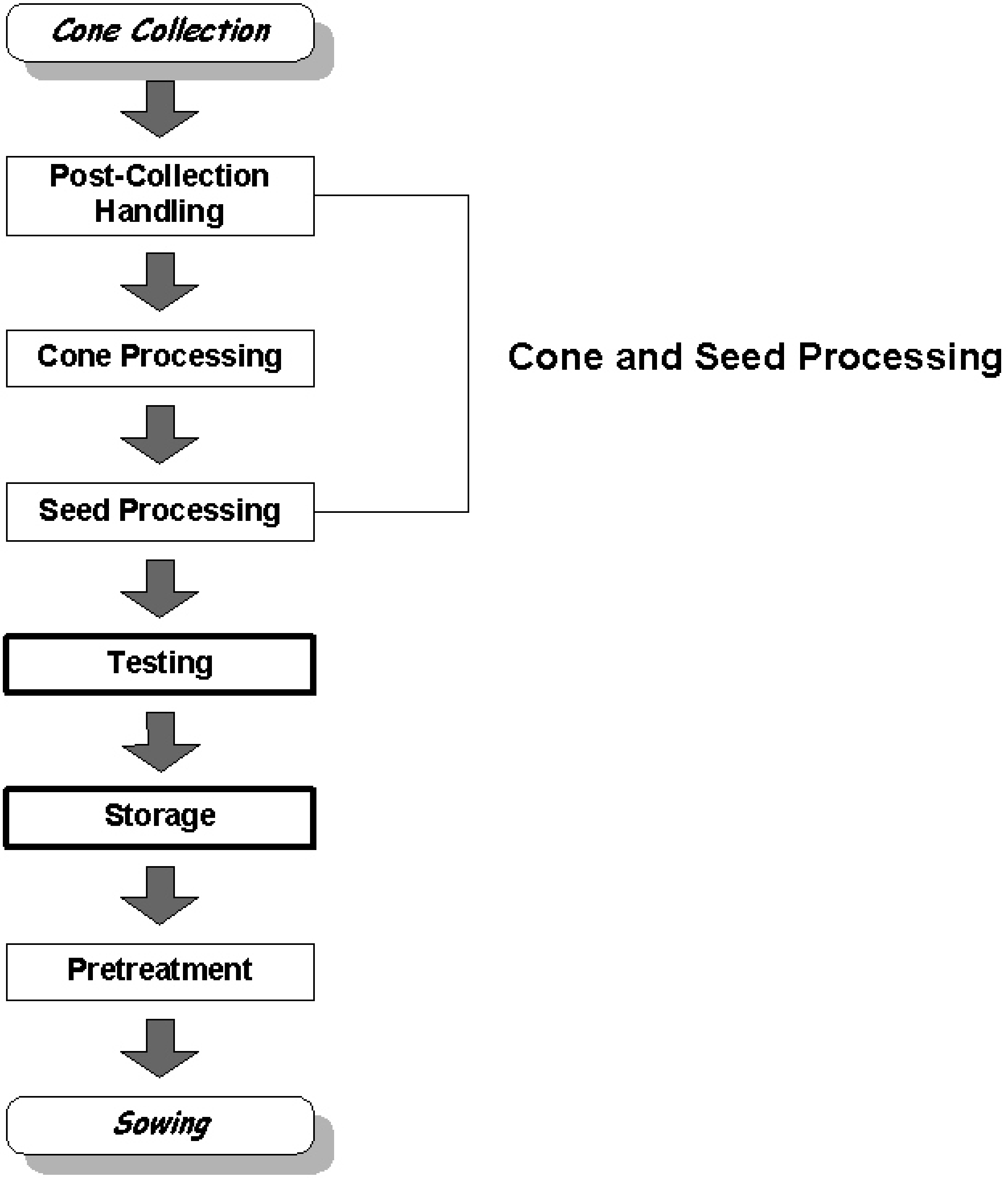
1. What is the largest source of variability at this stage going from the inputs to outputs?
I believe that by identifying the largest source(s) of variability one can go a long way to targeting QA points and improving efficiency (i.e., reducing process variability).

2. What step is most critical to delivery of the output?
The most variable stage may not be the most critical to product delivery. Is there one stage that can make or break your product?

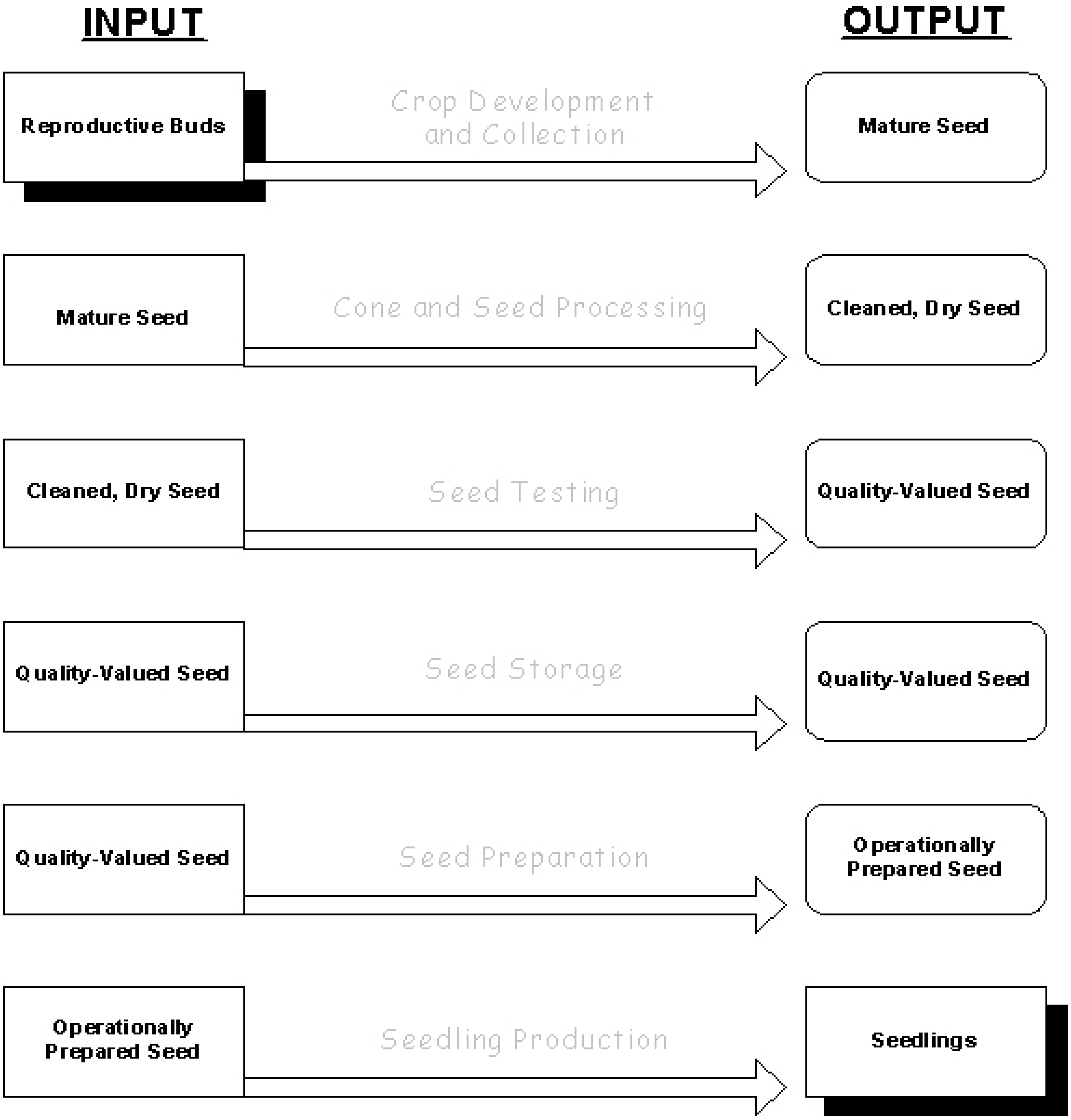
I hope you enjoy the session this morning. I think it is important to us running efficient operations, being good stewards and making advances in our understanding of tree seed biology. Thank you for your interest. Just one final thought as it is very important that you actually use the information you generate through your QA program.

Data are not Information
Information is not knowledge
Knowledge is not Wisdom

The Seed Handling System



Quality Assurance in the Seed Handling System



INPUT		OUTPUT
Reproductive Buds	Crop Development and Collection	Mature Seed
Mature Seed	Cone and Seed Processing	Cleaned, Dry Seed
Cleaned, Dry Seed	Seed Testing	Quality-Valued Seed
Quality-Valued Seed	Seed Storage	Quality-Valued Seed
Quality-Valued Seed	Seed Preparation	Operationally Prepared Seed
Operationally Prepared Seed	Seedling Production	Seedlings

1. What is the largest source of variability at each stage going from the inputs to outputs?

2. What step is most critical to delivery of <u>each</u> output?

CROP MAINTENANCE AND COLLECTION IN SEED ORCHARDS

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Regular orchard maintenance is important for producing a quality crop. Healthy trees are more likely to produce healthy seeds. The trees' needs are provided for through appropriate irrigation, fertilization, general pest protection and site maintenance. Orchard tree identities must be maintained to allow pickers to find the right trees.

Protect the developing crop from cone and seed pests. Regular, diligent monitoring is essential. Some pests dealt with at Kalamalka include *Leptoglossus, Cydia, Strobilomyia,* and *Dioryctria*

Harvest timing can have a significant effect on seed quality. Cones collected too early may contain seed that will germinate poorly or not store well. Cones left too late can open and shed valuable seed. Strategies to help achieve optimum timing include factors such as an experienced labour supply, crew safety, and motivation. The seed cutting test is the final word in determining seed maturity but to judge cone ripeness on a large scale we use the cone cutting test: the cone is cut in half longitudinally and the cut surface examined, paying particular attention to the cone axis. We prioritize picking throughout the harvest using this method.

Safe cone storage and shipping to the extractory ensure that the quality of a well cared for crop is preserved. Ventilation, temperature control, pest protection, and maintaining room for cone expansion are all addressed.

QUALITY ASSURANCE IN SEED TESTING

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Seed testing is conducted according to international standards such as the International Seed Testing Association's "International Rules for Seed Testing." Obtaining a random, representative sample of seed is the starting point for testing. The working sample is used to determine moisture content, purity, 1000-seed weight, and germination. The oven method is typically used to determine moisture content. Purity analysis is conducted to determine the percentage, by weight, of pure seeds of the crop species, seed of other species, and inert matter. Thousand-seed weight is determined by counting and weighing eight replicates of 100 seeds each, calculating the mean, and multiplying by ten. Germination tests are the most important assessment of a seedlot's quality. It is important that standards be adhered to in order for the results to be as repeatable as possible. Dormancy is commonly encountered with a number of species and is usually alleviated by a period of moist chilling. Seeds are considered to have successfully germinated when all essential structures necessary for continued normal development can be evaluated (radicle, hypocotyl/epicotyl, cotyledons). Viability tests are useful to quickly indicate if seeds are capable of germinating.

QUALITY ASSURANCE OF SEED STORAGE

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The Alberta Tree Improvement and Seed Centre (ATISC) is a Government of Alberta Sustainable Resource Development facility located 150 kilometres northeast of Edmonton. ATISC manages two seed programs both of which have their own storage facility and database management system. The Reforestation Seed Program is responsible for the registration, storage, distribution and tracking of all operational tree seed used for public land reforestation. Currently there are about 42 000 kg of seed of which about ⅔ is owned by forest industry and oil sands companies with the remaining ⅓ belonging to the government. The majority of seed is from wild collections with improved seed accounting for about 2% of the inventory. Average lot size is 25 kg. The Research Seed Program is responsible for the processing, testing, storage, and maintaining pedigree records of research and conservation seedlots in support of the provincial tree improvement program. There are presently about 5 500 seedlots about 4 800 of those being single tree collections. Average lot size is 20 g.

Three functions of seed storage are to: 1) provide storage conditions to minimize loss of seed quality, 2) maintain correct seedlot identity, inventory, and location, and 3) protect seed from harm and/or loss.

Reforestation seed is stored in an underground storage facility built in 1979. Being underground aids in maintaining low temperatures in case of mechanical failure and reduces energy costs. Because the facility is apart from the rest of ATISC's infrastructure and made of concrete there is added protection from fire. Storage temperature is maintained at -18ºC except during defrost cycles when the temperature rises to -16ºC. The bunker has four individual walk-in freezers and has a storage capacity of 84 000 kg of seed. Seed is stored in plastic bags inside waxed cardboard boxes. The 5 mil plastic bags are expelled of excess air and heat-sealed to prevent moisture absorption and spillage if boxes are dropped. The bags are replaced every 10 years. Withdrawals are carried out in the anteroom where temperature is +5ºC which minimizes temperature fluctuations in the seed and excessive moisture absorption.

Because of small lot size, research seed is stored in either glass or high-density polyethylene bottles and sealed with electrical or Teflon tape. The research storage facility is a -18ºC walk-in freezer located in the technical building where seed processing and testing take place. Seedlots are held at +2˚C for two hours and then at room temperature for two hours prior to withdrawal to minimize moisture absorption. Where amounts allow, portions of seedlots are withdrawn and held in the underground bunker for duplicate storage protection.

ATISC has on-site staff that maintain the storage facilities on a day-to-day schedule. Both facilities have back-up power generators and both are monitored 24 hours a day, seven days a week for temperature fluctuations. Should temperatures rise above or fall below the desired set points, a call-out system notifies an ATISC staff member of the situation.

All reforestation seedlots are initially tested for germination, moisture content, purity, and 1000-seed weight prior to storage. Proper moisture content is critical for long-term storability and the desired moisture content range is between 4 and 8%. Government seedlots are retested for germination every 4 to 5 years. Every tenth seedlot that is selected for germination testing is tested for moisture content as well. Industry clients are advised to retest their seed every five years. Because of small lot size, research seed quality is monitored through a reference seedlot testing program where 2% of the total seedlots are selected and tested annually (deciduous) or biennially (conifers).

Reforestation seedlot bags are tagged inside and out with the seedlot number. All boxes are labelled with the seedlot number and the current amount. Seed is stored by company by collection year. A new storage system is currently under review that will allow a company's seed to be stored throughout the four freezers instead of being concentrated in one freezer and will prevent seedlots with similar numbers from being stored adjacent to each other. Reforestation seedlots are inventoried annually to reconcile seed amounts with record amounts. Research seedlot bottles are labelled inside and out with assigned accession numbers and are arranged in numerical sequence.

The ATISC work site is fenced and gates are locked after hours and on weekends. Both storage facilities are locked and the reforestation seed bunker is equipped with an intrusion alarm system.

QUALITY ASSURANCE IN SEED PREPARATION

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Operational seed preparation is concerned with overcoming dormancy (or improving germination characteristics) and facilitating sowing. The treatments are intended to mimic lab testing procedures that determine the quantity of seed required. Four Quality Assurance (QA) foundations are the main supports for seed preparation and all services at the BCMoF Tree Seed Centre: 1) Avoid Physical Contamination (i.e., avoid introduction of debris = **cleanliness**), 2) Avoid Seedlot Contamination (i.e., avoid mixing of seedlots = labelling + attention), 3) Information Management (**organization**), and 4) Handling a perishable product (**exercise due care**).

The last foundation is especially important with imbibed seed as seed can be more easily damaged at elevated moisture contents. The first step for all BC species (except western redcedar that is pellet-coated) is to soak the seed. A minimum amount of moisture must enter the seed before dormancy can be overcome and/or germination initiated. A running water soak is used to reduce the quantity of seed-borne pathogens. Surface drying is subsequently employed to provide a free flowing product that can be easily mechanically sown and not promotive to fungal growth. It is critical that only surface moisture is removed and that internal moisture is not removed during this process. Optimum moisture contents appear to vary by species, but most appear to fall within the 30–35% window. Moisture content can be calculated non-destructively if one knows the storage moisture content, storage weight and hydrated weight of the seed.

The second critical step following appropriate hydration is to provide the correct duration of stratification. Most conifers have some degree of physiological dormancy, but mechanical dormancy is also implicated in western white pine and yellow cedar. Species requirements range from no stratification (western redcedar) to 98 days for western white pine. Naked stratification (i.e., no moisture-retaining media is involved) is conducted at our facility in 4 mil (0.1 mm) polyethylene bags. This thin material allows some gas exchange, but the bags should also have approximately a 4 cm opening at top to allow additional exchange. It is important to perform some germination testing to evaluate the effectiveness of your operational treatments.

Some species have specialized pretreatment methods. In subalpine, Amabilis, and Noble fir we are usually using a split stratification system in which a high moisture content is maintained for 28 days, the seed is then dried back to 30–35% moisture content at this stage and then placed back into stratification for an additional 56 days. In yellow cedar, an imbibed warm period (28 days) precedes cold stratification. In western white pine a 14-day soak is used and in western redcedar no soaking or stratification is performed, but the seed is pellet-coated due to difficulties in mechanically sowing the light-weight winged seed.

Some additional keys to successful seed preparation involve periodic inspection of seed condition and the mixing of seeds within a request to ensure uniform distribution of moisture and access to oxygen. Problems such as mold growth can usually be easily resolved if caught early enough. A well documented set of procedures and troubleshooting processes can be extremely helpful during the hectic sowing season. Tools should be in place to deal with potential problems. At shipping the seed bags need to be closed to avoid contamination and should be performed using an overnight courier service.

SEED QUALITY ASSURANCE IN THE NURSERY

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A seed handling protocol has been developed at Pelton Reforestation Ltd. to ensure the efficient use of seed in seedling production. All the procedures undertaken during seedling production are documented and tracked using an "order"-based Management Information System (PREMIS). Seed information on arrival date, amount, cleanliness, presence of insect/disease damage, stratification, seed treatment, and seeding factor, among others, is incorporated into a database for future reference. Different seed handling procedures were described and discussed in relation to "seed/seedling use efficiency".

THERMO-KINETICS OF WATER ABSORPTION, WITH SPECIAL REFERENCE TO NOBLE FIR SEEDS

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The role of imbibition in water uptake by tree seeds is discussed. Emphasis is placed on the effect of temperature on the rate and, more importantly, the completeness of imbibition. A theory is presented to show how the weak attractive force between water molcules and particles of the absorbing substrate (the seed coat), and the kinetic energy of the water molecules, are altered by changes in temperature. Based on this theory it is concluded that, as all text books state, imbibition occurs more slowly at lower temperature than at higher temperatrure. However, to date, no text book has been found that states that given suffcient time, the amount of water absorbed at low temperature is significantly higher than that absorbed at high temperature. Data from a study on noble fir seeds are used to support the theory and the conclusion.

EFFECT OF MOISTURE CONTENT DURING PRE-TREATMENT OR STORAGE ON THE GERMINATION RESPONSE OF ALDER, BIRCH AND OAK SEEDS

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Alder (*Alnus glutinosa* [L.] Gaertn.), birch (*Betula pubescens* Ehrh.), and pedunculate oak *(Quercus robur* L.) now form an important part of the planting program in Ireland. However, seed germination in the nursery bed is often low and/or slow. To this end, the effect of seed moisture content (MC) during pre-treatment on the germination performance of these species was investigated. Alder and birch have orthodox seed characteristics (easy to store at MC < 12%), whereas oak is difficult to store successfully (relatively high MC levels must be maintained during storage). Seeds of each species were adjusted to various MC levels and stored at 4 C for various periods. Acorns were also stored at -3 and 1 C. The optimum or target MC (TMC) during prechilling was about 30% in alder and 35% in birch. Germination increased following up to 24 weeks of prechilling for seeds at TMC levels in alder and 12 weeks in birch, significantly better than achieved using the standard method (fully imbibed for shorter periods). Thereafter, germination remained almost unchanged for seeds that received up to 36 weeks of prechilling, whereas the fully imbibed seeds deteriorated or germinated prematurely. In oak, acorns adjusted to the highest MC level (46%) and stored for 4–6 months at -3 C had the highest germination (76%) while the non-soaked controls and those adjusted to 37% MC has the lowest values (17% for both treatments). Interestingly, the control acorns had significantly lower germination than seeds that were soaked and then dried back to similar levels.

IUFRO UNIT 7.01.14
RESISTANCE BREEDING WORKSHOP
ABSTRACTS

EFFECTS OF GENOTYPE AND SILVICULTURE ON EXTENT OF TERMINAL WEEVIL DAMAGE TO JUVENILE SITKA SPRUCE

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Provenance-based resistance to terminal weevil damage was noticed in IUFRO spruce trials that were established by the BC Ministry of Forests in the 1970's. Subsequently, parent trees were selected from resistant sources and areas of similar climate, then screened at disease garden sites. Extra plants from these open-pollinated progeny tests were used to investigate the effects of silvicultural treatments and establish if they supported or detracted from the genetic effects. In 1994, resistant and susceptible families of Sitka spruce (*Picea sitchensis*) were inter-planted with western hemlock (*Tsuga heterophylla*) at rates of 10, 50, and 100% spruce. The following year similar genotypes were planted at 1, 2, and 3 m spacing. Lastly spruce differing in resistance were deployed to 10 sites that varied in weevil hazard (degree-days). Results from the spacing and inter-planting experiments are reported, and the weevil hazard series is described.

MAJOR AND 'R' GENE RESISTANCE – POSSIBILITIES AND PARALLELS BETWEEN PATHOGENS AND INSECTS

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Large gene effect resistance including 'R' gene resistance is noted widely in resistances to pathogens and an extensive literature has developed for this. In forest trees the resistance to white pine blister rust (*Cronartium ribicola*) by both western white pine (*Pinus monticola*) and sugar pine (*P. lambertiana*) provide classic examples of this type of resistance. These large gene effect resistances have not been as widely reported in insect resistance and entomologists have concentrated their efforts in describing the mechanisms of resistance rather than investigating such gene effects. One noted exception has been with wheat resistance to the Hessian fly (*Mayetiola destructor*). Large gene effects though do appear to be present in the resistance of Sitka spruce (*Picea sitchensis*) populations to the white pine weevil (*Pissodes strobi)* as indicated by some large phenotypic effects in our data investigations. We report here this evidence from our phenotypic data investigation and look at some of the techniques that can be used in detecting genes of large effects from such phenotypic data.

OVERVIEW OF *Phytophthora lateralis* RESISTANCE PROGRAM IN PORT-ORFORD-CEDAR

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Phytophthora lateralis is a non-native, invasive root pathogen that has infected 8% of federal lands throughout the range of Port-Orford-cedar (*Chamaecyparis lateralis*) in southwest Oregon and northwest California. Some local populations have had very high mortality and riparian communities on ultramific soils are at risk. An operational program to develop populations of Port-Orford-cedar that are resistant to *P. lateralis* is underway. Phenotypic selections from forest stands are screened using a stem dip test and the top 10% are re-tested using a root dip technique. Over 11 000 field selections have been tested since 1997. Thus far, approximately 100 selections with strong resistance have been identified in the root test. Full-sib families (including selfs) are generated to characterize resistance mechanisms and enhance resistance. Several types of resistance appear to be present in seedling testing: 1) high survival and 2) slower rates of mortality. A single dominant resistant gene is suggested by mendelian segregation ratios for the high survival families. Work is underway to further characterize the slow dying families and to pyramid with the high survival resistance. A Fain’s test suggests a single dominant resistant gene is influencing lesion length in the stem dip test.

The phenotypic correlation between stem dip and root dip resistance is moderate, while the genetic relationship is low suggesting the traits are unlinked. Early results from field studies show good survival of resistant families relative to susceptible controls. An important component of the resistance program is maintaining high genetic diversity in the Port-Orford-cedar populations. Genetic studies are underway to characterize genetic structure and diversity in pre-epidemic, post-epidemic, and *P. lateralis* resistant orchard populations. Initial efforts to map resistant genes using an outbred F2 mapping population is in preparation.

EARLY SURVIVAL, HEIGHT, AND BLISTER RUST PERFORMANCE OF *Pinus albicaulis* SEED SOURCES FROM THE INLAND NORTHWEST

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One hundred ten populations from eastern Washington, Idaho, and Montana from 1 900–3 300 m in elevation, were sown in a common garden study (nursery rust screening) in 1999 to evaluate genetic differentiation. First-year survival varied from 0.4 to 93.4% with a mean of 37.7%, with no differentiation based on geography or elevation. Third-year baseline measurements were obtained (survival, height, and presence of *Fusarium* spp.) prior to artificial inoculation with *Cronartium ribicola* in September 2001. Approximately half of the seedlings of each population were uninoculated to serve as controls. Inoculation efficiency as measured by percent spotting (82.7%) and spots per meter (0.37) was comparable to *Pinus monticola*; however, average number of spots per meter (0.37) typically should be higher (5–20) to accurately assign resistance traits to individual trees. Percent resistant *P. alibcaulis* seedlings (57.3%) is within the range of those reported for *P. monticola*. Preliminary analysis of individual-tree traits is showing low percent bark reaction (3.1%) and needle shed (8.8%) and similar no-spot (17.3%) and short shoot (28.1%) seedlings as compared to *P. monticola*. The majority of the horizontal traits (spot frequency, early stem symptoms, canker alive (tolerance)) are significant ($p < 0.0001$) among all populations except for adjusted bark reaction ($p < 0.6659$). Unlike *P. monticola*, four-year height was significant ($p < 0.0001$) among populations, and *P. albicaulis* is showing both longitudinal and elevation gradients, which likely follow the distribution of mountain ranges in the Inland Northwest. Following the final rust inspection later the fall of 2004, the rust resistance index will be finalized and populations will be ranked by performance. Based on the outcome of regression models, seed transfer guidelines may need to be updated. Survivors of the study will be planted in a long-term performance test in northern Idaho and scion collections will begin from above-average populations to establish seed orchards for the Bitterroots-Idaho Plateau, Selkirk-Cabinets, and Central Montana seed zones. Seed orchards will be located in *P. alicaulis* habitat types rather than low elevation tree improvement areas in an effort to promote flowering.

THE BASIS FOR SELECTION OF PARASITE-SPECIFIC, NON-HOST RESISTANCE

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Related plants host related fungal parasites, many of which are narrowly specialized. So plants can be nonhosts to many specialized parasites of congeners. According to theory, plants owe this general, nonhost resistance to genes that are not parasite-specific. It is presumably only when a parasite of a congener overcomes basic, non-host resistance that a coevolutionary arms race ensues. The initial, extreme susceptibility is thought to spark many generations of selection in both host and parasite, that ultimately results in parasite-specific, gene-for-gene interactions. But, evidence from many studies of resistance in *Populus* suggest that nonhost resistance is parasite-specific. This, and other evidence to be discussed, leads away from the accepted explanation for the existence of parasite-specific, major genes for resistance.

TRAUMATIC RESINOSIS IN SITKA SPRUCE – A RESISTANCE MECHANISM AGAINST ATTACK BY THE WHITE PINE WEEVIL?

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White pine weevil (*Pissodes strobi* Peck) is a serious pest of Sitka (*Picea sitchensis*) and interior spruce (*P. glauca* x *engelmannii*) in BC. This pest damages the terminal leader causing growth loss and stem deformities that severely impact tree value. Thus far there are no effective methods to control the white pine weevil. As a result, selection and breeding for weevil resistant genotypes hold promise to minimize weevil damage associated with reforestation programs.

In spruce, weevil attack induces a traumatic resinosis response that is characterized by the *de novo* synthesis of oleoresin that is sequestered in newly formed resin canals. Oleoresin is a complex mixture of monoterpenes, sesquiterpenes, and diterpene resin acids that provide chemical and physical protection against herbivores and pathogens. To determine whether traumatic resinosis is an important determinant of resistance we have examined this response in Sitka spruce genotypes that are resistant or susceptible to weevil attack. To achieve this we undertook molecular, histological, and chemical approaches to examine: 1) the expression of genes that encode enzymes responsible for terpenoid formation, 2) the formation of resin canals in the xylem, and 3) qualitative and quantitative changes in resin profiles. The data are presented and discussed as they relate to the response of susceptible and resistant Sitka spruce to artificial (achieved by stem drilling) and real weevil attack.

RESISTANCE BREEDING IN SITKA SPRUCE AGAINST THE GREEN SPRUCE APHID – RESULTS FROM THE DANISH BREEDING PROGRAM

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The paper summarizes a joint European project: Improving protection and resistance of forests to the spruce aphid (*Elatobium abietinum*), with special reference to the Danish investigations and their consequences for the Sitka spruce (*Picea sitchensis*) breeding program in Denmark. Factors investigated were needle loss, needle anatomy, content of phenols and terpenes, and RAPD markers linked to major genes behind field resistance.

The needle loss was studied in a 20-year-old open-pollinated progeny test from 15 selected clones. The ortets were selected in a heavily attacked Danish stand of Washington origin as healthy escapes, i.e., not attacked and included in a clonal seed orchard. Attacks were recorded in the progeny trial in three separate years 1990, 1992, and 1999, in which the progenies developed from a juvenile to a more mature stage with flowering, seed set, and closed canopy. There were significant difference between progenies demonstrating family heritabilities of 0.6–0.7, but all progenies showed a degree of resistance. The seed orchard offspring showed 50% less needle loss, compared to a commercial standard. In conclusion this investigation showed a consistency in resistance to *Elatobium abietinum* over generations and through different onthogenetic stages.

The possibility to characterise resistant trees by needle anatomy or content of phenols or terpenes was tried, but results were not clear. Two intermediate attacked families were used in the search for RAPD markers co-segregating with field resistance. Three markers co-segregated with needle loss, one in one family and two in the other. In the family in which two markers co-segregated with field resistance, apparent epistatic gene effects on field resistance were observed.

Selection for aphid resistance, either direct phenotypic or marker aided, appears to result in persistent gains throughout the entire rotation of Sitka spruce.

IDENTIFICATION OF GENES INVOLVED WITH WEEVIL RESISTANCE IN SPRUCE

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Forest health is one of the main areas of interest for the GenomeBC forestry project. We have utilised various approaches to further basic understanding of the genetic mechanisms involved and to develop tools for use in forest health improvement. These approaches include the use of microarrays to identify the genes involved in resistance and the use of DNA markers for genetic mapping and genetic variation surveys. The microarray and marker development has been based on a spruce Expressed Sequence Tag (EST) sequencing project that has identified over 20 000 unique genes expressed in various spruce tissues. Development of highly informative DNA markers in conifers has been viewed as a formidable task due to the large, highly repetitive, and mostly uncharacterized genome. Using our EST database and through the integration of bioinformatic and genetic tools we have developed informative markers that will be highly transferable both within spruce species and among other conifers. The combination of information from a wide variety of sources will expedite the development of molecular genetic tools for use in spruce.

BREEDING WESTERN REDCEDAR FOR HERBIVORE RESISTANCE

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Deer and elk browsing on western redcedar (*Thuja plicata* Donn) in the Pacific Northwest can result in delayed regeneration, and in severe cases, plantation failure. In addition, it can cost up to $6 CAN per tree to protect seedlings from browse and bring a plantation to free-to-grow. We are in the process of developing populations of deer resistant and deer preferred trees to help alleviate this problem.

Foliage samples from over 2 000 trees in a western redcedar genetic trial composed of 60 open-pollinated families from 14 populations on southern Vancouver Island were analyzed for 22 monoterpene compounds. In addition, browsing pressure (percent and intensity) and height growth were measured in the field. Browsing pressure was high with approximately 22% of the trees browsed with a mean family range from 5 to 40%. Narrow-sense heritabilities of the seven most prevalent monoterpenes varied from 0.33 to 0.56 and additive CV from 21 to 31%. Genetic correlations among these seven compounds were all positive and most were greater than 0.80. Genetic correlations with total and individual terpene content with growth were all not significantly different from zero.

A combined family within-family index, adjusted for replication effects, was constructed for total foliage terpene concentration. Individuals have been selected for two divergent populations: 1) deer resistance, selected for both absence of deer browse and high needle monoterpenes and 2) deer preferred, selected based on both heavy browse and minimal or no needle monoterpenes. We are currently testing foliage from these putatively resistant trees by feeding them alongside the preferred foliage to penned deer in feeding choice experiments. This will help to explain if specific needle monoterpenes alone result in resistance to deer browsing or if other factors such as primary sugars are also involved. Selections will then be bred for increased resistance based on the above feeding choice experimental results.

Once we are confident in calling these selections deer resistant, the next step is to outplant seed lot mixtures of varying levels of resistance in different percentages in operational trials. If deer pressure is high mixtures of deer resistant with wildstand seed lots would give the deer something to eat and perhaps the resistant trees will be left alone. The preferred trees, which taste just like lettuce, would most likely be gone the day they were planted, leaving the deer no choice but to eat the bitter resistant trees. Although they are high in toxic chemicals, the deer will make a choice on the balance between energy input and cost of detoxification. If deer pressure is moderate but still present, and volume production is a goal, then mixtures of deer preferred seed lots with elite growth seed lots may give the deer enough foliage to browse on and the elite trees may be left alone or browsed minimally.

WEEVIL RESISTANCE OF PROGENY DERIVED FROM PUTATIVELY RESISTANT AND SUSCEPTIBLE INTERIOR SPRUCE PARENTS

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The white pine weevil, (*Pissodes strobi*), has a major impact on spruce regeneration in western North America. Silvicultural, chemical, and biological controls have proven to be inadequate or impractical and genetic resistance is now being considered as a promising tool for weevil management. A collaborative program (Canadian Forest Service and BC Ministry of Forests) to screen BC spruce for resistance to white pine weevil is described. The results of screening controlled-cross progeny derived from weevil resistant and susceptible parents are presented and bark resin canal characteristics of three cross types of differing weevil resistance status are described.

NATIONAL SURVEY OF FOREST GENETIC RESOURCES MANAGEMENT WORKSHOP

A SURVEY OF FOREST GENETIC RESOURCES MANAGEMENT PROCESSES AND PRACTICES IN CANADA

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BACKGROUND

In 2002, the Alberta Forest Genetic Resources Council proposed a study to review how the management of genetic resources of forest trees in the province compared with that of other provinces and to learn from the experience of others. To initiate a comparison, a sub-committee developed a list of topics chosen for relevancy to the management of forest genetic resources and forwarded that list to other Councils in Canada (British Columbia, New Brunswick, and Ontario). The Councils expressed interest in a comparative study and requested additional details. The Alberta Council then assigned a committee to develop a survey that would include the specified topics.

The potential for a survey was explored further at a meeting of representatives from the Alberta Council and the Forest Genetics Council of British Columbia. Two issues were immediately apparent: 1) the operating environment of each Council was poorly understood by the other Council and 2) differences in operating environments would be likely to pose challenges to the comparison of specific operations for some topics. The challenges were expected to increase if some topics were expanded to include technical details.

Despite the expected difficulties, it was deemed useful to recommend a proposal to the Alberta Council. That proposal was as follows:

> *To circulate a very general survey of topics focused at the policy and planning level. The intent of the survey would be to prompt an exchange of ideas and discussion of issues both at the level of policy and, if desired, at more technical levels.*

The Alberta Council accepted the recommendation and directed that all Canadian provinces and territories with forests, regardless of whether a council was in place, should be invited to participate. A survey was developed and all provinces and territories, except Nunavut, were contacted.

Initial responses to the Survey showed that several of the questions were open to different interpretations. Most respondents attached comments to clarify their responses and correspondence with them provided additional information.

At an October 2003 meeting of representatives from the Alberta and British Columbia Councils, it was decided to contact respondents again with a note having the following objectives: 1) distribute an initial, general summary of results, 2) provide an opportunity to change responses (especially those of “not sure”), 3) obtain additional information (number of seed zones, average annual planting numbers, percentage of reforestation by planting) as rough measures of the complexity of forest genetic resource management in each jurisdiction, and 4) indicate the possible extent of public distribution of Survey results and determine whether jurisdictions would choose to have their responses identified.

APPROACH

Completed surveys were received from 11 of 12 jurisdictions. All surveys included comments that helped to clarify responses about specific topics.

The 11 surveys were numerically summarized by the process outlined below:

1. Tally survey responses in 8 classes. The initial tally represented only entries provided by respondents.
    a. Yes
    b. Yes with attached comment

   c. No
   d. No with attached comment
   e. Respondent is “not sure”
   f. Item is being developed
   g. Submitted response is unclear
   h. Topic is not applicable

2. Identify contradictions and uncertainties.

3. Contact respondents for clarification of items under 1.g above.

4. Revise survey tally and array by jurisdiction as “Yes” or “No”.

5. For each Survey question, consolidate the tally as follows:

   a. For jurisdictions choosing to be identified, present all “Yes” and “In Progress” responses (Appendix I)

   b. For jurisdictions choosing anonymity, present sums of “Yes” and “In Progress” responses (Appendix I)

6. List some apparent contradictions:

   a. The interpretation of whether policies and plans exist varied because the Survey did not specify whether policies and plans must be written. Therefore, a response of “No” to the query “Does the province have....” is not necessarily contradictory to a response of “Yes” to implementation of a plan.

   b. Similarly, a response of “Not Applicable” might or might not be appropriate when applied to a topic whose apparent prerequisite was tallied as non-existent.

INTERPRETATION

The following interpretations were made from Appendix I. Note that the proportion of “Yes” replies would be increased if the uniformly negative responses from one jurisdiction were omitted. In that jurisdiction, there is virtually no commercial timber harvest at present.

Section 1.1 Seed Transfer – Most jurisdictions have policies and plans for seed transfer. Seed transfer rules are generally implemented and implementation is monitored. The two jurisdictions reporting an absence of policy have guidelines. On questions of implementation, attached comments indicate that control of seed transfer is lacking in three jurisdictions, one of which has legally binding rules under development.

Note that the number of seed zones per jurisdiction (see Program Statistics at the end), as one measure of the complexity of gene resource management, varies widely.

Section 1.2 Conservation – Jurisdictions are fairly evenly split between those that have formal provincial activity in conservation of forest genetic resources and those that do not. Attached comments, however, including responses to question 1.2d suggest that conservation is a neglected topic in only two jurisdictions. Responsibility for gene conservation is vested in Parks Ministries in some provinces.

Section 1.3 Genetic Diversity – Planning for maintenance of genetic diversity is, or will be, in place for about half of the jurisdictions. Implementation and monitoring, however, are much less common.

Section 1.4 Tree Improvement – Planning has been accomplished in most jurisdictions and standards are in place. Less attention has been given to issues of estimation and verification of genetic gain.

Section 2.0 Genetically-modified Organisms – Less than one-third of jurisdictions have a policy on GMOs. The federal government has the responsibility for testing GMOs to determine whether operational use can be allowed. A rigorous protocol for testing is in place.

Section 3.0 Non-native Tree Species – About half of the jurisdictions have a policy but few cover ecosystem impacts. Response to proposals for introduction of non-native species on public lands often seems to be handled on a case-by case basis. Monitoring plans are not generally required.

Section 4.0 Education in Forest Genetics and Tree Improvement – Education in forest genetics and tree improvement is not generally required at the undergraduate level. Graduate-level training is available in about one-half of the jurisdictions. Continuing education for practitioners and extension information are available in most jurisdictions. Communication with the general public is less common.

Section 5.0 Forest Genetic Advisory Council/Board – Formal advisory organizations exist in about one-half of the jurisdictions. Topical focus is somewhat more on tree improvement than on seed transfer, conservation, and use of GMOs. The apparent lack of interest in seed transfer is less apparent when it is recognized that some jurisdictions have decided that one seed zone is adequate.

Representation of primary stakeholders in advisory organizations is common, even without a formal plan for representation. The opportunity for public involvement is less common, however, and this raises the question of who is defined as a primary stakeholder.

SUMMARY

In summarizing the results of the Survey, three points need to be kept in mind. First, the Survey questions reflected, to some extent, a lack of expertise on the part of the authors in developing surveys. Responses, therefore can be open to interpretation. Second, there is a wide range among jurisdictions in the need for and in the complexity of, formal approaches to gene resource management of forest tree species. Third, the existence of a policy or plan might be considered to be a “first level” measure that a given issue has been addressed in some fashion. Whether the details of that policy or plan would be considered to be adequate at a technical level cannot be determined here.

The Survey reveals a general appreciation of issues in forest genetics and tree improvement although several of the respondents have job titles that emphasize silviculture or ecology. The actualization of that appreciation in organizational structures and formal plans varies widely among jurisdictions.

As might be expected, jurisdictions in which the implementation of tree improvement is shared in public/private cooperative formats have the most codified activities. Where implementation of tree improvement is an exclusively governmental function, written standards are less common and, perhaps, viewed as unnecessary or undesirable.

Even where written policies and standards are in place, the resources and commitment to implement and monitor seem rarely to be available.

Possibly the most surprising results from the Survey are the responses of “Not sure”.

At a minimum, the Survey results offer a preliminary “directory” of identified jurisdictions where specific issues have been addressed.

ACKNOWLEDGMENTS

Following is a list of respondents to the Survey. Thanks to each respondent for participating.

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Jack Woods, Forest Genetics Council of BC, BC
Debra Wortley, Forest Management Branch, Energy, Mines and Resources, YK

POSTSCRIPT

This report was presented at an informal workshop of interested persons at the 29th Meeting of the Canadian Tree Improvement Association (CTIA), July 26, 2004, in Kelowna, BC. The following points were abstracted from the discussion following that meeting:

1. The fulfillment of national and international requirements for surveying and monitoring natural resources is a federal responsibility.

2. Provincial activities in management of genetic resources of forest trees could be coordinated with federal activities but that would require a lot of work. The amount of work required would arise from differences among provinces and from the distribution of responsibility among several federal agencies.

3. There is no current cooperative effort on the topic at the federal level that corresponds to activity by the Canadian Council of Forest Ministers.

4. Activities in forest certification may move toward standards for gene resource management but that process is slow.

5. In addition to discussing technical issues of gene resource management, exchange of information on administration of Councils could be useful.

6. A Council of Councils might fill a role similar to that of provincial councils providing advice to a Chief Forester.

7. A resolution proposing formation of a Working Group to meet on issues in gene resource management of forest trees will be developed and presented at the CTIA Business Meeting.

Editors Note: Following is the motion that was accepted at the CTIA Business Meeting:

> *That the CTIA endorse a committee of representatives from all provinces and territories, including reps from existing Councils, to be known as the Canadian Forest Genetics Councils Working Group of the CTIA and that this working group advocate and communicate, as needed, on matters related to federal-provincial/territorial policy interactions regarding the management of forest gene resources.*

Appendix I. Summary of "Yes" responses “Y” from 11 jurisdictions. "IP" represents "In Progress". Where sums of "Yes" responses are less than 11, actual responses were mostly "No", a few were "Not sure", and some were "Not applicable".

		Provinces/Territory						Remainder
1.0 Native Species		AB	BC	QC	NB	ON	YK	Yes
1.1 Seed Transfer								
	a. Does the Province have a policy on seed transfer?	Y	Y	Y	Y	Y	Y	3
	b. Does the Province have a plan for seed transfer issues?	Y	Y	Y	Y	Y	Y	2
	c. Has the plan been implemented?	Y	Y	Y	Y		Y	1
	d. Has significant progress been made on implementation?	Y	Y	Y	Y	Y	Y	1
	e. Is implementation monitored?	Y	Y	Y	Y		Y	1
1.2 Conservation								
	a. Does the Province have a policy on conservation?	Y	Y	Y	Y		Y	2
	b. Does the Province have a plan for conservation?	IP	Y	Y	Y	IP	Y	2
	c. Does the plan include coordinated *in situ* and *ex situ*	Y		Y	Y	Y		1
	d. Does the plan include protection for threatened species/populations?	Y	Y	Y	Y	Y	IP	2
	e. Has the plan been implemented?	Y	Y	IP	Y			2
	f. Has significant progress been made on implementation?		Y		Y		Y	2
	g. Is implementation monitored?	Y	Y		Y		Y	2
1.3 Genetic Diversity								
	a. Does the Province have a policy on genetic diversity?	Y	Y	Y	Y			2
	b. Does the Province have a plan for maintenance of genetic diversity?	Y	Y	Y	Y	IP		0
	c. Does the plan include both improved and unimproved species?	Y	Y	Y	Y	Y		0
	d. For improved material does the plan cover both stand-level and landscape-level diversity?	Y		Y		Y		0
	e. Has the plan been implemented?	Y	Y	Y				0
	f. Has significant progress been made on implementation?		Y		Y			0
	g. Is implementation monitored?	Y	Y		Y			0
1.4 Tree Improvement								
	a. Is there a long-term provincial improvement plan?	Y	Y	Y	Y	Y		2
	b. Are written breeding plans required?	Y	Y		Y	Y		2
	c. Are there standards for breeding-plan development?	Y	Y		Y	Y		2
	d. Does the Council monitor progress?	Y	Y		Y	Y		3
	e. Does the Council make recommendations on technical protocols?		Y		Y			3
	f. Is there a protocol for estimation of genetic gain including timber supply modeling?	Y	Y	Y	Y			2
	g. Is there a protocol for monitoring and verifying genetic gain?	Y	Y	Y	Y			2

		Provinces/Territory						Remainder
		AB	BC	QC	NB	ON	YK	Yes
2.0 Genetically-modified Organisms								
	a. Does the Province have a policy on the use of GMO's?	Y	Y	IP				0
3.0 Non-native Tree Species								
	a. Does the Province have a policy on use of non-native species?	Y	Y		Y			2
	b. Does the policy cover ecosystem impacts of non-native species?	Y						0
	c. Does the Province require monitoring plans for non-native species?	Y			Y			0
4.0 Education in FG and TI								
	a. Is education required at the undergraduate level in the Province?		Y	Y		?		0
	b. Is education available at graduate level in the Province?	Y	Y	Y	Y	Y		1
	c. Is continuing education available to practitioners?	Y	Y	Y	Y	Y		2
	d. Is extension information available to practitioners?	Y	Y	Y	Y	Y		3
	e. Is information communicated to the general public?	Y	Y	Y	Y			1
5.0 Forest Genetic Advisory Council/Board								
	a. Does the Province have a Forest Genetic Council?	Y	Y		Y	Y		3
	b. Does Council make recommendations on seed transfer issues?							
	seed transfer issues		Y		Y			2
	conservation	Y	Y		Y			1
	genetic diversity	Y	Y		Y			2
	use of GMO's	Y	Y					1
	tree improvement objectives	Y	Y		Y			3
	tree improvement planning		Y		Y			3
	c. Does Council include representation from primary stakeholder groups?	Y	Y		Y	Y		2
	d. Does Council have a formal plan for sectoral representation?	Y	Y					1
	e. Is there an opportunity for public involvement in planning for forest genetics resources management?	Y			Y			1
	Program Statistics							
	Number of Seed Zones (Number)	74	80	*a*	1	38	13	
	Average Annual Planting (Million)	65	220	130	60	120	0.5	
	Percent of Reforestation by Planting	80	80	18	50	50		
a Quebec uses transfer zones (distance from origin) rather than seed zones								
AB - Alberta, BC - British Columbia, QC - Quebec, NB - New Brunswick, ON - Ontario								

POSTER ABSTRACTS

IS BRITISH COLUMBIA’S SILVICULTURE PPLICY FRAMEWORK ADEQUATE FOR RESPONDING TO CLIMATE CHANGE?

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The Government of British Columbia recently revamped its *Forest Practices Code* by introducing new results-based forest management legislation. In this simplified regulatory model, government establishes objectives for conserving and protecting forest values. Forest licensees are responsible for developing and implementing results and strategies that will achieve those objectives. With the exception of a few default environmental standards (e.g., riparian areas, soil disturbance, and seed use) forest practices are to be prescribed by professionals.

Climate change has not been considered in establishing these objectives and environmental standards. Furthermore, licensees and foresters are not required to incorporate climate change scenarios into their forest management plans; nor would they necessarily have the expertise or resources to do so if they were obligated.

Scientists have suggested a number of adaptive management strategies to reduce the vulnerability of managed forests to climate change. These strategies include planting different species, modifying the seed transfer protocols, increasing the number of genotypes and seedlots used to reforest an area, and higher stocking densities.

This poster is intended to stimulate discussion regarding the adequacy of British Columbia’s silviculture policy framework for responding to climate change. For example, will forests managed under today’s policies be more or less at risk to climate change than unmanaged forests? What are the current opportunities and barriers to implementing the aforementioned silviculture strategies? What adaptation policies could be undertaken today at a reasonable cost that provide benefits under the present climate as well as the future? Will professional reliance be sufficient to implement these changes?

This poster and discussion will be used in refining the topic for a Master of Arts thesis in Environment and Management.

Ex situ CONSERVATION STRATEGY FOR BUTTERNUT (*Juglans cinerea* L.)

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Butternut (*Juglans cinerea* L.) survival is threatened in North America by the fungus *Sirococcus clavigignenti-juglandacearum*. To date, control for this fungal disease does not exist and long-term seed storage, as a means to assure survival of the species, is not a viable option. For these reasons, there is a requirement to develop *ex situ* conservation strategies for butternut. One such strategy involves developing storage using embryonic axes from seed collected from non-infected butternut. Embryonic axes, when excised from the nut with approximately 3 mm of cotyledonary tissue, will tolerate exposure to -196°C and subsequently germinate, forming a viable seedling. Water content of 4.8% appears to be a threshold below which some of the axes will germinate following cryopreservation. These results suggest that ultra low temperature storage of embryonic axes may be a viable method for butternut *ex situ* conservation. The use of other *ex situ* conservation methods such as the cryopreservation of apical and lateral buds, and somatic embryogenesis are presented.

GENETIC STRUCTURE AND MATING SYSTEM OF ARBUTUS (*Arbutus menziesii*)

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Arbutus (*Arbutus menziesii* Pursh) is the only broadleaved evergreen tree native to Canada. It belongs to four red- or blue-listed plant communities. Primary threats are urban encroachment, fire suppression, grazing, and exotic invasive species. Its growth is highly sensitive to environmental conditions; therefore more severe summer drought due to future climate change could further threaten this species. No data are available on pollination biology or population genetics of arbutus. Amplified fragment length polymorphisms (AFLPs) were used for the first genetic examination of *A. menziesii* in BC. Ten populations were studied throughout its range and one in Washington, USA. Genetic diversity estimates within populations were low (mean $H = 0.094$) relative to other long-lived perennials (0.25); there were no significant differences among populations. Genetic variation among populations ($F_{ST} = 0.15$) was comparable to the average in long-lived perennials and frugivore-dispersed species ($F_{ST} = 0.19$ and 0.16, respectively). The Gold River, BC population differed the most from other populations, but not significantly. Isolation by distance was significant based on kinship coefficients ($p < 0.01$); half-sibs were ~3 m apart. Mating system analysis of one BC island population revealed high outcrossing ($t = 0.97$); 10–20% of mating was biparental inbreeding. Conservation strategies and future research directions are presented.

EFFECTS OF FRAGMENTATION ON GENETIC STRUCTURE AND INBREEDING IN BIGLEAF MAPLE POPULATIONS

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Some plant populations including forest tree species have small geographical populations. As land use by man increases, the distribution of several tree species has become fragmented. In fragmented populations, the overall numbers of individuals are drastically reduced and remaining forest populations are restricted to small forest patches. Population genetic theory predicts that habitat fragmentation will result in an erosion of genetic variation in small remnant populations through the combined effects of genetic drift, inbreeding, and random extinctions of local populations. Almost all investigations of habitat fragmentation have used habitats that have been fragmented for close to a century or less. This study uses populations from habitats that have been naturally fragmented throughout the species history to examine the effects of fragmentation on a much longer time scale. Using isozyme markers, two questions were addressed:
1) What are the effects of forest fragmentation on the genetic structure of these populations?
2) Are changes in mating systems the mechanisms through which fragmentation is affecting bigleaf maple populations?

To address these questions, genetic variation and structure of continuous populations were compared to genetic variation and structure of fragmented populations.

Results for genetic diversity indicate that bigleaf maple (*Acer macrophyllum*) exhibits similar levels of genetic diversity as other maple species.

GENETIC GAIN AND GENE DIVERSITY UNDER THINNING SCENARIOS IN A SEEDLING SEED ORCHARD OF *Quercus accutissima*

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Genetic gain and gene diversity were estimated in a 12-year-old *Quercus accutissima* seedling seed orchard under three thinning scenarios. Both genetic gain and diversity of each scenario were estimated and compared to those of before thinning. These scenarios were based on genetic, systematic, and truncation thinnings. Gene diversity was assessed utilizing the status number concept (i.e., accumulation of coancestry). Genetic thinning involved the removal of individuals within families and the removal of entire families. Genetic thinning was based on the utilization of the family genetic values (GCA) generated from conventional progeny test trials. Truncation thinning produced the highest genetic gain that was coupled with the lowest gene diversity, while genetic thinning produced the optimum balance between genetic gain and diversity. Systematic thinning, on the other hand, produced the lowest genetic gain and the highest diversity. Under the genetic thinning option, the number of families completely removed was intentionally minimized to maintain higher gene diversity and to maintain options for further genetic evaluation and selection. Genetic thinning was accomplished by applying a within-family thinning regime that was proportional to the reverse of every family's genetic gain (i.e., low numbers of trees removed from high genetic gain families and higher numbers from trees from lower genetic gain families). Additionally, the effect of genetic relatedness among families and possible pollen contamination on both genetic gain and diversity, although not studied, their impact, is presented.

GIS-BASED SEED ZONES FOR WHITE SPRUCE IN ONTARIO

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To properly match seed sources to planting sites according to expressed patterns of adaptive variation, a focal point seed zone methodology was developed for white spruce (*Picea glauca* [Moench] Voss.) in Ontario. One hundred thirty-two provenances from Ontario and western Québec were established at a greenhouse and five field trials throughout Ontario. Growth and phenological variables were measured over two growing seasons and variables expressing variation among provenances were regressed individually against geographic and climate variables to assess whether they exhibited adaptive variation. Principal components (PC) analysis was used to summarize the main components of variation. The first PC axis mainly represented growth potential. PC axes 2 and 3 were strongly determined by phenological traits. PC axis scores for the provenances were regressed against climate variables and the resulting equations were used to model the PC axes. These models were converted to spatial data and reproduced as contoured grids using GIS. For any given point in Ontario the 3 PC axis grids are standardized and intersected, creating zones of adaptive similarity to that point. Focal point seed zones created for 9 example points selected from across the province show strong latitudinal trends and more regional longitudinal trends. Seed transfer for white spruce across traditional site region boundaries may be possible in most of north-central and north-eastern portions of Ontario.

MICROSATELLITE ANALYSIS OF GENETIC EFFECTS OF DOMESTICATION IN LODGEPOLE PINE

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Genetic diversity along the domestication process of lodgepole pine (*P. contorta* spp. *latifolia*) was investigated using microsatellite (SSRs) genetic markers. Genetic variability of 10 natural populations, each with 30 individuals, from the Prince George Breeding Zone provided the benchmark for comparison. The genetic diversity of the breeding (92 parents) and production (44 parents) populations as well as a representative seed crop was assessed. It was hypothesized that the domestication process may cause a gradual reduction of genetic diversity through several bottlenecks starting with phenotypic selection followed by the production population and the production of seed crops caused by the steady reduction of individuals included in each population. The number of alleles observed in natural, breeding, and production populations and the seed lot was 195, 166, 150, and 146, respectively. Alleles were grouped into four classes based on their frequencies (high: $P > 0.75$, intermediate $0.25 \leq P < 0.75$, low: $0.01 \leq P < 0.25$, and rare: $P < 0.01$). The majority of alleles fall into the low and rare frequency classes. A small amount of genetic variability was observed among the 10 natural populations studied ($F_{ST} = 0.008$), thus allowing using their collective genetic diversity as a benchmark for comparison. The total number of alleles (A_T) showed a steady reduction along the domestication process; however, most of the alleles lost were rare ($P < 0.01$) and expected heterozygosity (H_e) did not change substantially among the studied populations (range: 0.757 – 0.783). This was expected due to the minuscule effect of the rare allele's contribution to overall diversity. The results from the present study demonstrate that lodgepole pine has not experienced any major reduction of genetic diversity along the domestication process. However, more intensive breeding practices can result in a further erosion of genetic variability, especially the rare alleles.

INTER- VS. INTRA-PROVENANCE CROSSES IN *Pinus monticola*: EARLY PLANTATION RESULTS, WITH RECOMMENDATIONS FOR SEED TRANSFER IN BRITISH COLUMBIA

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Intra- and inter-provenance crosses of western white pine (*Pinus monticola*), using pollen mixes, were planted on two sites in British Columbia. Age 7 heights (five-years after planting) were analysed for the effect of seed tree, pollen source, and plantation. Although planting site affected population height and rank, interior seed parents and pollens generally produced trees 2–4% taller and Oregon, USA (Cascade Mountains) pollen reduced mean height of crosses consistently by 3–7%. Both positive and negative heterosis among crosses and significant genotype X environment interaction were found. Tentative recommendations for seed and pollen transfer are made.

REPRODUCTIVE AND GENETIC CHARACTERISTICS OF RARE, DISJUNCT PITCH PINE POPULATIONS AT THE NORTHERN LIMITS OF ITS RANGE IN CANADA

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Pitch pine (*Pinus rigida* Mill.) is a rare species in Canada, existing as a disjunct population in the St. Lawrence River Valley in eastern Ontario and as two northern outlier stands in southern Québec along Canada's southern border with the United States. Reproductive and genetic characteristics of these small, scattered stands were investigated to develop a foundation for management and restoration in the event of a northward range expansion under anticipated climate warming. Seed yields and seed quality appeared to be comparable to other eastern conifers, and to pitch pine at the center of its geographic range. For seed and seedling growth traits, most of the variation was attributable to differences among trees within stands and, to a lesser extent, among stands within a population. The population effect was non-significant. For reproductive traits, such as numbers of filled and empty seeds per cone, reproductive efficiency, and inbreeding estimates, high levels of variation (ranging from 26–33%) were found among stands, suggesting that stand structural features, such as stand size and tree density within stands, play an important role in pollination environment and overall reproductive success. Estimates of genetic diversity at 32 allozyme gene loci indicate that these small, isolated stands have maintained high levels of genetic diversity compared to populations at the center of the geographic range and also relative to other widely dispersed eastern conifers. Such comparatively high levels of genetic diversity suggest that Canada's extant pitch pine population may represent a remnant of a much wider distribution during warmer climates of the present interglacial period, rather than a population expanding its range northward. The relatively high levels of viable seed production and genetic diversity in native pitch pine populations indicate that native Canadian populations may be suitable seed sources for species restoration and expansion in Canada. Representative samples of these native Canadian populations have been established in New Brunswick, Prince Edward Island, and Nova Scotia to assess potential environmental limitations to the introduction of pitch pine across the Maritimes. The first series of such tests was established in 1996 and has demonstrated the excellent growth potential of this species for both industrial wood supply and ecological restoration in eastern Canada.

GENE RESOURCE INFORMATION MANAGEMENT IN BRITISH COLUMBIA – BUILDING A RESOURCE INFORMATION STRATEGY FOR GENETIC RESOURCE MAPPING, LAND-BASED STRATEGIC AND OPERATIONAL PLANNING AND EFFECTIVENESS MONITORING

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Gene resource information management (GRIM) forms a critical link to the long-term stewardship and sustainable resource management of the province's forest tree gene resources. GRIM goals and objectives will be met through the development of a Gene Resource Information Strategy. The Strategy will set direction and information management priorities over the next 2 to 5 years.

GRIM objectives include: 1) development of a provincial GRM framework (GRM-based Seed Planning Zones) to support forest stewardship plans, silviculture regeneration (seed deployment) strategies, forest tree genetics research, and gene conservation strategies; 2) development and support of forest tree genetic resource mapping, registries, and data warehouse repositories; 3) increased access to tree improvement program products (seed and vegetative material for operational use); 4) development of an integrated GRM effectiveness monitoring program linked to broader forestry initiatives (criteria and indicators, climate change) and land-based resource management issues (species conversion); and 5) incorporation of genetic gain into timber supply analyses through forest inventory updates and the use of GIS-ready spatial and attribute GRM data sets.

VEGETATIVE PROPAGATION OF *Fagus grandifolia* Ehrh. (AMERICAN BEECH) RESISTANT TO BEECH BARK DISEASE

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American beech (*Fagus grandifolia*) is an important tree species in eastern North America that has been severely affected by beech bark disease (BBD), a complex disease that involves the interaction of a scale insect (*Cryptococcus fagisuga* Lind.) and a *Nectria* fungus. While many trees have been killed, some show resistance to the disease. Resistance is believed to be of genetic origin and this provides an opportunity to propagate disease-free trees, introduce them to natural forests, and increase resistance levels. The purpose of this project is to use vegetative propagation on mature beech trees that appear resistant to BBD and test if the resistance is due to genetic factors. Three propagation techniques are being applied: micropropagation of buds, root sprouts and epicormic roots from branches, and grafting. Due to the difficulty of propagating this species in the past, a pilot study was carried out in 2003 to determine the feasibility of different propagation methods. It was determined that grafting success was low (30%) and was related to diameter of the rootstock. Contamination of *in vitro* cultured buds was high for some genotypes (more than 50% for 45% of the genotypes), and rooting of plantlets was low (less than 25%). Cuttings of root sprouts and shoots induced from branches were unsuccessful and epicormic shoots induced from branches were not vigorous and didn't survive *in vitro*. The grafted material is currently being tested for resistance by inoculating the scale insect on the bark of the seedlings.

DEFINING BLACK SPRUCE GROWTH OPTIMA IN ONTARIO: PRESENT AND FUTURE

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Height data from 19 range-wide black spruce (*Picea mariana* [Mill.] BSP) provenance trials were regressed against monthly minimum and maximum temperatures and monthly precipitation using the Cauchy function. Response functions were developed for individual populations to predict the climate value that will maximize performance for each source. Transfer functions were developed for individual test sites to predict climate values of populations that maximize performance at each of the test locations. Mid-spring and mid-to late-winter temperature data generally yielded the best fitting response and transfer functions. For each population/climate variable combination, a grid was developed to map predicted height growth of that population at all points within the region. Likewise, for each test site/climate variable combination, a grid was developed to predict height growth of all potential seed sources planted at that test site. Contours indicating maximal height growth for present and predicted 2040–2069 climate variables were added to these grids. Excluding the southern part of its range, black spruce seed sources produce better growth when moved south and should achieve better growth under warmer predicted future temperature regimes provided that other factors are not limiting. The incorporation of more southerly seed sources into today's northerly reforestation efforts will result in more rapidly growing trees today, and will also yield trees better adapted to predicted future temperatures.

RESPONSE FUNCTIONS OF LODGEPOLE PINE TO TEMPERATURE AND CO_2

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This project-in-progress is a short-term growth chamber experiment to establish norms of reaction to temperature and carbon dioxide. Seedlings of ten populations of lodgepole pine are being subjected to four temperature regimes and two CO_2 levels (ambient and elevated). Each population is represented by open-pollinated families, B+ seed lots, control-pollinated families, and seed orchard seed lots. The four temperature regimes correspond to the growing season of 4 locations with mean annual temperatures (MAT) of 1, 4, 7, and 10°C. Two of these regimes, MAT 4 and 10, receive both ambient and elevated CO_2 concentrations. Daylength is the same for all chambers, but varies from week to week as the season progresses. Water and nutrients are provided in excess. Height is measured periodically, while dry mass, allocation, photosynthetic rate, and water-use efficiency will be measured at the end of the season. Genotypes will be compared in order to determine which populations perform best in future climate scenarios and if there is rank change of genotypes among the scenarios. Differences between natural populations and improved seed lots, if any, will be identified. Gas exchange measurements will reveal whether photosynthetic acclimation to enriched CO_2 (downscaling) occurs. The underlying aim is to understand the physiological basis of these response functions and to determine if norms of reaction in growth chambers resemble those found in long-term field trials in different climates, such as the large-scale Illingworth lodgepole pine trials in BC.

CLIMATE CHANGE AND FORESTRY IN SWEDEN – A LITERATURE REVIEW

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The scope of the study was to review the relevant literature regarding the impact of climate change on forestry in Sweden, to synthesise the current knowledge, to draw conclusions on likely effects of climate change, and to identify the need for new research and knowledge. We have limited the study to the effects on a short and medium time span (20–100 years). We focused on the impact on the trees, both direct and indirect, through the climatic impact on soils, herbivores, insects, pests, and diseases. We made sharp delimitations to other aspects of forests and climate change.

This literature review has revealed major shortcomings in our knowledge about impacts that climate change will have on the forest ecosystems. Not only are the nature and magnitude of climate change uncertain, but even more its potential effects on the structure and processes of forest ecosystems.

However, the most likely effects of climate change can be predicted. They generally include an increase in potential biomass production, possibilities to grow new species commercially, and increased risk for damage of several kinds. It seems that climate change offers new opportunities to forestry in Sweden. At the same time the risk for calamities increases. This calls for demanding new approaches to forest- as well as risk-management.

Future research on the effects of climate change on forestry and forest ecosystems has to take account of a broad spectrum of scientific fields, but most important is probably the need for a multidisciplinary, scientific approach.

INTRASPECIFIC RESPONSES TO CLIMATE IN *Pinus albicaulis*

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Provenance tests of 42 populations of *Pinus albicaulis*, originating from inland northwestern United States revealed genetic differentiation for growth potential and phenology in relation to climate. The provenance tests were established at Priest River Experimental Forest, Idaho in 2000 using 2-year-old seedlings. Patterns of shoot elongation were recorded beginning in the second growing season. Hutchinson's thin plate splines were used to make point predictions for climate at each provenance. These climate predictions were then used to describe genetic variation. Genetic variation was significantly correlated with climate effects derived from temperature. Correlations were strongest for degree days > 5°C and timing of last spring frost. The relationship between growth potential and degree days > 5°C was negative. The analyses suggest that genetic differentiation for growth potential and phenology is controlled by the relative mildness of climate in relation to temperature.

POPLAR LEAF RUST CAUSED BY *Melampsora* SPECIES IN KOREA

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The severity of poplar leaf rust caused by *Melampsora* species on 15 poplar clones was investigated to select resistance in clones to the pathogens and to see whether the pathogens exhibit specificity toward the poplar clones. Cuttings of 15 poplar clones were planted at a nursery bed in Suwon, Korea, in March of 2003. Three rusted leaves per clone were collected from each of the 15 clones, and 10 urediniospores per leaf were observed with both scanning electron microscopy (SEM) and light microscopy (LM). Rust severity was rated on September 2 and 27 and October 20, 2003, using the Schreiner scale (0–100).

Urediniospores from all clones except 72-30, 72-31, Bong-wha 1, and Hyunsasi 3 were oval and tended to be clavate to broadly ellipsoid. Both apices and bases were mostly rounded, but the wall surface of the urediniospore was echinulate except for a smooth patch on the apex. However, urediniospores from the rest of the 4 clones had uniform echinulation. The size of the spores from two groups was also different from each other. The former (11 clones) measured 24-46 X 13-23 ìm, and the latter (4 clones) measured 20-29 X 13-20 ìm. On September 2, 2003, the first rust severity rating date, only two clones, 97-17 and Eco 28, rated a Schreiner score of 100. However, by October 20, 2003, a total of 12 clones rated 100. Bong-wha 1, Dorskamp, and Hyunsasi 3 were only lightly rusted (all 20 on October 20, 2003). All of the leaf rust samples taken from the 11 clones were identified as *M. larici-populina*; however, samples from the 4 clones were not exactly identified. It seems that they belong to the difficult species complex of *Populus* section *Populus.*

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PHOTOS

Andreas Hamman, Isabelle Chuine, and Makiko Mimura with empty plates at the ice breaker.

Kathy Tosh says "When you've got the "best", who needs the "rest?"

"We'll drink to that!" A jovial table enjoying the festivities at Summerhill Winery. Seated are Louise Corriveau, Tannis Beardmore, Kathy Tosh, Dale Simpson, Dana Howe, and Marilyn Cherry

Marilyn Cherry congratulates Cherdsak Liewlaksaneeyanawin for best student poster

Marilyn Cherry congratulates Mark Lesser for best student oral presentation.

Invited symposium speakers. From left to right, Jerry Rehfeldt, Isabelle Chuine, Steven Jackson, Dave Spittlehouse, Nadja Tchebakova, Andrew Weaver.

CTIA sponsored students: Nicolas Ukrainetz (UBC), Marienela Ramirez (UNB), Adriana Almeida-Rodriguez (UA), Stéphanie Beauseigle (ULaval), Jessica Courtier (UNBC), Jean-François Carle (UdeM), Claire Riddell (Lakehead U).

BC Ministry of Forests, Tree Improvement Branch. Left to right. Bottom row: Chris Walsh, Leslie McAuley, Ron Planden, Rita Wagner. Second row: Dale Draper, Dave Kolotelo. Third row: Cheri Tayler, Heather Rooke, Carolyn Lohr, Don Summers. Fourth row: Robb Bennett, Dawn Stubley, David Reid. Fifth row: Penny Draper, Debbie Poldrugovac, Spencer Reitenbach, Brian Barber, Roger Painter.