PROCEEDINGS OF THE THIRTIETH MEETING
OF THE
CANADIAN TREE IMPROVEMENT ASSOCIATION

PART 1 Minutes and Members' Reports
PART 2 Symposium

Canada's Forests – Enhancing Productivity, Protection & Conservation

Les forêts du Canada : mise en valeur de la productivité, de la protection et de la conservation

COMPTES RENDUS DU TRENTIÈME CONGRÈS
DE
L'ASSOCIATION CANADIENNE POUR L'AMÉLIORATION DES ARBRES

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

National Library of Canada cataloguing in publication data

Canadian Tree Improvement Association. Meeting (30th : 2006 : Charlottetown, PEI)

Proceedings of the Thirtieth Meeting of the Canadian Tree Improvement Association : Canada's forests – enhancing productivity, protection & conservation

Includes preliminary text and articles in French.
Contents : Part 1. Minutes and Member's Reports. Part 2. Symposium.

ISBN 978-0-662-46567-6
Cat. No. Fo1-16/2006E-MRC

1. Forest genetics – Congresses.
2. Trees – Breeding – Congresses.
3. Forest genetics – Canada – Congresses.
I. Atlantic Forestry Centre.
II. Title.
III. Title : Proceedings of the Thirtieth Meeting of the Canadian Tree Improvement Association : Canada's forests – enhancing productivity, protection & conservation

Données de catalogage avant publication de la Bibliothèque nationale du Canada

Association canadienne pour l'amélioration des arbres. Conférence (30e : 2006 : Charlottetown, ÎPE)

Comptes rendus du trentième congrès de l'Association canadienne pour l'amélioration des arbres : les forêts du Canada – mise en valeur de la productivité, de la protection et de la conservation

Comprend des textes préliminaires et des articles en français.
Sommaire : 1ère Partie. Procès-verbaux et rapports des membres. 2e Partie. Colloque.

ISBN 978-0-662-46567-6
No de cat. Fo1-16/2006E-MRC

1. Génétiques forestières – Congrès.
2. Arbres – Amélioration – Congrès.
3. Génétiques forestières – Canada – Congrès.
I. Centre de foresterie de l'Atlantique.
II. Titre.
III. Titre : Comptes rendus du trentième congrès de l'Association canadienne pour l'amélioration des arbres : les forêts du Canada – mise en valeur de la productivité, de la protection et de la conservation

PROCEEDINGS

OF THE

THIRTIETH MEETING

OF THE

CANADIAN TREE IMPROVEMENT ASSOCIATION

PART 1

Minutes and members' reports

Charlottetown, Prince Edward Island
July 24–27, 2006

Editor
J.D. Simpson

Additional copies of this
publication are available from:

Dale Simpson
Editor, CTIA
Natural Resources Canada
Canadian Forest Service - Atlantic
P.O. Box 4000
Fredericton, New Brunswick, Canada
E3B 5P7

Produced by

Natural Resources Canada
for the
Canadian Tree Improvement Association
2007

Financial Contributions

Bowater Maritimes Inc.
J.D. Irving, Limited
Jiffy Products
Natural Resources Canada
Neenah Paper of Canada (Pictou Woodlands)
New Brunswick Department Natural Resources
Nova Scotia Department Natural Resources
PEI Dept. of Environment, Energy and Forestry
PEI Model Forest Network Partnership Ltd.
Weyerhaeuser Ltd.

COMPTES RENDUS

DU

TRENTIÈME CONGRÈS

DE

L' ASSOCIATION CANADIENNE POUR L' AMÉLIORATION DES ARBRES

1re PARTIE

Procès-verbaux et rapports des membres

Charlottetown, Île-du-Prince-Édouard
24–27 juillet 2006

Rédacteur
J.D. Simpson

Des copies supplémentaires de cette publication
sont disponibles de:

Dale Simpson
Rédacteur, ACAA
Ressources naturelles Canada
Service canadien des forêts - Atlantique
C.P. 4000
Fredericton, Nouveau-Brunswick, Canada
E3B 5P7

Préparé par

Ressources naturelles Canada
pour
l'Association canadienne pour l'amélioration des arbres
2007

Sous le patronage de

Bowater Maritimes Inc.
J.D. Irving, Limited
Jiffy Products
Ministère des Ressources naturelles du Nouveau-Brunswick
Neenah Paper of Canada (Pictou Woodlands)
Nova Scotia Department Natural Resources
PEI Dept. of Environment, Energy and Forestry
PEI Model Forest Network Partnership Ltd.
Ressources naturelles Canada
Weyerhaeuser Ltd.

PROCEEDINGS OF THE THIRTIETH MEETING OF THE CANADIAN TREE IMPROVEMENT ASSOCIATION

Enquiries may be addressed to the authors or to Mr. Dale Simpson, Editor CTIA, Natural Resources Canada, Canadian Forest Service - Atlantic, P.O. Box 4000, Fredericton, New Brunswick, Canada, E3B 5P7. E-mail: Dale.Simpson@nrcan.gc.ca

IF YOUR ADDRESS ON THE LABEL IS INCORRECT OR INCOMPLETE, PLEASE RETURN THE CORRECTION SLIP BELOW.

Others interested in receiving Proceedings, notice of meetings, etc. may return the slip to be listed as Corresponding Members (Canadian) or be placed on the mailing list for the Proceedings only (libraries, institutions, international addresses). If you no longer wish to receive the Proceedings, please check "Delete" and return the completed slip to the Editor.

To: Dale Simpson
Editor, CTIA/ACAA
Natural Resources Canada
Canadian Forest Service - Atlantic
P.O. Box 4000
Fredericton, New Brunswick, Canada
E3B 5P7

PLEASE PRINT

Name: Prof. Ms.
Dr. Mr. ______________________________

Address: ______________________________

____

____

______________________ **Postal Code** __________

Please check one:
☐ Correction
☐ New addressee
☐ Delete from CTIA mailing list

COMPTES RENDUS DU TRENTIÈME CONGRÈS DE L'ASSOCIATION CANADIENNE POUR L'AMÉLIORATION DES ARBRES

Les demandes de renseignements peuvent être adressées aux auteurs ou à Dale Simpson, Rédacteur, ACAA, Ressources naturelles Canada, Service canadien des forêts - Atlantique, C.P. 4000, Fredericton, Nouveau-Brunswick, Canada, E3B 5P7. Courriel: Dale.Simpson@ rncan.gc.ca

SI VOTRE ADRESSE SUR L'ÉTIQUETTE EST INEXACTE OU INCOMPLÈTE, VEUILLEZ RETOURNER LA FICHE DE CORRECTION CI-DESSOUS

Les personnes qui aimeraient recevoir les comptes rendus, les avis de réunions, etc., sont priées de retourner la formule pour que leurs noms soient ajoutés à la liste des membres correspondants (canadiens), ou à la liste d'envoi pour les comptes rendus seulement (bibliothèques, institutions, destinataires à l'étranger). Si vous ne désirez plus recevoir ces comptes rendus, veuillez cocher "rayer" et retourner la formule completée au rédacteur.

À: Dale Simpson
Rédacteur, ACAA/CTIA
Ressources naturelles Canada
Service canadien des forêts - Atlantique
C.P. 4000
Fredericton, Nouveau-Brunswick, Canada
E3B 5P7

LETTRES MOULÉES S.V.P.

Nom: Prof. Mme
D^r M ______________________________

Adresse: ______________________________

____

____

______________________________ **Code postal** ____________

Veuillez cocher une seule case:

☐ Correction

☐ Nouveau destinataire

☐ Rayer le destinataire de la liste d'envoi de l'ACAA

TABLE OF CONTENTS

Alberta – Western Boreal Aspen Corporation

Alberta – University of Alberta

Alberta – Alberta Sustainable Resource Development

British Columbia – Western Forest Products Inc.

British Columbia – Isabella Point Forestry Ltd.

British Columbia – University of British Columbia

British Columbia – Ministry of Forests and Range

British Columbia – Ministry of Forests and Range

CTIA/ACAA ACTIVE MEMBERS

Greg Adams
JD Irving, Limited
181 Aiton Road
Sussex, New Brunswick
E4G 2V5

Dr. Sally Aitken
University of British Columbia
3041-2424 Main Mall
Vancouver, British Columbia
V6T 1Z4

Chris Atack
Fibre Max Forestry
111 Greeningdon Dr.
Timmins, Ontario
P4R 1G3

Brian Barber
B. C. Ministry of Forests and Range
P.O. Box 9518 Stn. Prov. Govt.
Victoria, British Columbia
V8W 9C2

Leonard K. Barnhardt
Alberta Sustainable Resource
Pine Ridge Nursery Box 750
Smoky Lake, Alberta
T0A 3C0

Dr. Tannis Beardmore
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3B 5P7

Dr. Jean Beaulieu
Ressources naturelles Canada
1055 rue du PEPS C.P. 3800
Ste. Foy, Québec
G1V 4C7

Michele Bettez
Min. des Ressources naturelles
1690, chemin Grande-Côte
Berthier, Québec
J0K 1A0

Dr. Anne-Christine Bonfils
Natural Resources Canada
580 Booth St., 7th floor
Ottawa, Ontario
K1A 0E4

Dr. Jean Bousquet
C. R. B. F.
Université Laval
Ste. Foy, Québec
G1K 7P4

Kathleen Brosemer
Forest Genetics Ontario
510 Queen St. East, Suite 24
Sault Ste. Marie, Ontario
P6A 2A1

Mike Butler
Dept. of Environment, Energy and Forestry
P.O. Box 2000
Charlottetown, PEI
C1A 7N8

Dr. Stewart E. Cameron
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3B 5P7

Dr. Mike Carlson
B. C. Ministry of Forests and Range
3401 Reservior Road
Vernon, British Columbia
V1B 2C7

Paul Charrette
Lakehead University
955 Oliver Road
Thunder Bay, Ontario
P7B 5E1

Fabienne Colas
Min. des Ressources naturelles
2700, rue Einstein
Sainte-Foy, Québec
G1P 3W8

Louise Corriveau
Weyerhaeuser Saskatchewan Ltd.
P.O. Box 1720
Prince Albert, Saskatchewan
S6V 5T3

Dr. Bruce Dancik
University of Alberta
855 General Services Bldg.
Edmonton, Alberta
T6G 2H1

Gaetan Daoust
Ressources naturelles Canada
1055 rue du PEPS C.P. 3800
Ste. Foy, Québec
G1V 4C7

Dr. Campbell G. Davidson
Agriculture and Agri Food Canada
Floor 7th, Room 770 930 Carling Ave.
Ottawa, Ontario
K1A 0C5

Marie Deslauriers
Ressources naturelles Canada
1055 rue du PEPS C.P. 3800
Ste. Foy, Québec
G1V 4C7

Dr. Narinder Dhir
Alberta Sustainable Resource
9920-108 Street, 8th Floor
Edmonton, Alberta
T5K 2M4

Franco Di-Giovanni
AirZone One Inc.
2240 Speakman Drive
Mississauga, Ontario
L5K 1A9

John Dojack
Manitoba Forestry Branch
Box 70, 200 Saulteaux Cres.
Winnipeg, Manitoba
R3J 3W3

Eric Earle
Department of Natural Resources
P.O. Box 2006, Fortis Building
Corner Brook, Newfoundland
A2H 6J8

Dr. Yousry A. El-Kassaby
University of British Columbia
3030-2424 Main Mall
Vancouver, British Columbia
V6T 1Z4

Gordon Falk
Dept. of Natural Resources
Box 70, 200 Saulteaux Cres.
Winnipeg, Manitoba
R3J 3W3

Dr. W. H. Fogal
Ecology Products and Service
P.O. Box 293
Chalk River, Ontario
K0J 1J0

Al Foley
Ministry of Natural Resources
141 King Street, Box 2028
Angus, Ontario
L0M 1B0

Randy D. Ford
Northeast Seed Management Inc.
P.O. Box 730
Englehart, Ontario
P0J 1H0

Howard M. Frame
Dept. of Natural Resources
P.O. Box 68
Truro, Nova Scotia
B2N 5B8

Michele Fullarton
N.B. Department of Natural Resources
Kingsclear Tree Nursery, 3732 Rte. 2
Island View, New Brunswick
E3E 1G3

Scott Green
University of Northern BC
3333 University Way
Prince George, British Columbia
V2N 4Z9

Tim Gylander
Weyerhaeuser Canada Ltd.
P.O. Box 7739
Drayton Valley, Alberta
T7A 1S8

Andreas Hamann
University of Alberta
775 General Services Building
Edmonton, AB
T6G 2H1

Christine Hanson
Alberta Sustainable Resource
P.O. Box 750
Smoky Lake, AB
T0A 3C0

Dr. Nathalie Isabel
Ressources naturelles Canada
1055 rue du PEPS C.P. 3800
Ste. Foy, Québec
G1V 4C7

Dr. Sally John
Isabella Point Forestry Ltd.
331 Roland Road
Salt Spring Island, British Columbia
V8K 1V1

Dr. John King
B. C. Ministry of Forests and Range
P.O. Box 9519, Stn. Prov. Govt.
Victoria, British Columbia
V8W 9C2

Dr. Marek Krasowski
University of New Brunswick
P.O. Box 44555
Fredericton, New Brunswick
E3B 6C2

Dr. Judy Loo
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3B 5P7

John Major
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3B 5P7

Dr. Alexander Mosseler
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3B 5P7

Mary Myers
Dept. of Environment, Energy and Forestry
P.O. Box 2000
Charlottetown, PEI
C1A 7N8

Greg O'Neill
B.C. Ministry of Forests and Range
3401 Reservoir Road
Vernon, British Columbia
V1B 2C7

Dr. Barry Jaquish
B. C. Ministry of Forests and Range
3401 Reservoir Road
Vernon, British Columbia
V1B 2C7

Dr. Dennis Joyce
Ministry of Natural Resources
70 Foster Drive, Suite 400
Sault Ste. Marie, Ontario
P6A 6V5

Dave Kolotelo
B.C. Ministry of Forests and Range
1879 - 32 Avenue
Surrey, British Columbia
V3S 0L5

Barry Linehan
Department of Natural Resources
P.O. Box 616
Grand Falls-Windsor, Newfoundland
A2A 2K2

Dr. Pengxin Lu
Ontario Ministry of Natural Resources
1235 Queen Street East
Sault Ste. Marie, Ontario
P6A 2E5

Gwen McGimpsey
Dept. of Natural Resources
Box 70, 200 Saulteaux Cres.
Winnipeg, Manitoba
R3J 3W3

Marie-Josee Mottet
Min. des Ressources naturelles
2700 rue Einstein
Ste. Foy, Québec
G1P 3W8

Florence Niemi
Daishowa-Marubeni International Inc.
Postal Bag 6500
Peace River, Alberta
T8S 1V5

Donna Palamarek
Alberta Sustainable Resource
P.O. Box 750
Smoky Lake, AB
T0A 3C0

Dr. Yill Sung Park
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3B 5P7

Dr. William Parker
Faculty of Forestry and Forest
Thunder Bay, Ontario
P7B 5E1

Pierre Périnet
Min. des Ressources naturelles
2700, rue Einstein
Sainte-Foy, Québec
G1P 3W8

Dr. Sharon Pond
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3P 5P7

John Quinn
Alberta Forest Service
P.O. Box 750
Smoky Lake, Alberta
T0A 3C0

André Rainville
Min. des Ressources naturelles
2700 rue Einstein
Ste. Foy, Québec
G1P 3W8

Dr. Om P. Rajora
University of New Brunswick
P.O. Box 44555
Fredericton, New Brunswick
E3B 6C2

Dave Reid
B.C. Ministry of Forests and Range
7380 Puckle Road
Saanichton, British Columbia
V8M 1W4

Dr. Kermit Ritland
University of British Columbia
2424 Main Mall
Vancouver, British Columbia
V6T 1Z4

Dr. John Russell
B.C. Ministry of Forests and Range
P.O. Box 335
Mesachie Lake, British Columbia
V0R 2N0

Deogratias Rweyongeza
University of Alberta
Dep. Agric., Food and Nutritional
Edmonton, AB
T6G 2P5

Darryl Sande
Weyerhaeuser Saskatchewan Ltd.
P.O. Box 1720
Prince Albert, Saskatchewan
S6V 5T3

William Schroeder
Shelterbelt Centre, P.F.R.A.
Indian Head
Saskatchewan
S0G 2K0

Dale Simpson
Natural Resources Canada
P.O. Box 4000
Fredericton, New Brunswick
E3E 5P7

Dr. Ron F. Smith
ValFor Ltd.
12 Chateau Drive
McLeod Hill, New Brunswick
E3A 5X2

David G. Steeves
Dept. of Natural Resources
P.O. Box 68
Truro, Nova Scotia
B2N 5B8

Dr. Michael Stoehr
B.C. Ministry of Forests and Range
1320 Glyn Road
Victoria, British Columbia
V8W 3E7

Kathleen Tosh
N.B. Department of Natural Resources
Kingsclear Forest Nursery, 3732 Rte. 2
Island View, New Brunswick
E3B 4X7

Denise Tousignant
Min. des Ressources naturelles
2700, rue Einstein
Sainte-Foy, Québec
G1P 3W8

Laurence Tremblay
Min. des Ressources naturelles
2700 rue Einstein
Ste. Foy, Québec
G1P 3W8

Richard Trudel
INRS - Institut Armand-Frappier
Laval, Québec
H7N 4Z3

Annette van Niejenhuis
Western Forest Products
8067 East Saanich Road
Saanichton, BC
V8M 1K1

Yuhui Weng
N.B. Department of Natural Resources
Kingsclear Forest Nursery, 3732 Rte. 2
Island View, New Brunswick
E3B 4X7

Dr. Jack H. Woods
Forest Genetics Council of BC
3370 Drinkwater Road
Duncan, British Columbia
V9L 5Z2

Dr. Alvin Yanchuk
B.C. Ministry of Forests and Range
P.O. Box 9519 Stn. Prov. Govt.
Victoria, British Columbia
V8W 9C2

Dr. Francis Yeh
University of Alberta
855 General Service Bldg.
Edmonton, Alberta
T6G 2H1

Dr. S. Y. Zhang
Forintek Canada Ltd.
319 rue Franquet
Sainte-Foy, Québec
G1P 4R4

BUSINESS MEETING MINUTES

CTIA/ACAA 30th Business Meeting Minutes

Kathy Tosh chaired the 30th Business Meeting of the CTIA/ACAA held at the Delta Prince Edward, Charlottetown, Prince Edward Island on Tuesday July 25, 2006. Thirty Active and 4 Honorary members were present.

346 Minutes of the 29th Meeting

(as printed in the proceedings from the 29th meeting, Part I)

Motion: That the minutes of the 29th Business Meeting be approved as published.
Moved by: Dave Kolotelo
Seconded by: Dave Reid
Carried.

347 Membership

347.1 Honorary Membership

No nominations received.

347.2 Active Membership

The name of one nominee was presented as follows:

Laurence Tremblay	Ministère des Ressources naturelles Sainte-Foy, QC

Motion: That the nominated Active Member be duly elected.
Moved by: Jean Beaulieu
Seconded by: Paul Charrette
Carried.

347.3 Corresponding Membership

No nominations received.

348 Chair's Report

The 30th meeting of the association was held for the first time in its history in Prince Edward Island and was also the first time it was co-hosted by three provinces. The meeting was truly a "joint" effort from all the committee members. The meeting was held in conjunction with the IUFRO Seed Symposium in Fredericton and the 1st Forum on the Conservation of Forest Genetic Resources.

On behalf of the 2006 organizing committee I would like to thank the many individuals that contributed to the success of the 30th CTIA meeting. The organizing committee did a great job in putting the conference together over the last two years. In particular I would like to thank the following committee members (names underlined), and many individuals and their respective employers who generously supported the conference.

PEI Department of Environment, Energy and Forestry
<u>Mike Butler</u> (field tour and local arrangements)
Mary Myers (support)
J. Frank Gaudet Tree Nursery Staff

NS Department of Natural Resources
Howard Frame (coordination of registration and gifts)
Sandy Anderson (web design and updating)
Lisa Patton (registration)

NB Department of Natural Resources
Michele Fullarton (conference binder)
Yuhui Weng (committee member)
Tree Improvement Staff

Natural Resources Canada
Yill-Sung Park (sponsored students)
Judy Loo (invited speakers)
Tannis Beardmore (CTIA treasurer)
Dale Simpson (posters and papers)
Debra Perry (logo design)

J.D. Irving, Limited
Greg Adams (committee member)

Workshop Organizers
Dave Kolotelo (Tree Seed Workshop)
Tony Zhang (Wood Quality Workshop)
Alvin Yanchuk (Wood Quality Workshop)

The support of ten sponsors allowed us to invite first class speakers and host a top notch conference. The sponsorship also allowed us to continue our student sponsorship program.The following sponsors provided much appreciated financial support for the 2006 meeting:

Bowater Maritimes Inc.
J.D. Irving, Limited
Jiffy Products
Natural Resources Canada
Neenah Paper of Canada (Pictou Woodlands)
New Brunswick Department Natural Resources
Nova Scotia Department Natural Resources
PEI Dept. of Environment, Energy and Forestry
PEI Model Forest Network Partnership Ltd.
Weyerhaeuser Ltd.

Thanks very much to these organizations for their generous contributions.

Lastly I would like to thank all the participants, the invited speakers, and the students who attended the 2006 conference. It is your participation and contributions to the meeting that resulted in a successful and enjoyable conference. Good luck to the next CTIA planning committee and I hope to see you in Québec in 2008!

Kathy Tosh
Chair

349 Treasurer's Report

The financial statement for the period of June 2004 to June 2006 was presented by Treasurer Tannis Beardmore and tabled for information and acceptance by the membership (see Attachment #1). The statement shows a balance of $30,143.89 in the Association's account plus GIC's totaling $23,000.00. Tannis suggested that additional GICs may be purchased after invoices have been paid for this meeting in order to obtain more interest.

Motion: That the financial statement be accepted as presented.
Moved by: Judy Loo
Seconded by: Sally Aitken
Carried.

350 Financial Contributions

Bowater Maritimes Inc.
J.D. Irving, Limited
Jiffy Products
Natural Resources Canada
Neenah Paper of Canada (Pictou Woodlands)
New Brunswick Department Natural Resources
Nova Scotia Department Natural Resources
PEI Dept. of Environment, Energy and Forestry
PEI Model Forest Network Partnership Ltd.
Weyerhaeuser Ltd.

Motion:	That the CTIA/ACAA executive of the 30th meeting express our sincere appreciation to these contributors.
Moved by:	Yousry El-Kassaby
Seconded by:	Yill Sung Park
Carried.	

351 Editor's Report

The proceedings were printed and distributed during October 2005 to all active members, honorary members, Canadian universities and libraries, registrants, and financial contributors of the 29th meeting. Two hundred and sixty-nine proceedings were mailed. For the first time, the proceedings were made available on CD-ROM. Sixteen copies were sent to Active members who requested this alternate medium.

A letter advising of the theme of the 29th 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 10 Canadian, 10 USA and 12 International addresses. No copies remain on inventory.

The mailing list contains 446 addresses comprised of: 18 Honorary, 87 Active, 95 Corresponding, 59 Canadian libraries, 70 USA, and 117 International.

Dale Simpson

352 Education Committee

As in the past, the organizing committee of the CTIA 2006 meeting sponsored students from Canadian Universities with an accredited undergraduate forestry program. This sponsorship is encouraged by CTIA members and financially supported by conference registration fees. Seven universities were contacted to nominate a student to attend the meeting in Charlottetown. With the exception of University of Alberta and Laval University, all others replied and the following students attended the meeting:

Erin Hamanishi	University of British Columbia
Cheryl Johnson-Schuetz	University of Northern British Columbia
Natacha Sénéchal	University of Moncton
Ashley Thomson	Lakehead University
Laurie Webster	University of New Brunswick

Sponsorship covered costs of attendance, including return flights, accommodation, and conference registration.

The Gene Namkoong Award is presented to a student with the best poster. Two students tied to receive this award which was presented to Erin Hamanishi from University of British Columbia for a poster titled "The accumulation of anthocyanins in juvenile *Pinus contorta* dougl. ssp. *latifolia* seedlings: Are phenotypic differences among provenances due to an adaptation to local environments?" co-authored with Sally Aitken and Karolyn Keir, University of British Columbia, who had a poster titled "Population genetics of Pacific dogwood (*Cornus nuttallii*)" co-authored with Sally Aitken.

The Carl Heimburger Award is presented to a student for the best oral presentation. The winner was Marianela Ramirez, University of New Brunswick, for her paper titled “Assessing genetic resistance of American beech to the beech scale insect” co-authored with J. Loo and M. Krasowski.

353 Working Group Reports

353.1 Tree Seed Working Group

The primary focus of the Tree Seed Working group has been in exchanging information through our biannual Newsbulletin and through the biennial Tree Seed Workshop. Since our last report we have published four editions of the News Bulletin (#40–43) on the following topic areas:

#40	Problems and Information Needs for Tree Seed
#41	Cone and Seed Pests
#42	Cone and Seed Processing
#43	Information Management

The News Bulletin has been well received and now reaches **250** people worldwide electronically. The topic for our 44th edition is “Seed Dormancy” and we welcome contributions from all. Appreciation is extended to all who contribute to the News Bulletin. Anyone who wishes to be on the distribution list can contact me (Dave.Kolotelo@gov.bc.ca) or Dale Simpson (dsimpson@nrcan.gc.ca). Past electronic versions of the News Bulletin can also be downloaded in pdf format from the following link: http://www.for.gov.bc.ca/hti/treeseedcentre/tsc/tswg.htm

The workshop in Charlottetown was titled “**Appreciating, Quantifying and Utilizing Family Differences**” with the following speakers presenting a wealth of information on the topic.

Introduction	Dave Kolotelo
25+ years of family-block planting in the Southern US – From novelty to standard operating procedure	Steve McKeand
Quantifying genetic differences in Newfoundland’s breeding population of white spruce seeds and cones	Barry Linehan
Processing family seedlots	Al Foley
Parental contribution estimation methods for orchard seedlots in British Columbia: why, how and does it work?	Jack Woods
Family variation in white spruce seed and seedling characteristics	Jean Beaulieu
BC experience of processing by family	David Kolotelo
Tree improvement delivery system: critical evaluation with emphasis on seed and seedling production	Yousry El-Kassaby

The workshop was well attended and provided a forum for some interesting discussion on genetic variability and its integration into our tree improvement programs. I look forward to our next workshop that will be held in Québec City in 2008.

Dave Kolotelo
Chair

353.2 Wood Quality Working Group

Eleven papers were presented at the workshop, organized by Tony Zhang, held on Monday. A variety of topics on wood quality and properties were included. The Working Group is 21 years old.

Alvin Yanchuk
Tony Zhang
Co-chairs

353.3 Canadian Forest Genetics Councils Working Group

The Working Group was created at the CTIA meeting held in Kelowna in 2004 as a result of a survey conducted by Don Lester on which he reported at that meeting. The recommendation was to form a Council composed of representatives from provinces and territories which could respond to issues having a national context. The Council was created and a contact list confirmed. No issues arose. Jack Woods will update and maintain the contact list.

Jack Woods
Chair

354 New Business

354.1 Canadian Institute for Science and Technical Information

Bruce Dancik outlined that the purpose of CISTI is to collect and subscribe to obscure journals as well as serving as a data depository for journals that may have had data submitted in conjunction with a paper but the data set was too large to publish. The service could be of useful for depositing a person’s or institution’s data. It could also be a means of storing the historical CTIA records.

The consensus was that it is worthwhile to investigate. The BC Ministry of Forests and Range is undertaking a large database project to store BC genetics data. Another suggestion was that it could serve as a catalogue of data of who has what, allowing somebody to contact the specific person for the data. Bruce agreed to follow up.

354.2 Change Name of Canadian Tree Improvement Association

Sally John brought this forward saying that a name change was suggested at the meeting held in 2000 but the motion was defeated. Sally Aitken agreed that a name change is long over due. Bruce Dancik also agreed with Sally Aitken and felt that people are inhibited to attend the meeting due to the stigma of the current name. Gaëtan Daoust pointed out that changing the name has been discussed at two past meetings. The current name was adopted in 1973.

Motion:	Change the name of Canadian Tree Improvement Association to Canadian Forest Genetics Association.
Moved by:	Sally John
Seconded by:	Om Rajora

Dave Reid felt that production and tree improvement people may feel out of place with the proposed name. Kathleen Brosemer felt the public perception of tree improvement and genetics is bad. Kris Morgenstern felt the current name is too narrow. Don Fowler did not see any advantage to changing the name. Kit Yeatman was “on the fence” over the name change.

Motion defeated: Yeas 18, Nays 8, Abstentions 2. The motion was defeated because Article IX, section b of the Constitution and Bylaws states “An amendment proposed during a business meeting ... shall require for adoption an affirmative vote of no fewer than 20 members, and of not less than two-thirds of those present and voting.”

Motion:	An electronic poll of the Active Members will be undertaken within a 3 month period following the business meeting regarding changing the name of Canadian Tree Improvement Association to Canadian Forest Genetics Association.
Moved by:	Jack Woods
Seconded by:	Kathleen Brosemer
Carried	

Sally John will produce a one page document in favor of Canadian Forest Genetics Association. Dave Reid will produce a one page document in favor of Canadian Tree Improvement Association. These documents will accompany the e-mail to be sent to Active Members polling them on the proposed name change.

355 Future Meetings

355.1 Location of the 2008 Meeting

Jean Beaulieu confirmed to host the meeting in Québec City possibly jointly with an IUFRO genomics conference.

355.2 Location of the 2010 Meeting

Ontario, possibly Thunder Bay.

355.3 Location of the 2012 Meeting

Vancouver.

356 Election of New Executive

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

Chairperson:	Jean Beaulieu Canadian Forest Service
Vice-Chairperson: Symposium	Jean Bousquet Laval University
Vice-Chairperson: Local arrangements	André Rainville Quebec Ministry of Natural Resources
Treasurer:	Tannis Beardmore Canadian Forest Service
Editor:	Dale Simpson Canadian Forest Service
Executive Secretary:	Dale Simpson Canadian Forest Service

357 Adjournment

Motion:	That the 30th business meeting of the CTIA/ACAA be adjourned.
Moved by:	Bruce Dancik

Attachment # 1

CTIA/ACAA
Financial Statement
June 2004 – June 2006

Cash balance	$28,744.58
GIC	$8,000.00
Total Holdings - June 12, 2004	**$36,744.58**

Credits

Interest (account)	$29.08
Interest (GIC)	$231.75
Sale of proceedings	$572.87
Surplus from 2004 CTIA meeting	$10,787.59
2006 CTIA meeting deposits:	
Province of Nova Scotia	$3,540.00
Bowater	$500.00
Neenah Paper	$1,260.00
Registrations	$11,068.00
Total Credits	$27,989.29

Debits

Supplies for proceedings mailout	$370.84
Printing of proceedings of 2004 meeting	$8,280.00
Bank fees	$36.43
Deposit for 2006 meeting at Delta Hotel	$1,500.00
Airline tickets for invited speaker, 2006 meeting	$1,402.71
GIC purchase	$8,000.00
GIC purchase	$7,000.00
Total Debits	$26,589.98

Guaranteed Investment Certificates

GIC (matures Feb 07)	$8,000.00
GIC (matures Jun 08)	$7,000.00
GIC (matures Jun 09)	$8,000.00

Holdings - June 27, 2006

Cash balance	$30,143.89
GIC	$23,000.00
Total	**$53,143.89**

ACTIVITY REPORTS
FROM ACTIVE MEMBERS

COOPERATIVE TREE BREEDING IN NOVA SCOTIA

Howard Frame and David Steeves

Department of Natural Resources
PO Box 68
Truro, NS
B2N 6P6
E-mail: hmframe@gov.ns.ca

Keywords: *Picea mariana*, *P. glauca*, *P. rubens*, *P. abies*, 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 (DNR), Bowater Mersey Paper Company Limited, Neenah Paper (formerly 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 from the program's inception. Meetings are held in the spring and fall of each year to review progress and plans. 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.), and Norway spruce (*P. abies* [L.] Karst.).

The industrial cooperative members have taken the lead role in the day to day tree breeding activities formerly carried out by the DNR. With first-generation seed orchards able to supply the current seed demand for reforestation within the province, the DNR stepped away from second-generation orchard development. The industrial cooperators however, are proceeding with second-generation breeding and orchard development. Neenah Paper has leased the DNRs' Tree Breeding Centre and is using that facility for orchard propagation as well as for housing their woodlands staff.

The data analysis function of any tree improvement program is of paramount importance. With the reallocation of the Department's staff formerly assigned to tree improvement, no significant data analyses have been conducted over the past two years. Scheduled measurements of field tests have, however, been made as required in anticipation that the staffing issue will be resolved, hopefully by the summer of 2006. Meanwhile, the industrial cooperators have been doing what they are able to do by moving the breeding programs forward, particularly for white spruce, black spruce, and Norway spruce. Look to the next Progress report in two years for a more detailed update of cooperative tree breeding in Nova Scotia.

GROWTH AND JUVENILE CHARACTERISTICS OF IMPROVED BLACK SPRUCE OF DIFFERENTIAL LONG-TERM PERFORMANCE POTENTIAL

Marek J. Krasowski

Faculty of Forestry and Environmental Management
University of New Brunswick
PO Box 4455
Fredericton, NB
E3B 6C2
E-mail: marek@unb.ca

Research and educational activities in tree genetics and improvement are on the rise in our faculty. Dr. Om Rajora has been appointed the Canada Research Chair in Genomics and Conservation Genetics. He is still based in Halifax, at Dalhousie University, pending the completion of his research lab in Fredericton. This report focuses only on the activities of its author, but stay tuned for news on research evolving in our faculty as a result of Dr. Rajora's appointment. At the moment, I am the only regular faculty member in residence pursuing research and teaching in the areas of tree improvement and forest genetics. Relevant topics are covered in a core course on the Structure and Development of Woody Plants and in an elective course on the Principles of Forest Nursery Production. The courses introduce students to seed biology, reproductive biology of woody plants and their vegetative propagation, pollen management, flower and cone induction, as well as describe the goals and approaches to tree improvement. In my research, I have collaborated with researchers from the Canadian Forest Service affiliated with our faculty as adjunct professors or honorary research associates. Most of them are submitting their own reports to these proceedings; therefore, I will limit my reporting to the activities not described elsewhere. I will concentrate on a project testing the early growth characteristics of improved black spruce (*Picea mariana* [Mill.] BSP) by examining traits, rarely if ever evaluated in trials aimed at predicting the performance potential from measurements made at the juvenile stage. Ten-year results of progeny trials, in which the families used in this study were evaluated, are used as the basis for classifying their performance potential. However, this project intends to evaluate potential usefulness of different juvenile morphological and developmental traits as predictors of longer-term growth performance rather than to evaluate particular individual families.

STUDY ON JUVENILE BLACK SPRUCE

Dr. Ron Smith, formerly of Canadian Forest Service, collaborated in this study. Seeds of half-sib families from controlled polycrosses were collected in 1989–1990 for the 1991 progeny tests (Akerley 1992). Fifteen families were chosen from 79 of the half-sib families such that seven represented the better and eight the worse performers in height growth evaluated in the 10-year assessment of the progeny trials (McInnis 2001). The better families were all above the median and had positive breeding values while the worse families were below the median and had negative breeding values. The seeds were germinated in a greenhouse in June 2002 and the germinants were potted into 4L pots that were buried in soil outdoors. Collections were made five times during the growing season. Each family was sampled at each time (there were also some one-time measurements, such as the number of leaf primordia in terminal buds) but the number of measurements varied for different morphological characteristics. The measurements were compared mainly for the two groups of performance potentials (PP) and individual families were compared only when 10 or more samples per family were assessed for an individual characteristic at a given time. The measurements included: germination capacity, cotyledon numbers and surface area, height, stem-base diameter, dry weights of stems and foliage (summed to shoot dry weights), projected leaf surface area, number of leaves, taproot length, projected surface area and dry weight of the roots, numbers of root tips, numbers of leaf primordia in terminal buds at the end of the first and second growing season, and dry biomass of whole plants at the end of the first and second growing season.

There was very little deterioration in seed germination capacity after 10–13 years of freezer storage. PP grouping had no significant effect on most of the measured characteristics although in some cases the effect of grouping was close to being significant. On the other hand, the effect of family x date of collection interaction was significant for the majority of the morphological characteristics. This indicated that for these characteristics, the families ranked differently on different dates. The following exceptions were found. Seedlings had 3–7 cotyledons and those of the better PP group had significantly ($p < 0.0001$) more cotyledons than those in the worse PP group. Five of the seven better families were among those with more than four cotyledons but two high PP families were among those with mostly less than four cotyledons, including family #076, that was #2 in the ranking for 10-year height. Despite the significant difference in the numbers of cotyledons, their projected surface area was significantly affected by PP. Seedlings of the better PP group were on average taller and their stems were thicker across all dates in the first growing season than those in the worse group and the effect of PP was not far from being significant for both variables (p 0.11 and 0.1, respectively). This was also true for other characteristics indicative of the size of the shoot system including dry weights of shoots, dry weights of foliage, and number of leaves, but all these differences were deemed as not significant at $\alpha = 0.05$ (p values between 0.9–0.13) and only the effect of PP on projected leaf surface area was significant, (p 0.05). The root systems also tended to be larger in the better PP group especially their dry weights although the difference between the two groups was again not significant (p 0.11) at $\alpha = 0.05$. However, other root system characteristics were less affected by PP grouping while family or family x date effects were typically significant. On average, dry weights of whole plants were larger in the better PP group and the difference between the groups was not far from being statistically significant (p 0.096) at the end of the first season and even more so at the end of the second growing season (p 0.082). Shoot to root dry weight ratios and the ratios of the projected leaf surface area to projected root surface area were very similar in both PP groups however, they were both affected by the date x family interaction indicative of changes in the ranking of families from one sampling date to another. Measurements of photosynthesis at the beginning of the second growing season were made on the previous-year foliage showing no significant difference between the rates of carbon fixation per unit of leaf area between the two PP groups and no significant effect of the family.

The numbers of leaf primordia in terminal buds of the leaders at the end of the first growing season were almost significantly affected by PP grouping (p 0.07) with the better PP seedlings having 133 leaf primordia (standard error (SE 6.9)) while the worse group seedlings had only 114 (SE 6.4). The family effect was also significant (p 0.02). When the analysis was repeated with the family treated as a fixed rather than a random factor in the design, the effect of PP became very significant (p 0.0015) but this precluded extending the results beyond the 15 families tested in this study. Listing the families in the descending order of leaf primordia numbers (Table 1) shows that if the median (120 leaf primordia) were taken to separate the families, expecting better performance from those at and above the median, all but one better PP family would be selected along with two of the worse performers.

Table 1. Means and their standard errors (SE) of leaf primordia in terminal buds of seedlings from better and worse performing (PP) families. The PP is based on the 10-the year results of provincial progeny tests (McInnins, 2001). The families are grouped as acceptable for potentially good performance if at or above the median or rejected otherwise. Means marked by the same letter are not significantly different from each other at $\alpha = 0.05$.

Acceptable				Rejected			
Family	PP	Mean	SE	Family	PP	Mean	SE
076	better	161a	11.8	20	worse	119bc	11.9
075	better	154ab	12.5	68	worse	115bc	12.5
072	better	144ab	11.8	13	worse	109bc	12.5
040	worse	137ab	11.8	34	worse	105bc	11.3
080	worse	133ab	11.3	39	better	105bc	11.9
010	better	122b	12.5	62	worse	105bc	12.5
030	better	122b	11.9	32	worse	89c	11.9
078	better	120bc	11.9				

Of the latter, families 040 and 080 were ranked in the 10-year survey as 74th and 71st (out of 79), respectively, hence they were among the families that performed the worst. The single better PP family that would be rejected based on Table 1 is family 039, which ranked as the 4th best in the 10-year progeny test results. If we extend the findings to make them generally applicable, then about 25% of families selected on the basis of leaf primordia number at the end of the first growing season would be wrongly selected as having a good performance potential while about 14% of potentially good families would be rejected. If the separation of the means (Table 1) were taken as a criterion for accepting or rejecting families with the "c" rank, family 078 would belong to the rejected group, increasing the number of rejected good PP families to two (about 28% wrongly rejected). The number of seedlings whose buds were dissected for estimating leaf primordia number was 9–11 per family, which is not many and the accuracy of prediction may be improved by increasing the number of dissected buds. However, estimates of leaf primordia numbers are time consuming, especially if there are many families to be assessed. Leaf primordia numbers reasonably conformed to the PP grouping only at the end of the first growing season and not at all at the end of the second season.

Bud set started to occur in early September, first in families 013 and 068 of the worse PP group. By mid-September, bud setting was in progress in most families except 032, 062, 075, and 080 (refer to Table 1 for PP group) in which it was noticed in the second half of September. In May 2003, terminal buds were late to break in families 010, 034, and 080, only the latter was among the late bud setting families. Families 010, 034, 039, and especially 075 were most behind in breaking lateral buds. The variation in the timing and progression of bud break in the spring was not affected by PP grouping for either terminals or laterals but family effects were highly significant ($p < 0.0001$) in all Chi-square analyses.

Many (960) seedlings remained outdoors through the winter in approximately similar numbers per family. Some of these seedlings were damaged while overwintering, probably due to frost desiccation. The PP grouping had a significant effect on susceptibility to injury (p 0.03) with a greater proportion of the better PP seedlings being injured than in the worse PP group. The family effect was also highly significant ($p < 0.0001$) with most injuries in families (in descending order) 010, 075, 040, and 039 and fewest in 030, 062, and 076. Both the phonological and the injury data indicate that phenology of shoot growth varies in families of the same PP potential, so the timing of their shoot elongation is not always reflected by greater or smaller growth in height. Although, overall, the susceptibility to injury during the winter after planting was greater in better PP families, representatives of both PP groups were among the most and least susceptible families. Hence, the risk of injury during overwintering may be more a family trait than be related growth performance.

In summary, plants in the families that performed better in the long run tended to be larger during juvenile growth. Hence, at least some of the examined traits (numbers of cotyledons, numbers of leaf primordia after the first growing season and whole-plant dry weights) should be explored further to confirm their usefulness as growth performance predictors. A manuscript based on this study will be submitted for publication to a refereed journal in June 2006.

REFERENCES

Akerley B. 1992. 1991 black spruce progeny tests. NB Tree Imp. Council, Estab. Rep. No. 33, 78 p.

McInnis, B. 2001. 1991 black spruce progeny (polycross) tests, 10-year results. Suppl. to Estab. Rep. No. 33. NB Tree Imp. Council, pp. 88–95.

TREE IMPROVEMENT PROGRESS BY THE NEW BRUNSWICK DEPARTMENT OF NATURAL RESOURCES

K.J. Tosh and M.S. Fullarton

NB Department of Natural Resources
Kingsclear Provincial Forest Nursery
3732 Route 102
Island View, NB
E3E 1G3
E-mail: Kathy.Tosh@gnb.ca

Keywords: cross-pollinations, progeny tests, seed orchards

The tree improvement program in New Brunswick (NB) is celebrating its 32nd 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 increased substantially 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 New Brunswick Department of Natural Resources (DNR) is a member of the New Brunswick Tree Improvement Council (NBTIC), a group of cooperators including 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.

In the past two years, we have continued to plant second-generation black spruce and jack pine progeny tests. The last series of progeny tests for black spruce will be planted in 2006. There is one more series left to complete jack pine.

Since 2004, one series of full-sib black spruce and one series of black spruce progeny tests were planted. The full-sib test series came from crossing done within sub-lines established from progeny test information. The older full-sib tests will be used for making third-generation selections within the next two to three years.

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. This is being done in selection plantations. Two hundred and ninety trees have been selected since 1998. This will continue until we have made 400–500 selections.

In 2005, the first-generation white spruce clonal orchards were rogued again, leaving 50–59% of the original 99 clones. 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[1]	Year of establishment	Area (ha)
White spruce	First	CSO	1985–1987	9
	First	SSO	1978–1982	8.6
	Second	CSO	2000–2004	5
Black spruce	First	SSO	1980–1987	32
	Second	CSO	1989–1997	11.8
Jack pine	First	SSO	1979–1986	25
	Second	CSO	1992–1998	7.9
Tamarack	First	CSO	1984–1986	8
Balsam fir	First	CSO	1990–1992	2.7
Red spruce	First + 1/2	CSO	1999–2001	2
Norway spruce	First	CSO	1999–2001	2
		SPA	1998	2

[1] CSO - clonal seed orchard; SSO - seedling seed orchard; SPA - seed production area

CONE COLLECTION IN ORCHARDS

The second-generation orchards are producing a substantial quantity of cones providing ample seed for our production nursery operation. Below is a table showing the production from second-generation orchards and also what has been harvested from first-generation orchards.

Table 2. Cone collection and seed yield from orchards in 2004 and 2005.

Species	Orchard	2004		2005	
		Cones (L)	Seeds (kg)	Cones (L)	Seeds (kg)
White spruce	First-generation SSO	3920	60	-	-
Jack pine	Second-generation CSO	8299	65	-	-
Black spruce	Second-generation CSO	4888	21	5919	33
Balsam fir	First-generation CSO	2740	80	-	-

NEW BRUNSWICK TREE IMPROVEMENT COUNCIL UPDATE

Kathy Tosh, Michele Fullarton and Yuhui Weng

c/o NB Dept. Natural Resources
Kingsclear Provincial Forest Nursery
3732 Route 102
Island View, NB
E3E 1G3
E-mail: Kathy.Tosh@gnb.ca

Keywords: breeding, second-generation, genetic gain, seed orchard, black spruce, jack pine, white spruce, red spruce, Norway spruce, tamarack

The New Brunswick Tree Improvement Council (NBTIC) celebrated its 30th year of operation in 2006. 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) selections is now complete 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 are producing substantial quantities of seed, and several second-generation crops of seedlings have been planted throughout the province.

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 Natural Resources 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 established. The first planting of second-generation white spruce orchards was started in 2000 and a total of 4.2 ha has been established. Four agencies will be participating in the establishment of second-generation white spruce orchards.

Seed production in 2004 was substantial, with a yield of 234 million seeds, one of the largest cone harvests in NBTIC history. As expected, the seed yield for 2005 was a modest 35 million seed.

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 planted in 2002. Polycrossing of second-generation black spruce and jack pine has made tremendous progress since the start of the tree breeding program in 1989, with the last series of black spruce polycrosses to be planted in 2006. The last series of jack pine remains to be planted. This success 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 15 years of breeding work. Pair-mating of black spruce and jack pine commenced in 1994 and 1996, respectively, producing material for third-cycle selections. The breeding and testing is 92% complete for black spruce and 47% for jack pine.

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 17 sub-lines has been established for black spruce and 18 for jack pine.

SELECTION PROGRESS

Second-generation selection 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 with each plot comprised of seedlings from a single full-sib cross. These selections are based on breeding values from 5,10, and 15-year polycross progeny test measurements. A total of 290 of 400–500 trees have been selected to date. A red spruce tree improvement program was initiated in 2003 and there have been 61 plus tree selections made to date.

TESTING AND DATA ANALYSIS

Testing continues to be an important component of the NBTIC program. Over the past 30 years, 322 tests were planted on over 365 ha. Since 1989, 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 2004, a black spruce progeny nursery test was planted in lieu of field tests. In 2004, the fourth series of black spruce full-sib progeny tests was planted and the fifth series was planted in 2005.

The data analyst position has continued to be funded by the NBTIC. A total of 13 NBTIC test series were analyzed in 2004 and 2005 which included 11 progeny tests and 2 gain tests.

OTHER

The NBTIC held a 2 day Tree Improvement Short Course for all its members in November of 2005. The Council has not done this before and it was well-received by the membership.

PUBLICATIONS

Tosh, K.J. 2006. Twenty-first annual report of the New Brunswick Tree Improvement Council. NB Dept. Nat. Res., 20 p.

GENETIC DIVERSITY AND GENE CONSERVATION RESEARCH AT THE ATLANTIC FORESTRY CENTRE

J. Loo, B. Daigle, K. Forbes, D. McPhee, S. Pond and D. Simpson

Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: Judy.Loo@nrcan.gc.ca

GENETIC DIVERSITY AND GENE CONSERVATION

J. Loo, K. Forbes, D. McPhee, S. Pond, C. Ramirez and N. Ramirez

The forest genetic resources group at AFC continues to work locally (through the informal NB Forest Tree Gene Conservation Working Group) and nationally to foster awareness and cooperation in addressing forest tree gene conservation issues. In collaboration with CFS employees in other regions and non-CFS experts, the foundation was developed to initiate a national program for the conservation of forest tree genetic resources, called CON**FOR**GEN. A forum was organized and held in conjunction with the 2006 CTIA meeting, to explain and seek input and support for the initiative.

Primary research areas include: vegetative propagation and breeding American beech (*Fagus grandifolia*) for resistance to beech bark disease, quantitative trait variation and allozyme diversity of weeping pinyon (*Pinus pinceana*) to develop a conservation strategy, and genetic diversity studies for several forest trees of interest.

American Beech

In collaboration with Dr. Marek Krasowski at UNB, research continued to develop vegetative propagation methods for trees having putative resistance to the scale insect that is one of the causative agents of beech bark disease. Nela Ramirez completed a Masters thesis examining three propagation methods: rooting cuttings, micropropagation and grafting, and testing clones having putative resistance. Little progress was made on rooting or micropropagation, although contamination was successfully reduced and rooting percentages of plantlets were increased. In collaboration with Sharon Pond, embryogenesis of beech seed and buds was explored and success was achieved in producing immature embryos. Grafting is somewhat successful but survival ranges only from 10 to 30%. Grafts were used for inoculation and screening for resistance to the beech scale.

Progeny were generated from crosses among and within groups of resistant and susceptible beech trees to provide material for assessing the inheritance of resistance. About 700 seedlings were inoculated in 2006 to screen for resistance to beech scale. Four full-sib families from susceptible x susceptible crosses, 11 families of resistant x susceptible crosses, and 20 families of resistant x resistant crosses were inoculated with scale eggs. The seedlings will be assessed for resistance levels and ratios of resistant:susceptible seedlings will be estimated for each family and cross type, in summer 2007. An inoculation study of grafted trees, with known resistance levels, to examine the timing of failure for the scale insect, indicated two possible resistance mechanisms, as the insect failed to become established on one clone, but became established then gradually failed to thrive on the other resistant clones. Scale colonies developed, insects grew to full size, and reproduction was observed for the susceptible clones.

Work has been initiated to evaluate differences in phenolic compounds and in proteins found in cells between the outer bark and cambium, in the zone where the scale feeds.

Weeping Pinyon

PhD student, Carlos Ramirez continued to study allozyme diversity and quantitative trait variation of weeping pinyon as part of a larger project under the auspices of the North American Forestry Commission Genetic Resources Working Group. The aim of the study is to contribute to developing and implementing a conservation strategy for the species which is endemic and endangered in Mexico.

The project had several components the first being to determine factors that influence germination and develope an approach to improve it. Seed that had been stored in cold temperatures had an induced dormancy that was difficult to break. The cause appeared to be the physical barrier imposed by the seed coat, in combination with some degree of chemical inhibition. Seed was germinated for both allozyme analysis and quantitative trait analyses, including standard growth measures as well as needle wax quantity and type and response to severe moisture stress. The patterns of variation were found to be similar for allozymes and quantitative traits, with very large differences found between regions.

Other species

Mature and regenerating hemlock exhibited very low genetic diversity, with no difference between the two groups, for all 15 populations studied across the Maritime provinces. The resolution of bands was poor when using vegetative material, and seed was collected from a subset of the populations for additional analysis. Additional populations were collected in Québec and Ontario. Results were very similar to the first study, with extremely low allozyme diversity observed. Seed has been shared with Jean Beaulieu at Canadian Forest Service - Laurentian Forestry Centre and with Jean Bousquet at Laval University, to examine diversity of mitochondrial and chloroplast DNA markers.

Populations have been identified and allozyme protocols worked out for beech and butternut allozyme analyses. The aim of the beech study is to determine whether greater diversity is found in susceptible than resistant groups of trees, as previously suggested. For butternut, the objective is to evaluate natural levels of genetic diversity over a small geographic area, where the butternut canker has not yet caused mortality. White ash seed has been collected from 10 populations in the Maritimes and allozyme analysis has commenced to determine the population genetic structure. The intention is that population genetic information will be used to develop an *ex situ* conservation effort for ash species prior to invasion of the Emerald ash borer (*Agrilus planipennis*).

NATIONAL FOREST GENETIC RESOURCES CENTRE

D. Simpson and B. Daigle

The National Tree Seed Centre continues to be a key activity of the National Forest Genetic Resources Centre. The Seed Centre collects, stores, and provides seed of know origin and quality for research. Another role is long-term storage of seed for *ex situ* gene conservation. The Centre aims to store seed of tree and shrub species from throughout their ranges in Canada. Seed from most species is stored at -20°C. Activities include collecting and processing seed, testing such as germination, moisture content, and 1000-seed weight, setting up and evaluating research trials, and supervising students conducting research projects for theses. The gene conservation component was formalized and a separate database set up for these accessions.

One of the major activities is seed collection to expand the geographic sampling for species and to add new species to the inventory. Since 2002, the focus has been on collecting seed from individual trees because many scientists prefer these types of collections, it is a means of sampling genetic variation, and it allows for evaluation of variation in storage ability among genotypes. A minimum of 15 trees is sampled in a population. During 2004 and 2005, 690 seedlots were collected and stored from 25 species. An additional 550 seedlots from 17 species were either donated or purchased from a number of agencies. Over 5,600 seedlots are available for research. The Seed Centre's gene conservation collection was formalized by creating a separate database and assigning unique numbers to these seedlots. These collections will be stored long-term and material will only be made available for unique research or for restoration. Samples are placed in this collection from species or populations that are unique or threatened as well as to preserve genetic variation of species. Sample sizes range from 1,000 to 10 000 seed per tree depending on species and seed size. Some species in storage are: white spruce (*Picea glauca*), limber pine (*Pinus flexilus*) - threatened by white pine blister rust, and Ash species (*Fraxinus* spp.) - threatened by Emerald ash borer. Just over 2,900 seedlots are in storage at -20°C.

The Seed Centre is participating in an ash seed collection project that involves other scientists at the Atlantic Forestry Centre. Ash trees are being attacked in Ontario by an introduced insect, the Emerald ash borer. The insect creates galleries in a tree causing the tree to die. It seems that all ash species are susceptible to this insect and the existence of the ash resource is threatened. There is an opportunity to collect seed and store it long-term to preserve the genes of ash species so that this material can be used to develop trees resistant to the insect and/or for small restoration plantings after the insect infestation has passed through an area. The material can also be evaluated to determine the pattern of genetic variation within the species and may help identify unique areas for additional sampling. Seed from throughout the range of these species in Canada is being collected from a minimum of 15 individual trees in a population and stored at -20°C. Collecting will continue over a period of years when there are good seed crops. To date, seed is in storage from 12 white ash (*F. americana*) and 6 black ash (*F. nigra*) populations.

Effort has been expended over the years to quantify the quality and quantity of material from several species for which data were outdated. One species was jack pine (*Pinus banksiana*) which included seedlots used in range-wide provenance trials established in the early 1960's. Some of the seed was collected in the late 1940's and early 1950's. Germination of these older seedlots averaged 61% and ranged from 3 to 80% indicating the long-term storage potential for seed of this species. Over 550 seedlots had been germination tested 20 years previously. Following retesting, the better quality seedlots showed an average decline in germination of 0.03% per year.

A preliminary germination trial conducted in 2002, using seed already in storage indicated that seed of sugar maple (*Acer saccharum*) from the Maritimes required a longer period of chilling to alleviate dormancy than what is prescribed by International Seed Testing Association (ISTA) Rules. The Rules recommend 8 weeks of chilling whereas the trial demonstrated that 12 to 15 weeks were required to maximize germination. This trial also included one seedlot from Ontario which indicated that a chilling time of 9 weeks was sufficient to alleviate dormancy. A more comprehensive experiment was set up using six seedlots from New Brunswick and two seedlots from each of Québec and Ontario. The experimental design consisted of: 2 constant germination temperatures of 20°C and 15°C, with 8 hrs light/16 hrs dark and 85% RH; 3 soaking treatments of 0, 72 hrs, and 14 days; and 3 moist chilling durations of 8, 12, and 16 weeks. As well, a control of no soak and no chill was tested. Seed was tested six months after collection and after 12 months storage at -20°C. Results showed there was no overall difference in seed germination between the two germination temperatures. Therefore, there is no reason to discontinue using ISTA's recommended germination temperature of constant 20°C. Seed from New Brunswick required 12 weeks of chilling to alleviate dormancy whereas eight weeks of chilling was adequate to alleviate dormancy of seed from Québec and Ontario. Soaking for 14 days damaged seed and caused mortality. Soaking seed for 24 hours is probably sufficient because of the rapid imbibition that takes place during this period of time.

PUBLICATIONS

Beardmore, T.; Loo, J.; McAfee, B.; Malouin, C.; Simpson, D. 2006. A survey of tree species of concern in Canada: the role for genetic conservation. For. Chron. 82: 351–363.

Betts, M.G.; Diamond, A.W.; Forbes, G.J.; Frego, K.; Loo, J.A.; Matson, B.; Roberts, M.R.; Villard, M.-A.; Wissink, R.; Wuest, L. 2005. Plantations and biodiversity: a comment on the debate in New Brunswick. For. Chron. 81: 265–269.

Bourgoin, A.; Simpson, J.D. 2004. Soaking, moist-chilling, and temperature effects on germination of *Acer pensylvanicum* seeds. Can. J. For. Res. 34: 2181–2185.

Daigle, B.; Simpson, D. 2004. Effects of chilling duration and germination temperature on germination of eastern hemlock seed. *In* Can. Tree Imp. Assoc., Tree Seed Work. Group News Bull. No. 39: 10–11.

Loo, J., Beardmore, T., Simpson, D.; McPhee, D. 2004. Developing gene conservation strategies for tree and shrub species. Pages 20–25. *In* J. Beaulieu, ed. Silviculture and conservation of genetic resources for sustainable forest management. Nat. Res. Can., Can. For. Serv., Inform. Rep. LAU-X-128.

Loo, J.A.; Beardmore, T. 2005. Butternut may be doomed. Can. Silvi. (Spring): 15.

Loo, J.A. 2005. Importance of setting objectives for biodiversity conservation. Pages 61–62. *In* B. McAfee and C. Malouin, eds. Conservation lands: integrating conservation and sustainable management in Canada's forests. Nat. Res. Can., Can. For. Serv., Sci. Pgm. Br., Ottawa, ON.

Loo, J.A.; Basquill, S.; Betts, M.G. 2005. Maintaining forest community groups at coarse and fine resolutions. Chapter 3, Pages 27–32. *In* M.G. Betts and G.J. Forbes, eds. Forest management guidelines to protect native biodiversity in the Greater Fundy Ecosystem. N.B. Co-op. Fish Wildlife Res. Unit, Univ. New Brunswick. 110 p.

Loo, J.A.; MacDougall, A.S.; Wissink, R. 2005. Ecologically significant areas. Chapter 7, Pages 53–60. *In* M.G. Betts and G.J. Forbes, eds. Forest management guidelines to protect native biodiversity in the Greater Fundy Ecosystem. N.B. Co-op. Fish Wildlife Res. Unit, Univ. New Brunswick. 110 p.

Loo, J.A.; Beardmore, T.L.; Simpson, J.D.; McPhee, D.A. 2005. Special status species. Chapter 10, Pages 69–78. *In* M.G. Betts and G.J. Forbes, eds. Forest management guidelines to protect nNative biodiversity in the Greater Fundy Ecosystem. N.B. Co-op. Fish Wildlife Res. Unit, Univ. New Brunswick. 110 p.

Ramirez, N. 2005. Screening for genetic resistance and vegetative propagation of disease-free American beech (*Fagus grandifolia*). Unpubl. Masters Thesis, Univ. New Brunswick. 62 p.

Simpson, J.D.; Wang, B.S.P.; Daigle, B.I. 2004. Long-term seed storage of various Canadian hardwoods and conifers. Seed Sci. Technol. 32: 561–572.

Wang, Ben S.P.; Simpson, J. Dale. 2004. Factors affecting tree seed storage. Pages 3–15. *In* Proc. IUFRO Tree Seed Symp., Seed Physiol. and Technol. Res. Grp. 2.09.00, 20–22 Sep. 2004, Nanjing, China.

Wang, B.S.P.; Simpson, J.D. 2006. Factors affecting tree seed storage. J. Nanjing For. Univ. 30(1): 1–7.

GENETIC DIVERSITY: IMPACTS AND ADAPTATION RESEARCH AT THE ATLANTIC FORESTRY CENTRE

Alex Mosseler and John E. Major

Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: Alex.Mosseler@nrcan.gc.ca

Keywords: climate change, adaptation, genetic diversity, cold hardiness, drought tolerance, elevated CO_2, G x E*, Picea mariana, Picea rubens,* hybrids, *Pinus rigida*, *Pinus strobus, Salix*, provenance, genetic variation, genomics, ecological restoration, population viability, gas exchange, water relations, allometry, adaptive traits, inbreeding, fitness

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 (*P. rigida*), and 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 are significant and positive 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, white spruce (*Picea glauca*), 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 is necessary in order to minimize the effects of inbreeding and genetic drift and 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 (NS) and New Brunswick (NB). Based on the excellent growth performance observed in these tests, further testing 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 local seed sources of jack pine (*Pinus banksiana*) and red pine (*P. 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 our population genetics study of pitch pine is to conserve the gene pool of this 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 rare 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 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, NB, and NS). Results 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 a gene sequence database and genetic maps, and identify, isolate and map genes and genetic factors controlling traits related to productivity, adaptation to abiotic stresses, 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 carbon inventory in a 35-year-old (F1) first-generation cross black spruce experiment with distinct differences in above-ground volume growth. 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 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 silviculture 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 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. In 2005, this project was expanded to include three other species: *S. amygdaloides*, *S. interior*, and *S. nigra*. A short-term (3–5 year) objective is to select clones for site and habitat restoration (e.g., mines, oil sands, pits and quarries, etc.), afforestation of difficult-to-manage sites (e.g., riparian zones, abandoned agricultural lands), and to provide forage for pollinators to assist in the blueberry industry in Atlantic Canada. The long-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 targets.

PUBLICATIONS

Major, J.E.; Mosseler, A.; Johnsen, K.H.; Rajora, O.P.; Barsi, D.C.; Kim, K.-H.; Park, J.-M.; Campbell, M. 2005. Reproductive barriers and hybridity in two spruces, *Picea rubens* and *Picea mariana*, sympatric in eastern North America. Can. J. Bot. 83: 163–175.

Major, J.E.; Barsi, D.; Mosseler, A.; Rajora, O.P.; Campbell, M. 2006. Predominant paternal inheritance pattern of light-energy processing adaptive traits in red and black spruce hybrids. Can. J. For. Res. (in press)

Major, J.E.; Barsi, D.; Mosseler, A.; Campbell, M. 2006. Genetic variation and control of chloroplast pigment content in *Picea rubens*, *Picea mariana*, and their hybrids. I. Under ambient and elevated CO_2 environments. Tree Physiol. (in press)

Mosseler, A.; Rajora, O.P.; Major, J.E.; Kim, K.-H. 2004. Reproductive and genetic status of disjunct pitch pine populations in Canada. Conserv. Gen. 5: 571–583.

Mosseler, A.; Pendrel, B.; Wang, W.; Niu, Y.; Park, Y.-S.; Gao, C.-Q.; Song, L.-W. 2005. Observations on forest restoration in Jilin, China. J. For. Res. 16(4): 331–334.

O'Connell, L.M.; Mosseler, A.; Rajora, O.P. 2006. Impacts of forest fragmentation on the mating system and genetic diversity of white spruce (*Picea glauca*) at the landscape level. Heredity 97: 418–426.

O'Connell, L.M.; Mosseler, A.; Rajora, O.P. 2006. Impacts of forest fragmentation on the reproductive success of white spruce (*Picea glauca*). Can. J. Bot. 84: 956–965.

TREE IMPROVEMENT PROGRESS BY THE DIRECTION DE LA RECHERCHE FORESTIÈRE

Roger Beaudoin, Marie-Josée Mottet, Mireille Desponts,
Pierre Périnet, Martin Perron and André Rainville

Direction de la recherche forestière
Ministère des Ressources naturelles et de la Faune
2700, rue Einstein
Sainte-Foy, QC
G1P 3W8
E-mail: andre.rainville@mrnf.gouv.qc.ca

Keywords: white spruce, Norway spruce, black spruce, jack pine, hybrid larch, hybrid poplar, Septoria canker, controlled crosses, tree improvement, tree selection, provenance tests, progeny tests, molecular certification, hardwoods, forest yield, seed orchards

WHITE SPRUCE TREE IMPROVEMENT

André Rainville

In the past two years, seedlings necessary to evaluate general combining ability (GCA) of the remaining 140 trees of the first-generation white spruce (*Picea glauca*) base population were cultivated in the nursery and will be planted in 2006 on five test sites representing the ecological diversity of the province. Meanwhile, specific combining ability (SCA) seeds of the same 140 trees were sown in 2005; tests are expected to be established in 2007. Clones in 14 first-generation seed orchards (out of 18 established) are now evaluated. Collecting cones from the best clones is expected to give additional gains in height of 15–25% over natural stand collections.

On a more operational level, two major advances took place in plant production operations in Québec, one of which had an influence on the white spruce tree improvement strategy. In light of the genetic gains achieved by material derived from control crosses, it was decided to increase the number of stecklings produced and consequently, two new facilities were established in provincial nurseries. The second one concerns embling production, derived from somatic embryogenesis. Successes obtained in the last 10 years led to the first steps of plant production at an operational scale, on a large number of clones, for the establishment of clonal tests with the first tests planned for 2007.

Measurements of two full-sib progeny tests at 8 years were used to recommend the best crosses to be performed in the future, thus fulfilling needs of reforestation by cuttings; gains of 11–15% over the mean of the crosses can be achieved by reproducing the 10 best crosses and propagating them by cuttings.

NORWAY SPRUCE TREE IMPROVEMENT

Marie-Josée Mottet

Total height of the best Norway spruce (*Picea abies* [L.] Karst.) families and white pine weevil (*Pissodes strobi*) resistance make up the principal selection criteria. Wood density will be another criterion in the near future. Four progeny tests were established in 2006 to measure SCA and four other SCA progeny tests will be established in 2007. An exceptional flowering year in 2006 allowed us to almost complete our specific cross program. In 2005, we completed the selection of 164 trees as the new population for the regions of Bas Saint-Laurent and Gaspé. A total of 1,640 grafts were done in March 2006 at the Duchesnay grafting centre near Québec City.

JACK PINE TREE IMPROVEMENT

Mireille Desponts and Roger Beaudoin

In 2005, selection of 300 superior jack pine (*Pinus banksiana*) trees in first-generation progeny tests was completed in both central and northern improvement zones. The establishment of new clonal seed orchards and clone banks will be completed in 2007. For each breeding zone, polycross and controlled crosses will be carried out in elite as well as the main breeding populations.

LARCH TREE IMPROVEMENT

Martin Perron

In spring 2004, an intra and interspecific 10 x 10 factorial design was initiated with five European larch (*L. decidua* Mill.) (EL) and five Japanese larch (*L. kaempferi* [Lamb.] Carr.) (JL) as males. The scientific goal of this mating design is to study heterosis in larch hybrids between EL and JL. Moreover, this mating design will produce one part of our second-generation hybrid progenies that will be used to recommend the best progenies for rooted cutting propagation.

In 2005, four full-sib progeny tests, composed of 79 progenies, were established to determine the best hybrid type for the northern Québec boreal forest (three sites planted above 49° N and one control in the south). They originated from controlled crosses between Siberian larch (*Larix siberica* Ledeb.) (SL) as male or female and EL and JL. Open pollinated progenies of SL, EL, and JL parents were used as controls.

In winter 2006, a sub-group of 20 EL and 20 JL from our second-generation breeding populations was constituted to form the new hybrid larch seed producion population.

Finally, we started organizing LARIX 2007: International Symposium of the IUFRO Working Group S2.02.07 (http://www.mrnf.gouv.qc.ca/carrefour/english/larix.asp).

HYBRID POPLAR IMPROVEMENT PROGRAM

Pierre Périnet and Marie-Josée Mottet

Since 1969, the hybrid poplar improvement program has been active testing populations through former breeding programs, 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, the program is mainly focussed on 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, respectively).

Since 2004, four clonal tests were outplanted in forest sites in northeastern Québec (domains 4 and 5) for clonal evaluation of the selections from the 1996 breeding program. Selection is planned in 2006 in three other progeny tests planted in 2000 in the Bas-Saint-Laurent area from the 1998 breeding program. In 2005, two other plantations of *P. maximowiczii* were also established in domain 4 near La Tuque and Chicoutimi.

A new population was bred in 2004 for the Abitibi-Témiscamingue area, using parents from local and Alberta balsam poplar (*P. balsamifera*) provenances, selected hybrid poplar clones, and progenies of *P. deltoides* and *P. maximowiczii* from northern locations. In May 2006, approximately 23 000 seedlings were planted in three progeny tests and established as family collections at the Trécesson nursery near Amos.

A special effort was conducted to monitor *Septoria musiva* in areas traditionally free of the canker (domains 3, 4, and 5). Unfortunately, some leaf spots or cankers caused by *S. musiva* were found outside the range of the disease with no evidence, up to now, of being epidemic. In 2005, an eradication operation was undertaken in a clonal test in the Lac-Saint-Jean area where a sudden presence of cankers occurred in a single location. The unforeseen presence of *S. musiva* in Témiscamingue, noted in 2001, seems to have now reached a plateau with some signs of canker healing and a limited spread of the disease. Monitoring of those sites is maintained through litter inspection and leaf spot and canker identification.

The provincial list of selected clones for planting is revised regularly based on results from the clonal tests in different regions. Several projects are going on within the network Réseau Ligniculture Québec in collaboration with scientists, forest industry partners, and provincial nurseries for steckling production (1-0 rooted cuttings). The poplar research team contributes to different projects on Septoria canker, wood quality, and molecular genetics studies with scientists from Université Laval, Concordia University, University of Alberta, Forintek Canada Corp., and Canadian Forest Service.

HARDWOOD TREE IMPROVEMENT
André Rainville

In hardwood tree improvement, work is still in progress to evaluate white ash (*Fraxinus americana*) provenances for quality and growth characteristics across its distribution in Québec. This represents most of the efforts devoted to hardwood tree improvement in the last years.

REALIZED GENETIC GAIN TESTS
André Rainville, Mireille Desponts and Guy Prégent

This new project, evaluating long-term gains of productivity (volume) and quality associated with first-generation seed orchards, is now ongoing with the first trees being planted. In 2005, five black spruce (*Picea mariana*) tests were established in northern Québec. In 2006, three additional black spruce tests and three jack pine tests will be established in the central improvement zone with the same objective.

On the other hand, we also measured four 10-year-old black spruce tests from the northern zone in 2005. These tests included seedlings from three unrogued local seed orchards. Gains of 5–10% in height were obtained from seed orchard material compared to natural sources.

PUBLICATIONS

Beaulieu, J.; Rainville, A. 2005. Adaptation to climate change: genetic variation is both a short- and a long-term solution. For. Chron. 81(5): 704–709.

Daoust, G.; Mottet, M-J. 2006. Impact du charançon du pin blanc (*Pissodes strobi* Peck) dans les plantations d'épinettes de Norvège (*Picea abies* [L.] Karst.) Partie 1 : Productivité et qualité des sciages. For. Chron. (accepté)

Desponts, M.; Beaudoin, R.; Mottet, M.-J.; Périnet, P.; Perron, M.; Rainville, A. 2005. L'amélioration génétique des arbres au MRNF : un outil de performance pour la forêt du Saguenay-Lac-Saint-Jean. Les pages 7–9. *Dans* Résumé des présentations : forum de transfert de connaissances. Le 29 novembre 2005, Saguenay, QC.

Khasa, D.P.; Pollefeys, P.; Navarro-Quezada, A.; Périnet, P.; Bousquet, J. 2005. Species-specific microsatellite markers to monitor gene flow between exotic poplars and their natural relatives in eastern North America. Mol. Ecol. Notes 5: 920–923.

Pliura, A.; Yu, Q.; Zhang, S.Y.; Mackay, J.; Périnet, P.; Bousquet, J. 2005. Variation in wood density and shrinkage and their relationship to growth of selected young poplar hybrid crosses. For. Sci. 51(5): 472–482.

Rainville, A. 2005. Adaptation aux changements climatiques : la génétique peut-elle nous servir? Les pages 18–21. *Dans* Actes du Colloque "Changements climatiques et adaptation : impacts et adaptation". Les 20– 21 avril 2005, Baie-Comeau, QC.

ORAL AND POSTER PRESENTATIONS

Desponts, M.; Beaudoin, R.; Mottet, M.-J.; Périnet, P.; Perron, M.; Rainville, A. 2005. L'amélioration génétique des arbres au MRNF : un outil de performance pour la forêt du Saguenay-Lac-Saint-Jean. Conférence présentée par Mireille Desponts dans le cadre du "Forum de transfert de connaissances". Le 29 novembre 2005, Saguenay, QC.

Daoust, G.; Beaulieu, J.; Perron, M.; Pâquet, R.; Aerni, C. 2006. Les mélèzes dans le réseau de démonstration des gains génétiques : résultats de 10 ans. Colloque RLQ, SCF, MRNF et RGDF « La ligniculture : une solution d'avenir! », Orford, QC. (poster)

Lamhamedi, M.; Colas, F.; Tousignant, D.; Tremblay, L.; Rainville, A.; Guay, J-Y.; Ouellet, C.; Rioux, M. 2006. Intégration de l'embryogenèse somatique dans la filière de production de plants forestiers du Québec. Affiche présentée dans le cadre du 4e atelier sur la production de plants forestiers au Québec. Les 15–16 mars 2006, Sainte-Foy, QC. (poster).

Mottet, M.-J. 2005. Rendement en sciage et caractéristiques du bois de l'épinette de Norvège en plantation - Rencontre annuelle des conseillers forestier Bas Saint-Laurent. Le 14 avril 2005, Rimouski, QC.

Mottet, M.-J. 2005. Le programme d'amélioration génétique de l'épinette de Norvège : des résultats prometteurs pour la région du Bas-St-Laurent-Gaspésie-Rencontre annuelle des conseillers forestier Bas Saint-Laurent. Le 14 avril 2005, Rimouski, QC.

Mottet, M.-J. 2005. Rendement en sciage et caractéristiques du bois de l'épinette de Norvège en plantation - Cours amélioration génétique. Le 11 avril 2005, Univ. Laval, QC.

Périnet, P. 2005. Diversité et renouvellement des variétés de peuplier hybride au Québec. Colloque du RLQ, Congrès de l'ACFAS. Les 9–11 mai 2005, Chicoutimi, QC.

Perron, M. 2004. Le devenir d'une des sources de la ligniculture au Québec : le programme d'amélioration génétique des mélèzes du Québec. A.C.F.A.S., 72e Congrès, UQAM, Montréal, QC.

Perron, M. 2006. Le mélèze hybride et la sylviculture intensive des résineux : parce que le temps c'est de l'argent ! Colloque RLQ, SCF, MRNF et RGDF « La ligniculture : une solution d'avenir! », Orford, QC.

Perron, M. 2006. Retombées des 35 années d'amélioration génétique des mélèzes au MRNF: qualité et productivité de la prochaine variété de mélèze hybride du Québec. Colloque RLQ, SCF, MRNF et RGDF « La ligniculture : une solution d'avenir! », Orford, QC.

Rainville, A. 2005. Adaptation aux changements climatiques : la génétique peut-elle nous servir ? Conférence présentée dans le cadre du Colloque "Changements climatiques et adaptation : impacts et adaptation". Les 20–21 avril 2005, Baie-Comeau, QC.

RECENT ADVANCES IN TREE REPRODUCTION IN QUÉBEC

Denise Tousignant and Fabienne Colas

Ministère des Ressources naturelles et de la Faune
Direction de la recherche forestière
2700, rue Einstein
Québec, QC
G1P 3W8
E-mail: Denise.Tousignant@mrnf.gouv.qc.ca

Keywords: seed orchard management, indoor orchard, pollen, mass pollination, seeds, germination, cutting propagation, stockplants, stecklings, nursery culture, *Picea glauca, Picea mariana, Picea abies, Larix decidua, Larix kaempferi, Larix marschlinsii, Pinus banksiana*

This report summarises ongoing research and recent results on sexual and vegetative propagation of conifers by the Direction de la recherche forestière (DRF) of the Ministère des Ressources naturelles et de la Faune of Québec (MRNFQ). Topics include a new concept of indoor seed orchard for larches, spruce seed orchard management techniques, optimisation of seed allocations for containerized nursery production, characterisation of family differences for controlled crosses, improved cutting propagation facilities and refinements of the culture techniques for stockplants, rooted cuttings, and transplanted stecklings.

SEED ORCHARD MANAGEMENT

Research on indoor larch seed orchards is being completed, in collaboration with Dr. Martin Perron, head of the larch improvement program. We have developed a new and unique concept of sheltered orchards, enabling large-scale production of hybrid larch (*Larix marschlinsii* Coaz.) seeds. Potted grafts of European larch (*Larix decidua* Mill.) and Japanese larch (*Larix kaempferi* [Lamb.] Carrière) are cultivated in separate cold frames. A "pot in pot" culture regime favours regular production of both male and female flowers. Pollen is applied using an electrostatic pistol adapted by the DRF. An abundant production of certified hybrid seed can thus be obtained, using only a small work team. This orchard concept has now been transferred to an operational scale at the Berthier provincial nursery.

Ongoing research on mass pollination of white spruce (*Picea glauca* [Moench] Voss) and black spruce (*P. mariana* [Mill.] BSP) is currently aimed at increasing seed orchard productivity.

GERMINATION OF CONIFER SEEDS AND SEEDLING PRODUCTION

Until 2005, the allocation of seeds for containerized nursery production was determined by the nature of the seed sources. Regardless of germination percentage, the MRNFQ provided nurseries with 2.5 viable seeds per cavity for genetically improved seed sources, and 3.2 viable seeds per cavity for non-improved sources. Recent improvements in the germination percentage of seedlots extracted at the Centre de semences forestières de Berthier (CSFB) incited the MRNFQ to examine the possibility of reducing the amount of seeds distributed for seedling production. Studies were conducted during three years, in collaboration with Michèle Bettez (CSFB), Anne Savary (Direction de la production des semences et des plants) and several public nurseries of the province. Results confirm that seed allocations can be reduced by 20% for genetically improved sources of black spruce, jack pine (*Pinus banksiana* Lamb.), and white spruce (in this case, only for highly improved sources), with a germination percentage of at least 90%. This leads to significant savings for the MRNFQ, without compromising nursey seedling production objectives.

CONTROLLED CROSSING: CHARACTERIZATION OF FAMILY DIFFERENCES

A major study was initiated in 2005 with Dr. Mohammed Lamhamedi (DRF) and the Pépinière de Saint-Modeste on the characterization of the main controlled crosses used for white spruce cutting propagation. Currently, prior to seeding the donor stockplants, all seeds are mixed together without taking into account genetic origin (cross), proportion of each cross in the mixture (varies with the year), or seed size (caliber). The result is wide variation in terms of germination kinetics, growth, and crown architecture. The nursery manager thus faces major problems in attaining production objectives for cutting propagation. The number of productive donor stockplants is variable, as is the yield of cuttings from donor stock, depending on the cross. It becomes necessary to adapt the cultural regime (irrigation and fertilization) to the heterogeneity of the stockplant lot, and most likely, of the cuttings produced. Each of the crosses used in the cutting program must be subjected to a multi-criteria, morpho-physiological and phenological selection process before it can be definitively integrated into the cutting production program. Our goal is to reduce growth variation of white spruce stockplants and to select the best crosses to allow the nursery grower to optimise stockplant and cutting culture.

MASS PROPAGATION OF CONIFERS BY CUTTINGS

The need for genetically improved plants from cuttings continues to increase, with a production objective of 4 million plants in 2006 (1 950 000 for white spruce, 1 500 000 for black spruce, 50 000 for Norway spruce (*Picea abies* [L.] Karst.) and 500 000 for hybrid larch). Our recent work has led to better control of the rooting conditions, significantly improving propagation success of hybrid larch and white spruce in the outdoor rooting enclosures at the Pépinière de Saint-Modeste. The propagation system is now being implemented in two other nurseries, where the first white spruce cutting production will begin in 2006.

A new research project has been initiated, with three objectives: 1) to improve the quality of root systems on conifer cuttings, before and after being transplanted in the nursery, 2) to determine optimal characteristics of a transplantable cutting, in order to reach large-sized plant quality standards, two years later, and 3) to characterize the growth, root, and shoot morphology of cuttings during the transplant phase in the nursery, both for bareroot and large (> 300 cm^3) container-grown stecklings.

PUBLICATIONS

Bettez, M.; Colas, F. 2005. Seed processing at the Centre de semences forestières of Berthier (Québec). Can. Tree Imp. Assoc., Tree Seed Work. Group Newsbull. 42: 8–9.

Colas, F.; Bettez, M. 2004. The biggest problems or information needs with respect to tree seed for the province of Québec. Can. Tree. Imp. Assoc., Tree Seed Work. Group Newsbull. 40: 3–4.

Colas, F.; Bettez, M. 2006. L'ensemencement et la germination: des étapes cruciales dans la réussite d'une culture en pépinière forestière. *In* 4^e atelier de production de plants forestiers du Québec : Facteurs et techniques culturales influençant le développement racinaire des plants en pépinière forestière, 15–16 March 2006, Québec, QC. CD-ROM. ISBN 2-550-46934-8.

Colas, F.; Tousignant, D.; Perron, M. 2004. La biologie florale, un élément capital à la pratique de la ligniculture du mélèze hybride. (Abstract). *In* 72^e congrès de l'ACFAS : La ligniculture aux quatre coins du Québec : de la théorie à la pratique. 11–13 May 2004, Montréal, QC.

Colas, F.; Bettez, M.; Savary, A. 2005. Suivis d'ensemencement et de germination en pépinière des semences d'épinette blanche, d'épinette noire et de pin gris selon différents facteurs d'ensemencement. Avis technique, Ministère des Ressources naturelles et de la faune, Direction de la recherche forestière, 18 p.

Colas, F.; Tousignant, D.; Lamhamedi, M.S.; Gagnon, J. 2005. La recherche sur la production de semences et de plants au Québec : l'innovation au service du reboisement. Les pages 11–12. *In* Résumés des présentations : Forum de transfert de connaissances. 29 November 2005, Saguenay. Ministère des Ressources naturelles et de la faune, Direction de la recherche forestière, Québec, QC.

Colas, F.; Bettez, M.; Savary, A. 2006. La précision de l'ensemencement : première étape pour des cultures réussies! *In* 4^e atelier de production de plants forestiers du Québec : Facteurs et techniques culturales influençant le développement racinaire des plants en pépinière forestière, 15–16 March 2006, Québec, QC. CD-ROM. ISBN 2-550-46934-8.

Gouvernement du Québec and Office des producteurs de plants forestiers du Québec 2006. Actes du 4^e Atelier en production de plants forestiers au Québec : Facteurs et techniques culturales influençant le développement du système racinaire des plants en pépinière forestière. 15–16 March 2006, Québec, QC. CD-ROM. ISBN 2-550-46934-8.

Lamhamedi, M.S.; Colas, F.; Tousignant, D. 2005a. Caractérisation de la croissance des pieds-mères d'épinette blanche issus de croisements dirigés : 1. Approche méthodologique. Avis technique. Ministère des Ressources naturelles et de la faune, Direction de la recherche forestière, 10 p.

Lamhamedi, M.S.; Colas, F.; Tousignant, D. 2005b. Vers une nouvelle optimisation de l'utilisation des croisements dirigés pour la production de pieds-mères en bouturage. Des plants et des hommes 8(1): 21–26.

Lamhamedi, M.S.; Colas, F.; Tousignant, D.; Tremblay, L.; Rainville, A.; Guay, J.-Y.; Ouellette, C.; Rioux, M. 2006. Intégration de l'embryogenèse somatique dans la filière de production de plants forestiers du Québec. *In* 4^e atelier de production de plants forestiers du Québec : Facteurs et techniques culturales influençant le développement racinaire des plants en pépinière forestière, 15–16 March 2006, Québec, QC. CD-ROM. ISBN 2-550-46934-8.

Richer, C.; Rioux, J.-A.; Tousignant, D.; Brassard, N. 2004. Improving vegetative propagation of sugar maple (*Acer saccharum.* Marsh.). Acta Hort. 630: 167–175.

Tousignant, D. 2006. Particularités des systèmes racinaires des plants résineux issus de boutures. *In* 4^e atelier de production de plants forestiers du Québec : Facteurs et techniques culturales influençant le développement racinaire des plants en pépinière forestière, 15–16 mars 2006, Québec, QC. CD-ROM. ISBN 2-550-46934-8.

Trudel, R.; Guertin, C.; de Groot, P.; Grant, G.; Colas, F. 2005. Development of biological control methods against seed orchard insect pests. Can. Tree Imp. Assoc., Tree Seed Work. Group Newsbull. 42: 16–18.

RECENT ADVANCES IN TREE AND FOREST GENOMICS AT LAVAL

Jean Bousquet, P. Damase Khasa and John J. Mackay

Canada Research Chair in Forest and Environmental Genomics,
***ARBOREA*, and Forest Biology Research Centre**
Faculté de foresterie et de géomatique
Université Laval
Québec, QC
G1K 7P4
E-mail: bousquet@rsvs.ulaval.ca

Keywords: comparative structural and functional genomics, chloroplast DNA, ectomycorrhiza, ESTs, ESTPs, genome mapping, marker-aided selection, microsatellites, mitochondrial DNA, molecular ecology, molecular population genetics and breeding, phylogeny, phylogenomics, phylogeography, poplars, SNPs, spruces, tree improvement, wood formation, xylem

INTRODUCTION

The last two years have seen many positive developments in the research areas of fungi, tree and forest genetics, and genomics. Our major genomic research program *ARBOREA I*, which aimed to better understand the functional genomics of wood formation and defense mechanisms in white spruce (*Picea glauca*) and poplars (*Populus* spp.), has been renewed by Genome Canada and Genome Québec for another three-year period (*ARBOREA II*). The new emphasis is on developing molecular breeding tools to improve growth and wood characters of white spruce based on the basic knowledge generated by phase I of the project. *ARBOREA II* is also supported by the Canadian Biotechnology Strategy (CBS), the Canadian Forest Service (CFS), and the Fonds québécois de la recherche en nature et technologie (FQRNT). Following proof-of-concept studies in the previous period, projects in molecular phylogeography and on the genetic consequences of large-scale introduction of exotics in the landscape have leveled off and are now recognized and supported by the National Science and Engineering Research Council of Canada (NSERC), CBS, and other organizations. All these projects involve the intensive collaboration of our colleagues from CFS (J. Beaulieu, N. Isabel, and A. Séguin), and from Forêt Québec (M. Perron, P. Périnet, A. Rainville, and M. Desponts). *ARBOREA II* also involves other major collaborators, including J. Cooke, who has recently moved to University of Alberta as assistant professor, P. Watson from PAPRICAN in Vancouver, J. Dean from University of Georgia, P. Rigault from CHUQ (formerly at Illumina, California), and E. Retzel from University of Minnesota.

During the last two years, the group has hosted several postdoctoral researchers, including C. Bomal, J.-L. Jany (now at Cornell), N. Pavy, C. Guillet-Claude (now back to France), J.P. Jaramillo-Correa, F. Lafarguette, L. Tarca, and M.-C. Namroud. Many graduate students were involved in the various research projects, including at the MSc level: S. Beauseigle, H. Bérubé, F. Boileau, E. Campagnac, C. Côté, A. Gagné, S. Girardi, A. Noël, and C. Ouinsavi and at the PhD level: F. Bedon, G. Bois, M. Bouillé, J. Godbout, S. Legay, B. Pelgas, F. Pitre, J. Prunier, and R. Sibout. Many of these students were co-supervised by the adjunct professors J. Beaulieu, N. Isabel, and A. Séguin (CFS).

PHYLOGEOGRAPHY

J. Bousquet

Major progress has taken place under this theme. We pursued the development of mtDNA markers and have succeeded in resolving the large-scale geographical structure of broadly distributed Canadian conifers and identifying ancestral lineages. This work is part of the theses of J.P. Jaramillo-Correa and J. Godbout. 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. Several ancestral lineages have been discovered for black spruce (*Picea mariana*) (Jaramillo-Correa et al. 2004) and for jack pine (*Pinus banksiana*) (Godbout et al. 2005). For black spruce, a distinct western lineage was identified, from a glacial population inferred to be located west of the Rocky Mountains. For both species, a correlated pattern of geographical location was also observed, involving the existence of genetically distinct refugia on the east and the west sides of the Appalachian Mountains as well as distinct lineages in the northeast, implying the existence of glacial refugia on the North Atlantic continental shelf. Recent (Holocene) mtDNA recombination was also identified in the zone of contact in Eastern North America between black spruce and red spruce (Jaramillo-Correa et al. 2005). Natural hybridization and introgression were identified as the most likely factors for such genetic instability.

A major NSERC strategic grant (Phylogeographical Atlas of Canadian Conifers) has been obtained in collaboration with J. Beaulieu (CFS) to pursue these studies on broadly distributed Canadian conifers.

Western (*Larix occidentalis*) and alpine larche (*L. lyallii*) were also investigated, in collaboration with B. Jaquish (BC Ministry of Forests and Range) (Khasa et al. 2006). At least two distinct lineages could be identified for each of the species, presumably arising from refugia located east and west of the Rocky Mountains. Quite divergent patterns of nuclear microsatellite diversity were observed between the two species, with alpine larch being genetically less diverse and more structured. The signature of recent bottlenecks was evident in alpine larch while it was not observed in the more widespread western larch, indicating that the former species would have suffered more from post-glacial recolonization. The Mexican endemic *Picea chihuahuana*, which grows at high elevations, was also studied in collaboration with T. Ledig (USDA, California) and J. Beaulieu (CFS) (Jaramillo-Correa et al. 2006). This study was commissioned by the Forest Genetics Resources Working Group of the North American Forest Commission of the FAO. Two ancestral disjunct mtDNA lineages were observed. The mtDNA and cpDNA patterns obtained were disconnected and cpDNA diversity indicated recent bottlenecks and very little gene flow between residual stands, suggesting a population collapse of this conifer species following the Holocene warming. Under the leadership of D.P. Khasa, an international project on the genomics of Mexican species of the Pinaceae family is also underway with L. Eguiarte (Autonomous University of Mexico). This project is being funded by the Ministère du Développement Économique et Régional et de la Recherche du Québec. Informative mtDNA and SSRcp markers were first developed to study the phylogeographic structure of Mexican *Abies* species (Jaramillo-Correa et al. 2006, in preparation).

Another range-wide phylogeographical study was completed on Scots pine (*Pinus sylvestris*) in collaboration with K. Naydenov and F. Tremblay (Université du Québec in Abitibi-Témiscamingue) and J. Beaulieu (CFS) (Naydenov et al. 2006). A new mtDNA marker indicated the existence of genetically distinct glacial populations in Asia Minor and in North Central Europe, in addition to previously known lineages from the Balkans and the Iberian Peninsula. A large suture zone between two ancestral lineages was also delineated from Western Europe to Central Russia. Range-wide studies are currently being conducted for other broadly distributed conifers including lodgepole pine (*Pinus contorta*) (in collaboration with F. Yeh, C. Newton, and A. Fazekas), white spruce, balsam fir (*Abies balsamea*), eastern white pine (*Pinus strobus*), eastern hemlock (*Tsuga canadensis*), and Canada yew (*Taxus canadensis*), with colleagues from the CFS (J. Beaulieu and J. Loo).

MOLECULAR ECOLOGY, ENVIRONMENTAL, AND POPULATION GENETICS

D. Khasa

With funding from NSERC and Ligniculture Québec, and the collaboration of P. Périnet (Forêt Québec), several SSR markers were developed and optimized for poplar species. Some of these microsatellite markers have been shown to be species-specific to identify five commercially important poplars and their interspecific hybrids in North America (Khasa et al. 2005a). With funding from CBS and in collaboration with N. Isabel (CFS) and P. Périnet, these diagnostic markers and others were used to assess potential gene flow from plantations of exotic poplar species into coexisting stands of native species and between native species hybridizing naturally (*Populus deltoides* and *P. balsamifera*) (Gigou et al., in preparation). In collaboration with N. Isabel, MSc student M.-C. Gros-Louis developed nuclear, cpDNA, and mtDNA diagnostic markers for the recognition of larch species and their hybrids, and the cpDNA and mtDNA phylogenies of the genus were inferred (Gros-Louis et al. 2005). With the collaboration of M. Perron (Forêt Québec), these markers were used to certify hybrid progenies and to estimate the extent of gene flow between exotic plantations and natural populations of indigenous species. This work has been supported by CBS, Forêt Québec, and Ligniculture Québec. At the international level and with the funding of AUF and NSERC, our research group has contributed to the development of novel microsatellite DNA markers for the threatened African endemic tree species, *Milicia excelsa* (Moraceae) and its closely related ally, *Milicia regia* (Ouinsavi et al. 2006).

The molecular ecology and ecophysiology of mycorrhizal fungi are also an important aspect of our research program. Research on the effects of partial cutting on the ectomycorrhizal biodiversity of white spruce forests in northwestern Alberta was completed (Lazaruk et al. 2005). Using both an enriched cDNA library for single- or low-copy sequences and data mining strategies, we were successful in developing single-locus codominant microsatellite markers for several ectomycorrhizal fungi including *Laccaria bicolor* (Jany et al. 2006). These sets of hypervariable markers are valuable in environmental genomics studies for the monitoring of the persistence of introduced mycorrhizal strains into the environment (Gagné et al. 2006), to measure the potential introgression of alien genes into the gene pool of native ectomycorrhizal species, and for 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 identify mycorrhizal and root endophytic fungi of pure reclamation materials and revegetated tailing sands from the Canadian oil sand industry (Bois et al. 2005). As well, we assessed the early growth response of container-grown selected woody boreal seedlings in amended composite tailings and tailing sand (Khasa et al. 2005b). In collaboration with Syncrude Canada and financial support from NSERC, a research project investigating the ecophysiology of ectomycorrhizal tree seedlings in oil sand tailings has been successfully completed (Bois et al. 2006a, b). Based on these results, a new project on isolation, identification, and selection of arbuscular and ericoid mycorrhizal fungi for reclamation of oil sands tailings is now being developed.

FUNCTIONAL GENOMICS

J. Mackay

J. Mackay has established a functional genomics research program focused primarily on issues related to wood properties and formation. For the past three years, a large-scale initiative lead by J. Mackay, project *ARBOREA* (www.arborea.ulaval.ca) funded by Genome Canada and Genome Québec, has been investigating 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. For example, putative regulators of secondary metabolism and lignin biosynthesis were analysed within the MYB family of transcripton factors (Bedon et al. 2006).

Gain-of-function experiments were conducted for many genes through over-expression studies in spruce or poplar in collaboration with A. Séguin (CFS). Results obtained to date have identified genes involved in the regulation of plant growth and development, and effect on vascular development either directly or indirectly. An integrated RNA analysis laboratory has been established to support diverse studies of gene expression, from high-resolution studies of individual genes to large-scale analyses of thousands of genes using microarray technologies (e.g., Egertsdotter et al. 2004, Tarca et al. 2005). RNA profiling methods are being used 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. Our group has also participated in research on the quantitative genetics of wood quality in hybrid poplar in collaboration with T. Zhang (Forintek) (Pliuria et al. 2005). This research was sponsored by the Ligniculture Québec Network.

As part of *ARBOREA I*, a large-scale EST sequencing effort was completed in white spruce. High quality sequences were obtained for approximately 80 000 ESTs from 17 cDNA libraries created from diverse organs and tissues. About 15 000 distinct transcripts were identified and, for the most part, they could be classified into various gene ontology classes. Part of the new sequence information is now publicly available at the SpruceDB and ForestTreeDB databases which were developed in collaboration with the University of Minnesota (Center for Computational Bioinformationcs and Genomics) and are easily accessed via www.arborea.ulaval.ca. Large-scale analyses of expressed conifer genes were conducted in pine (Pavy et al. 2004) and spruce (Pavy et al. 2005). An analytical pipeline has also been established for studying the functional diversity of regulatory genes and it is being applied to various conifer gene families (e.g., Guillet-Claude et al. 2004)

STRUCTURAL AND EOLUTIONARY GENOMICS WITH IMPLICATIONS FOR MOLECULAR BREEDING

J. Bousquet

Composite genetic maps of black spruce and white spruce have been assembled with nearly 1,000 markers each, including markers of anonymous position (AFLPs), SSRs, and markers of expressed genes (ESTP) (Pelgas et al. 2005, 2006) in collaboration with N. Isabel (CFS). This work is part of the theses of B. Pelgas and S. Beauseigle. Dozens of anchor markers were positioned, which allowed for the comparison of the genome macro-structure between these species and *Picea abies* (in collaboration with V. Acheré and S. Jeandroz from University Nancy, France), and with other Pinaceae including Douglas-fir (*Pseudotsuga menziesii*) and loblolly pine (*Pinus taeda*). Chromosome fission, segmental duplications, and translocations were identified. To accelerate the developement of ESTPs and identify useful SNPs for mapping, we relied on DNA pool sequencing (DPS) to sample sequence 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).

These joint marker development and mapping projects with N. Isabel (CFS) were funded by the NSERC genomic program, the Canadian Biotechnology Strategy, as well as Genome Canada and Genome Québec through *ARBOREA*. As part of the *ARBOREA I* project, large-scale searches of SNPs in contigs derived from ESTs have also been conducted in white spruce, with over 12 000 SNPs identified (Pavy et al. 2006). The conditions to minimize the rate of false positives have been determined as well as categorization of SNPs under various schemes. A registry of SNPs has been created as part of ForestTreeDB (accessible via www.arborea.ulaval.ca). These SNPs will be most useful for gene mapping as well as in association and population studies aimed at finding markers of adaptive significance. We have recently completed the testing of a high-throughput SNP genotyping approach where hundreds of SNPs were called for hundreds of individuals using the Illumina bead-array technology. A success rate of 70% of the SNPs with callrate higher than 98% was obtained. As part of *ARBOREA II* and in collaboration with N. Isabel and J. Beaulieu (CFS), current studies with these SNP arrays involve the mapping of hundreds of regulatory genes in the white spruce genome, co-localization with QTLs, association studies, and identification of outlier loci in natural populations. Similar studies have been initiated in black spruce (funded by FQRNT, CFS, and NSERC) in collaboration with J. Beaulieu and N. Isabel.

Studies have also been pursued to characterize the patterns of neutral variation at the intraspecific and interspecific levels in the genus *Picea*. As part of her thesis, M. Bouillé has recently shown that transpecies shared polymorphisms at the DNA level are numerous among distantly related spruce species, indicating incomplete lineage sorting, long allele coalescence time, and large historical population sizes (Bouillé and Bousquet 2005). These observations 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 systems and high gene flow. We also completed the estimation of the phylogeny of the complete *Picea* genus using chloroplast and mitochondrial genes. The use of maternally inherited mitochondrial genes for the estimation of phylogenies in the Pinaceae is an innovation and is more likely to be indicative of speciation processes related to dispersion, vicariance, and isolation than paternally inherited chloroplast genes. The results obtained indicate that none of the traditional morphological classifications is right. At the same time, mtDNA and cpDNA phylogenies were incongruent. They pointed at several cases of reticulation and mtDNA capture, which indicates that patterns from cpDNA are not reliable to estimate congeneric phylogenies in old genera of the Pinaceae (supported by NSERC).

Phylogenomics studies under *ARBOREA I* were also conducted for white spruce, black spruce, Norway spruce, white pine and loblolly pine for a number of regulatory genes, in collaboration with N. Isabel. These studies indicate that gene duplication and ensuing translocation is a major force driving neofunctionalization, and that patterns of diversification of gene families observed in conifers are not necessarily following those seen in Angiosperms (Guillet-Claude et al. 2004). The study of several regulatory genes at the population level for each of white spruce, black spruce, and Norway spruce did not allow us to decipher short-term effects of natural selection, but intragenic recombination was high, generating low LD and high haplotype diversity (Guillet-Claude et al. 2006). Under such circumstances, association studies involving markers of expressed genes appear more promising to develop molecular breeding systems than QTL approaches based on anonymous markers or markers of non coding regions. Differential demographic effects were also detected among the three spruces for the various regulatory genes analysed, with recent population expansion detected for Norway spruce. Fine scale association studies of regulatory genes resulted in positive associations between allelic variants and traits related to seed germination and induction in somatic embryogenesis in white spruce. Theses various studies were conducted in collaboration with N. Isabel and they will be expanded to additional genes and characters.

PUBLICATIONS

Andalo, C.; Beaulieu, J.; Bousquet, J. 2005. The impact of climate change on growth of local white spruce populations in Québec, Canada. For. Ecol. Manage. 205: 169–182.

Beaulieu, J.; Perron, M.; Bousquet, J. 2004. Multivariate patterns of adaptive genetic variation and seed source transfer in black spruce (*Picea mariana*). Can. J. For. Res. 34: 531–545.

Bedon, F.; Grima-Pettenait, J.; MacKay, J. 2006. Conifer R2R3-MYB transcription factors: sequences analyses and genes expression relative to wood formation in white spruce *(Picea glauca*). (submitted)

Bois, G.; Piché, Y.; Fung, M.Y.P.; Khasa, D.P. 2005. Mycorrhizal inoculum potentials of pure reclamation materials and revegetated tailing sands from the Canadian oil sand industry. Mycorrhiza 15: 149–158.

Bois, G.; Bertrand, A.; Piché, Y.; Fung, M.Y.P.; Khasa, D.P. 2006a. Ectomycorrhizal fungi affect the physiological response of *Picea glauca* and *Pinus banksiana* seedlings exposed to a NaCl gradient. Tree Physiol. (in press)

Bois, G.; Bertrand, A.; Piché, Y.; Fung, M.Y.P.; Khasa, D.P. 2006b. Growth, compatible solute and salt accumulation of five mycorrhizal fungal species grown over a range of NaCl concentrations. Mycorrhiza 16: 99–109.

Bouillé, M.; Bousquet, J. 2005. Trans-species shared polymorphisms at orthologous nuclear gene loci among distant species in the conifer *Picea* (Pinaceae): implications for the maintenance of genetic diversity in trees. Am. J. Bot. 92: 63–73.

Bouillé, M.; Bousquet, J. 2006. Discordant mtDNA and cpDNA phylogenies in the conifer *Picea* indicate ancient reticulate evolution. (submitted)

Egertsdotter, U.; van Zyl, L.; Mackay, J.; Whetten, R.; Peter, G.; Sederoff, R. 2004. Gene expression profiling during formation of earlywood and latewood in loblolly pine: expression profiles of 350 genes. Plant Biol. 6: 654–663

Gagné, A.; Jany, J.-L.; Bousquet, J.; Khasa, D.P. 2006. Ectomycorrhizal fungal communities of nursery-inoculated seedlings outplanted on clearcut sites in northern Alberta. Can. J. For. Res. 36: 1684–1694.

Godbout, J.; Jaramillo-Correa, J.P.; Beaulieu, J.; Bousquet, J. 2005. A mitochondrial DNA minisatellite reveals the postglacial history of jack pine (*Pinus banksiana*), a broad range North American conifer. Mol. Ecol. 14: 3497–3512.

Gros-Louis, M.-C.; Bousquet, J.; Pâque, L.E.; Isabel, N. 2005. Species-diagnostic markers in *Larix* sp. based on RAPDs and nuclear, mtDNA, and cpDNA gene sequences, and their phylogenetic implications. Tree Genet. Genom. 1: 50–63.

Guillet-Claude, C.; Isabel, N.; Pelgas, B.; Bousquet, J. 2004. The evolutionary implications of *knox-I* gene duplications in conifers: correlated evidence from phylogeny, gene mapping, and analysis of functional divergence. Mol. Biol. Evol. 21: 2232–2245.

Guillet-Claude, C.; Isabel, N.; Mackay, J.; Bousquet, J. 2006. Molecular evolution of regulatory genes in the conifer *Picea*: evidence for frequent intragenic recombination, selection, and recent population expansion. (submitted)

Jany, J.-L.; Bousquet, J.; Gagné, A.; Khasa, D.P. 2006. Simple sequence repeat (SSR) markers in the ectomycorrhizal fungus *Laccaria bicolor* for environmental monitoring of introduced strains and molecular ecology applications. Mycol. Res. 110: 51–59.

Jaramillo-Correa, J.P.; Beaulieu, J.; Bousquet, J. 2004. Variation in mtDNA reveals multiple glacial refugia in black spruce (*Picea mariana*), a transcontinental North American conifer. Mol. Ecol. 13: 2735–2748.

Jaramillo-Correa, J.P.; Bousquet, J. 2005. Mitochondrial genome recombination in the zone of contact between two hybridizing conifers. Genetics 171: 1951–1962.

Jaramillo-Correa, J.P.; Beaulieu, J.; Ledig, F.T.; Bousquet, J. 2006. Decoupled mitochondrial and chloroplast DNA population structure reveals Holocene collapse and population isolation in a threatened Mexican-endemic conifer. Mol. Ecol. (in press)

Khasa, D.P.; Pollefeys, P.; Navarro-Quezada, A.; Périnet, P.; Bousquet, J. 2005a. Species-specific microsatellite markers to monitor gene flow between exotic poplars and their natural relatives in eastern North America. Mol. Ecol. Notes 5: 920–923.

Khasa, D.P.; Fung, M.; Logan, B. 2005b. Early growth response of container-grown selected woody boreal seedlings in amended composite tailings and tailings sand. Bioresour. Technol. 96: 857–864.

Khasa, D.P.; Jaramillo-Correa, J.P.; Jaquish, B.; Bousquet, J. 2006. Contrasting microsatellite variation between subalpine larch and western larch, two closely related species with different distribution patterns. Mol. Ecol. (in press)

Koubaa, A.; Isabel, N.; Zhang, S.Y.; Beaulieu, J.; Bousquet, J. 2005. Transition from juvenile to mature wood in *Picea mariana*. Wood Fiber Sci. 37: 445–455.

Lazaruk, L.W.; Kernaghan, G.; Macdonald, S.E.; Khasa, D.P. 2005. Effects of partial cutting on the ectomycorrhizae of *Picea glauca* forests in northwestern Alberta. Can. J. For. Res. 35: 1442–1454.

Mackay, J.; Bérubé, H.; Regan, S.; Séguin, A. 2003. Functional genomics in forest trees: application to the investigation of defense mechanisms and wood formation. Pages 163–180. *In* C. Walter and M. Carson, eds. Plantation Forest Biotechnology for the 21st Century.

Naydenov, K.; Senneville, S.; Beaulieu, J.; Tremblay, F.M.; Bousquet, J. 2006. Pan-Eurasian variation in mitochondrial DNA reveals multiple distant glacial populations and the postglacial history of Scots pine (*Pinus sylvestris*). (submitted)

Ouinsavi, C.; Sokpon, N.; Bousquet, J.; Newton, C.H.; Khasa, D.P. 2006. Novel microsatellite DNA markers for the threatened African endemic tree species, *Milicia excelsa* (Moraceae), and cross-species amplification in *Milicia regia.* Mol. Ecol. Notes 6: 480–483.

Pavy, N.; Laroche, J.; Bousquet, J.; Mackay, J. 2004. Large-scale statistical analysis of secondary xylem ESTs in pine. Plant Mol. Biol. 57: 203–224.

Pavy, N.; Paule, C.; Parsons, L.; Crow, J.A.; Morency, M.-J.; Cooke, J.; Johnson, J.E.; Noumen, E.; Guillet-Claude, C.; Butterfield, Y.; Barber, S.; Yang, G.; Liu, J.; Stott, J.; Kirkpatrick, R.; Siddiqui, A.; Holt, R.; Marra, M.; Séguin, A.; Retzel, E.; Bousquet, J.; Mackay, J. 2005. Generation, annotation, analysis, and database integration of 16,500 white spruce EST clusters. BMC Genomics 6: 144. 19 p.

Pavy, N.; Parsons, L.; Paule, C.; Mackay, J.; Bousquet, J. 2006. Automated SNP detection from a large collection of white spruce expressed sequences: contributing factors and approaches for the categorization of SNPs. (submitted)

Pelgas, B.; Isabel, N.; Bousquet, J. 2004. Efficient screening for expressed sequence tag polymorphisms (ESTP) by DNA pool sequencing and denaturing gradient gel electrophoresis in spruces. Mol. Breed. 13: 263–279.

Pelgas, B.; Bousquet, J.; Beauseigle, S.; Isabel, N. 2005. A composite linkage map from two crosses for the species complex *Picea mariana* [Mill.] B.S.P. x *P. rubens* (Sarg.) and analysis of synteny with other Pinaceae. Theor. Appl. Genet. 111: 1466–1488.

Pelgas, B.; Beauseigle, S.; Acheré, V.; Jeandroz, S.; Bousquet, J.; Isabel, N. 2006. Comparative genome mapping among *Picea glauca*, *P. abies* and *P. mariana X rubens*, and correspondance with other Pinaceae. (submitted)

Pliura, A.; Yu, Q.; Zhang, S.Y.; Mackay, J.; Périnet, P.; Bousquet, J. 2005. Variation in wood density and shrinkage and their relationship to growth of selected young poplar hybrid crosses. For. Sci. 51: 472–482.

Tarca, A.L.; Cooke, J.E.K.; Mackay, J. 2005. A robust neural network approach for spatial and intensity dependent normalization of cDNA microarray data. Bioinform. 21: 2674–2683.

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

Jean Beaulieu, Gaëtan Daoust, Nathalie Isabel, Marie Deslauriers and Manuel Lamothe

Natural Resources Canada
Canadian Forest Service
Laurentian Forestry Centre
PO Box 10380, Stn. Sainte-Foy
Québec, QC
G1V 4C7
E-mail: Jean.Beaulieu2@nrcan.gc.ca

Keywords: white spruce, black spruce, eastern white pine, Canada yew, Norway spruce, larches and poplars, *Picea glauca*, *Picea mariana*, *Picea abies*, *Pinus strobus*, *Taxus canadensis*, *Larix* spp., *Populus* spp., growth-related traits, wood quality, warp, shrinkage, lumber, open-pollinated families, climate change, pedigree, ESTPs, AFLPs, microsatellites, RAPDs, SNPs, mtDNA markers, genomic mapping, association mapping, QTLs, species-specific markers

This report summarizes the progress of the Canadian Forest Service, Laurentian Forestry Centre (CFS) research in forest genetics, genomics, molecular ecology, and biodiversity for the period 2004–2006. Our activities have mainly focussed on advanced genetics and breeding work in three spruces and eastern white pine (*Pinus strobus*). We have also continued to invest considerable time and effort in population genetics studies of forest tree species and in genomics in collaboration with J. Bousquet from Université Laval and as part of our participation in the activities of the Canada Research Chair in Forest and Environmental Genomics (Tier I) and via a strategic grant obtained from Natural Sciences and Engineering Research Council (NSERC) for the development of a phylogeographic atlas of Canadian conifer tree species. Research was also done in collaboration with our colleagues from Forintek Canada Corporation and Université Laval on genetic variation and control of wood characteristics. One of the projects was funded by the Fonds québécois de recherche sur la nature et les technologies. We are also co-investigators of the genomics research program *ARBOREA* (Mackay, Bousquet, et al.), a major initiative, funded by Genome Canada and Genome Quebec for developing molecular breeding in softwood trees. On another front, in collaboration with Université Laval (J. Bousquet and D. Khasa) and Forêt Québec (P. Périnet et al.), nuclear diagnostic markers for the recognition of *Populus* species and their hybrids have 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, Sébastien Clément, France Gagnon, Marie-Claude Gros-Louis, Patrick Meirmans, Karine Plante, Esther Pouliot, Patricia Sylvestre, Michèle Bernier-Cardou, Pamela Cheers, and many summer students.

WHITE SPRUCE

Quantitative Genetics

Over the last 2 years, we completed a study initiated in collaboration with Tony Zhang (Forintek Canada Corp.) and André Rainville (Ministère des Ressources naturelles et de la Faune (MRNF)) 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 processed into 2 x 4 studs for analysis of lumber mechanical properties. As expected, the mechanical properties of lumber from young plantation-grown trees were low (Beaulieu et al. 2006, in press). The low wood density, the occurrence of numerous large dimension knots, and a high proportion of juvenile wood are the main factors contributing to low lumber stiffness and strength properties. The narrow-sense heritability for lumber stiffness was low to moderate (0.279) whereas that of strength was hardly different from zero (0.016). The environmental growing conditions appear to highly influence young white spruce wood mechanical properties. Strong negative correlations between stem volume and lumber stiffness and strength at the family means (-0.43 and -0.34, respectively) suggest that selection for stem volume would have an indirect negative effect on lumber quality. The white spruce reforestation program is one of the most important in Quebéc with close to 30 million seedlings planted yearly. 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.

In order to estimate the potential impact of climate change on growth of white spruce populations, transfer models were developed to predict the performance of seed sources based on temperature and summer precipitation differentials between the geographical origin of seed sources and experimental site locations. To do so, data were collected in a genecological test, replicated on three sites, and involving 45 distinct geographical seed sources from the province of Quebéc, most of them represented by five open-pollinated families. We found that white spruce populations located within the sampled area were optimally adapted to their local environment for thermal conditions but not for moisture conditions; populations that originated from sites receiving more precipitation generally showed higher tree growth than the local sources (Andalo et al. 2005). We predicted that the adaptive lag related to precipitation would increase under global warming conditions. Simulations of growth under various climate change scenarios indicated that it would be tangibly diminished under more intense warming.

Thanks to a grant from the Fonds québécois de recherche sur la nature et les technologies awarded to one of us and J. Bousquet, a biophysical site index model was developed for white spruce plantations in Québec. This model makes it possible to predict the white spruce site index (average height of dominant trees at 25 years) for any location based on degree-days and summer precipitation. A GIS-tool was then developed to map both site index and plantation yield at any age for a given spacing. Moreover, using data of selected families from a series of progeny tests, we estimated a genetic-gain multiplier for height which can be used to multiply the predicted site index in order to estimate genetically improved plantation yield. Results will be presented in a scientific paper that is in preparation.

The seed source transfer model and the biophysical site index model described above, both based on temperature and precipitation, were combined to obtain realistic estimates of white spruce plantation yield under future global warming conditions. Both models as well as white spruce yield tables were incorporated into BioSIM, a climate simulator developed by J. Régnière from CFS, to estimate and map plantation yield up to 2070 (Beaulieu and Rainville 2005). Our simulation results predict that global warming should favour a slight increase in white spruce plantation yield in southern Québec. However, one cannot expect to obtain similar yields from a seed source rapidly exposed to warmer conditions compared with a seed source that is presently growing under climatic conditions to which it has become adapted. The simulator is used to revise seed source transfer rules.

A comparison of early height growth between seedlings and rooted cuttings was carried out using annual measurements collected over 5 years in a farm-field test replicated on three sites. The experiment included 148 full-sib families and 15 open-pollinated families used as controls. Average total heights of seedlings and rooted cuttings were 186 cm and 171 cm, respectively, after the 5-year period. The difference in height between both types of plants at the end of the testing period was about of the same magnitude as that at out-planting. The average growth rate of seedlings was slightly larger than that of rooted cuttings and the yearly growth rate increased over time. It did so at a somewhat higher rate for the seedlings. Variance components associated with families suggested that important gains in early growth might be achieved by bulking up superior families through cuttings. Producing rooted cuttings is more expensive than producing seedlings. This is why this vegetative propagation method can be efficient only when there is a need to bulk-up scarce seed supplies. However, as family ranking based on rooted cuttings is similar to that of seedlings, it could be used to obtain better estimates of breeding values.

Genomics

During the period under review, two grants were obtained from the Canadian Biotechnology Strategy to initiate one project on QTL mapping and an association study of growth-related traits and another one on association mapping of wood traits, both in white spruce. These grants were also used as co-funding for two of the research activities of the *ARBOREA* Project, a major initiative, funded by Genome Canada and Genome Québec for developing molecular breeding in softwood trees and co-led by J. Mackay and J. Bousquet from Université Laval. So far, primer pairs to amplify DNA sequences of candidate genes for wood traits have been developed for over 200 genes. Discovery of SNPs in gene sequences is underway. Our goal is to design primers to amplify DNA sequences of over 500 candidate genes for both growth-related traits and wood traits. We will identify favourable alleles responsible for a significant proportion of variation in traits related to growth (budset), wood formation, and quality. For growth-related traits, two mapping populations of more than 300 individuals each were developed. For wood traits, a discovery population of 495 trees was assembled as well as a validation population of 200 trees. Increment cores were collected from these trees and phenotypic values for a variety of wood traits and properties are being assessed at Paprican's facilities in Vancouver. Association studies will be carried out over the next 2 to 3 years thanks to the grant from Genome Canada and Genome Québec.

The development of pedigree populations continued. Single-pair matings were carried out in order to have access to a large number of unrelated families for the genomics studies. A population of 1,000 trees, one from each of 1,000 unrelated families, was assembled to carry out an association study between candidate genes and growth and phenology traits. Seeds were sown in February 2005 and seedlings were submitted to accelerated growth in a heated greenhouse during winter 2006. Cuttings will be collected from each of the seedlings and rooted during summer 2006 with the collaboration of Michel Rioux from the Saint-Modeste cutting centre.

BLACK SPRUCE

Quantitative Genetics

There is still some controversy about the determination of transition from juvenile wood to mature wood in conifers. Several methods have been proposed including visual examination of pith-to-bark profiles and mathematical approaches such as Gomperts function, segmented regression techniques or polynomial regression models. A study was carried out to characterize the average trend in growth and wood density as a function of age and to obtain consistent estimates of transition age from juvenile to mature wood in black spruce (*Picea mariana*) using about 1000 trees from a 50-year-old plantation (Koubaa et al. 2005). Radial patterns of wood density, ring width, latewood density, and latewood proportion obtained by X-ray densitometry of increment cores were modeled with polynomial regressions. It was found for all traits measured that the radial profiles were typical of those previously reported for *Picea* species. Significant differences among the various classes of diameter observed in the plantation were also disclosed for all the traits. The juvenile wood production period varied with growth rate and transition age for a given diameter class also varied, depending on the trait. Hence, it appears that in black spruce, transition age needs to be defined based on physiological processes.

Structural Genomics

In collaboration with J. Bousquet (Université Laval), individual and composite linkage maps of the black-red spruce complex species have been published (Pelgas et al. 2005). Over the past two years, PhD student B. Pelgas and MSc student S. Beauseigle, supervised by J. Bousquet (Université Laval) and co-supervised by one of us, have focused on further mapping the genome of white spruce (one composite map) and establishing a composite map for black spruce. In collaboration with colleagues from the Université de Nancy (S. Jeandroz and V. Achere), macro-synteny and macro-collinearity among divergent spruce species, including black spruce, white spruce, and Norway spruce (*Picea abies*), were estimated (Pelgas et al. submitted). This joint project with J. Bousquet was funded by a NSERC-genomic grant and the Canadian Biotechnology Strategy.

JACK PINE

Phylogeography

A highly variable minisatellite locus was discovered in the mitochondrial DNA of jack pine (*Pinus banksiana*) and the pattern of intra- and interpopulation variation was studied using this marker by Julie Godbout, a PhD student supervised by J. Bousquet and one of us (Godbout et al. 2005). By examining the modern population structure of mitochondrial DNA diversity along its natural range, three relatively homogeneous groups of populations could be delineated and they are presumably representative of genetically distinct glacial populations. The first one covers the region extending from Lake Huron to the Yukon. The second one is located in the southeast and mainly gathers populations located in eastern Ontario and south of the St. Lawrence River in Québec. The third group is located in the Maritimes. The last distinct group was observed in central Québec, which harbours a higher level of genetic diversity within populations and a lower degree of population differentiation than other groups. This region is likely a zone of suture between migration fronts of the three ancestral populations colonizing the three other zones. Based on these results and on the available fossil record, it was possible to put forward hypotheses regarding the number and the location of glacial populations and refugia for jack pine during the Last Glacial Maximum. Because of startling differences between western and southeastern populations, it is likely that there was a glacial population located west of the Appalachian Mountains in the United States, which was genetically distinct from another one located east of the mountain range. Because of the genetic distinctiveness of Maritimes populations, a third glacial population was presumably located on the unglaciated northeastern coastal area in Canada. This last hypothesis is also supported by botanists and entomologists. Recommendations about seed source movement were also made. Hence, it was recommended to avoid any transfer between the Maritimes and the regions west of the province of Québec, and vice versa. Moreover, any *in situ* conservation decisions should take into account the phylogeographical structure reported in that study.

ENVIRONMENTAL GENOMICS

Estimation of effective gene flow levels towards native species represents the first step in the assessment of ecological risks linked to the introduction of GMO trees in Canada. In order to evaluate the risks of such gene flow, several authors have recently suggested assessing spontaneous introgression levels using old exotic material already established in the field. A grant was obtained from the Canadian Regulatory System of Biotechnology to estimate the level of spontaneous hybridization between exotics and their native counterparts to develop an alternative method for measuring the impact of the introduction of genetically modified trees on the integrity of local populations. The study is being conducted by one of us and a postdoctoral fellow (P. Meirmans, University of Amsterdam), and also a M.Sc. student (G. Guigou) supervised by D. Khasa and J. Bousquet. For larches, species-specific markers already developed by us (Gros-Louis et al. 2005) were used to monitor the rate of gene flow from plantations of exotic species of *Larix* into natural populations of their respective native congeners. For *Larix*, we use Primer Extension and CAPS techniques to genotype paternally inherited chloroplast markers and maternally inherited mitochondrial markers, allowing for a rapid identification of first-generation hybrids. For *Populus*, we use SNP stream technology to simultaneously genotype 12 nuclear, species-specific, SNPs (Meirmans et al., in preparation) allowing for a high power of identification of first- and second-generation hybrids. Preliminary results for *Larix* show that the rate of hybridization is quite low: genotyping 1,779 offspring produced by 98 trees of native *L. laricina*, we found 2.2% hybrids. The funding has just been renewed and the next phase of the project will focus on population genetics and hybridization of poplar species across Canada in collaboration with B. Schroeder (AgriFoodCan, Saskatchewan) and B. Thomas (University of Alberta).

ÉPINETTE DE NORVÈGE

Les efforts concertés du Service canadien des forêts (SCF) et du MRNF ont permis de poursuivre le programme conjoint d'amélioration génétique. Au cours de la dernière période, les efforts du SCF ont surtout été consacrés à l'entretien et au mesurage des dispositifs mis en place au cours des dernières années. Par la suite, plusieurs dispositifs établis avec des espacements restreints ont fait l'objet d'éclaircie systématique. Le parc d'hybridation de Valcartier, regroupant plus de 350 clones, a été éclairci afin de permettre un meilleur développement des cimes et une plus grande production de cônes à long terme. Ce parc d'hybridation est utilisé pour la production de semences et de croisements dirigés devant servir au programme d'amélioration et au programme de reboisement et de production de boutures du MRNF.

L'étude entreprise pour étudier l'impact du charançon sur la productivité et la qualité du bois a été complétée et sera publiée sous peu (Daoust et Mottet 2006). Plusieurs présentations de cette étude ont été faites auprès des aménagistes et des utilisateurs de cette ressource. L'étude a permis de faire ressortir, malgré l'impact du charançon, le potentiel de cette espèce lorsqu'on la compare à l'épinette blanche tant pour la productivité que pour les caractéristiques du bois.

PIN BLANC ET PINS HYBRIDES

Le programme d'amélioration du pin blanc s'est poursuivi au cours de la dernière période. La majorité des ressources disponibles a été consacré à l'établissement et au maintien des dispositifs expérimentaux en région et à Valcartier. Des efforts soutenus pour lutter contre le charançon du pin blanc et la rouille vésiculeuse dans les jeunes dispositifs expérimentaux ont été maintenus.

Les tests de descendances issues de pollinisations libres entre les clones de notre population d'élevage ont été mesurés après 5 ans. Les analyses préliminaires ont permis de formuler des recommandations à la Division des semences et des plants (DPSP) du MRNF afin de mieux cibler les descendances les plus performantes à récolter dans leurs vergers à graines ayant du matériel commun avec notre population d'amélioration et débuter des éclaircies dans ces derniers.

Soixante-quinze clones d'un verger à graines de l'Outaouais, constitué de sélection locale, ont été échantillonnés en 2004, une excellente année semencière. Un test de descendances a été démarré à partir de ce matériel et les semis seront repiqués en pépinière sous forme de dispositif expérimental en vue d'une évaluation à trois ans. Par la suite, les résultats seront transmis à la DPSP pour la récolte sélective et l'éclaircie du verger. Éventuellement, le dispositif mis en place à la pépinière sera utilisé pour l'établissement de tests de descendances dans la région ciblée pour ce verger à graines.

Plusieurs croisements dirigés et libres entre le *P. wallichiana* et *strobus* ont été ensemencés en 2005 en vue de vérifier la résistance à la rouille vésiculeuse du pin blanc. Les tests d'inoculation artificielle seront réalisés en 2006.

IF DU CANADA

Les tests clonaux mis en place dans Charlevoix et à Valcartier par la Société d'aide au développement de la collectivité de Charlevoix et le SCF ont été échantillonnés pour des analyses de taxanes. La croissance relativement lente des plants n'a pas permis de faire un échantillonnage complet tel que planifié au départ. Les analyses chimiques des contenus en taxanes ont été réalisées. Ces résultats seront comparés avec les données des populations de départ et devraient permettre de valider si le contenu en taxanes est sous contrôle génétique. Une affiche scientifique portant sur ce projet a été présentée à la première conférence internationale portant sur les « Crop Wild Relative Conservation and Use » tenue en Italie à l'automne 2005.

PUBLICATIONS

Andalo, C.; Beaulieu, J.; Bousquet, J. 2005. The impact of climate change on growth of local white spruce populations in Québec, Canada. For. Ecol. Manage. 205: 169–182.

Beaulieu, J.; Rainville, A. 2005. Adaptation to climate change: Genetic variation is both a short- and a long-term solution. For. Chron. 81(5): 704–709.

Beaulieu, J. 2005. Transferencia de Fuentes de Semilla de Picea en QUEBEC, Canada : Linaemientos y Herramientas. Pages 1–14. *In* G. Vera C., J.J. Vargas H., and J. Dorantes L., eds. Memoras del Simposium « Uso y Conservación de Recursos Genéticos Forestales ». 5 Nov 2002, Colegio de Postgraduados - Comisión Nacional Forestal Jalapa, Veracruz, Mexico.

Beaulieu, J.; Godbout, J.; Jaramillo-Correa, J.P.; Bousquet, J. 2006. Sur la trace du passé de nos conifères. Santé et biodiversité des forêts : Nouvelles. Serv. can. for. Printemps 2006.

Beaulieu, J.; Godbout, J.; Jaramillo-Correa, J.P.; Bousquet, J. 2006. On the track of the past of our conifers. Can. For. Serv., Forest Health and Biodiversity News, Spring 2006.

Beaulieu, J.; Bernier-Cardou, M. 2006. Comparison of early height growth between white spruce seedlings and rooted cuttings. Can. J. For. Res. (in press)

Beaulieu, J.; Zhang, S.Y.; Yu, Q.; Rainville, A. 2006. Comparison between genetic and environmental influences on lumber bending properties in young white spruce. Wood Fiber Sci. (in press)

Daoust, G.; Mottet, M.-J. 2006. Impact du charançon du pin blanc (*Pissodes strobi* Peck) dans les plantations d'épinettes de Norvège (*Picea abies* [L.] Karst.), Partie 1 : Productivité et qualité des sciages. For. Chron. (in press)

Godbout, J.; Jaramillo-Correa, J.P.; Beaulieu, J.; Bousquet, J. 2005. A mitochondrial DNA minisatellite reveals the postglacial history of jack pine (*Pinus banksiana*), a broad-range North American conifer. Mol. Ecol. 14: 3497–3512.

Gros-Louis, M.-C.; Bousquet, J.; Paques, L.E.; Isabel, N. 2005. Species-specific diagnostic markers in *Larix* spp. based on RAPDs and nuclear, cpDNA, and mtDNA gene sequences, and their phylogenetic implications. Tree Genet. Genom. 1: 50–63.

Guillet-Claude C.; Isabel, N.; Pelgas, B.; Bousquet, J. 2005. The evolutionary implications of knox-I gene duplications in conifers: correlated evidence from phylogeny, gene mapping, and analysis of functional divergence. Mol. Biol. Evol. (6.4) 11: 2232–2245.

Jaramillo Correa, J.P.; Beaulieu, J.; Bousquet, J. 2004. Variation in mitochondrial DNA reveals multiple distant glacial refugia in black spruce (*Picea mariana*), a transcontinental North American conifer. Mol. Ecol. 13: 2735–2747.

Jaramillo-Correa, J.P.; Beaulieu, J.; Ledig, F.T.; Bousquet, J. 2006. Postglacial history, population structure and considerations for the conservation of a threatened Mexican-endemic conifer inferred with mitochondrial and chloroplast DNA markers. Mol. Ecol. (in press)

Koubaa, A.; Isabel, N.; Zhang, S.Y.; Beaulieu, J.; Bousquet, J. 2005. Transition from juvenile to mature wood in *Picea mariana* (Mill.) B.S.P. Wood Fiber Sci. 37(3): 445–455.

Lamothe, M.; Meirmans, P.; Isabel, N. 2006. A set of polymorphic EST-derived markers for *Picea* species. Mol. Ecol. Notes (on line)

Pelgas B.; Bousquet, J.; Beauseigle, S.; Isabel, N. 2005. A composite linkage map from two crosses for the species complex (*Picea mariana* x *Picea rubens*) and analysis of synteny with other Pinaceae. Theor. Appl. Genet. 111: 1466–1488.

Pelgas B.; Isabel, N.; Bousquet, J. 2004. Efficient screening for expressed sequence tag polymorphisms (ESTP) by DNA pool sequencing and denaturing gradient gel electrophoresis in spruces. Mol. Breed. 13: 263–279.

Rainville, A.; Beaulieu, J. 2005. Adaptation aux changements climatiques : la génétique peut-elle nous servir? Les pages 18–21. *Dans* Actes du colloque « Changements climatiques et foresterie : impacts et adaptation, 20 et 21 avril 2005, Baie-Comeau, QC.

Sotelo Montes, C.; Hernández, R.E.; Beaulieu, J.; Weber, J.C. 2006. Genetic variation and correlations between growth and wood density of *Calycophyllum spruceanum* Benth. at an early age in the Peruvian Amazon. Silvae Genet. (in press)

Zhang, S.Y.; Yu, Q.; Beaulieu, J. 2004. Genetic variation in veneer quality and its correlation to growth in white spruce. Can. J. For. Res. 34: 1311–1318.

ORAL AND POSTER PRESENTATIONS

Beaulieu, J.; Ung, C.-H.; Rainville, A.; Zhang. S.Y.; Bousquet, J. 2004. Allométrie de la biomasse des familles supérieures d’épinette blanche en fonction de leur site d’implantation. 72e congrès de l’ACFAS. 13 mai 2004, Université du Québec à Montréal, Montréal, QC.

Beaulieu, J. 2004. Les caractéristiques du bois d’épinette blanche de plantation : de la fibre à la seconde transformation. In La ligniculture au Québec : de la théorie à la pratique. Réseau Ligniculture Québec. Colloque organisé par le Réseau Ligniculture Québec. 12 mai 2004, Montréal, QC.

Beaulieu, J.; Prégent, G.; Raulier, F.; Bousquet, J. 2005. Prédiction du rendement des plantations d’épinette blanche en fonction des caractéristiques biophysiques des sites à reboiser. 73e congrès de l’ACFAS. 13 mai 2005, Université du Québec à Chicoutimi, Saguenay, QC.

Beaulieu, J. 2005. Genetic diversity: subtle differences that matter. International Day for Biological Diversity. 18 May 2005, Ottawa, ON.

Beaulieu, J.; Watson, P.; Isabel, N.; Bousquet, J.; Mackay, J. 2006. Association mapping for candidate genes in white spruce. Page 229. *In* Plant and Animal Genome XIV,14–18 Jan 2006, San Diego, CA.

Beaulieu, J. 2006. Qualité des bois résineux de plantation : connaissances et perspectives. Colloques du SCF-CFL, 16 mars 2006.

Beauseigle, S.; Pelgas, B.; Bousquet, J.; Isabel, N. 2004. La cartographie génétique chez les épinettes. Colloque CRBF-GREFI. mars, Sainte-Foy, QC.

Belleau, P.; Daoust, G. 2005. Programme de réintroduction du pin blanc dans le Bas-Saint-Laurent. Journée de la Forêt modèle du Bas-Saint-Laurent, 30 mars 2005, Sainte-Foy, QC.

Bousquet, J.; Beaulieu, J.; Rainville, A.; Ung, C.-H.; Zhang, S.Y. 2006. Optimisation du choix et du rendement des sources améliorées d'épinette blanche en fonction des caractéristiques biophysiques des sites à reboiser. Les pages 173–180. *Dans* Forum de transfert sur l'aménagement et l'environnement forestiers. 6 avril 2006, Québec, QC.

Bousquet J.; Isabel, N.; Pelgas, B.; Guillet-Claude, C. 2005. The evolutionary implications of knox-1 gene duplications in conifers: correlated evidence from phylogeny, gene mapping, and analysis of functional divergence. September, Asilomar, CA.

Carles, S.; Beaulieu, J.; Lamhamedi, M.S.; Margolis, H.A. 2005. Improving root development : Genetic selection, cultural pracites or both? The Thin Green Line: A Symposium on the State-of-the-Art in Reforestation. 26–28 July 2005, Thunder Bay, ON.

Carles, S.A.; Beaulieu, J.; Lamhamedi, M.S.; Stowe, D.; Margolis, H.A. 2006. Contrôle génétique et effets de la fertilité du substrat sur la croissance des racines de plants d'épinette blanche (1+0). 4e Atelier sur la production de plants forestiers au Québec. Facteurs et techniques culturales influençant le développement racinaire des plants en pépinière forestière. 15–16 mars 2006, Québec, QC.

Coulombe, C.; Bélanger, G.; Lavallée, R.; Laflamme, G.; Daoust, G. 2004. Un outil de contrôle simple et efficace contre le charançon et la rouille vésiculeuse du pin blanc sur l'épinette de Norvège et le pin blanc. Partenariat Innovation Forêt. 8p.

Daoust, G. 2004. Concerto pour pins et épinettes, variation en gènes majeurs. Présentée le 23 février 2004 lors de l'activité interne du CFL-SCF sur la Science de mon voisin.

Daoust, G. 2005. Amélioration génétique du pin blanc au Québec, Bilan des progrès accomplis. Colloques du CFL-SCF. 17 nov 2005.

Daoust, G.; Mottet, M.-J. 2004. Impact du charançon du pin blanc sur les propriétés du bois de l'épinette de Norvège en plantation. Présentée le 12 mai 2004 lors du 72^{e} Congrès annuel de l'ACFAS dans le cadre du Colloque de Ligniculture.

Daoust, G.; Mottet, M.-J. 2004. Rendement en sciage et caractéristiques du bois de l'épinette de Norvège en plantation. Présentée le 28 septembre 2004 à la pépinière de Sainte-Luce lors de la journée-clients.

Daoust, G.; Mottet, M.-J. 2004. Rendement en sciage et caractéristiques du bois de l'épinette de Norvège en plantation. Présentée le 14 avril 2005 lors de la rencontre annuelle des agents livreurs du Bas-Saint-Laurent, Rimouski.

Daoust, G.; Mottet, M.-J. 2004. Rendement en sciage et caractéristiques du bois de l'épinette de Norvège en plantation. Présentée le 29 septembre 2004 à la pépinière de Saint-Modeste lors de la journée-clients.

Daoust, G.; Beaulieu, J.; Perron, M.; Pâquet, R.; Aerni, C. 2006. Les mélèzes dans le réseau de démonstration des gains génétiques : Résultats à 10 ans. Les pages 28–29. *Dans* La ligniculture : une solution d'avenir. 23–24 mars 2006, Orford, QC.

Guigou, G.; Meirmans, P.; Lamothe, M.; Gros-Louis, M.-C.; Bousquet, J.; Khasa, D.; Isabel, N. 2006. Evaluation of gene flow between exotic and native *Populus* species using microsatellites (SSRs) and SNPs. Plant and Animal Genome Conference. January, San Diego, CA.

Guillet-Claude, C.; Isabel, N.; Pelgas, B.; Bousquet, J. 2004. The evolutionary implications of knox-I gene duplications in conifers: correlated evidence from phylogeny, gene mapping, and analysis of functional divergence. June, Penn State. Univ.

Isabel, N. 2006. Flux de gènes entre espèces exotiques et indigènes: duel à armes égales? Chaire de recherche en développement durable, Université du Québec en Abitibi. February.

Isabel, N. 2005. What is a genetic marker? Genomics to Production Workshop. Poplar Council of Canada. March, Edmonton, AB.

Isabel, N. 2005. Les produits dérivés de la génomique : les marqueurs moléculaires à valeur ajoutée. Colloque de Ligniculture Québec. ACFAS. May, Chicoutimi, QC.

Isabel, N.; Rutledge, R. 2004. Genomics in spruce species: discovery of genes involved in meristematic activities. September, Ottawa, ON.

Isabel, N. 2004. Direct access to the spruce genome via composite genetic maps. Treenomix' Workshop. August, Vancouver, BC.

Lamothe, M.; Gros-Louis, M.-C.; Senneville, S.; Dubois, P.; Khasa, D.; Bousquet, J.; Isabel, N. 2004. Evaluation of gene flow between exotic and native tree species. Poplar Council of Canada. August, Vancouver, BC.

Meirmans, P.; Lamothe, M.; Gros-Louis, M.-C.; Périnet, P.; Isabel, N. 2006. Using SNPstream technology to distinguish poplar species and their hybrids. Plant and Animal Genome Conference. January, San Diego, CA.

Meirmans, P.; Gros-Louis, M.-C.; Lamothe, M.; Guigou, G.; Khasa, D.; Bousquet, J.; Isabel, N. 2005. Evaluation of gene flow between exotic and native tree species; developing an alternative method for measuring the impact of the introduction of genetically modified trees on the integrity of local populations. IUFRO Tree Biotechnology 2005. November, Pretoria, South Africa.

Mackay, J.; Bousquet, J.; Cooke, J.; Isabel, N.; Pavy, N.; Regan, S.; Retzel, E.; Séguin, A. 2005. Functional genomic investigations of wood formation and defense response in trees and beyond. Plant and Animal Genome Conference. January, San Diego, CA.

Pelgas, B.; Bousquet, J.; Beauseigle, S.; Isabel, N. 2005. Comparative mapping within the genus *Picea* and analysis of synteny with other Pinaceae. IUFRO Tree Biotechnology 2005. November, Pretoria, South Africa.

Pelgas, B.; Beauseigle, S.; Gosselin, I.; Lamothe, M.; Bousquet, J.; Isabel, N. 2004. Towards composite genetic maps of the spruce genome. 2nd Canadian Plant Genomics Workshop. September, Québec, QC.

Sotelo Montes, C.; Hernandez, R.; Beaulieu, J.; Webber, J.C. 2006. Variation in growth, juvenile wood density and color of *Calycophyllum spruceanum* Benth. Society of Wood Science and Technology (SWST). 48th Annual Convention and Forest Products Society (FPS) and 59th International Convention, 19–22 June 2005, Québec, QC.

MODELLING AIRBORNE POLLEN DISPERSAL TO AID REDUCTION IN POLLEN CONTAMINATION

Franco DiGiovanni

AirZOne One Ltd.
222 Matheson Boulevard East
Mississauga, ON
L4Z 1X1
E-mail: fdi-giovanni@airzoneone.com

Keywords: pollen dispersal, pollen contamination, gene flow, seed production, modelling

Pollen contamination (PC) can reduce the genetic quality of seed used for forest replanting and thus 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 (SOs). Current models for estimating wood volume production from improved seed assume maximal genetic gain from seed sired in SOs and ignore reductions in gain due to PC (pers. comm., 2002, Randy Ford, Northeast Seed Management Association). We describe the development and demonstrate the application of a computer model of PC that will eventually be used to assist in managing SOs in Ontario.

BACKGROUND

Work was initiated in the early 1990s on development of the prototype POLDISP software program (POLDISP v1.0). The dispersal model software was developed to simulate airborne pollen dispersal from the natural stand into a seed orchard and can be used to simulate the effect of various anti-contamination strategies (work funded by the Ontario Tree Improvement Council and Ontario Tree Improvement Board). With the "best" methods predicted by POLDISP v1.0, the orchard manager could decide on the economics and practicality of the methods suggested by the model. Work on assessing pollen emissions from trees and providing model validation data was conducted at the Island Lake Tree Improvement Area (ILTIA), near Chapleau, Ontario, during that same period.

Further work was funded by Forest Genetics Ontario in 2000/2001 aimed at continuing model validation by using the field data gathered at ILTIA. General model validation work was continued under a contract to the Canadian Food Inspection Agency (CFIA). That work addressed issues of the environmental impact of genetically modified wheat. The result of the CFIA contract (completed July 2004) was the production of an operational version of the model for agricultural purposes (POLDISP v2.0).

Northeast Seed Management Association (NESMA) has funded the work reported here in order to apply these modelling approaches to determine how genetic gain is affected and suggest appropriate anti-contamination methods for existing seed orchards across Ontario. In addition, the modelling may be used for the selection of future orchard sites to ensure pollen contamination is adequately dealt with in the planning stages.

The initial aim and the subject of the work completed over 2005–06 was a demonstration of these approaches at the Edward Bonner Tree Improvement Centre (EBTIC). This work was subdivided into two tasks: 1) to estimate pollen contamination in two black spruce (Sb) SOs at EBTIC, using long-term meteorological data to simulate multiple years of PC information and 2) to suggest strategies to reduce wild pollen influx and quantify reductions by the various strategies.

The first task involved deriving estimates of relative Sb pollen emissions from the surrounding area. Then, the dispersal model was run with 30 years of hourly meteorological data input from the nearest meteorological station in order to simulate 30 years worth of PC data. The provision of multiple years' worth of PC data allows calculation of averages as well as variability of PC over time. The assessment of variability was required in determining the probability of success of any anti-contamination method.

MODEL APPLICATION AND RESULTS

Worst-case (assuming no controls) PC was estimated to be 70–100% with averages of 80% in the two SOs at EBTIC, with individual PC values varying with location within the two SOs. More refined input data would likely allow less conservative predictions to be made.

The control methods assessed were: 1) the use of a buffer zone within the orchard, 2) isolation zones outside the orchard, 3) a windbreak-like vegetative barrier, and 4) pollination desynchronization between the natural stand and the SO. The control simulations were applied as conservatively low (in most cases) estimates of their effectiveness.

For the buffer zone control, the scenario modelled was one where no physical gap existed between natural stand trees and the SO, but where some width of the SO seed crop adjacent to the contaminating trees (CT) would constitute the buffer. For such a situation “probability of failure” (PoF) graphs can be examined and, with some prescribed critical PC threshold in mind, one can identify the distance at which that threshold occurs. A PoF must be prescribed because of annual variations in PC. An example is shown in Fig. 1. To illustrate, if 80% PC is considered acceptable and a 10% (≡ 0.1) chance of failure of the buffer is acceptable (failure 1 year out of 10, on average), then an approximate 135 m buffer width would be required. In other words, if a seed orchard manager were attempting to grow seed with less than 80% PC, then the manager would reject the seeds harvested within 135 m of the SO edge, but the SO manager should realize that this method will fail 1 year out of 10 on average. In this case, however, note that to have ~ 0% failure rate (on average) the manager would only need to increase the buffer zone width to ~150 m. This sensitivity to distance is caused by the steepness of the PoF curves for higher PC thresholds.

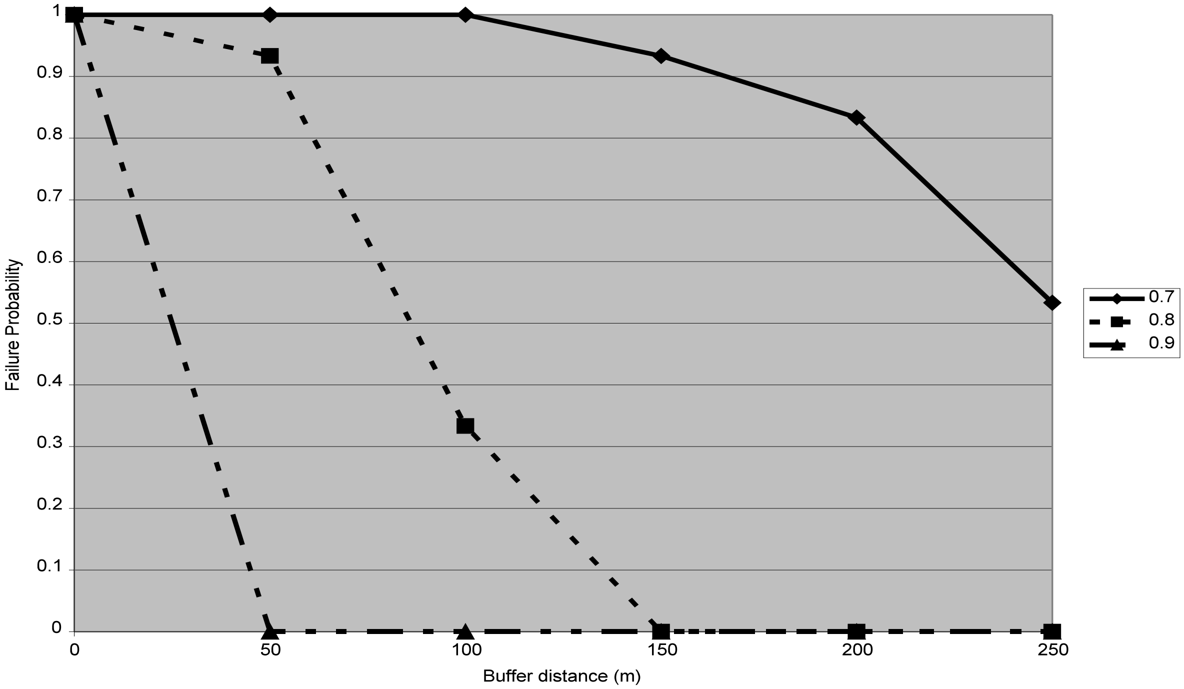

Figure 1. Variation in Probability of Failure within the SO with increasing distance downwind of the CT/SO edge and PC threshold. Results are shown for PC thresholds of 70% (0.7), 80% (0.8) and 90% (0.9).

As a further example, Fig. 2 shows the effect of temporal desynchronization. The 6-day difference causes a reduction in PC of approximately 50% across the SO. Imposition of desynchronization also causes greater variability in the annual PC values indicated by wider data ranges.

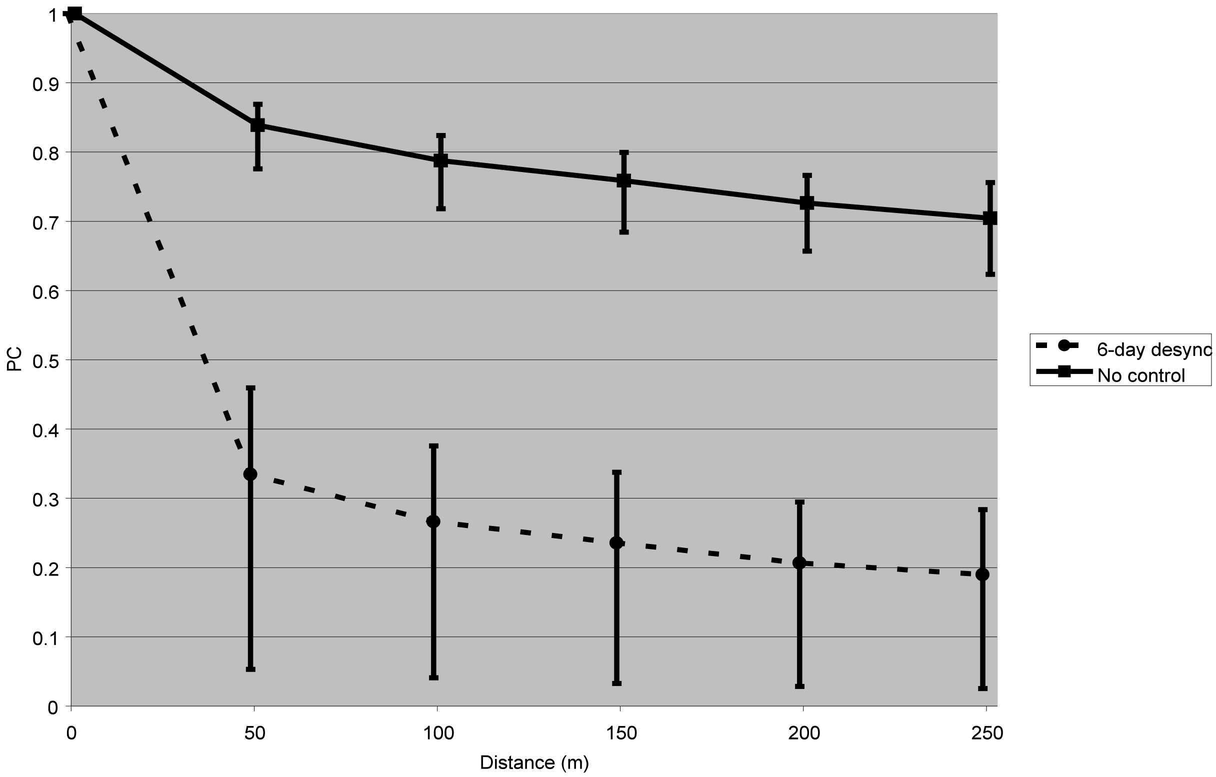

Figure 2. Comparative pollen contamination (PC) variation for a 6-day desynchronization scenario. Vertical bars indicate data extremes.

No attempt to combine control methods was attempted but it was thought that it may be useful to do so at certain seed orchards.

This work should be linked to seed quality standards defined for the forestry community. Control methods adopted will depend upon the degree of tolerance of PC allowable and the “risk” acceptable to the forestry community; a risk which was quantified in this work by examining pollen dispersion variability. Upper-limit (worst-case) PC values were estimated, but what constitutes “tolerable” must be linked to a forest industry objective to set seed quality standards similar to agricultural seed production.

NORTHEAST SEED MANAGEMENT ASSOCIATION (NeSMA)

Randy Ford, Chris Atack, Marya Laine and Sandra Gordon

Northeast Seed Management Association
P.O. Box 730
Englehart, ON
P0J 1H0
Email: nesma@ntl.sympatico.ca

The past years have seen the completion of the second-generation breeding program that was started in 2002. Sufficient seed from controlled crosses has been collected and processed that will allow for the establishment of the second-generation elite and infusion tests. In addition, strides have been made in the development of second-generation clonal orchards and archives. Management cycles, that will maximize potential seed collections, have been developed for all of the first-generation orchards. To date, the 13 seed orchards have produced over 230 million improved seed for NeSMA's forest company partners. In addition, biologically sound second-generation breeding zones have been created.

FIRST-GENERATION PROGRAMS

NeSMA actively manages eight black spruce (*Picea mariana*) and five jack pine (*Pinus banksiana*) seed orchards located throughout northeastern Ontario.

Cone crop management cycles have been developed for all first-generation orchards. The cone crop management cycle is similar to crop rotation in farming; it's a scheduling of flower induction, crown management, and cone collection geared towards optimizing seed yield over time. Other activities such as fertilizer application, pest management, and periodic thinning are incorporated to ensure seed yield targets are achieved. These were developed in response to the requirements of orchard field operations, management planning, and budgeting. Advantages of these management cycles include regular cone crops and a standardized framework of field activities for planning and budgeting. The cycle also lends itself to pest management with the removal of most of the mature cones in any given year. Cost efficiencies are realized by focusing on field activities that reduce geography within an orchard and the cycle satisfies the biological timeline for flower recovery in crown-managed trees.

Crown management (topping) and flower inductions were carried out at several orchards (as outlined by the management cycles). As well, general spring orchard nutrient applications were completed. Annual soil and foliar samples, collected in the fall and analyzed over the winter, determine which orchards require fertilizer.

A total of 151.57 hL of jack pine cones and 34.64 hL of black spruce cones were collected in 2005. Just over 28.3 million improved seed was distributed to NeSMA's forest company partners. A final roguing of the Edward Bonner black spruce Breeding Zone 2 (field 27) was completed in 2005. Selections for thinning were based on family breeding values; approximately 20% of the original trees now remain in the orchard.

Genetic gain estimates for all of the orchards have been completed or are in the process of being completed. These new genetic gain percentages will provide NeSMA's partners with better information to use in their forest modeling practices.

NeSMA is moving ahead with the development of a white pine (*Pinus strobus*) tree improvement program. Second-year seedlings, to establish 3 new tests (in addition to the 3 tests that were planted in 2001) were over-wintered and planted in the spring of 2006. Site preparation was completed during the summer of 2004 and 2005. The layout for one test was also completed in the fall of 2005.

SECOND-GENERATION PROGRAMS

Historically, tree improvement practices in the northeast have been based on first-generation breeding zones that were created in the early 1970's. These were largely defined by administrative boundaries with limited information on the adaptive variation of the target species (black spruce and jack pine). In recognition of the inefficiencies of the first-generation program breeding zones, two older genecology studies provided information to produce biologically sound second-generation breeding zones. This work was completed by Dr. Dennis Joyce in early 2004. These new zones will be more effective at addressing adaptability concerns (climate model vs. administrative boundaries). The new zones will also be more cost effective by increasing the land area supported by individual programs.

In 2004, six Elite and four Infusion population tests were established at various locations throughout northeastern Ontario. Seeds for the Elite tests came from controlled crosses made in 2002 and 2003. NeSMA's breeding program goal was to collect sufficient seed from 50 controlled crosses and 300 Infusion populations to establish three Elite and two Infusion tests for each of the four second-generation programs. With the exception of controlled cross cone collections scheduled for one jack pine program in 2006, all of the breeding work has now been completed. In the near future, NeSMA plans to begin test establishment for all of the remaining programs. In 2004–2005, irrigation and vegetation management was carried out at the 10 established test sites.

ONTARIO FOREST RESEARCH INSTITUTE: FOREST GENETICS AND TREE IMPROVEMENT 2004–2006

Pengxin Lu

Ontario Forest Research Institute
Ministry of Natural Resources
1235 Queen Street East
Sault Ste. Marie, ON
P6A 2E5
E-mail: pengxin.lu@mnr.gov.on.ca

BREEDING EASTERN WHITE PINE FOR BLISTER RUST RESISTANCE

Pengxin Lu, Robert W. Sinclair and Darren Derbowka

The breeding and screening of eastern white pine (*Pinus strobus* L.) and its interspecific hybrids for blister rust (caused by *Cronartium ribicola*) resistance continued to be a research focus at the Ontario Forest Research Institute. The objectives of this project were to: 1) study the inheritance of blister rust resistance in pure *Pinus strobus* and its interspecific hybrids with Eurasian white pine species, 2) develop white pine genotypes with strong resistance to *C. ribicola* that can be deployed in moderate to high blister rust hazard zones, and 3) test the selected white pine genotypes for adaptation, growth, and wood quality traits under varying climatic conditions.

Controlled crosses (CP) were made each year since 2003. A major breeding objective was to backcross the interspecific hybrids to eastern white pine with an expectation of enhancing climatic adaptation and growth performance while retaining resistance to *C. ribicola*. We have obtained a few B_2 backcrosses of interspecific hybrids between *P. strobus* and *P. wallichiana* (Himalayan blue pine) which averaged about 87.5% parentage from *P. strobus*. Seedlings of full-sib families are being artificially inoculated with *C. ribicola* and data will be used to validate some patterns of inheritance in *C. ribicola* resistance observed on open-pollinated (OP) families.

Six runs of artificial blister rust inoculation experiments have been carried out since 2001, involving more than 16 000 6- to 18-month-old seedlings from OP and CP families. Included in the last two inoculation experiments were also some pure *P. strobus* and *P. monticola* selections for *C. ribicola* resistance obtained from the USDA Forest Services. Post-inoculation seedling mortality was among the key criteria for blister rust resistance evaluation.

Five new field trials and two clone banks were established in central to northern Ontario in 2005 and 2006. These are to test the climatic adaptation and growth performance of the advanced generation white pine selections. Long-term field trials established across Ontario between the 1960s and 1980s showed that some interspecific hybrids between *P. strobus* and *P. wallichiana* outperformed pure *P. strobus* in southern Ontario with equivalent or greater wood specific gravity. Insufficient cold hardiness, however, was a deterrent for the pure *P. wallichiana* and the first-generation (F_1) interspecific hybrids to grow well on more northerly sites. Backcrossed interspecific hybrids to *P. strobus* gained considerable cold hardiness. We expect the advanced generation (e.g., B_1 and B_2) of backcrosses to adapt and grow well on more northerly sites.

Accelerated breeding is currently underway to create B_2 and B_3 generation backcrosses of interspecific hybrids between *P. strobus* and *P. wallichiana*. The B_3 backcrosses are expected, on average, to have about 94% parentage from *P. strobus*. This is feasible because early flower induction has been successful with eastern white pine with the application of $GA_{4/7}$ during the early part of the growing season.

WOOD DENSITY STUDY IN JACK PINE AND BLACK SPRUCE

Paul Charrette, Tony Zhang and Pengxin Lu

In collaboration with the Superior Woods Tree Improvement Association and Forintek Canada Corporation, genetic parameters between wood density and growth traits were investigated in jack pine (*Pinus banksiana* Lamb.) and black spruce (*Picea mariana* [Mill.] BSP) in northwest Ontario. Increment cores were collected from 2 field progeny trials for each species and wood quality attributes, including wood density, were measured in Forintek's laboratory using an x-ray densitometer. Preliminary results indicated that wood density is under moderately strong genetic control and is weakly and negatively correlated with growth traits, such as height, DBH, and volume in black spruce. Strong, negative genetic correlations between wood density and growth traits, however, exist in jack pine. Implications of wood density to selection in tree improvement vary, depending 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 serious 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 in both species, which had desirable candidates possessing both faster growth and high wood density.

PUBLICATIONS

Lu, P.; White, T.L. 2004. Determining test and block numbers in consideration of progeny testing quality and cost: an example of half-sib families with RCB design and single-tree plots. For. Gen. 11: 27–42.

Lu, P.; Sinclair, R.W.; Boult, T.J.; Blake, S.G. 2005. Seedling survival of *Pinus strobus* and its interspecific hybrids after artificial inoculation of *Cronartium ribicola*. For. Ecol. Manage. 214: 344–357.

Lu, P.; Colombo, S.L.; Sinclair, R.W. 2006. Cold hardiness of interspecific hybrids between *Pinus strobus* and *P. wallichiana* revealed by post-freezing needle electrolyte leakage. Tree Physiol. (in press)

Lu, P.; Sinclair, R.W. Survival, growth and wood specific gravity of interspecific hybrids of *Pinus strobus* and *P. wallichiana* grown in Ontario. For. Ecol. Manage. (submitted)

TREE SEED AND TREE IMPROVEMENT ACTIVITIES AT PETAWAWA, 2004–2006

Ben Wang and Steve D'Eon

Natural Resources Canada
Canadian Forest Service
Great Lakes Forestry Centre
Petawawa Research Forest
PO Box 2000
Chalk River, ON
K0J 1J0
E-mail: Ben.Wang@nrcan.gc.ca

APPLICATION OF PUBLISHED SEED GERMINATION RESULTS

Dormancy in white spruce (*Picea glauca*) seeds is known to vary with individual trees within a stand, between stands within the same crop year, between crop years, and between locations (Wang 1976). Dormancy in seed from various sources in Canada has always been effectively overcome by 21 days of moist chilling (cold stratification). However, several published reports suggested that a 14-day cold soaking treatment was as effective as 21 days of cold stratification in breaking seed dormancy of white spruce from Great Lakes sources. For curiosity, two white spruce seed lots from outside of the Great Lakes region were obtained from the National Tree Seed Centre (NTSC): 1996 seed crop from Lac Belisle, Québec and 2000 seed crop from Porcupine Mountain, Manitoba. Four replications of 50 seeds each were randomly drawn from each lot and treated with 14-day cold soak, 21-day moist chill, 18-week moist chill, and control. The germination test results are presented in Table 1.

Table 1. Germination of white spruce seed from two provenances following three durations of pre-treatment

		Germination % by pre-treatment			
Seed Source	Germinability (%) and year tested at NTSC	14-day soak	21-day chill	18-week chill	Control
Lac Belisle, QC.	76 (2000)	41	51	84	48
Porcupine Mt., MB.	94 (2003)	40	78	96	25

This test was carried out on a dry laboratory bench top with room temperature ranging from 22 to 29.7°C. The results clearly indicate that the 14-day cold-soak treatment had the same effect on both seed lots but it cannot replace the 21-day moist chilling treatment. From this test result, one has to be cautious in applying published findings in seed research where seed lot, crop years, and geographic locations are different. The difference in germination percentage between the 21-day and 18-week moist chill is due to the germination temperature because a longer period of moist chilling will reduce the seed's requirement for optimum temperature and light (20–30°C alternating with 8-hour light) for maximum germination (ISTA 1996).

PROGRESS ON THE INTRODUCTION OF CANADIAN TREE SPECIES TO NORTHEAST CHINA

Canadian tree species growing in Liaoning province (northeast China) show early promising results with very strong adaptability for survival and fast growth in height and diameter. For example, 4-year-old jack pine (*Pinus banksiana*) seedlings planted as 1+1 nursery bare-root stock reached an average height of 2.5–3.0 m. Eastern white pine (*Pinus strobus*) not only grows very well but also is currently free from any local disease or insect attacks. Eastern white pine cones in Ontario have to be cured for several months by a cold period in order to crystallize the resin before extracting the seeds. The first-generation cones in Liaoning are less resinous and they can be processed shortly after collection indicating an adaptation to the local climate.

EXTRA CURRICULAR ACTIVITIES

Ben was invited as a keynote speaker to the IUFRO International Seed Symposium held in Fredericton, NB to talk about “Highlights of my experience in tree seed research and development at Petawawa”. While there he chaired a session on informal discussion of emerging issues in seed science. He is currently compiling a handbook on subtropical tree seeds in Taiwan with Drs. C.T. Chien of the Taiwan Forestry Research Institute and T.P. Lin of the National Taiwan University.

SEED COLLECTION

It was a bumper seed crop year in 2006 for many tree species. To ensure the collection of seed of high genetic and physiological quality, it is best to follow the diversity principle by harvesting seeds only in good crop seed years. For this reason, were collected by Petawawa staff in order to establish a local seed bank for maintaining a 10-year seed inventory of major reforestation species. Individual tree collections for research were also made:

- White spruce: Douglas and Ottawa Valley.
- Eastern hemlock: Petawawa Research Forest and Deep River areas.
- Eastern white cedar: Petawawa Research Forest and Deep River areas.
- Tamarack: Petawawa Research Forest.

FIELD EXPERIMENTS

The 194G range-wide white spruce provenance test was measured in 2002 and the results published (Morgenstern et al. 2006). The 12 x 12-tree plots employed in this experiment allowed for the calculation of volume per ha at half rotation age and comparison with early results based upon individual tree heights. The 255-E-2 range-wide jack pine test was re-measured in 2005 and data forwarded to Lakehead University for inclusion in their work based upon the 255 experiment series (see abstract of voluntary paper by Thomson et al. in Part 2 of these Proceedings). All genetics experiments at the Sturgeon Lake plantation area were cleaned in the fall of 2005. Several spruce experiments at the Unit Creek plantation area were thinned and cleaned in the winter of 2005. A new test of 180 white pine progeny from northern Ontario sources was installed in the spring of 2006 in cooperation with Randy Ford’s group, Northeast Seed Management Association.

PUBLICATIONS

Morgenstern, K.; D’Eon, S.; Penner, M. 2006. White spruce growth to age 44 in a provenance test at the Petawawa Research Forest. For. Chron. 82(4): 572–577.

Simpson, J.D.; Wang, B.S.P.; Daigle, B.I. 2004. Long-term seed storage of various Canadian hardwoods and conifers. Seed Sci. Technol. 32(2): 561–572.

Wang, B.S.P.; Simpson, J.D. 2004. Factors affecting tree seed storage. Pages 3–15. *in* Proc. IUFRO Tree Seed Symp., Seed Physiol. Technol., Res. Grp. 2.09.00, 20–22 Sep. 2004, Nanjing, China.

Wang, B.S.P.; D’Eon, S.; Dong, J. 2006. Introduction of Canadian tree species to the Northeast of China. For. Chron. 82(2): 219-225.

Wang, B.S.P. 2007. Highlights of my experience in tree seed research and development at Petawawa. *in* Proc. IUFRO Tree Seed Symp., Seed Physiol. Technol., Res. Grp. 2.09.00, 18–22 July 2006, Fredericton, NB. (in press)

REFERENCES

ISTA. 1996. International rules for seed testing, 1996. Seed Sci. Technol. 24, suppl.

Wang, B.S.P. 1976. Dormancy and laboratory germination criteria of white spruce seed. Pages 179–188. *in* Proc. 2nd Int. Symp. Physiol. Seed Germ., Fuji, Japan, 1976.

MANITOBA'S TREE IMPROVEMENT PROGRAM

G. Falk[1], G. McGimpsey[1] and K. Broughton[2]

[1] Manitoba Conservation
Forestry Branch
Box 27 Group 8 R.R. 2
Dugald, MB
R0E 0K0
E-mail: GoFalk@gov.mb.ca

[2] LP Canada Ltd
Swan Valley Forest Resources
P.O. Box 998
Swan River, MB
R0L 1Z0

Keywords: jack pine, black spruce, white spruce, hybrid poplar

Manitoba Conservation – Forestry has established tree improvement programs in breeding zones across the province for the three main coniferous reforestation species: jack pine (*Pinus banksianna* Lamb.), white spruce (*Picea glauca* [Moench] Voss), and black spruce (*Picea mariana* [Mill.] BSP). Tree improvement work in many of these zones is accomplished through cost-sharing agreements with the three forest companies holding Forest Management Licences (FML's); Tolko Manitoba, Louisiana-Pacific Canada Ltd. (LP), and Tembec Forest Resources. This report will highlight the major activities completed in 2004/2005.

TOLKO MANITOBA – MANITOBA CONSERVATION CO-OPERATIVE PROGRAMS

Sixteen-year measurements of the four black spruce family tests in the Saskatchewan River Breeding Zone were completed in fall of 2005. The data were sent for analysis in 2006 and further roguing of the Prospector seed orchard is scheduled for the fall of 2006. Cone induction treatments using gibberellin injections were done in half the orchard in the spring of 2005. The clone bank for this zone was treated for a low level spruce beetle attack with an application of Prelude™ (2005) and removal of dead trees (2004 and 2005).

In the Nelson River Breeding Zone, the Axis Lake black spruce seedling seed orchard was rogued in 2004 based on ranking information from the 10-year measurements. The bottom 25% of families (4901 trees) were removed and then an additional 3322 trees were selectively rogued based on spacing, family rank, size, and condition.

Maintenance continued on the three black spruce family tests and one seedling seed orchard established in the Highrock Breeding Zone in 1997/98.

The white spruce clonal seed orchard and breeding garden in the Saskatchewan River Breeding Zone were maintained through fertilizing and mowing.

TEMBEC FOREST RESOURCES – MANITOBA CONSERVATION CO-OPERATIVE PROGRAM

Analysis of the 15-year family test measurements in the Lake Winnipeg East Breeding Zone was completed in 2005. The priority at the Brightstone Seed Orchard is to build up the seed supply for the zone. Further intensive roguing will be delayed until this is accomplished, although some roguing to improve spacing will be done in 2006. Cone collections were conducted at the seed orchard in 2004 (3.0 hL) and 2005 (2.9 hL) in conjunction with crown management. Cone induction treatments using gibberellin injections were conducted on trees from top-ranked families in selected reps in the spring of 2005. Conducting these treatments on only selected trees was found to be much more time-consuming than doing treatments on all the trees in a selected area. Selective cone induction treatments will likely only be used in the future for orchards in which seed supply is already being met and seed lots with increased gain are requested.

LP CANADA LTD. – MANITOBA CONSERVATION CO-OPERATIVE PROGRAMS

Maintenance, including mowing and application of Vantage™, continued in the black spruce family tests and seedling seed orchard that were established in the Mountain Breeding Zone in 2001.

In the Mountain White Spruce Breeding Zone, 15-year measurements were completed in four family tests in the fall of 2004. The data were analyzed in 2005 giving family ranking information for roguing and genetic gain estimates for various future roguing scenarios. The extent of roguing at the Birds Hill Clonal Seed Orchard will depend on seed requirements and ensuring a supply of improved seed is available for that zone. Cone induction treatments using gibberellin injections were done in the spring of 2005 at the Birds Hill Orchard on about half of the ramets for clones from the top 25% of families (based on 10-year data). Cones were collected from the orchard in the fall of 2004 (6.0 hL) and 2005 (1.5 hL). The clone bank for this zone was treated for spruce beetle attack with an application of Prelude™ (2005) and removal of dead trees (2004 and 2005).

MANITOBA CONSERVATION PROGRAMS

The Mantagao black spruce mass selection seed orchard (MSSO) in the Interlake Breeding Zone was rogued in the spring of 2004. The Lake St. George MSSO was rogued in 2005. Cone collections (2.1 hL) were conducted at these two orchards in the fall of 2004 in conjunction with a topping operation. Another cone collection (4.8 hL) was completed in 2005 in conjunction with roguing and topping.

Jack pine cone collections were conducted at the Interlake MSSO (17.0 hL in 2005), the Cranberry Portage MSSO (6.3 hL in 2005) in the Northern Breeding Zone, and the Hillside Pedigreed seed orchard (9.8 hL in 2004 and 15.0 hL in 2005) in the Eastern Breeding Zone.

A black spruce seed production area in the Southeast Breeding Zone produced 4.3 hL of cones in 2005.

The province cooperated with the Canadian Forest Service in the establishment and maintenance of hybrid poplar trials across southern Manitoba testing the performance of eleven clones.

The percentage of stock for provincial and industrial reforestation that originates from improved seed continues to increase. In 2007, it is expected that improved stock will outnumber unimproved for the first time (Fig 1).

The tree improvement GIS database continues to be updated with family test measurement, family ranking, and orchard roguing data. This allows for such things as the mapping of the locations of plus trees for top ranked families (See Fig 2).

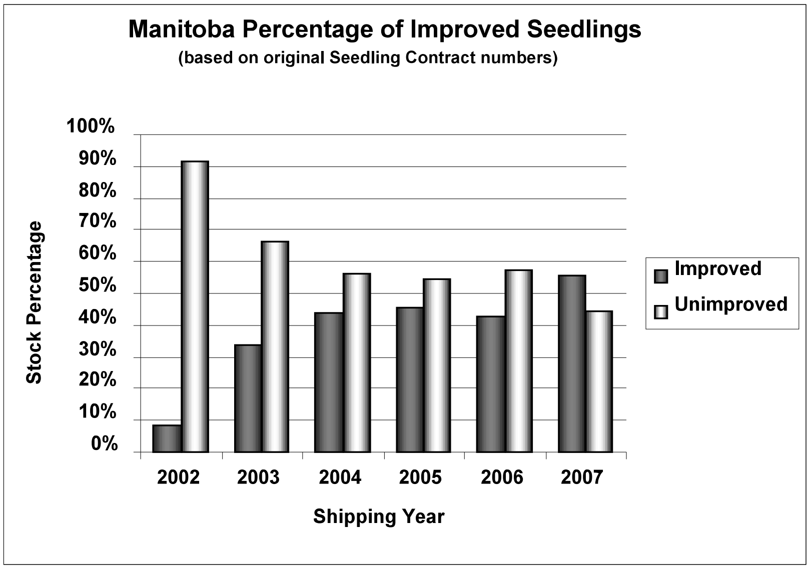

Figure 1. Proporton of improved and unimproved stock used for reforestation.

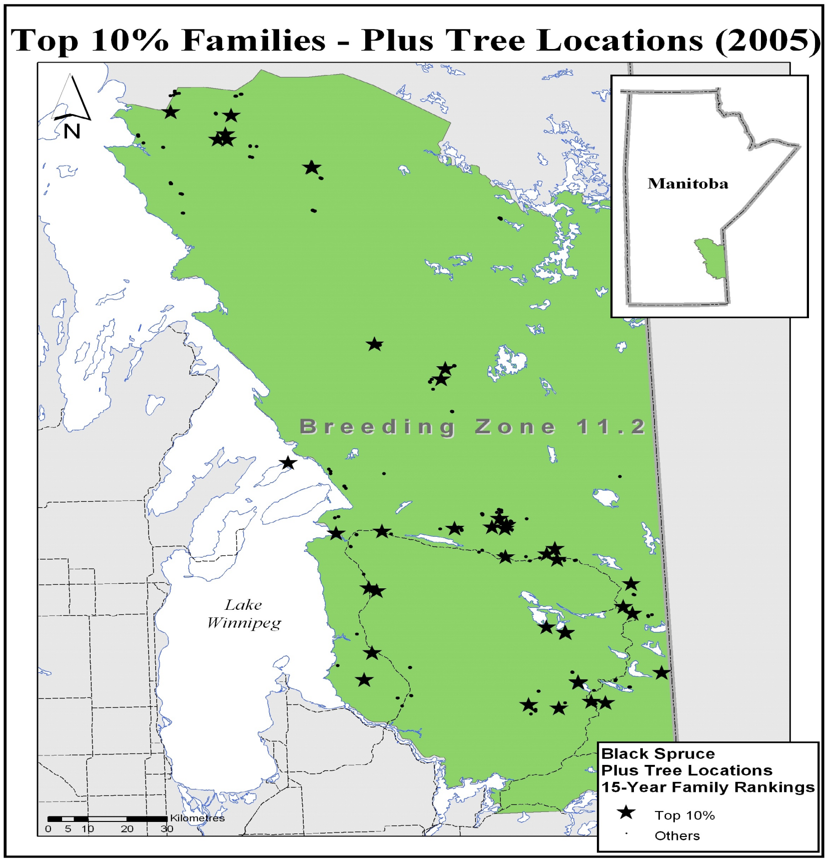

Figure 2. Location of the black spruce plus trees for the top 10% of families in the Lake Winnipeg East Breeding Zone.

AAFC-PFRA SHELTERBELT CENTRE – TREE IMPROVEMENT SUMMARY

Bill Schroeder, Dan Walker, Salim Silim and Don Reynard

Agriculture & Agri-Food Canada
PFRA Agroforestry Division
Indian Head, SK
SOG 2K0
E-mail: schroederb@agr.gc.ca

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

The AAFC-PFRA Agroforestry Division (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. These projects increase our knowledge on the adaptability of tree and shrub populations to prairie growing conditions and provide genetic material for selection and breeding. Genetically improved trees and shrubs enhance the value and function of agroforestry systems by providing woody plants that have increased survival, higher biomass accumulation, and higher economic value. New initiatives include a *Salix* improvement program and a range-wide collection of *Populus balsamifera*. The Division also continued to be active in development of hybrid poplar and maintains germplasm collections of prairie woody plant genera. Improved trees and shrubs developed in the program are used for shelterbelts, wildlife habitat planting, riparian buffers, phyto-remediation, and afforestation. From 2004 to 2006, the tree improvement program focussed on *Populus* and *Salix* genera as well as genetic resource collections.

Larix IMPROVEMENT

Seed representing four species *Larix sukaczewii* Dyl, *L. sibirica* Ledeb., *L. cajanderi* Mayr., and *L. gmelinii* Rupr. was obtained from the Swedish University of Agriculture Sciences. This seed originated from collections from individual *Larix* trees distributed over 16 regions and 45 stands in Russia. This collection represents a very wide genetic and geographic distribution of *Larix*. The Agroforestry Division was selected as the Canadian participant in the project. The objectives of this project are to evaluate the adaptability of exotic *Larix* seed populations to prairie growing conditions, study genotype x environment interactions of the *Larix* species, and to provide genetic material for future selection and breeding.

Populus IMPROVEMENT AND CONSERVATION

Populus Breeding

The poplar breeding program has involved controlled-pollinations using *Populus deltoides* Marsh. var. *occidentalis* Rydb., *P. balsamifera* L., *P. maximowiczii* A. Henry, *P. nigra* L., *P. laurifolia* Ledeb., *P.* x *petrowskyana* Schneid, and *P. deltoides* x *P.* x *petrowskyana* as the mother trees. Pollen sources included *P. deltoides* var. *occidentalis*, *P. nigra*, *P. maximowiczii*, *P. balsamifera*, *P. maximowiczii*, *P. laurifolia*, *P.* x *petrowskyana*, and *P. tristis* Fisch..

Seedlings from the controlled crosses have been planted in nursery trials at Indian Head. The individual families and genotypes are being screened using several criteria. Regardless of end use we are primarily concerned with biomass gain. *Populus* biomass is a function of many internal plant processes and their interaction with the environment. However, we are most interested in traits with high heritability and strong correlation with biomass accumulation that can be easily and efficiently scored early on during growth. Tree stem height and basal diameter have been strongly correlated with biomass as has leaf area. In the prairie region, water use efficiency (WUE) is linked to tree growth. We indirectly estimate WUE through carbon isotope discrimination. Therefore, initial screening of trees is based on tree height, basal diameter, leaf area, and carbon isotope discrimination.

Beginning in year two, following breeding, individual ortets are selected from within each family represented in the nursery trials. For each selected individual, multiple ramets are propagated for field trials. The field trials include riparian buffers and plantations. Of primary importance is evaluation of clones using traits that are most influential on tree architecture, biomass accumulation (stem height, diameter, number of stems, and number of sylleptic branches) as well as adaptation (cold and drought tolerance), and pest resistance. In addition, we will continue to evaluate leaf traits such as leaf area and number of leaves on the dominant stem as well as WUE. Other traits under consideration are listed in Table 1.

Table 1. Traits appropriate for poplar selection for the Canadian prairies

Biomass Accumulation	Maximum tree height
	Individual leaf area
	Diameter
	Whole-tree biomass
Tree Architecture	Number of sylleptic branches
	Crown and stem form
Adaptation	Vulnerability to low temperate damage
	Water use efficiency
	Nutrient Use efficiency
Pest	*Melamspora medusae* Thuem. rust assessment
	Septoria musiva Peck canker and leaf spot
	Herbivore damage

A summary of the plant pedigrees, successful crossing combinations (families), and subsequent individual genetic lines from the breeding program is presented in Table 2. The overall breeding success has averaged 53%. The program has generated 93 families and a gene pool of over 15 000 pedigree lines (genotypes).

Ex Situ Conservation of *P. balsamifera*

The distribution of *P. balsamifera* throughout its Canadian range has been determined as accurately as possible and populations that are physically isolated from the contiguous range have been identified. The project has chosen *P. balsamifera* to study the distribution of genetic diversity within its natural Canadian range. A set of predictions regarding the genetic diversity from close to the centre of the species range outward to the fringes, including isolated populations, is being tested by collecting and analyzing vegetative samples from selected populations.

Our primary purpose is to obtain a genetically representative sample of balsam poplar germplasm over a wide geographic region for climate change research and *ex situ* conservation. For this reason phenotypic selection during sampling is not important. The intent is to sample the geographic range of the species. We have sampled 37 populations from different ecoregions across the native range. Within each population 15 individual non-related trees were sampled. To minimize the possibility of sampling related individuals a reasonable distance (100 – 200 meters) between sample trees was maintained. Sample trees were of various ages including young trees. Because the objective is to obtain a genetically representative sample, tree selection was not biased by phenotypic selection. A minimum of 30 hardwood cuttings per tree are collected from each sample tree. *Ex situ* conservation can be achieved using many different methods. We have chosen to preserve the assembled genebank in two common gardens. Each common garden includes 15 individuals from each population with three, two ramet replications for each individual tree collected. This network of trials will provide valuable information on growth potential, disease resistance, and suitability of hybrid poplar clones in Alberta and Saskatchewan. The trials have also been designed to provide estimations of growth and yield.

Table 2. Number of families and progenies produced in AAFC-PFRA breeding program

Pedigree	No. Families	No. Plants
P. deltoides x *P. balsamifera*	26	6550
P. deltoides x *P. maximowiczii*	11	1300
P. deltoides x *P.* x petrowskyana	3	100
P. deltoides x *P. laurifolia*	2	150
P. deltoides x *P. tristis*	3	600
(P. deltoides x *P. x petrowskyana)* x *P. balsamifera*	14	1600
(P. deltoides x *P. x petrowskyana)* x *P. maximowiczii*	8	1700
(P. deltoides x *P. x petrowskyana)* x *P. deltoides*	7	800
(P. deltoides x *P. x petrowskyana)* x *P. laurifolia*	2	200
(P. deltoides x *P. x petrowskyana)* x *P. tristis*	2	400
(P. deltoides x *P. x petrowskyana)* x *P. nigra*	3	400
P. balsamifera x *P. maximowiczii*	8	700
P. balsamifera x *P. laurifolia*	1	150
P. balsamifera x *P. tristis*	1	100
P. maximowiczii x *P.* x *petrowskyana*	2	100
Total	93	15 000

Clone Tests

One of the major areas of research being undertaken at the Division is testing hybrid *Populus* clones. At this time over 300 clones are being tested at 40 locations across the prairie provinces. 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.

Since 2000, poplar clone trials have been established at eight sites in Alberta and Saskatchewan. All trials are arranged in randomized complete block designs with four to five replications. Plot size ranges from five to 49 trees depending on the number of clones in the trial. Preliminary results show significant differences in performance between clones and sites. Although it is early to make definitive recommendations, several clones appear to be well adapted over a wide range of growing conditions. The Walker x petrowskyana hybrid, WP-69-86, was among the top clones at all sites. In addition, this clone has performed well at Indian Head where it has consistently shown superior hardiness and growth in shelterbelt trials under varying growing conditions.

Salix IMPROVEMENT

Salix is an important genera for agroforestry systems, particularly in riparian zones. Very little is known about the genetic variation of productivity-related traits of Canada's native *Salix* populations across their geographic range. In collaboration with the Canadian Forest Service, Fredericton, New Brunswick and Institut de recherche en biologie in Montreal a *Salix* improvement project for biomass production has been initiated. The main project activities are: 1) surveys for locations of natural populations of native *Salix* species with potential for use in riparian buffers and for biomass production, 2) collection and propagation of stem cuttings from selected individuals, 3) establishment of field tests to assess population genetic variation in growth-related traits, and 4) selecting superior clones for distribution and further testing and use in agroforestry plantings. The project was initiated in 2005 with collection and propagation of *Salix eriocephala* Michx. and *S. discolor* Muhl. from natural habitats in eastern Canada and continued in 2006 with collection and propagation of Saskatchewan *S. eriocephala* and *S. discolor* populations. The main deliverables at the end of the project will be an understanding of population genetic variation and structure for growth-related traits across *Salix* populations and geographic areas and selection of superior clones for next round of testing and breeding through a controlled crossing regime. We have assembled 90 clones representing 24 populations of *S. discolor* and 127 clones representing 23 populations of *S.*

eriocephala. These collections have been planted in common gardens at Indian Head and Saskatoon, Saskatchewan.

GENETIC RESOURCE COLLECTIONS

The Division is involved in conservation of woody genetic resources used in agroforestry. This includes sampling native populations and establishment of common gardens. These collections facilitate access to genetic resources for breeding and the study of genetic diversity. The collections provide for *ex situ* conservation of native woody plant populations which supports Agriculture and Agri-Food Canada's actions in biodiversity. The gene pool of collections is conserved in common gardens or gene banks established within the native range of the species. Garden design varies depending on species and site. The purposes of the gardens are to conserve the collection, provide data on adaptation and performance of the collection, and to provide genetic material for genomic studies. The vegetative collections include 756 populations and 24 500 individual genotypes of the following species: *Prunus virginiana* L. var. *melanocarpa* (A. Nels.) Sarg., *Cretaegus rotundifolia* Moench, *Shepherdia argentea* Nutt., *Symphoricarpos occidentalis* Hook., *Rosa woodsii* Lindl., *Quercus macrocarpa* Michx., *Fraxinus pennsylvanica* Marsh. var. *subintegerrima*, *P. deltoides* var. *occidentalis*, *P. balsamifera, Prunus nigra* Ait., and *Prunus americana* Marsh.

EVALUATION OF LONG TERM GENETIC TESTS

During the past 25 years over 200 genetic tests have been established in the prairie region. Genera included in the tests are *Pinus*, *Larix*, *Quercus*, *Populus*, *Salix*, *Prunus*, *Hippophae*, *Celtis*, *Symphoricarpus*, *Rosa*, *Shepherdia*, and *Fraxinus*. These tests are evaluated every five years for survival, growth, adaptability, and pest resistance. From 2004–2006 a total of 15 tests were evaluated. Information from the tests describes genetic variability within genera, is used to recommend new species, and/or to provide data to support release of new clones or seed strains.

WESTERN BOREAL ASPEN CORP. PROGRESS TO 2006

Jean Brouard, Lee Charleson, Tim Gylander, Peter Nicholson
Florance Niemi, Fred Radersma and Wil Sheidegger

Western Boreal Aspen Corp.
11420 -142 Street
Edmonton, AB
T5M 1V1
E-mail: wbac@telusplanet.net

The Western Boreal Aspen Corporation (WBAC) is an aspen and poplar genetics cooperative with four industrial members: Ainsworth Engineered Canada LP, Daishowa Marubeni International (DMI), Footner Forest Products, and Weyerhaeuser Company Ltd. Collectively, these four companies harvest 4.5 million cubic meters of hardwood (approximately 90% aspen : 10% balsam poplar) to supply three OSB mills and one pulp mill (DMI) in Alberta. WBAC has been working since 1992 to develop genetically improved aspen and support research towards achieving successful deployment to support the members' fiber needs. As a secondary focus, the corporation is also addressing poplar tree improvement. Significant achievements to date in pure species and hybrid tree improvement and applied silviculture are listed below.

NATIVE ASPEN AND BALSAM POPLAR TREE IMPROVEMENT

A seed-based provenance trial was established on five sites (one British Columbia, three Alberta, and one Saskatchewan). This is providing valuable information on adaptation and growth in native aspen. This work is being extended through provenance analysis of clone screening trials and the testing of non-local sources from Eastern Canada and the USA.

First-generation breeding of aspen (*Populus tremuloides)* was completed in 2004 and progeny tests are being established in 2005–07. A total of 224 controlled crosses was made in two breeding regions. The first two seedling based progeny tests with full-sib family structure were established in 2005; a further six progeny tests will be established with clonal replication.

Controlled pollination of balsam poplar (*P. balsamifera*), using the cut branch technique, was initiated in the winter of 2004–05 as part of an Alberta Forestry Research Institute (AFRI)-funded hybrid balsam poplar breeding project.

The goal for both of these native species breeding programs is to investigate the patterns of between-family and within-family genetic variation. Clonal replication allows for more precise genetic ranking. The genetic tests allow for the ranking of families, forward selection of outstanding clones, estimation of genetic parameters for optimizing selection, and the creation of the next generation for breeding, testing, and selection.

Clone testing of wild aspen selections continues. In the first phase, WBAC has made 1,088 selections of which 353 are in multi-location clone trials on a total of 13 sites. WBAC plans to test 300 wild selections from each of two breeding regions; future candidates for clonal screening will be sourced from controlled crosses in the breeding program.

WBAC members have begun assembling wild balsam poplar collections for multi-location clone screening trials.

HYBRID ASPEN AND HYBRID POPLAR BREEDING AND CLONE TESTING

Aspen Hybrids

A first cycle of aspen hybrids has completed four growing seasons in field trials. Some of the tested trees are achieving over 1 m in height increment per year. (This is about ten times the average height increment of white or black spruce of a similar age tested in Alberta). A second cycle of hybridization has begun with funding from AFRI. In all cases WBAC is using one locally adapted parent (usually female) crossed with exotic aspens such as *P. alba, P. grandidentata, P. canescens, P. tremula,* and *P. tremula* var. *davidiana.* Thus far, 85 new hybrid crosses have been made in 2006, with each cross generating up to 110 clones.

Balsam Poplar Hybrids

WBAC initiated a balsam poplar hybridization program in 2004 with funding assistance from AFRI. This will generate hybrids between local *P. balsamifera* and North American (*P. deltoides*) and Asian (*P. ussuriensis* and *P. simonii)* poplars.

Table 1. WBAC's long-term breeding

Year	Funding agency	No. crosses	Type	Parents
2006	AFRI	64	hybrid Aspen	*P. tremuloides, P. davidiana , P. tremula*
		21	hybrid Aspen	*P. tremuloides, P. davidiana , P. tremula*
		35	hybrid Poplar	*P. balsamifera P. deltoides, P. ussuriensis, P. simonii*
2005	AFRI	21	native Poplar	*P. balsamifera*
2004	WBAC	125	native Aspen	*P. tremuloides*
2003	WBAC	99	native Aspen	*P. tremuloides*
			hybrid Aspen	*P. tremuloides, P. alba, P. grandidentata, P. tremula*
2002	WBAC	187	hybrid Aspen	*P. tremuloides, P. alba, P. davidiana, P. tremula, P. canescens*
2001	WBAC	160	hybrid Aspen	*P. tremuloides, P. davidiana, P. tremula, P. canescens, P. alba x grandidentata*
2000	WBAC	71	native Aspen	*P. tremuloides*
1999	WBAC	53	native Aspen	*P. tremuloides*
			hybrid Aspen	*P. tremuloides, P. davidiana, P. tremula*
1998	WBAC	119	hybrid Aspen	*P. tremuloides, P. davidiana, P. tremula*

APPLIED SILVICULTURE

WBAC has conducted a wide variety of silviculture trials covering stock type, planting density, site preparation and timing of plantation, fertilizers, vegetation control, disease issues, browse control, flower induction, and plant vegetative propagation. Our research in rootling propagation has demonstrated the advantage of using juvenile root segments for economical and effective multiplication of selected clones (Niemi et al. 2003, Brouard et al. 2006). WBAC sponsored a graduate student to work on the physiology of early growth in aspen seedlings at the University of Alberta. Collaboration with the University of Alberta continues in this subject area.

PUBLICATIONS

Brouard, J.S.; Niemi, F.; Charleson, L.R. 2006. The effect of root segment origin, size and orientation in aspen rootling propagation. Pages 80–91. *In* Proc. 28th South. For. Tree Imp. Conf., Raleigh, NC, 21–23 June 2005. www.ncsu.edu/feop/sftic/proceedings.html

Niemi, F.; Charleson, L.R.; Brouard, J.S.; Hoyem, J. 2003. An effective, efficient, and economical method of mass propagation for aspen (*Populus tremuloides*). (Abstract) Page 81. *In* Proc. West. For. Gen. Assoc., Genomics and Adaptation, Whistler, BC, 28–31 July 2003.

POPULATION RESPONSE TO CLIMATIC TRANSFER AND FOREST PRODUCTIVITY IN THE CHANGING CLIMATE IN ALBERTA

D.M. Rweyongeza and R-C. Yang

Department of Agricultural
Food & Nutritional Science
University of Alberta
Edmonton, AB
T6G 2P5
Email: drweyong@ualberta.ca

Keywords: climate change, moisture index, height growth, survival, black spruce, white spruce, lodgepole pine, jack pine, tamarack

In cooperation with the Alberta Tree Improvement and Seed Centre (ATISC), we are studying the genetic variability of the main Alberta conifers, which include white spruce (*Picea glauca* [Moench.] Voss), black spruce (*Picea mariana* [Mill] BSP), tamarack (*Larix laricina* [Du Roi] K. Koch), lodgpole (*Pinus contorta* Dougl), and jack pine (*Pinus banksiana* Lamb.) as well as the responses of these species and their populations to climatic transfer and how productivity of these species could be affected by climate change. These studies are based on 31 ATISC field provenance trials: white spruce (8), black spruce (7), tamarack (7) and, lodgepole pine, jack pine and their natural hybrids (9), which contain a total of 132 Alberta populations.

Using height and survival as response variables, 1961–1990 site climate (Alberta Environment 2005) and a second degree polynomial regression, we have found that mean annual temperature (MAT), mean temperature for the coldest month (MTCM), growing degree days > 5°C (GDD), mean annual precipitation (MAP), and annual moisture index (AMI) are the main climate variables affecting survival and growth of conifers when transferred across sites in Alberta. AMI is expressed as GDD ÷ MAP, where high values indicate high heat units relative to moisture (potential drought), and low values indicate low heat units relative to moisture which is characteristic of regions with short growing seasons. For example, in white spruce, AMI response functions of individual populations had average r^2 of 0.71 (0.40–0.93) and 0.61 (0.23–0.87) for 24-year height (H24) and survival (S24), respectively. In lodgepole pine, jack pine, and hybrid populations, AMI response functions for 15-year height (H15) had average r^2 of 0.58 (0.41–0.78), 0.71 (0.59–0.79) and 0.62 (0.46–0.79), respectively. Survival (S15) of these species responded more to MAT and MTCM (average r^2 > 0.75) than to AMI. Tamarack had the greatest response to GDD where the population response functions had average r^2 of 0.78 (0.63–0.93) and 0.93 (0.86–0.98) for H15 and S15, respectively. For black spruce, H15 responded the greatest to MAT with average r^2 of 0.47 (0.29–0.69). However, black spruce response functions were linear and could not be used for extrapolation. Survival response functions for black spruce were very weak.

It is predicted that by the end of this century, MAT and MTCM in Alberta could, respectively, rise by 5°C and 5.6°C over the 1961–1990 temperature levels. During the same period, GDD, MAP, and AMI could increase by 69.2, 13.5, and 48.1%, respectively (Anon. 2004, Alberta Environment 2005,Barrow and Yu 2005). This shows that, in a changing climate, winters would become warmer, whereas summers could become increasingly drier. Therefore, Alberta Sustainable Resource Development (ASRD) has identified drought due to a disproportional increase in GDD and MAP (high moisture index) as the greatest potential cause of mortality and low annual growth in both young and old conifer forest stands in the future. As a result, AMI is currently being used to predict potential change in survival and growth for different regions of Alberta. For example, H15 of lodgepole pine, jack pine, and hybrids trees planted and grown in the AMI climate predicted for 2030 could attain only up to 40% of their achieved height in the 1961–1990 climate in central Alberta. In northern Alberta where summer drought already exists, it could be nearly impossible to attain natural regeneration and meaningful growth. On the contrary, in the Upper Foothills and Rocky Mountains region, growth could increase by up to 55%. In central and northern Alberta, white spruce could suffer larger declines in H24 (58.1–100%) and S24 (34.2–88.5%) than the pines. However, in the Upper Foothills and Rocky Mountains, increases in S24 (> 27%) and H24 (> 58%) could be expected for trees planted and growing in the AMI climate of the 2030s.

There are considerable uncertainties in predicting future climate (Burrow and Yu 2005) and many GCM models agree on temperature predictions but differ greatly in predicting future precipitation trends and the associated moisture loss by evaporation and transpiration (Loehle and LeBranc 1996). Therefore, the projected future survival and growth of Alberta conifers are only considered approximations within the assumptions of the Alberta Climate Model (Anon. 2004). Nevertheless, these predictions show that climate change could have serious impacts on survival and growth of Alberta forests and therefore a strategy is needed to cope with climate change.

PUBLICATIONS AND REFERENCES

Alberta Environment. 2005. Alberta Climate Model (ACM) to provide climate estimates (1961–1990) for any location in Alberta from its geographic coordinates. Alberta Environ., Edmonton, AB, Publ. No. T/749, 33 p.

Anonymous. 2004. Using the Alberta Climate Prediction Model and Global Climate Models to estimate future climates of Alberta. Unpubl. Rep., Alberta Environ. Sustain. Res. Devel., Edmonton, AB, 26 p.

Barrow, E.; Yu, G. 2005. Climate scenarios for Alberta. A report prepared for the Prairie Adaptation Research Collaborative (PARC) in co-operation with Alberta Environment. Available at: http://spatial.parc.uregina.ca/parc/www/research_pub_scenarios.htm

Loehle, C.; LeBranc, D. 1996. Model-based assessment of climate change effect on forests: a critical review. Ecol. Model. 90: 1–31.

Rweyongeza, D M. 2005. Geographic variation for height and diameter among black spruce (*Picea mariana*) provenances in Alberta. Meet. West. For. Gen. Assoc., July 2005, Corvallis, OR.

Rweyongeza, D.M.; Barnhardt, L.K. 2005. Provenance research results from Alberta trials and preliminary inferences regarding climate change impacts. Meet. Alberta For. Gen. Res. Council, April 2005, Edmonton, AB.

Rweyongeza, D.M.; Yeh, F.C.; Dhir, N.K. 2005. Heritability and correlations for biomass production and allocation in white spruce seedlings. Silvae Genet. 54: 228–235.

GENETICS AND TREE IMPROVEMENT PROGRAM, 2004–2006 ALBERTA SUSTAINABLE RESOURCE DEVELOPMENT

C.R. Hansen[1], N.K. Dhir[1], L. Barnhardt[1], J. Quinn[1], D. Rweyongeza[2], D. Palamarek[1], C. Andriuk[1], N. Antoniuk[1], T. DeCosta[1] and M.A. Mochulski[1]

[1] Alberta Tree Improvement and Seed Centre
Alberta Sustainable Resource Development
Smoky Lake, AB
T0A 3C0
E-mail: christine.hanson@gov.ab.ca

[2] Department of Agriculture
Food and Nutritional Science
University of Alberta
Edmonton, AB
T6G 2P5

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

This report summarizes the progress of the Forestry Division's genetics and tree improvement program for the period 2004–2006. 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, and British Columbia Ministry of Forests and Range (BC MoFR).

PROGRAM DEVELOPMENT

The Forest Genetics Alberta Association (FGAA) commenced operations in 2005. The objectives of the FGAA include cooperative development, management, and operation of selected projects involving the Alberta Tree Improvement and Seed Centre (ATISC) and industry. The Alberta Forest Genetic Resources Council continued its work. The council had several major initiatives during the report period: 1) development of a communications strategy, 2) forest genetics research gap analysis, 3) review of the climate change and genetic resources management issue and workshop, and 4) Post-harvest Stand Development conference organized in collaboration with the Foothills Growth and Yield Association and the Foothills Model Forest.

GENETIC IMPROVEMENT

Assembly of Breeding Stock

Superior parent tree selections, made as part of Sustainable Resource Development (SRD)/Industry cooperative breeding projects, included 10 lodgepole pine (*Pinus contorta* var. *latifolia* Engelm.) for Breeding Region J (Clear Hills outlier foothills) and 13 white spruce (*Picea glauca* [Moench] Voss) for Breeding Region E1 (northeast boreal lowland). Twelve forward selections from the Breeding Region E (northeast boreal lowland) white spruce progeny trials were completed based on 11-year height measurements. These selections will be incorporated into the Region E and E1 seed orchards.

Companies participating in these projects are Northland Forest Products Ltd. and Tolko Industries Ltd. (High Level Lumber Division).

Genetic Testing

In 2004, three progeny trials for white spruce Breeding Region G2 (northwestern outlier foothills) were assessed for survival and height at four years from seed. A total of 124 families are in the tests including 63 from Region G2, 37 from the interior spruce program in British Columbia, and 24 from adjacent white spruce breeding regions and associated progeny trials.

Fifteen-year assessments were completed on two Douglas-fir (*Pseudotsuga menziesii* [Mirb.] Franco) progeny trials in 2004. The trials consist of ten families from the Porcupine Hills in the southern montane region. The main objective of the tests was to develop an understanding of family variation in growth and yield, climatic hardiness, and disease resistance in Alberta interior Douglas-fir. Survival, height, and plant damage condition were assessed.

In 2005, three progeny trials for lodgepole pine Breeding Region J (Clear Hills outlier foothills) were assessed at six years from seed. Ninety-seven families are represented in the tests including 25 from Breeding Region J, 43 from the adjacent foothills region in British Columbia, and 29 from other Alberta lodgepole pine breeding regions and the Saddle Hills. Survival, height, vigor, and western gall rust infection were assessed. Individual and family mean heritabilities for six-year height were 0.24 and 0.67, respectively, and the family x site interaction was not significant.

Two Breeding Region K1 (southern upper foothills) lodgepole pine progeny trials were partially assessed in 2005 at nine years from seed. Survival, height, and vigor were assessed on bulk provenance seedlots and on the top three families for height (out of 102 families planted in the test) to get additional data in order to confirm the exceptional height superiority shown by one provenance (Clearwater) at age six. The growth superiority of the Clearwater provenance was maintained and, in ranking it against the families, it was similar to the top three percent. Analysis of the six-year measurements was also completed. Individual tree and family mean heritabilities for six-year height were 0.21 and 0.62, respectively. The family x site interaction was significant and the interaction variance was 30.5% of the family variance. The type B genetic correlation for six-year height between the two sites was 0.77.

A white spruce progeny trial for Breeding Region G1 (northern lower foothills) was assessed at 21 years from seed in 2005. Survival, plant vigor, height, dbh, and white pine weevil incidence were assessed on the 69 families represented in this test.

Seed Orchards

The Breeding Region D1 (Slave Lake area boreal) white spruce seedling orchard was rogued for the third time in 2005 based on 21-year progeny trial measurements. Established in 1982–83, the orchard was originally comprised of 3450 trees representing 150 families. By 2005, it had been rogued to 989 trees, representing 89 families. For the third roguing, families were ranked by breeding value for 21-year height and were rogued proportionately according to rank. Secondary consideration was given to white pine weevil (*Pissodes strobi*) resistance in the decision to rogue or retain a family. The main purpose of the roguing was to reduce seed tree numbers considering the surplus of seed from this orchard, but also to achieve some additional genetic gain while maintaining genetic diversity levels. A total of 337 trees (34%) were removed for the third roguing, leaving 652 trees representing 82 families.

The Breeding Region E (northeast boreal lowland) white spruce clonal seed orchard, established in 1989, was rogued for the first time in 2005 based on 11-year progeny trial results. Because families currently in test represent only about 55% of the parents in the orchard, roguing was limited to 7 clones with the lowest breeding values for 11-year height and 2 clones with the highest incidence of white pine weevil attack. In total, 153 trees (13%) were removed from the orchard leaving 1009 trees representing 92 parents. Grafting to increase numbers of high breeding value clones in the orchard commenced in 2005.

In 2005, 200 grafts were planted in the Breeding Region H (northwest boreal lowland) white spruce clonal orchard. Forty percent of the trees in the orchard, originally established in 1989, were killed by wildfire in 2002. The fire, although devastating, presented the opportunity to replant based on 11-year progeny trial results. Families were ranked according to 11-year height and clones were re-established in the orchard proportionate to rank. As of 2005, 724 ramets representing 67 clones are established in the orchard.

Seed production over the report period from the five white spruce orchards located at ATISC was just over 3 kg. Orchards are still recovering from the bumper crop of 2003 when a total of 447 kg of seed was produced.

PROVENANCE RESEARCH

In cooperation with the BC MoFR, Kalamalka Forestry Centre, a series of Siberian stone pine (*Pinus sibirica* Du Tour) provenance tests was established in 2005. Seed is from seven provenances, representing the northern, middle, and southern Siberian taiga. Provenances are represented by up to five stands and ten single-tree collections were made within each stand for a total of 310 single-tree seedlots. The material is tested on four sites: two in British Columbia and two in Alberta. The objectives of the study are to assess the feasibility of introducing Siberian stone pine as a reforestation species in Alberta, to collect information on survival, growth, pest resistance/susceptibility and adaptation of seed sources, and to identify promising seed sources.

Also in cooperation with the Kalamalka Forestry Centre, two Spruce Genecology-Climate Change field trials were planted in Alberta in 2005. These trials are part of a series of sixteen trials established primarily in BC. A total of 128 seedlots are in the tests including seed orchard seedlots from BC, Alberta, and Ontario and wild stand seedlots from BC, Alberta, Northwest Territories, Yukon, and the western United States. Species included are white and Engelmann spruce (*Picea engelmannii* Parry) and their hybrids.

Statistical and genetic analyses were carried out on 15-year measurements of tamarack (*Larix laricina* [Du Roi] K. Koch) provenance trials from seven sites. Significant ($P \leq 0.05$) differences were found for 15-year survival (S15) at two sites, and for height (H15) and diameter at breast height (D15) at three sites. On the latter sites, variation among populations was 6.2–20.3% of the total variance for H15 and 5.3%–17.8% of the total variance for D15. Regression analysis showed that height growth was significantly related to latitude and elevation of seed source ($r^2 = 0.41 – 0.76$). Across sites, the variance among populations was 5.1% and 2.7% of the total variance for H15 and D15, respectively. In addition, height and diameter showed significant population × site interaction; the population × site variance was 45.3% and 138.2% of the population variance for H15 and D15, respectively.

Analysis of 15-year survival (S15) for nine provenance trials combining lodgepole pine, jack pine (*Pinus banksiana* Lamb.), and their natural hybrids did not reveal significant ($P > 0.05$) variation among populations at all sites. However, variation among populations for 15-year height (H15) and diameter at breast height (D15) was significant ($P \leq 0.05$) at seven of the nine sites. On individual sites, the population variance for H15 and D15 was 5.7–37.0% and 6.0–34.2% of the total variance, respectively. Across sites, variation among populations was significant with the population variance accounting for 5.3% of the total variance for H15 and 7.3% of the total variance for D15. The population x site interaction was also highly significant with the interaction variance equivalent to 94.2% and 77.9% of the population variance for H15 and D15, respectively. The analysis also indicated significant ($P \leq 0.05$) variation among populations (12.4% of the total variance across sites) for incidence of western gall rust (*Endocronartium harknessii* [J.P. Moore] Y. Hirat.) and revealed that the fungus attacked lodgepole pine more than jack pine and the putative natural hybrids.

TREE GENE RESOURCES CONSERVATION

A draft of the “Gene Conservation Plan for Native Trees of Alberta” was completed in cooperation with Alberta Parks and Protected Areas. The plan describes a technical framework including concepts for tree gene conservation and a work plan for gap analysis, implementing, coordinating, and maintaining a provincial network of *in situ* reserves for 28 native tree species. The plan is expected to be implemented over a seven-year period. A formal protocol will be used to establish priorities by species. The initial emphasis is on white spruce and lodgepole pine, for which large tree improvement programs are in place, and on limber pine (*Pinus flexilis* James) and whitebark pine (*P. albicaulis* Engelm.), species that are on the provincial tracking list because of the increasing threat from white pine blister rust (*Cronartium ribicola*). A working group was formed to develop a strategy for conservation and restoration of limber pine which is known to have suffered serious mortality and population decline in southern Alberta.

In co-operation with Alberta Parks and Protected Areas, seed was collected from one population of jack pine in Richardson Dunes Provincial Park in northeastern Alberta and from one lodgepole x jack pine hybrid population in the Caribou Mountains. In continued cooperation with the Canadian Forest Service (CFS), seed was collected from one limber pine population in southwestern Alberta. Also in cooperation with the CFS, vegetative materials were collected from 40 balsam poplars (*Populus balsamifera* L.) from the southern limits of the boreal forest and 20 river valley cottonwoods (*P. deltoides* ssp. *monilifera* [Aiton] Eckenwalder) from the balsam poplar and western/plains cottonwood contact zone in the parkland.

Over the report period, 16 new clones were established in ATISC clone banks: three white spruce, nine lodgepole pine, three black spruce (*Picea mariana* [Mill.] BSP), and one tamarack. Four Douglas-fir clones and four western larch (*Larix occidentalis* Nutt.) clones were established in the clone banks for these species located at the Crop Diversification Centre at Brooks. Near Rocky Mountain House, five Douglas-fir clones were established in the clone bank for northern and outlier populations of Douglas-fir.

PLANT PROPAGATION, WOOD, SEED AND POLLEN TECHNOLOGY

Plant Propagation

In 2005 and 2006, stock production at ATISC included approximately 109 300 seedlings. A major project was the rearing of 2800 jack pine seedlings for a series of progeny trials for Breeding Region P1 (northeastern lowlands boreal). Under the conservation program, 95 000 seedlings and small potted stock were reared for projects including promotional trees for National Forestry Week, Arbor Day, and Junior Forest Wardens. Four thousand white spruce and lodgepole pine seedlings were grown for reforestation and reclamation plantings in Cypress Hills Provincial Park. Rootstock production for the grafting program was approximately 7500 seedlings.

Graft production consisted of 1487 grafts for establishment in seed orchards and clone banks. This included 797 white spruce, 392 lodgepole pine, 103 black spruce, 123 jack pine, 33 interior Douglas-fir, 28 western larch, 2 tamarack, and 9 red pine (*Pinus resinosa* Ait.).

Wood Technology

Samples were received from a total of 74 parent trees for fibre length and wood density determination including: 14 white spruce, 30 lodgepole pine, and 30 jack pine.

Seed Technology

Over the report period, 128 seedlots were added to the genetics seed bank. Single-tree collections from selected parent trees were: lodgepole pine (56), white bark pine(4), jack pine (30), white spruce (3), and limber pine(1). Collections from research tree improvement programs included the following species: Scots pine (*Pinus sylvestris* L.) (10), black spruce (14), white spruce (2), lodgepole pine (2), jack pine (1), and western larch (1). To date the seed bank contains 5669 seedlots.

Reference seedlots representing 2% of the seed bank entries have been monitored for 25 years. Initial average germination for lodgepole pine in1981 was 88.3% and in 2006 was 86.8%. Initial average germination for white spruce in 1981 was 91.7% and in 2006 was 86.1%. Average white spruce germination has declined slightly over the 25 year period. After 14 years of testing, mean germination of aspen (*Populus tremuloides* Michx.) has declined 62%, balsam poplar has declined 38%, and plains cottonwood (*Populus deltoides* Bartr.) has declined 58%.

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 19 tree and shrub species represented in seed storage by 1820 individual lots for a total of 42 280 kg of seed. During the reporting period, 2900 kg of seed were withdrawn for seedling production, direct seeding, research projects, and quality testing and 163 new seedlots were collected and registered for public land use.

Revisions of The Standards for Tree Improvement in Alberta, regulations that deal with collection, processing, testing, registration, storage, and deployment of tree seed for public land use, were implemented July 2005.

WESTERN FOREST PRODUCTS – COASTAL SEED DELIVERY

Annette van Niejenhuis

Western Forest Products Inc.
Saanich Forestry Centre
Saanichton, BC
V8M 1K1
E-mail: avanniejenhuis@westernforest.com

Keywords: seed orchard, clonal tests, controlled pollination

Western Forest Products delivers high quality seed to our forest regeneration programs and makes surplus seed available to other licensees operating in the Maritime Seed Zone of British Columbia. At our Saanich Forestry Centre we manage seed orchards for five conifer species: western redcedar (*Thuja plicata* Donn ex D. Don), coastal Douglas-fir (*Pseudotsuga menziesii* [Mirb.] Franco var. *menziesii*), western hemlock (*Tsuga heterophylla* [Raf.] Sarg.), Sitka spruce (*Picea sitchensis* [Bong.] Carr.), and yellow-cedar (Chamaecyparis nootkatensis [(D. Don] Spach). Additionally, Western Forest Products supports genetics, tree seed, and associated research conducted by Research Branch at the Ministry of Forests and Range (MoFR), the Universities of British Columbia (UBC) and Victoria (UVic), Canadian Forest Service, and associated consultants; and provides input to seed deployment policy development.

WESTERN REDCEDAR

A second-generation western redcedar seed orchard is in early production, with seed harvested in 2005 for a million plantable seedlings with projected gain of 5% volume at rotation. As more selections from the breeding program are anticipated in the next few years, this interim seed production orchard will be phased out and greater gains will be realized from replacement stock.

Western redcedar pollen handling techniques for year to year pollen storage, developed by O. Hak and others, were implemented and tested. Additional refinement of the techniques is required to get consistent results.

The interim orchard was established to examine management practices for reduction of self-pollination in western redcedar crops. A portion of the orchard is established as a standard randomized design. A second portion is designed for putatively male and female trees, with select clones restricted to male contribution and others restricted to female contribution. Based on previous research, and under the research limitations of the federal pesticide permit program, timing of GA_3 applications is being tested for its efficacy in producing putatively female trees. A third portion of the orchard has been grafted twice to layer one clone above another. Upon maturity, these techniques will be evaluated to determine cost-effective techniques to minimize self-pollination.

COASTAL DOUGLAS-FIR

Because seed supply in coastal Douglas-fir has been in short supply in recent years, aggressive development of second-generation Douglas-fir orchards at Saanich Forestry Centre has been deferred. High-gain replacement stock is being phased into the current orchard to replace mortality. The 2005 cone crop was small and suffered extensive insect damage, thus recoveries were poor. The crop is registered for a gain of 10% volume at rotation for 113 000 plantable seedlings.

Seed from the 2005 crop was provided to Y. El-Kassaby (UBC) for study of parental contribution estimates. DNA analysis will be used to evaluate various methods of estimating parental contribution. J. Webber has been studying pollen contamination at our orchards for the last three pollen seasons as well. New research was begun by P. von Aderkas (UVic) and associates to develop and refine techniques for cone crop induction in Douglas-fir; this team is using our orchard as one if its test sites.

Disease and insects can dramatically reduce the deployment of high-gain seed to regeneration programs. M. Petersen (consultant) is studying Douglas-fir seed pathogens and R. Bennett (MoFR) is developing Douglas-fir insect monitoring and control techniques. Saanich Forestry Centre is co-operating with these researchers and providing access to orchards and cones.

WESTERN HEMLOCK

The low-elevation second-generation western hemlock orchard at Saanich Forestry Centre produces seed for 14% volume gain at rotation. The 2005 crop produced seed for 325 000 plantable seedlings. A high-elevation second-generation western hemlock orchard is under development at this time. It will produce future seedlots of 8% volume gain at rotation.

SITKA SPRUCE

Combined tree improvement efforts of many agencies have led to the identification of naturally, weevil-tolerant Sitka spruce provenances and selections. These selections have been established in an orchard at the Saanich Forestry Centre that is entering production. The 2005 crop produced seed with a weevil resistance score of 87% and potential for 113 000 plantable seedlings.

Staff at the Saanich Forestry Centre have been co-operating with J. King, the MoFR Sitka spruce breeder, to provide controlled cross seed for progeny testing. From these progeny tests we anticipate more accurate estimates of the weevil resistance of selections included in the orchard and scores for volume, the secondary trait for selection in this species. Future orchard development will maintain the weevil resistance rating at the current level and improve growth through roguing and ramet replacement.

YELLOW-CEDAR

Western Forest Products initiated clonal evaluation of yellow-cedar cuttings more than two decades ago. Numerous test sites have been established and data have been collected repeatedly. J. Russell, the MoFR cedar breeder, has provided analysis of the data and developed genetic worth scores. At present, the Saanich Forestry Centre is delivering yellow-cedar cuttings to our regeneration programs with a projected volume gain at rotation of 20%.

Cuttings were selected for regeneration programs when it was realized that seed orchard production in yellow-cedar was not reliable, wild seed crops were costly and sporadic, and seed germination was challenging. Significant progress has been made in seed stratification techniques in recent years and new information regarding pollen viability and management techniques is coming available. Cuttings are more costly than seedlings to produce in the nursery. Western Forest Products is co-operating with O. Hak in developing seed production protocols, using MoFR and Western Forest Products high gain selections established in a seed orchard.

ISABELLA POINT FORESTRY LTD.: ACTIVITIES 2004 – 2006

Sally E.T. John and Jean S. Brouard

Isabella Point Forestry Ltd.
331 Roland Road
Salt Spring Island, BC
V8K 1V1
E-mail: ipf@saltspring.com

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 2004–2006 we were engaged in a range of activities in Alberta, British Columbia, Saskatchewan, Manitoba, and Ontario. Activities included program planning, trial design and analysis, and seed orchard research for tree breeding programs in Alberta and Saskatchewan, tree improvement strategy development for Forest Genetics Ontario, BLUP analysis of progeny test data for Manitoba, and investigation of the interaction of disease with genetics in north-central British Columbia.

Isabella Point Forestry celebrates its 10th anniversary in 2006.

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 genetic base for both breeding and production populations and error control through appropriate trial design and layout.

An interesting early result of a seed orchard fertilizer trial suggests that seed production in lodgepole pine can be significantly increased by adjusting nitrogen and phosphorus amendments. This trial is ongoing.

Sally John has represented a group of forest companies as councillor on the Alberta Forest Genetic Resources Council since its inception in April 2000 and continues to be involved in policy development for the province.

BRITISH COLUMBIA

Genetics of Disease Resistance

This project, planned and implemented in cooperation with Ministry of Forests and Range (MoFR) genetics and pathology staff and industry foresters, considers genetic variation in susceptibility to three common rust diseases of lodgepole pine.

Through earlier assessments of a 14–15 year-old-lodgepole pine MoFR 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. Data and results from this study have been used by MoFR genetics staff to identify several provenances as resistant comandra rust.

A series of trials established on five sites in the Bulkley Valley in the spring of 2004 is being assessed at the time of writing (May 2006). The incidence of comandra, gall, and stalactiform rust lesions is being tallied.

Preliminary estimates of total disease incidence on two sites are extremely high (30–40%), after only two seasons in the field. This trial series is expected to provide precise estimates of rust resistance of families produced in the Bulkley Valley seed orchard which will facilitate targetted deployment of rust-resistant stock on high-risk sites.

MANITOBA

In 2004–2005 we performed BLUP analysis of progeny test data from family trials of black and white spruce in Manitoba. Results were used by Manitoba Conservation - Forestry Branch to rogue existing seed orchards and to make forward selections in progeny tests for establishment of future seed orchards.

ONTARIO

Working with Forest Genetics Ontario, Ontario Ministry of Natural Resources, and industry personnel we are developing a comprehensive tree improvement plan for the province. This plan will incorporate breeding strategies for black spruce, jack pine, white spruce, and white pine, and will address conceptual issues such as breeding zone delineation, climate change, and gene conservation, as well as the more pragmatic considerations of mating design, field test design, selection method, rotation length, and realized gain trials.

FOREST GENETICS AT THE FACULTY OF FORESTRY, THE UNIVERSITY OF BRITISH COLUMBIA, 2004–2006

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

The University of British Columbia
Department of Forest Sciences
Vancouver, BC
V6T 1Z4
E-mail: y.el-kassaby@ubc.ca

GENE CONSERVATION, ECOLOGICAL GENETICS AND CLIMATE CHANGE

S.N. Aitken

Our group continues to characterize the genetic structure of forest tree populations in British Columbia (BC), to determine their potential for adaptation to climate change, to quantify their degree of protection for gene conservation purposes, and to identify variation at the nucleotide level involved in local adaptation. Two major projects on genetic structure were completed in the past two years: Makiko Mimura completed her PhD on core-peripheral structure and diversity using Sitka spruce (*Picea sitchensis*) as a model species and Andy Bower completed his PhD research on ecological genetics and inbreeding in whitebark pine (*Pinus albicaulis*). The relative diversity of peripheral compared to core populations is an important issue in gene conservation. Following the research of Makiko Mimura and Washington Gapare on range-wide genetic structure in Sitka spruce, Sally Aitken in collaboration with Bruno Fady, INRA, France analyzed all published data for 40 conifer species to determine general patterns of core-peripheral structure. New projects include a study of range-wide genetic structure and diversity in Pacific dogwood (*Cornus nuttallii*) using genetic markers is being conducted by MSc student Karolyn Keir and a study of local adaptation in Garry oak (*Quercus garryana*) was initiated by MSc student Colin Huebert.

We have been very active in the area of climate change research. Drs. Tongli Wang and Andreas Hamann (now at University of Alberta) developed a climate model for BC incorporating climate change predictions called ClimateBC. This model was then used to evaluate provenance response to climate and implications of climate change for lodgepole pine (*Pinus contorta*). Dr. Pia Smets characterized seedling temperature response curves for some of the same provenances in a growth chamber experiment. Sierra Curtis-McLane (MSc student) is studying inter-annual variation in tree rings in relation to climatic variation over a 30 year period in the Illingworth lodgepole pine provenance trial. Andreas Hamann conducted a detailed assessment of the *in situ* conservation of 50 tree species in BC in the Protected Areas Network. Christine Chourmouzis is continuing this work by preparing a detailed technical report evaluating protection of all these species in each major ecological zone in the province, as well as the extent of *ex situ* conservation.

A new area of research for our group is genomics. We are participating in the Genome Canada supported “Conifer Forest Heath” project led by Kermit Ritland and Jörg Bohlmann, with the ultimate goal of identifying single nucleotide polymorphisms (SNP) involved in phenotypic variation in adaptation to cold. PhD student Jason Holliday is characterizing patterns of gene expression in southern, central, and northern populations of Sitka spruce using the Treenomix microarray with ~22 000 unique expressed sequences to identify candidate genes for further characterization and potential use in an association study of SNP genotypes and phenotypes.

APPLIED FOREST GENETICS AND BIOTECHNOLOGY

Y.A. El-Kassaby

The main activity during the past two years was the creation of an NSERC Industrial Research Senior Chair in Applied Forest Genetics and Biotechnology. The focus of the Chair's research program is to create linkages between germplasm developers and operational users to enhance the efficiency of the tree improvement delivery system by incorporating new innovations, including appropriate biotechnologies. The Chair’s research program has two primary objectives: 1) delivery of higher genetic gains by augmenting the traditional tree improvement delivery system with biotechnology techniques and 2) studying wood quality traits. The research program is proceeding in close collaboration with the Chair sponsors to foster synergies including: 1) maximizing the relevance of the research to the end-users, 2) seamless implementation of results, and 3) creating a collaborative environment between germplasm developers and users. This program will train highly qualified personnel needed in the forest industry and the related biological sciences. The industrial partners include The Johnson Family Forest Biotechnology Fund, BC Ministry of Forests and Range, Pulp and Paper Research Institute of Canada, Forintek Canada Corp, Forest Engineering Research Institute of Canada, CellFor Inc., SelectSeed, Edoc Systems Group Ltd., Pacific Regeneration Technologies Inc. (formerly known as Pelton Reforestation Ltd.), and Western Forest Products Inc.

I have been engaged in a wide array of research projects including molecular breeding, seed orchard genetics (with emphasis on parental gametic contribution, development of alternative seed orchard designs, economic and biological modeling of seed orchards turnover), seed biology for improved utilization, theoretical development of seed germination and dormancy parameters, fine scale investigation of population structure and the mating system in Ponderosa pine (*Pinus ponderosa*), and genetic gain implications of somatic embryogenesis under variable induction rates. My research group is studying the genetics of poplar, estimating gametic contribution in a Douglas-fir (*Pseudotsuga menziesii*) seed orchard, pedigree reconstruction of a yellow-cedar (*Chamaecyparis nootkatensis*) production population, and wood attributes of 35-year-old Douglas-fir progeny test trials.

POPULATION GENETICS AND GENOMICS OF BC CONIFERS

K. Ritland

Together with Drs. Joerg Bohlmann, Carl Douglas, and Brian Ellis at UBC, we recently finished a large-scale Genome British Columbia research program involving spruce, poplar, and *Arabidopsis*. Over its four year timespan (Jan. 2002 – Dec. 2005), we developed genomics tools (ESTs, microarrays) for spruce and poplar, and applied these tools to understand the genomic basis of traits relating to forest health and wood quality. For details visit http://www.treenomix.ca. Some of the outcomes are included in the publication list below.

In January 2006, Joerg Bohlmann and I started a "second-generation" genome research program, involving only spruce but with some inclusion of loblolly pine (*Pinus taeda*) for comparative purposes. This program, also funded by Genome British Columbia and Genome Canada, has an emphasis on forest health, specifically resistance to the spruce budworm (*Choristoneura fumiferana*) and white pine weevil (*Pissodes strobi*). In addition to developing more ESTs, we will continue using the microarrays developed in the first project for a number of innovative studies involving the genomics of resistance. Included in this list is an "e-QTL" mapping study using material from the BC Ministry of Forests and Range's Kalamalka Research Station (Barry Jacquish and associates), and studies that integrate gene expression, protein expression, and metabolite expression (Shawn Mansfield and associates). Our project is also collaborating with the Genome Québec project (John Mackay and Jean Bousquet), which is also involved with spruce.

Two students are finishing their PhDs in tree genetics: Cherdsiak Liewlaksaneeyanawin (evolutionary genomics of lodgepole pine), and Dilara Ally (evolution of clonality in aspen), and a new PhD student in tree genetics, Rockney Albouyeh (evolution of gene expression in spruce). Two other students are working with monkeyflowers. In June 2006 my NSERC University-Industrial Research Chair ended its ten-year term. A number of publications in forest genetics have arisen or will arise from this work.

PUBLICATIONS

Beland, J.D.; Krakowski, J.; Ritland, C.E.; Ritland, K.; El-Kassaby, Y.A. 2005. Genetic structure and mating system of northern *Arbutus menziesii* populations. Can. J. Bot. 83: 1581–1589.

Bower, A.D.; Aitken, S.N. 2006. Changes in genetic structure of whitebark pine (*Pinus albicaulis* Engelm.) associated with inbreeding and white pine blister rust infection. Conserv. Genet. (submitted)

Bower, A.D.; Aitken, S.N. 2006. Genetics of cold hardiness in whitebark pine. Can. J. For. Res. 36: 1842–1850.

Chuine, I.; Rehfeldt, G.E.; Aitken, S.N. 2005. Height growth determinants in pines: a case study of *Pinus contorta* and *Pinus monticola*. Can. J. For. Res. 36: 1842–1850.

Ehlting, J.; Mattheus, N.; Aeschliman, D.S.; Li, E.; Hamberger, B.; Cullis, I.F.; Kaneda, M.; Mansfield, S.D.; Samuels, A.L.; Ritland, K.; Ellis, B.E.; Bohlmann, J.; Douglas, C.J. 2005. Global transcript profiling of primary stems from *Arabidopsis thaliana* identified candidate genes for missing links in lignin biosynthesis and transcriptional regulators of fiber differentiation. Plant J. 42: 618–640.

El-Kassaby Y.A.; Ritland, K.; Ritland, C.; Aitken, S.; Bohlmann, J.; Krakowski, J. 2005. Forest Genetics. Pages 474–486. *In* S.B. Watts and L. Tolland, eds. Forestry Handbook, 5th Edition. Faculty of Forestry, The University of British Columbia, Vancouver, BC.

El-Kassaby, Y.A.; Askew, G.R. 2004. A method for estimating expected genetic diversity of vegetatively propagated populations produced from commonly used mating designs. Pages 129–146. *In* C. Walter and M. Carson, eds. Plantation forest biotechnology for the 21st century. Research Signpost, Kerala, India.

El-Kassaby, Y.A.; Moss, I. 2004. Clonal forestry: options, deliverables and benefits. Pages 55–64. *In* B. Li and S. McKeand, eds. Forest Genetics and Tree Breeding in the Age of Genomics: Progress and Future. IUFRO Joint Conference of Division 2. Charleston, SC, 1–5 Nov 2004, Available online at: http://www.ncsu.edu/feop/iufro_genetics2004/proceedings.pdf.

El-Kassaby, Y.A.; Krakowski, J. 2004. Forest biotechnology deliverables: availability and benefits. Pages 53–69. *In* S. McCord and R. Kellison, eds. New Century, New Trees: Biotechnology as a Tool for Forestry in North America. Institute of Forest Biotechnology, Forest History Society, Pinchot Institute for Conservation, Resources for the Future, and Purdue University. Research Triangle Park, SC, 16–17 Nov 2004.

El-Kassaby, Y.A.; Krakowski, J. 2004. Methods of cloning forest trees. Pages 327–332. *In* B. Li and S. McKeand, eds. Forest Genetics and Tree Breeding in the Age of Genomics: Progress and Future. IUFRO Joint Conference of Division 2. Charleston, SC, 1–5 Nov 2004, Available online at: http://www.ncsu.edu/feop/iufro_genetics2004/proceedings.pdf.

El-Kassaby, Y.A.; Benowicz, A.; Edwards, D.G.W. 2004. Genetic variation in germination attributes and response to accelerated aging in western hemlock seeds. Seed Technol. 26: 38–50.

El-Kassaby, Y.A.; Prescher, F.; Lindgren, D. 2006. Advanced generation seed orchards turnover as affected by breeding advance, time to sexual maturity, and costs: special reference to Scots pine in Sweden. Scan. J. For. Res. (submitted)

El-Kassaby, Y.A.; Stoehr, M.U.; Reid, D.; Walsh, C.G.; Lee, T.E. 2006. Clonal-row vs. random seed orchard designs: interior spruce mating system evaluation. Can. J. For. Res. (submitted)

El-Kassaby,Y.A.; Lstibůrek, M.; Liewlaksaneeyanawin, C.; Slavov, G.T.; Howe, G.T. 2006. Breeding without breeding: approach, example, and proof of concept. *In* Low input breeding and genetic conservation of forest tree species. IUFRO Div. 2 Joint Conf., Antalya, Turkey, 9–13 Oct 2006. (in press)

Gapare, W. J.; Aitken, S.N.; Ritland, C.E. 2005. Genetic diversity of core and peripheral Sitka spruce (*Picea sitchensis* (Bong.) Carr) populations: implications for conservation of widespread species. Biol. Conserv. 123: 113–123.

Gapare, W.J.; Aitken, S.N. 2005. Strong spatial genetic structure in peripheral but not core populations of Sitka spruce (*Picea sitchensis* (Bong.) Carr.). Mol. Ecol. 14: 2659–2667.

Hamann, A.; Smets, P.; Yanchuk, A.D.; Aitken, S.N. 2005. An ecogeographic framework for *in situ* conservation of forest trees in British Columbia. Can. J. For. Res. 35: 2553–2561.

Hu, X-S.; Goodwillie, C.; Ritland, K. 2004. Joining genetic linkage maps using a joint likelihood function. Theor. Appl. Genet. 109: 996–1004.

Iddrisu, M.; Ritland, K. 2004. Genetic variation, population structure and mating system in bigleaf maple (*Acer macrophyllum* Pursh). Can. J. Bot. 82: 1817–1825.

Kang, K.S.; El-Kassaby, Y.A.; Chung, M.S.; Kim, C.S.; Kang, Y.J.; Kang, B.S. 2005. Fertility variation and effective number in a clonal seed orchard of *Cryptomeria japonica*. Silvae Genet. 54: 104–107.

Kang, K.S.; El-Kassaby, Y.A.; Han, S.U.; Kim, C.S. 2005. Genetic gain and diversity under different thinning scenarios in a breeding seedling seed orchard of *Quercus accutissima*. For. Ecol. Manage. 212: 405–410.

Kolosova, N.; Miller, B.; Ralph, S.; Ellis, B.E.; Douglas, C.; Ritland, K.; Bohlmann, J. 2004. Isolation of high-quality RNA from gymnosperm and angiosperm trees. BioTech. 36: 821–824.

Krakowski, J.; Benowicz, A.; Russell, J.; El-Kassaby, Y.A. 2005. Effects of serial propagation, donor age and genotype on *Chamaecyparis nootkatensis* physiology and growth traits. Can. J. For. Res. 35: 623–632.

Krakowski, J.; El-Kassaby, Y.A. 2005. Lodgepole pine and white spruce germination: effects of stratification and simulated aging. Silvae Genet. 54: 138–144.

Krakowski, J.; Park, Y.S.; El-Kassaby, Y.A. 2005. Early testing of Douglas-fir: wood density and ring width. For. Genet. 12: 99–105.

Liewlaksaneeyanawin, C.; Ritland, C.; El-Kassaby, Y.A.; Ritland, K. 2004. Single-copy, species-transferable microsatellite markers developed from loblolly pine ESTs. Theor. Appl. Genet. 109: 361–369.

Lippert, D.; Zhuang, J.; Ralph, S.; Ellis, D.; Gilbert, M.; Olafson, R.; Ritland, K.; Ellis, B.; Douglas, C.; Bohlmann, J. 2005. Proteome analysis of early somatic embryogenesis in *Picea glauca*. Proteomics 5: 461–473.

Lstibůrek, M.; Mullin, T.; El-Kassaby, Y.A. 2006. The impacts of positive assortative mating, differential success of somatic embryogenesis, and multi-trait selection on the outcome of clonal forestry programs. Can. J. For. Res. 36: 1376–1384.

Mimura, M.; Aitken, S.N. 2006. Increased selfing and decreased effective pollen donor number in peripheral relative to central populations in *Picea sitchensis* (Pinaceae). Amer. J. Bot. (submitted)

Mimura, M.; Aitken, S.N. 200_. Adaptive gradients and isolation by distance with postglacial migration in *Picea sitchensis*. Heredity (submitted)

Mullin, T.J.; Lstibůrek, M.; Pait, J.; El-Kassaby, Y.A. 2005. The impact of variable success of somatic embryogenesis among elite crosses on expected genetic gain and diversity of selected varieties. *In* Proc. 28th South. For. Tree Imp. Conf., Raleigh, NC, June 2005. (in press)

O'Connell, L. M.; Ritland, K. 2004. Somatic mutation rate at microsatellite loci in *Thuja plicata*. J. Hered. 95: 172–176.

O'Connell, L.; Russell, J.; Ritland, K. 2004. Fine-scale estimation of outcrossing in western redcedar with microsatellite assay of bulked DNA. Heredity 93: 443–449.

O'Connell, L.; Russell, J.; Ritland, K. 2005. Post-pollination mechanisms promoting outcrossing in a self-fertile conifer. Can. J. Bot. 83: 335–342.

Perscher, F.; Lindgren, D.; El-Kassaby, Y.A. 2006. Is linear deployment of clones optimal under different clonal outcrossing contributions in seed orchards? Tree Genet. Genom. 2: 25–29.

Ritland K. 2005. Multilocus estimation of pairwise relatedness with dominant markers. Mol. Ecol. 14: 3157–3165.

Ritland, K.; Travis, S. 2004. Inferences involving individual coefficients of relatedness and inbreeding in natural populations of *Abies*. For. Ecol. Manage. 197: 171–180.

Ritland, K. 2004. Pathways to plant population genomics. Pages 11–17. *In* Q.C.B. Cronk, J. Whitton, R.H. Ree and I.E.P. Taylor, eds. Proc. Molecular Genetics and Ecology of Plant Adaptation. Vancouver, BC, 11–13 Dec 2002. NRC Research Press, Ottawa, ON.

Ritland, K.; LeBlanc, M. 2004. Mating system of four inbreeding monkeyflower (*Mimulus*) species as revealed by "progeny-pair" analysis of highly informative microsatellite markers. Plant Species Biol. 19: 149–157.

Ritland, K.; Meagher, M.D.; Edwards, D.G.W.; El-Kassaby, Y.A. 2005. Isozyme variation and the conservation genetics of Garry oak. Can. J. Bot. 83: 1478–1487.

Rungis, D.; Hamberger, B.; Bérubé, Y.; Wilkin, J.; Bohlmann, J.; Ritland, K. 2005. Efficient genetic mapping of nucleotide polymorphisms based upon DNA mismatch digestion. Mol. Breed. 16: 261–270.

Rungis, D.; Bérubé, Y.; Zhang, Z.; Ralph, S.; Ritland, C.E.; Ellis, B.E.; Douglas, C.; Bohlmann, J.; Ritland, K. 2004. Robust simple sequence repeat (SSR) markers for spruce (*Picea* spp.) from expressed sequence tags (ESTs). Theor. Appl. Genet. 109: 1283–1294.

Sutton, B.C.S.; Attree, S.M.; El-Kassaby, Y.A.; Grossnickle, S.C.; Polonenko, D.R. 2004. Commercialisation of somatic embryogenesis for plantation forestry. Pages 275–301. *In* C. Walter and M. Carson, eds. Plantation forest biotechnology for the 21st century. Research Signpost, Kerala, India.

Travis, S.; Proffitt, E.; Ritland, C.E.; Ritland, K. 2004. The successional dynamics of fine-scale genetic structure and its effects on inbreeding in a facultatively clonal plant (*Spartina alterniflora*). Ecol. Appl. 14: 1189–1202.

van Kleunen, M.; Ritland, K. 2005. Estimating heritabilities and genetic correlations with marker-based methods: an experimental test in *Mimulus guttatus*. J. Hered. 96: 368–375.

Wahbe T.R.; Ritland, C.; Bunnell, F.L.; Ritland, K. 2005. Population genetic structure of tailed frogs (*Ascaphus truei*) in clearcut and old-growth stream habitats in south coastal British Columbia. Can. J. Zool. 83: 1460–1468.

Wang, T.; Hamann, A.; Spittlehouse, D.; Aitken, S.N. 2006. Development of scale-free climate data for western Canada for use in resource management. Int. J. Climat. 26: 383–397.

Wellman, H.; Ritland, C.; Ritland, K. 2004. Genetic effects of domestication in western hemlock, *Tsuga heterophylla*. For. Genet. 10: 229–240.

Wheeler, N.C.; Jermstad, K.D.; Krutovskii, K.V.; Aitken, S.N.; Howe, G.T.; Krakowski, J.; Neale, D.B. 2005. Mapping of quantitative trait loci controlling adaptive traits in coastal Douglas-fir. Mol. Breed. 15:145–156.

Wilkin, J.E.; Shamoun, S.F.; Ritland, C.; Ritland, K.; El-Kassaby, Y.A. 2005. Genetic diversity and population structure of *Valdensinia heterodoxa*, a potential biocontrol agent for salal in coastal British Columbia. Can. J. Plant Path. 27: 559–571.

Wilkin, J.E.; Shamoun, S.F.; Ritland, C.; Ritland, K.; El-Kassaby, Y.A. 2005. Population genetics of *Gaultheria shallon* in British Columbia and the implications for management using biocontrol. Can. J. Bot. 83: 501–509.

BC MINISTRY OF FORESTS AND RANGE TREE IMPROVEMENT BRANCH 2004–2006

Brian Barber[1], Dave Kolotelo[2] and David Reid[3]

[1] PO Box 9518 Stn Prov Govt
Victoria, BC
V8W 9C2
E-mail: Brian.Barber@gov.bc.ca

[2] Tree Seed Centre
18793 32nd Avenue
Surrey, BC
V3F 0L5
E-mail: Dave.Kolotelo@gov.bc.ca

[3] 7380 Puckle Road
Saanichton, BC
V8M 1W4
E-mail: David.Reid@gov.bc.ca

Keywords: policy, seed biology, seed production, seed planning, gene conservation, stratification, seed testing, extension, climate change

POLICY AND CLIMATE CHANGE

Brian Barber

Over the past several years I have been leading the development and implementation of regulations and standards that govern the disposition and use of the province's forest genetic resources and tree seed under the *Forest Act* and the *Forest Range Practices Act* (FRPA).

The regulations, technical standards, guidelines, and policies that pertained to the registration, storage, selection, and transfer of tree seed under the Forest Practices Code (now repealed) were updated and consolidated in the *Chief Forester's Standards for Seed Use* http://www.for.gov.bc.ca/code/cfstandards/. These standards were brought into force on April 1, 2005 with training and extension delivered province-wide in September 2005.

In addition to working on seed policy and planning matters, I have been involved in other provincial initiatives, such as the Forests for Tomorrow program http://www.for.gov.bc.ca/hfp/fft/, management of post-harvest species composition in Mountain Pine Beetle blocks http://www.for.gov.bc.ca/hfp/fft/species/index.htm, and the Future Forest Ecosystem of BC Initiative http://www.for.gov.bc.ca/hts/Future_Forests/.

I also lead the Ministry of Forests and Range Climate Change Task Team which produced its report and recommendations for public review and comment in May 2006 http://www.for.gov.bc.ca/mof/Climate_Change/. This report summarizes the potential impacts of climate change on the province's forest and range resources and identified a number of short-term and long-term actions that the Ministry could undertake in response to these impacts – including changes to species selection guidelines and seed transfer limits. In September 2006, I was appointed Deputy Director, and Manager, Policy, Planning and Climate Change, of the Ministry's Tree Improvement Branch.

CONE AND SEED IMPROVEMENT

Dave Kolotelo

Tree seed extension has been an active area of the past two years with four Tree Seed Workshops being offered in 2005, organization of the Tree Seed Working Group (TSWG) Workshop in 2006 "Appreciating, Quantifying and Utilizing Family Differences", and production of four TSWG News Bulletins:

#40 Problems and Information Needs for Tree Seed

#41 Cone and Seed Pests
#42 Cone and Seed Processing
#43 Information Management

Additional extension activities involved presentations at the IUFRO Tree Seed Symposium, Forest Nursery Association of BC (2004 and 2005), Forest Genetics Council, and Northern Silviculture Committee. In addition I have served on the following committees during this term: Gene Conservation **T**echnical **A**dvisory **C**ommittee (GC**TAC**), Interior TAC, Coastal TAC, Pest Management TAC, IUFRO Tree Seed Physiology and Technology Working Group, and the ISTA Forest Tree and Shrub Seed Committee. The Tree Seed Centre web page was updated and a Cone and Seed Improvement section added enabling users to download various newsletter articles and the latest issues of the News Bulletin: http://www.for.gov.bc.ca/hti/treeseedcentre/tsc/csio.htm.

The Quality Assurance (QA) program at the Tree Seed Centre was reviewed in 2004 and improvements are ongoing. Monitoring programs are active in the areas of germination and moisture content of operational sowing requests, pellet efficiency in western red cedar (*Thuja plicata*) and red alder (*Alnus rubra*), and fungal assay testing for *Fusarium* spp., *Caloscypha fulgens*, and *Sirococcus conigenus*. Research on *Fusarium* spp. trends during cone and seed processing was conducted and presented at the IUFRO Tree Seed Symposium. Testing continues to increase data confidence and efficiency through a variety of initiatives including elimination of three-replicate germination test results (tests must be redone), addition of seed weight tolerances, construction of a pellet assessment screen, improved reporting, and the replacement of destructive moisture content testing with target moisture content monitoring in QA.

Initiatives related to our seed inventory include an annual summarization of improved seed by Seed Planning Unit (SPU) and an analysis of the amount and distribution of lodgepole pine (*Pinus contorta* var. *latifolia*) seed available in relation to the Mountain Pine Beetle epidemic.

SEED PRODUCTION

David Reid

BC Ministry of Forests and Range seed orchards produce approximately 50% of the orchard seed in British Columbia annually. The Ministry has managed seed orchards since 1963 and currently operates six seed production sites in 3 regions of the province. These sites contain 30 seed orchards of ten species and approximately 40 000 seed producing trees. To date, Ministry Tree Improvement Branch (TIB) seed orchards have produced over 8,000 kg of seed which is equivalent to over two billion seedlings. The long-term goal in BC is to have 75% of seed used in Crown land reforestation to come from seed orchards and improved sources by 2014 and to increase the average genetic worth of the seedlots to 14% by 2020.

Significant time was dedicated to organizing and conducting the 2004 CTIA conference in Kelowna. My involvement included acting as Co-chair with Dave Kolotelo, Hotel and Catering Director, and Treasurer. The conference was a great success and over $10,000 was returned to the main CTIA account. Cost savings were realized through lower field trip expenses, lower guest speaker costs, and higher attendance which brought higher registration fee income.

Since the conference, regular work activities have focussed on improving gain in many of our seed orchards through roguing when new breeding values have been released from Research Branch and installation of entirely new seed orchards for several species. The Mountain Pine Beetle infestation that is devastating BC's lodgepole pine forests has created a huge demand for lodgepole pine seed. The 2006 sowing request was for a record 133 million lodgepole pine seedlings. There is insufficient seed orchard capacity to deal with this rapid need for seed. Thus TIB undertook a study to determine if lodgepole pine seed utilization could be improved. One main finding of the study was that by increasing the ISTA recommended stratification period by one week resulted in an increased germination capacity by 2%. If this was applied to the 2006 sowing above, then an additional 11 million seedlings would be generated or enough to re-plant 7,000 ha. Extension activities have revolved around attending Coast and Interior Technical Advisory Committees of the Forest Genetics Council and attending Northern and Southern Silviculture Committee meetings to promote use of improved seed.

BRITISH COLUMBIA MINISTRY OF FORESTS AND RANGE FOREST GENETICS SECTION

Michael Carlson, Charlie Cartwright, Barry Jaquish, John King,
Sylvia L'Hirondelle, Greg O'Neill, John Russell, Michael Stoehr,
Ward Strong, Chang-Yi Xie and Alvin Yanchuk

Ministry of Forests and Range
Research Branch
722 Johnson Street
Victoria, BC
V8W 9C2
E-mail: Alvin.Yanchuk@gov.bc.ca

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

TREE BREEDING

Coastal Douglas-fir (Michael Stoehr)

Coastal Douglas-fir (*Pseudotsuga menziesii* var. *menziesii*) remained the highest valued species in British Columbia (BC) based on product value (SPU 1), and seed needs have risen over the past years to more than 10.5 million seedlings planted per year. Breeding and testing for third-generation seed orchards continued over the last two years. In the spring of 2006, the third phase of sublines (out of a total of 4) was planted on four sites to obtain GCA estimates and on two sites for full-sib forward selections. Based on an index of family and within family performance, forward selections were made in full-sib family blocks of phase 1 tests (planted in 1999) in late 2005. From each subline, scions from three full-sib seedlings from each of three families were grafted to speed graft development before final selection decisions are made in two years. A subset of full-sib families is being evaluated with respect to frost hardiness and growth rhythm patterns to determine the effects of selection on these traits. We are currently looking at the use of optimum selection techniques to better balance gain and genetic diversity in the breeding populations.

In the interior-coast transition (submaritime) zone (SPU 19) (Seed Planning Unit 19), three progeny tests were planted in 2005 with poly-crossed seedlings of 93 parents of a newly established seed orchard. GCA estimates will be used to rogue the orchard which will also be supplemented with forward selections from open-pollinated genecology tests located in the submaritime zone. Twenty genotypes have been selected from one site based on BLP estimates of individual trees (using family and within-family information from 5 test sites). Seed needs for this SPU are 2.4 million seedlings.

In SPU 31, high-elevation coastal Douglas-fir (700–1200 m), two open-pollinated progeny trials, to test parents in Canadian Forest Products Ltd.'s (Canfor) high elevation seed orchard, were measured (age 11) and final backward selections were made based on BLP estimates. Selected parent trees will be re-grafted from clones in Canfor's orchard at Sechelt and re-established in Saanichton in Western Forest Product's orchard complex. Expected gain for this orchard is around 10% for volume at rotation (60 yrs). As seed production is limited for this zone and natural seed crops are sparse, a severe seed shortage led to a change in seed transfer guidelines. Based on performance of low elevation A-class seed at higher elevations, maritime coastal seed from SPU 1 can be used up to 900 m with a penalty in genetic gain of 3%/100 m upwards movement.

Interior spruce (Barry Jaquish)

The Interior spruce (*Picea glauca* x *engelmannii)* tree breeding program is structured in two phases. Phase one began in the mid-1960s and focussed on three geographic regions: Prince George, Bulkley Valley, and the East Kootenays. Phase two began in the mid-1970s and focussed on other geographic regions where Interior spruce is commercially and ecologically important. The program has progressed to the point where much of the current planting stock (more than 80 million per year) comes from rogued first-generation seed orchards and full-sib second-generation progeny tests are in place for three seed planning units (SPUs). In 2005, 65 trees in the 10-year-old Series I Prince George Selection Unit second-generation progeny tests were selected, grafted, and established in holding beds where they will be held for 1–2 years and then moved into seed orchards.

In the mid-1990s' Interior seed planning zone review, the Prince George Interior spruce SPU was expanded to include six small seed planning units from the Phase II program and the Prince George Selection Unit from the Phase I program. This merger resulted in a composite breeding population for the Prince George SPU that included 1,140 tested parent trees.

The second-generation crossing plan for this new Prince George zone consisted of crossing the top 144 parents in a 5-tree incomplete partial diallel crossing plan where each parent was crossed with four other parents. This plan resulted in 24 partial diallel units and a maximum of 288 crosses. Crossing was completed over four breeding seasons and progeny tests were planted on four sites in spring 2006. These tests were established in an incomplete block Alpha design with ten replicate blocks per site, 13 blocks per replication and 20 seedlots per block. Experimental units consisted of three-tree row plots with trees planted at 2 x 2 m spacing.

In spring 2006, four realized gain tests were established in the Prince George SPU. These tests will compare the growth performance on an area basis of elite families, seed orchard seedlots, and a wild stand seedlot comprised of a composite of ten wild stand seedlots.

Controlled crossing to produce full-sib families for second-generation selection is ongoing in the Nelson SPU.

Western Larch (Barry Jaquish)

Commercial planting of western larch (*Larix occidentalis)* continues to increase with over 6.6 million seedlings planted in 2006. Sixty-eight percent (4.5 million) of these seedlings originated from rogued first-generation seed orchards located in Vernon. Second-generation crossing in the East Kootenay and Nelson SPUs is over 70% complete and we anticipate completion of the crossing program within three years. In spring 2006, grafting was completed for the establishment of a new high elevation seed orchard for high elevation sites in the Nelson SPU. Realized gain tests were established in the East Kootenay and Nelson Low SPU in 2005 and 2006, respectively.

Interior Douglas-fir (Barry Jaquish)

Second-generation controlled crossing in interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca)* continued in the Nelson low elevation SPU and is near completion. In 2006, four 15-year-old open-pollinated progeny tests in the East Kootenay SPU were maintained and measured, and two 20-year-old sites in the Nelson SPU were measured. Various supportive research plantations were maintained and measured. These included the 20-year-old seedling/steckling study and five Submaritime Douglas-fir adaptation plantings.

The pilot interior Douglas-fir *Armillaria* genetic resistance study was completed and data analysis is in progress. This test included 1,566 trees from 88 open-pollinated families and four SPUs. The artificial inoculation technique proved very effective as inoculum was present on 1,408 of the 1,566 treated trees. After three years, 83% of the trees had been killed by *Armillaria* and 6% of the living trees were completely girdled and near death. Family mortality ranged from 44–100%. In general, families from warmer and drier environments were more tolerant than trees from colder and wetter environments.

Western Hemlock (Charlie Cartwright)

The western hemlock (*Tsuga heterophylla)* forest genetics program has been focussed on measurements and selections from the F_1 testing of material shared with the Hemlock Tree Improvement Cooperative (HEMTIC). Age 10 data have been collected from 2 of 8 BC test sites while 200 forward selections have been selected based on age 5 measurements. It is intended that these will be rogued once all the age 10 numbers are in for the purpose of development of new orchards and perhaps a further round of recurrent selection. For high elevation hemlock the last series of first-generation trials is now going into the ground bringing the number of high elevation parent trees tested to 325. New breeding values from 2 earlier series (1995 and 2001) are being released. In support of tree breeding work, a broad array of genecology trials combining a practically range-wide spread of seed sources along with improved materials are being tended and measured for refinement of seed transfer guidelines. Other supporting research includes screening of current low elevation orchard parents for resistance to mistletoe, wood studies, and a genotype-by-shade interaction nursery bed study.

True Firs (Charlie Cartwright)

The true firs (*Abies* spp.) have proven to be remarkably poor candidates for development of seed orchards. Several small trials researching methods of inducing cone crops (such as varied environments, fertilization, and micro-tenting) have been completed with limited success. Despite this, due to considerable variability in growth characteristics by provenance, sizeable genetic gains are still attainable with selection of best seed sources. To date, data to age 15 have been collected for grand (*A. grandis*) and noble fir (*A. procera*) test series with gains between 5 and 10% in volume at rotation attributable to best sources (after accounting for age/age correlation and test repeatability). Farm field trials have been measured to 5 years old for Pacific silver *(A. amabilis*) and sub-alpine firs (*A. lasiocarpa*) with 5-year-old data for wild site provenance tests of the former becoming available before 2007. Now that a gap in our seed collections from Idaho, Utah, and Colorado has been filled, a series of field trials for the latter will hopefully proceed within a couple of years.

Lodgepole Pine (Michael Carlson)

Interior lodgepole pine (*Pinus contorta* var. *latifolia*) has, for the past several years, been under ever increasing attack by the Mountain Pine Beetle (*Dendroctonus ponderosae*) with an estimated 10 million ha currently affected. By 2013 it is expected that 80% of the mature lodgepole pine trees in the province will be dead. Salvage harvesting has greatly accelerated over the past 5 years with approximately 44% of the provincial AAC now lodgepole pine (61% of the interior volume cut). Over 134 million pine seedlings were requested in 2006 representing one-half of all seedlings requested for 2007 planting. One and one-half percent of lodgepole pine seedlings currently planted are of seed orchard origin, 9.5% are from tested superior-provenance seed collections, and 89% from wild stand collections.

Over the past 6 years lodgepole pine seed orchard capacity has been increased with an intensive orchard parent selection program concentrating on 16–20 year-old first-generation wind-pollinated progeny trials for 7 SPUs. A total of 35 000 ramets has been grafted and 8 new orchards planted. In 2006 we continued selection work in two southern interior SPUs; the Nelson low and high elevation units. A single-tree weighted index score for total tree height (age 10 years) was used to rank progeny test trees. The index is based on family mean height and deviations of individual trees within family, with adjustments made for block(site) and site effects. Stem and crown form as well as disease and insect resistance traits were also integrated into the selection process. In addition, selections were made from a central interior SPU test series (the CP or Central Plateau) for a western gall rust resistance seed orchard to be grafted in 2007/08. This will be the first lodgepole pine disease resistance seed orchard in BC.

All second-generation SPU family test series are now planted (5) and the first planted (the PG) was measured in 2006 after 5 field seasons. Each SPU family test series consists of sets of factorial crossings for volume growth and for wood relative density. Genetic variation for resistance to Mountain Pine Beetle attack has been documented in a first-generation progeny test series (wind-pollinated families) and in two lodgepole pine seed orchards (at clonal, full-sib family, and provenance levels) (see Alvin Yanchuk's submission).

Western White Pine (Michael Carlson)

Enhancement of existing western white pine (*Pinus monticola*) seed orchards (2) continued with the selection of 26 parents from a 23-year-old blister rust resistance demonstration plantation and the continued selection of parents from our rust inoculation and screening program.

Ponderosa Pine (Michael Carlson)

Climate change predictions suggest increasingly drier and warmer conditions for the southern interior of BC. Ponderosa pine (*Pinus ponderosa*) inhabits the driest parts of the southern interior now and numbers of seedlings planted have increased gradually to over 1 million in 2006. In 2002, a 1992 planted 73 seed-source trial (2,400 trees) was thinned to the best trees within the best seed sources (450/2,400 based on total tree heights) to create a seed production stand/orchard. In 2005, based on 13-year stem volume data, an elite subset of 41 parents was re-selected from this population (41/450). These trees were grafted in 2006 and will be planted as a seed orchard in 2007. Final selection intensity is approximately 1 in 60 (41/2,400).

Weevil Resistance Program (John King)

The first-generation screening of Sitka Spruce (*Picea sitchensis*) for weevils (*Pissodes strobi*) is near completion and we are summarizing these results in a technical report that we hope to publish spring 2007. From this screening we have established two phases of an F_1 breeding program for weevil resistance and a third and final phase will be sown next year (2007). Parents were designated by their phenotypic resistance to the weevil and their source (mainly Haney or Big Qualicum). Some susceptible parents were also used. The trials were established in medium to high hazard sites but we also established a site in each of the phases on the Queen Charlotte Islands that are weevil free.

Selection and breeding work continues but our focus in the future for the breeding program will be to identify parents for specific traits. They will still be field assessed for resistance after weevil augmentation but a more detailed microscopic evaluation is being undertaken in order to classify parents according to putative mechanisms. This is particularly valuable for 'constitutive' types 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.

Ongoing also, for deployment, is evaluating weevil hazard. A series of trials has been established to test resistance over a variety of ecological and potential weevil hazard areas. The main objective is to aid in determining deployment guidelines. This exercise is being carried out with Don Heppner, the Coast Regional entomologist, and we hope to provide Regional guidelines for spruce over the next year.

Queen Charlotte Islands North West Hybrid Program (John King)

The Queen Charlotte Islands (QCI) program allows us to assess Sitka spruce growth free from weevil attack and supports the seed orchard program (SO142 and its replacement). Our major difficulty has been in getting 'free-to-grow' conditions, in this case not from weevil or brush but from deer browse, and a good deal of our maintenance effort is on browse protection. We are planning on completing height measurements in 2007.

The transition program is designed mainly to test seed transferability in a very environmentally heterogeneous area with pressures from both frost and weevil. We completed 5-year height and frost assessments and are now evaluating these trials for weevil attack. We hope to complete our assessment of this trial series in 2007. We continued to make some selections of good hybrid weevil resistant trees for possible orchard deployment.

Coastal Western White Pine (John King)

A dual strategy is proposed for white pine that in the main program involves selection and breeding for 'horizontal resistance' mechanisms. These mechanisms include such things as slow canker growth: the rust can invade the tree but cankers are slow to form and grow thus allowing the tree to have cankers but to survive to them. We constructed pedigreed F_1 populations from such resistant trees from all three of the western white pine programs (BC, Idaho, and Oregon). The second strategy will seek to isolate and determine major gene resistant genotypes. The production population will come from seed orchards where the female ramets are selected from the parental or F_1 population but the pollen would come from a separate major gene population. This provides a pyramided approach where the major gene resistant genotypes can provide 'up-front' resistance but trees will also have been selected for 'horizontal' mechanisms that provide for 'downstream' resistance if virulence arises.

The next few years will see us refine our inoculation and testing program. New *Ribes* spp. gardens are being established at Cowichan Lake Research Station. We also hope to establish a ‘stone pine’ species and provenance testing program. Whitebark pine (*Pinus albicaulis*), which is the North American stone pine and is highly valuable as a high mountain ecological keynote species, is under heavy pressure from both blister rust and Mountain Pine Beetle. Understanding how the ecological equivalents in Eurasia handle blister rust in an endemic environment may help us to preserve this species.

Coastal Broadleaf Species (Chang-Yi Xie)

Interest in the commercial management of native broadleaf tree species in BC is increasing rapidly. Questions relating to seed transfer, seed source selection, potential genetic gain in growth and wood quality, seed (or cutting) production and management, and gene conservation once had little relevance to broadleaf tree species in the province but are now burning issues. At the present time, there are only a few applied gene resources management trials for broadleaves and very limited information on which to base gene resource management policy decisions.

Red alder (Chang-Yi Xie)

There are two long-term red alder (*Alnus rubra*) provenance-progeny test trials, one located at Bowser on Vancouver Island and another at Thunderbird near Terrace. Forty-two provenances, each with 5 families, are tested at each site. Ten-year results suggest that two seed zones (breeding zones), one for the southern and another for the northern region, should be delineated to minimize maladaptation and maximize gain in seed deployment and tree breeding. The proper boundary between the two zones seems to be latitude 52°N. Significant latitudinal patterns of adaptive genetic variation in growth and survival suggest about a 5% increase in mortality for each degree of northward and about a 1.5 dm^3 decrease in stem volume for each degree of southward transfer of seed sources. Two base populations are constructed, one for each breeding zone. The base population for the northern zone consists of 800 trees of 68 families from 24 provenances north of 50°N at Thunderbird, while the base population for the southern zone consists of 929 trees of 116 families from 36 provenances south of 54°N. Ninety forward selections have been made for the southern zone based on stem volume and other quality characters such as form and branch number and size. The average breeding value of the selections is about 18%. Selection for the northern zone will be conducted in 2007.

Black Cottonwood (Chang-Yi Xie)

Two long-term black cottonwood (*Populus balsamifera* var. *trichocarpa*) provenance-clonal trials have been established with about 450 clones from 120 provenances. One site is located near Terrace and another at Red Rock, near Prince George. A southern site at Harrison Mills will be established in the spring of 2007. Gene conservation, long-term genecology studies, and clonal selection are the main objectives of these tests.

Big-leaf Maple (Chang-Yi Xie)

Seeds from 43 bigleaf maple (*Acer macrophyllum*) provenances were collected in 2005. Thirty provenances are located in BC, 4 in Washington, 4 in Oregon, and 5 in California. Ten trees were sampled in each provenance and seeds from each tree were bagged separately. Seedlings have been raised and four provenance-progeny test trials are going to be established in the spring of 2007, two on Vancouver Island and two on the coastal mainland.

Black Cottonwood and its Hybrids (Michael Carlson)

Clonal testing of native black cottonwood and its hybrids (mostly with *P. deltoides*, eastern cottonwood) began in 1989. The most recent testing effort involves 50+ hybrid clones of central BC interior origin black cottonwoods with northern origin eastern cottonwoods. Growth and adaptation comparisons with eastern shelterbelt *Populus* spp. clones will be made in this trial. This effort is an adjunct to the black cottonwood genecology trial described above by Chang-Yi Xie. Growth and adaptation studies of a small number of hybrids continue in the Kootenay River valley near Creston. One clone in the 1997 plantings has produced approximately 350 m^3 of stem wood per ha.

Interior Broadleaved Species - Paper Birch (Michael Carlson)

Heretofore paper birch (*Betula papyrifera* var. *papyrifera*) has received little commercial attention (firewood mostly) but, like red alder (*Alnus rubra*) on the BC coast, this species is getting more attention annually with increased utilization for flooring, furniture, and small milled products. Experimentation with paper birch started with an 18 seed-source genecology trial in 1996, a 195 family wind-pollinated family trial in 1998, and a second genecology trial in 2001. All three trials were measured in 2006. The oldest trial data will be used to derive the first seed transfer guidelines for the species. The family trial at 9 years in the field will be the source of selected parents (approximately 20–40) for the first paper birch seed orchard(s) for BC. Cuttings for grafting and rooting will be collected from selected test trees in winter of 2006/07 with propagation in spring of 2007. We will be following the advice of the much experienced Finnish birch breeding program staff in the development of indoor (greenhouse) seed orchards for paper birch. Extension work with European silver birch (from Finland's breeding program) continues with private landowners.

Western Redcedar (John Russell)

Management of the western redcedar (*Thuja plicata*) gene resource, a major component of BC's coastal mixed-coniferous forests is in its infancy. The program had it's beginnings in 1990 focussing on gene conservation and genecology. A tree breeding program was initiated in 1996.

Tree breeding for western redcedar involves the development of three overlapping breeding populations from first-generation selections: 1) volume growth (main population), 2) heartwood durability, and 3) deer resistance. Volume Growth: Breeding for first-generation polycross testing, involving approximately 1,000 parents for the maritime low SPU, is complete. Seven annual series of tests have been established totalling 46 sites covering six SPUs. Parental breeding values for volume at rotation are currently available for series 1 through 5 based on 7-year-heights (615 parents). Rogued and new seed orchards are currently producing seedlots with a genetic worth of up to 7%. Approximately 50 parents from the first three series have been selected based on volume growth for the advanced generation population and established into breeding orchards. Assortative mating with selfing is currently ongoing. Heartwood Durability: The original 350 BC parent trees selected in the early 1970's (also represented in the first three series of polycross testing, described above) were assessed for heartwood durable chemicals using wood cores from grafted ramets established in the Cowichan Lake Research Station (CLRS) clonebanks and industrial seed orchards. Fifty selections based on gamma- and beta-thujaplicin concentration have been cloned and established in the advanced generation breeding orchard. Deer Resistance*:* Selections for a deer resistant population were made from both the Holt Creek family/population study (within-family forward selections) and the CLRS clonebank (parental backward selections). Approximately 100 selections for high needle monoterpene concentration and low deer browse have been cloned and established into a breeding orchard. In addition, approximately 50 genotypes have been selected for low monoterpenes and high deer browse. This population will serve as a control for deployment trials with the resistant population. Assortative mating with selfing is currently ongoing.

Yellow-cedar (John Russell)

Yellow-cedar (*Chamaecyparis nootkatensis*) is a major component of high elevation coastal BC forests. Yellow-cedar propagates vegetatively in nature and, in addition, cone crops are usually infrequent and seed viability and germination, historically poor. The genetic management of this valuable species which includes gene conservation, genecology, and tree breeding has focussed on a clonal strategy. Recent advances in pollen and seed management will assist in advanced generation breeding and future rejuvenation of select clones through sexual recombination for operational stock.

Fifteen-year measurements were completed for the yellow-cedar provenance trials, which are comprised of approximately 50 populations established on 10 sites throughout BC. Preliminary analyses indicate the lack of a correlation between seed-origin climatic and geographical descriptors and mean provenance performance as seen in the 10-year data as well. Current liberal seed transfer guidelines reflect this random provenance genetic variation.

First-generation cloned progeny tests have been established and the focus is currently on maintenance and measurements. The first two series of trials have been measured at eight years in the field and the third series, five years. Clonal values from approximately 5,000 clones including genetic material from Western Forest Products' (WFP) clonal trials have been released and the best clones established in operational hedge orchards. Advanced generation selections based on volume growth from the WFP clonal program and from Ministry genetic trials have been established in three breeding orchards including one high elevation site for pollen production. Maintenance continued in 2006 in these orchards, as well as monitoring pollen performance and production for advanced generation breeding.

FOREST GENETICS, SEED TRANSFER AND PHYSIOLOGY AND PEST RESEARCH

Resistance to Mountain Pine Beetle (Alvin Yanchuk)

As noted above under Mike Carlson's submission, we are experiencing a dramatic impact on our genetic resources of lodgepole pine in BC due to Mountain Pine Beetle (MPB). Dozens of genetic trials are being heavily attacked and mortality is almost total in many of them. As unfortunate as this is, it is allowing us the opportunity to look for genetic variation in attack and resistance to MPB. One particular open-pollinated (OP) trial was hit with MPB where ~50% of the trees had signs of attack, which is optimum for initial genetic discrimination. Provenance effects and family effects were highly significant, so it appears that MPB does make choices with respect to initial colonization of trees it ultimately bores into. Other 'sister' tests (i.e., with the same families) are currently being assessed for resin flow and bark chemistry (by D. Ott, a graduate student at University of Northern BC) to help elucidate which phenotypes MPB stays away from, at initially a moderate attack level. In the summer of 2006, the same OP trial was further attacked and assessed for survival and all provenance effects disappeared, which suggests that when the pressure increases the MPB ignores previous mechanisms. However, family effects were still significant suggesting that some strong genetic variation is present, more along the lines of resistance rather than initial choice. (A manuscript has been submitted on this research). Many other trials are being further assessed for differential attack among genotypes (e.g., seed orchards) and we will continue to examine what the underlying mechanisms of MPB genotypic choice and resistance may be.

Climate Change (Greg O'Neill)

New tools in genecology (GIS, fine-scale climate models, new analytical techniques) and the spectre of climate change have resulted in a resurgence of interest in adaptation in tree breeding programs. Opportunities may exist to mitigate (and in some locations to reverse) negative forest health and productivity impacts due to climate change, by better matching of seedlot and site climates, facilitated migration of seedlots and species, increased genetic diversity through deployment of multiple species and seedlots on a landscape, and by implementing transfer function-based seed transfer systems.

Since CTIA 2004, key adaptation initiatives in the BC MoFR include: 1) Establishment of a large trial (18 test sites) of improved and natural stand seedlots of interior spruce. 2) Data collection from an interior spruce provenance trial (4 sites, 150 populations from western North America) that will furnish the first province-wide adaptive map of spruce. 3) Re-measurement and first stage of analysis of Illingworth's lodgepole pine provenance tests (43 sites; 32 years old). 4) Completion of two manuscripts that examine climate change impacts to lodgepole pine productivity and analytical approaches to estimating population response functions. 5) Completion of research developing an approach to accounting for non-climatic impacts in population response functions.

Physiology (Sylvia L'Hirondelle)

The adaptive physiology program tests genetic variation in phenology, frost hardiness, heat tolerance, photosynthetic potential, and other stress tolerances of BC tree species with a goal of maximizing field performance of planted seedlings while minimizing the risk of maladaptation. Recent projects include genetic variation in frost and heat tolerance in wild-stand and seed-orchard sources of interior spruce, frost hardiness testing of coastal conifer seedlings from genetically-improved seed sources for increased post-planting vigour, and changes in photosynthetic potential in interior spruce in response to changing photoperiod and temperature.

Cone and Seed Pest Research (Ward Strong)

The new cone and seed pest research program is situated at the Kalamalka Research Station. An office and lab have been set up, and 5 major projects started in 2006: 1) *Leptoglossus* host-finding. Cooperator: Gerhard Gries's lab, Simon Fraser University. The Gries lab has demonstrated a novel host-finding mechanism in *Leptoglossus* which has very strong management implications for monitoring and control of this insect. 2) *Leptoglossus* mark-release-recapture. Cooperator: Sylvie Desjardins, University of British Columbia (UBC)-Okanagan. Marking methods, marking effects on longevity and behaviour, and preliminary data gathering on dispersal and population densities resulted from the first year of this project. 3) *Adelgid* species and life history. Cooperator: John McLean's lab, UBC-Vancouver. A graduate student has been trained in *adelgid* identification, has gathered species identification and flight periods from 21 000 specimens of a 1996 insect collection at Kalamalka, and has plans in place for species' diversity, host plant associations, and life history traits in the future. 4 *Dioryctria* life history. Cooperators: Gary Grant, Natural Resources Canada and Jocelyn Millar, University of California-Riverside. Pheromone optimization, flight phenology, and life history traits were determined. 5) Pesticide trials. Four systemic active ingredients were tested with sprayable and injectable formulations, at both Interior and Coastal BC sites. Seed extraction should be completed by the end of 2006.

MOLECULAR GENETICS

Seed Orchard Research (Michael Stoehr)

Application of molecular markers to seed orchard management issues is continuing. Recent work included the evaluation of supplemental mass pollination in a lodgepole pine orchard and the estimation of pollen contamination. The molecular markers of choice for these studies are chloroplast DNA derived markers, as these are inherited paternally in conifers (i.e., via the pollen grain). The current practice of pollen monitoring in coastal Douglas-fir orchards is assessed using paternal analysis of orchard seed.

PUBLICATIONS

Alfaro, R.I.; van Akker, L.; Jaquish, B.; King, J.N. 2004. Weevil resistance of progeny derived from putatively resistant and susceptible interior spruce parents. For. Ecol. Manage. 202: 369–377.

Chen, X.-Y.; Hawkins, B.; Xie, C.-Y.; Ying, C.C. 2004. Age trends in genetic parameters and early selection of lodgepole pine provenances with particular reference to the Lambeth model. For. Gen. 10(3): 249–258.

Grossnickle, S.G.; Russell, J.H. 2005. Yellow-cedar and western redcedar ecophysiological response to fall, winter and early spring environmental conditions. Ann. For. Sci. 62: 1–8.

Grossnickle, S.G.; Fan, S.; Russell, J.H. 2005. Variation in gas exchange and water use efficiency patterns among populations of western redcedar. Trees Structure and Function 19(1): 32–42.

Hak, O.; Russell, J.H. 2004. Environmental effects on yellow-cedar pollen quality. For. Gen. Council Extension Note No. 5, 9p.

Hamann, A.; Aitken, S.N.; Yanchuk, A.D. 2004. Cataloguing *in situ* protection of genetic resources for major commercial forest trees in British Columbia. For. Ecol. Manage. 197: 295–305.

Johnson, G.R.; Cartwright, C. 2005. Genotype x shade effects for western hemlock. Can. J. For. Res. 35: 1496–1501.

Khasa, D.P.; Jaramillo-Correa, J.P.; Jaquish, B.; Bousquet, J. 2006. Contrasting microsatellite variation between subalpine larch and western larch, two closely related species with different distribution patterns. Mol. Ecol. (in press)

Kimball, B.A.; Russell, J.H.; Griffin, D.L.; Johnston, J.J. 2005. Response factor consideration for the quantitative analysis of western redcedar (*Thuja plicata*) foliar monoterpenes. J. Chromatog. Sci. 43: 253–258.

King, J.N.; Hunt, R. 2004. Five needle pines in British Columbia, Canada: Past, present and future. Pages 12–19. *In* R.A. Sniezko, S. Samman, S.E. Schlarbaum, H.B. Kriebel, eds. Breeding and genetic resources of five-needle pines: growth, adaptability, and pest resistance. IUFRO Work. Party 2.02.15, Medford, OR, 23–27 July 2001, USDA, For. Serv., Rocky Mountain Res. Sta. RMRS-P-32, 259 p.

King, JN.; Alfaro, R.I. 2004. Breeding for resistance to a shoot weevil of Sitka spruce in British Columbia, Canada. *In* M.J. Carson and C. Walter, eds. Plantation Forest Biotechnology for the 21st Century. 2004 Forest Research, New Zealand.

King, J.N.; Alfaro, R.I.; Cartwright, C. 2004. Genetic resistance of Sitka spruce (*Picea sitchensis*) populations to the white pine weevil (*Pissodes strobi)*: distribution of resistance. Forestry 77: 269–278.

King, J.N.; David, A.; Smith, J.A. Genetic approaches to the management of blister rust in White Pines. For. Ecol. Manage. (accepted)

Krakowski, J.; Benowicz, A.; Russell, J.H.; El Kassaby, Y.A. 2005. Effects of serial propagation, donor age and genotype on *Chamaecyparis nootkatensis* physiology and growth traits. Can. J. For. Res. 35: 623–632.

L'Hirondelle, S.J.; Binder, W.D. 2005. Temperature stress tolerance of conifer seedlings after exposure to UV-B radiation. Photochem. Photobiol. 81: 1094–1100.

L'Hirondelle, S.J.; Simpson, D.G.; Binder, W.D. 2006. Overwinter storability of conifer planting stock: operational testing of fall frost hardiness. New For. Published online Oct. 26, 2006. http://www.springerlink.com/content/w6647100745564r8/

L'Hirondelle, S.J.; Simpson, D.G.; Binder, W.D. 2006. Predicting planting stock quality. BC Min. For. and Range, Res. Br., http://www.for.gov.bc.ca/hfd/pubs/Docs/P/P078.htm

L'Hirondelle, S.J.; Simpson, D.G.; Binder, W.D. 2006. Chlorophyll fluorescence, root growth potential, and stomatal conductance as estimates of field performance potential in conifer seedlings. New For. (accepted)

Millar, J.G.; Grant, G.G.; McElfresh, J.S.; Strong, W.B.; Rudolph, C.; Stein, J.D.; Moreira, J.A. 2005. (3Z,6Z,9Z,12Z,15Z)-Pentacosapentaene, a key pheromone component of the Fir Coneworm moth, *Dioryctria abietivorella*. J. Chem. Ecol. 31: 1229–1234.

McKay-Byun, A.; Godard, K.-A.; Toudefallah, M.; Martin, D.M.; Alfaro R.I.; King J.N.; Bohlmann, J.; Plant, A.L. 2006. Wound-induced terpene synthase gene expression in Sitka spruce that exhibit resistance or susceptibility to attack by the white pine weevil. Plant Physiol. 104: 1009–1021.

Namkoong, G.; Lewontin, R.C.; Yanchuk, A.D. 2004. Plant genetic resource management: The next investments in quantitative and qualitative genetics. Gen. Res. Crop Evol. 51: 853–862.

O'Connell, L.M.; Russell, J.H.; Ritland, K. 2004. Fine-scale estimation of outcrossing in western redcedar with microsatellite assay of bulked DNA. Heredity 93: 443–449.

O'Neill, G.A.; Russell, J.H.; Hooge, B.D.; Ott, P.K.; Hawkins, C.B.D. 2005. Estimating gains from genetic tests of somatic emblings of interior spruce. For. Gen. 12: 57–66.

Russell, J.H.; Burdon, R.D.; Yanchuk, A.D. 2004. Inbreeding depression and variance structures for height and adaptation in self and outcross *Thuja plicata* families in varying environments. For. Gen. 10: 171–185.

Russell, J.H.; Hak, O. 2006. Effect of gibberellin A_3 inductions on male and female cone production and seed quality in western redcedar (*Thuja plicata*). West. J. Appl. For. (in press)

Stoehr, M.U.; Mehl, H.; Nicholson, G.; Pieper, G.; Newton, C. 2006. Evaluating supplemental mass pollination efficacy in a lodgepole pine orchard in British Columbia using chloroplast DNA markers. New For. 31: 83–90.

Stoehr, M.U.; O'Neill, G.A.; Hollefreund, C.C.A.; Yanchuk, A.D. 2005. Within- and among-family variation of orchard and wild-stand progeny of interior spruce in British Columbia. Tree Gen. Genom. 1: 64–68.

Stoehr, M.U.; Webber, J.E.; Woods, J. 2004. Protocol for rating seed orchard seedlots in British Columbia: quantifying genetic gain and diversity. Forestry 77: 297–303.

Stoehr, M.U.; Webber, J.E.; Hollefreund, C.C.A.; Painter, R.A. 2004. Potential pollen contamination effects of progeny from an off-site Douglas-fir seed orchard. 9-year field results. Can. J. For. Res. 34: 981–984.

Strong, W.B. 2006. Seasonal changes in seed reduction in Lodgepole pine cones caused by feeding of *Leptoglossus occidentalis* (Hemiptera: Coreidae). Can. Ent. (accepted)

Wang, T.; Hamann, A.; Yanchuk, A.D.; O'Neill, G.A.; Aitken, S.N. 2006. Use of response functions in selecting lodgepole pine populations for future climates. Global Change Biol. 12: 1–13.

Wang, T.; Russell, J.H. 2006. Evaluation of selfing effects on western redcedar growth in operational plantations using Tree and Stand Simulator (TASS). For. Sci. 52(3): 281–289.

Xie, C.-Y.; Fu, Y.-B.; Yanchuk, A.D. 2006. Accuracy of ranking individuals for forward selection in advanced generation progeny testing with different field designs: a computer simulation. Silvae Genet. 55(2): 70–77.

Xie, C-Y.; Murphy, J.C.; Carlson, M.R. 2006. Predicting individual breeding values and making forward selections for seed production of interior lodgepole pine (*Pinus contorta* ssp. *latifolia*) in British Columbia. New For. (in press)

Ying, C.C.; Yanchuk, A.D. 2006. The development of British Columbia's tree seed transfer guidelines: Purpose, concept, methodology, and implementation. For. Ecol. Manage. 227: 1–13.

Yanchuk, A.D.; Bishir, J.; Russell, J.H.; Polsson, K.H. 2006. Variation in volume production through clonal deployment: results from a simulation model to minimize risk for both a currently known and unknown future pest. Silvae Genet. 55(1): 25–37.

PROCEEDINGS

OF THE

THIRTIETH MEETING

OF THE

CANADIAN TREE IMPROVEMENT ASSOCIATION

PART 2

Symposium

CANADA'S FORESTS – ENHANCING PRODUCTIVITY, PROTECTION & CONSERVATION

Charlottetown, Prince Edward Island
July 24–27, 2006

Editors
J.A. Loo and J.D. Simpson

COMPTES RENDUS

DU

TRENTIÈME CONGRÈS

DE

L' ASSOCIATION CANADIENNE POUR L' AMÉLIORATION DES ARBRES

2^e PARTIE

Colloque

LES FORÊTS DU CANADA : MISE EN VALEUR DE LA PRODUCTIVITÉ, DE LA PROTECTION ET DE LA CONSERVATION

Charlottetown, Île-du-Prince-Édouard
24–27 juillet 2006

Rédactrice/Rédacteur
J.A. Loo et J.D. Simpson

TABLE OF CONTENTS

KEYNOTE

INVITED SYMPOSIA PAPERS

PANEL PERSPECTIVE

VOLUNTEER PAPER ABSTRACTS

TREE SEED WORKING GROUP WORKSHOP ABSTRACTS

WOOD QUALITY WORKSHOP ABSTRACTS

POSTER ABSTRACTS

KEYNOTE

CTIA 1953–2006; WHAT LIES AHEAD?

Bruce Dancik

Devonian Botanic Garden
University of Alberta
Edmonton, AB
T6G 2E1
E-mail: Bruce.Dancik@afhe.ualberta.ca

This paper reviews some of the history, highlights, and accomplishments of the Canadian Tree Improvement association (CTIA) over the past half-century and presents some challenges that face us as we look ahead to the next few decades.

THE PAST

The first activity related to what later become CTIA was the First Conference on Forest Tree Breeding and Propagation, that was held in 1937 at the National Research Council of Canada (NRC) Laboratories, probably the classic building at 100 Sussex Drive. A grand total of five people attended! There were several more meetings held over the next year-and-a-half. Finally in June of 1939, the Subcommittee on Forest Tree Breeding under the Associate Committee on Forestry of NRC held its first meeting. Over the next 14 years, there were 24 such meetings.

In 1953, after the Associate Committee on Forestry ceased to function, the first meeting of the Committee on Forest Tree Breeding (which would later become the CTIA) was held in Ottawa in the old Forest Products Laboratory at Metcalfe and Isabella Streets. Twelve people attended. This committee had been set up under the Forestry Branch, Department of Resources and Development, and its main function "…should be to meet and to discuss the various phases of forest tree breeding". After much discussion at that meeting, it was agreed that a committee of H.D. Heaney, Mark Holst, and Carl Heimburger would draw up terms of reference for the committee. They discussed their work, set up a membership committee consisting of the Chair and Secretary, and retained the Chair (H.D. Heaney) and Secretary (Carl Heimburger) for another year. The meeting lasted a full day and the minutes included appendices with reports from five of the members (5/12 or about 40% submitted reports). They talked about seed viability, vegetative propagation, looking for polyploids of *Populus*, provenance studies, inter- and intra-specific crosses, selection for disease resistance (Dutch elm disease, blister rust), among other things.

In 1954 the second meeting of the committee took place in the same location, and much of the discussion reminded me of graduate student seminars today. At the meeting, the attendees presented reports, and then questioned each other about those reports and work completed. They adopted terms of reference. They talked about giving lectures in the forestry schools and having visiting lecturers. They suggested inviting an outstanding geneticist from U.S. to a future meeting. They adopted several membership categories (Active, Sponsoring, Corresponding), that still stand today.

The third meeting was held over a day-and-a-half in 1955 in the same place. At this meeting, Kit Yeatman became a new member. During the business part of the meeting, members started a tradition, which many of us continue to be amused about, of making multiple, detailed corrections of the minutes of the last meeting! There also was much discussion about possible lectures at universities, preservation of superior stands, inviting visitors, and the format of future meetings. There was a suggestion of having two-day meetings, with a brief business meeting and longer discussion of topics, and the rotation of meetings at different locations across the country. It was suggested that members submit their reports prior to the meetings, so that there would be adequate time to peruse and discuss the reports at the meeting. Someone wanted minutes to be marked confidential, as were the minutes of the old subcommittee. They started worrying about funding for activities and someone remarked that the NRC used to pay the costs of meeting attendance! The appended reports got longer (11 pages each for Heimburger and Carmichael, 12 pages for Mark Holst, and 1 to 6 pages for each of the others).

The fourth meeting was held at Maple, Ontario in 1956. During the meeting, Carl Heimburger suggested that 200 acres could be obtained at Turkey Point for a substation for genetics field trials, if costs of clearing and fencing could be met. There was an attempt to have the first standardized reports at the meeting. Fifteen member reports were submitted for the meeting, and the meeting included a symposium on poplar breeding in North America. There were now 22 Active, 16 Sponsoring, and 1 Corresponding members.

At the fifth meeting in 1957 at Petawawa, a motion was passed that the Proceedings of the meetings would be in two parts, bound separately, containing minutes for members only and reports for general distribution, respectively. By this time Active members were distributing annual reports in advance of the meeting and the minutes reflected the discussion of those reports at the meeting. As might have been expected, this led to good, detailed discussions of the work of various members at their respective stations. This fifth meeting featured a large Round Table Discussion of Provenance Problems in Tree Species, chaired by Jack Farrar. Notes from that discussion took up 10 pages in the minutes. The meeting also featured a small symposium.

In 1958 at the sixth meeting at Macdonald College, Ste. Anne de Bellevue, Québec, a motion to have meetings in two-year cycles was passed, along with another (proposed by Heimburger, seconded by Holst) that removed the requirement of a report from those members who attended other tree breeding meetings where their reports would be published elsewhere as part of those other proceedings. For an old editor like me, this showed that Heimburger and Holst recognized the problems of duplicate publication! This meeting had the first mention of a banquet (C. Syrach Larsen was the guest speaker), and also featured a seminar on Timber Quality and Genetics, along with a tour of Morgan Arboretum. There were eight guests from U.S. and Europe, and many of the guests participated in an informal talk on the development of forest tree breeding throughout the world, and in the seminar. Carl Heimburger reported on “The role of “Rhubarb” in forest tree breeding”.

The seventh meeting in 1960 was the first one held out west – at Lake Cowichan, BC. New members included Oscar Sziklai. In the good traditions of the many members who religiously followed Roberts Rules of Order, a subcommittee was formed to review and revise the terms of reference. During the technical meeting, reflecting the male chauvinistic traditions of the time, “Dr. Orr-Ewing called the meeting to order…and asked that each man present should introduce himself to the meeting”.

In 1964 the ninth meeting was held back at Petawawa, Ontario. Highlights included a panel discussion on red pine (*Pinus resinosa*) breeding, with noted panelists Mark Holst, Don Fowler, Don Lester, Hans Nienstaedt, and Johnny Wright. Stan Rowe led a discussion on his paper, “Environmental preconditioning with special reference to forestry” that had appeared in Ecology (45: 399–403) earlier that year.

The 1966 meeting (10th) was held at the University of British Columbia in Vancouver. Mark Holst reported on seed and plant certification and Bob Kennedy (from UBC) reported on the subcommittee on wood properties. New members included Al Gordon, Jerry Klein, and Marie Rauter. There was a technical meeting with presentations by Jack Duffield, Tom Greathouse, and Bob Campbell, among others, on selection, seed orchard establishment and management, and flower induction. Gene Namkoong was an attendee and was involved in lots of the discussion.

At the 12th meeting in 1970 at Laval University, Québec, there was a symposium on Tree Breeding and Silviculture. New members included Doug Pollard and Keith Illingworth. Jerry Klein moved that the next meeting be held a year earlier (1971).

The 13th meeting was held in 1971 in Prince George, BC, and included a symposium on Conservation of Forest Gene Resources. In the business meeting, there was a big report from the subcommittee on procedures, which included 25 proposals. A motion was passed to have the next and subsequent meetings held on a two-year cycle.

In 1973 (the 14th meeting, in Fredericton, NB) I attended my first meeting and this was the first meeting under a new name, the Canadian Tree Improvement Association. A Constitution and By-laws for the new association were approved. A working party for conservation of endangered arboreal germplasm was set up. Tom Ledig chaired a symposium on interspecific and interprovenance hybridization that included contributions from Kris Morgenstern, Mark Holst, Don Fowler, Howard Kriebel, Don Lester, Bill Critchfield, Louis Zsuffa, and many others.

In 1977 at the 16th meeting in Winnipeg, Manitoba, a symposium was held on the contribution of forest genetics to the urban environment (jointly with Genetics Society of Canada and the Canadian Botanical Association). Until I reviewed all of these proceedings, I had forgotten that I had made the introduction to that symposium.

At the 17th meeting in 1979 in Gander, Newfoundland, a forest genetics scholarship fund committee was established. During the business meeting, it was decided to plan for the next three meetings at each meeting. This meeting also included a symposium on tree improvement in the boreal forest.

The 18th meeting at Duncan, BC, in 1981 was chaired by Chris Heaman. New members included Bill Cheliak, Yousry El-Kassaby, Barry Jaquish, Sally John, Don Lester, Glen Dunsworth, Dale Simpson, Steve Ross, Don Lester, and Bill Parker. The education committee reported that it had not been successful in raising funds for a scholarship. The meeting included a panel discussion on spruces, hard pines, west coast species, along with a symposium on seed orchards and strategies for tree improvement.

In Toronto in 1983, the 19th meeting featured a symposium on clonal forestry, along with a discussion on gene conservation led by Kit Yeatman.

Without continuing, I think that I have provided you with some of the flavour of these meetings. More recent ones had themes like maintaining biodiversity, evolution and tree breeding, genetic resources management, integrating tree improvement with sustainable forest management practice, enhancing productivity, etc. You can see a pattern in all of these themes and symposia, in which typically they were particularly timely, because of the issues in forestry and society at the time.

CHALLENGES FOR THE FUTURE

Let us now look at a few issues, ideas, and challenges that I think will face the CTIA and you as forest geneticists and breeders in the future. Some of these have been developing for some time, and others have more recently appeared on the horizon.

Before, I get too far, I strongly believe that traditional testing of populations, provenances, and families, and selection and breeding, especially using traditional technologies will continue to be the core of what many of us do, and will not diminish in importance.

Yes, biotechnology will be used – it's even becoming mainstream! – but I think more for special situations , such as introduction of a gene for specific resistance, and even then, more as a supplement to traditional breeding activities. For example, we might not be able to find a gene or genes for resistance to a particular pest in one species, but can find it in another. In that case, instead of working through hybridization, we may instead try to insert the desired gene in some individuals of our species, and then use traditional breeding methods to increase our output of individuals carrying the gene.

And in any forest genetics or tree breeding work, you're certainly going to have to be more aware of genetics in terms of ecosystems and landscapes in your thinking, and well aware of the world around you and not just the species you are working with.

On the other had, I'm also aware that some big changes will come, and things we have accepted and expected will not be relevant or around anymore. I was reminded of this when I listened to a couple of Futurists recently, who were commenting on the questions/comments they got from young people around them – and I quote:

> "Dad, what's a cassette?"
>
> (and overheard from a young colleague) "It is SO inconvenient to lug around a notebook computer!"

In forestry, only 10 or 15 years ago (or even less), when there were quite a few prominent voices saying that (for much of the country, anyway, where there are large tracts of crown land) we had to sell or privatize crown land to ensure investments in tree improvement or any forestry activities – that tenure was not enough. And they used the U.S. example as a model. Well, it appears that industrial ownership isn't as secure as we were led to believe. Many companies are dumping forest lands, primarily for vacation properties – some for mega-estates, as discussed in this article.

I recently read an article in National Geographic where, in Florida, the St. Joe Company is developing many acres of their forest lands in Gulf and Bay counties for sale for housing/vacation properties. They are actually moving 13 miles of U.S. highway 98 more than a mile inland so they can develop and sell prime oceanfront lots. So much for the advantages of industrial ownership of forest lands! So, be ready for anything.

There are several challenges or opportunities that I see for CTIA.

The biggest one certainly is climate change or global warming, and for those of us dealing with long-lived perennials like trees this is a huge issue – probably the one that overrides any other issue. We're not talking about losing an annual crop or even moving people or communities – we're talking about plants that can't walk away, that may be half-way through their lives or half-way to maturity possibly finding conditions not so great for growth or even survival. The question is: what do you plant now? What do you breed for?

The answers aren't exactly clear. For most of us, in most areas, it will be warmer, but how much? When? Will it be drier or moister? Lots of questions, even with the variety of models most of us have seen. On the anecdotal level, we've all been seeing some changes already. Where I live, for example, the birches have taken a real beating, and even the spruces are suffering – with far greater mortality in the last couple of years than had been seen over several decades. In British Columbia and now Alberta, the mountain pine beetle has ravaged many stands of lodgepole pine (*Pinus contorta*), and there is a real concern that it will jump to jack pine (*P. banksiana*) and proceed eastward across the boreal forest and most of the other provinces. On the other hand, oaks, which had been kind of an introduced novelty in our Alberta cities (in spite of my joke to students in my woody plants course that if we could wait another 10 000 years (since glaciation), we'd probably see bur oak marching up the rivers from Winnipeg all the way to the Rockies), are looking more vigorous and happy than I've ever seen them. So maybe we can plan ahead if we're careful – and lucky.

Another consequence of climate change is fire frequency. Mike Flannigan of the Canadian Forest Service reports that up to the 1970s, fires had been burning around 1M ha/year in Canada. In the past thirty years, the area burned has averaged 2.6 M ha/year! This has tremendous implications for rotation calculations and certainly for the area harvested and regenerated, and for how we handle regeneration or if we plant selected stock or different species.

By the way, there is a recent short perspective on Permafrost and the Global Carbon Budget by Zimov, Schuur, and Chapin in the 16 June 2006 issue of Science that suggests that climate warming will thaw permafrost, releasing trapped carbon from this high-latitude reservoir and further exacerbating global warming.

If global warming is not enough of a challenge, let's combine that with economics of the forest industry. The long-expected paperless office may not be here, but it certainly is starting to have an effect, as has internet news on newspapers. North American newsprint sales fell 8.5% as of January 2006 compared with a year ago. The New York Times just announced that it plans to eliminate 250 jobs and reduce the size of its pages by 3.8 cm in 2008, reducing the space devoted to news by at least 5.5%. USA Today and the Washington Post already have reduced their size, pointing to newsprint costs and the loss of readers and advertisement dollars to the Internet. All across the continent, newspaper circulation is falling, and they are losing their share of advertisements to other media, especially the Internet. For the year up to March 2006 we have seen 31 full or partial closures of pulp and paper mills in Canada, 13 of them in Ontario. Increased demands in China may take up some of the slack in demand but they may supply all of the demand from their own sources.

And now let's look at opportunities. We've all seen (or even planted) the variety of neat yard, garden, and street trees we see in our cities and towns. Some of us like the fastigiate form trees like *Populus tremula* c.v. *erecta* or even pines, like *Pinus resinosa* "Bancroft". In addition, all sorts of other shapes of various clones or cultivars have been popular literally for hundreds of years. Some of them are rather low and shrubby, fitting into lots of gardens and a few are really compact

I think we've often passed up great opportunities to propagate and sell these in conjunction with tree breeding programs. Those of you who are breeders see these odd-balls all of the time, but I think they represent a golden opportunity. Horticulture is the fastest growing activity on the continent (#1 activity now!) – something like $3.5B in sales in Canada last year.

Finally, I have a challenge for CTIA. As I reviewed a lot of notes and minutes for old Committee on Forest Tree Breeding/CTIA meetings, I got to thinking about all of the data in files and boxes left behind by long-gone geneticists and breeders. How much is there? Who knows? Where is it? Who knows?
I have a proposal: that CTIA promote a data registry (electronic, preferably) at a maintained site for all of the data all of you and your predecessors have generated, and your successors will generate, so that it can be available and useful for future generations of workers, so we don't keep re-inventing the wheel. Some journals, notably those published by the Ecological Society of America, are encouraging deposition of original data on a site maintained by the journal. If you publish in any of our NRC journals, such as the Canadian Journal of Forest Research, you can ask the editor about depositing your original data, which would then be linked to the on-line version of your article.

INVITED SYMPOSIA PAPERS

THE IMPORTANCE OF TREE IMPROVEMENT TO J.D. IRVING, LTD.'S FOREST MANAGEMENT STRATEGY

Blake Brunsdon

J.D. Irving, Limited
300 Union Street
Saint John, NB
E2L 4M3
E-mail: brunsdon.blake@jdirving.com

INTRODUCTION

J.D. Irving, Limited, headquartered in Saint John, NB, is an integrated company consisting of 12 sawmills, 7 pulp, paper, and tissue production facilities, and two nurseries. As well, the company owns 1.4 million ha of land in New Brunswick, Nova Scotia, and the State of Maine and manages one million hectares of Crown land in New Brunswick. We produce a variety of forest products and are ideally situated to serve the eastern United States market. The company embraces the following business principles: to remain competitive by continually modernizing and improving and to continue making investments that requires a secure and increasing future supply of timber. Intensive silviculture is the key in order for J.D. Irving to remain competitive and to meet important ecological and social goals. Tree improvement is a cornerstone of our intensive silviculture strategy.

GROWTH AND PRODUCTIVITY

Some of J.D. Irving's forest land is highly productive. Productivity today averages 3.5 m^3/ha/yr and is expected to rise to 4.5 m^3/ha/yr by 2030. This is in comparison to current productivity of 1.5 m^3/ha/yr on NB Crown land and 2.25 m^3/ha/yr for Finland and 3.0 m^3/ha/yr for Sweden. Productivity can be significantly impacted through silviculture. For example, if no silviculture is applied, average yield will be 100 m^3/ha at 50 years. If thinning is employed, productivity increases to 210 m^3/ha at 50 years and planting further increases it to 350 m^3/ha at 50 years. If genetically improved seedling are planted then yield is further increased to 425 m^3/ha at 50 years. Therefore, it is clear that tree improvement can substantially impact the annual allowable cut by providing the company with an allowable cut effect allowing us to harvest more now knowing that there will be sufficient volume to harvest in the future.

Increases in growth and volume in plantations established using genetically improved seedlings occurs over time in a step-wise fashion as gains are acquired from such factors as seed orchard roguing and moving from one generation to the next. For example, we anticipate an increase in volume of 18% from plantations of genetically improved white spruce at age 60 years as opposed to plantations planted with non-improved stock. Stem and crown form is also improved which undoubtedly affects harvesting costs and enhances utilization. Tree improvement also provides us with the means to mitigate impacts from climate change by allowing us to select and breed trees that will be better adapted to grow under changing climatic conditions. Another way that the company is accelerating the capture of gains from tree improvement is by practicing multi-varietal forestry on the most productive sites using highly productive, valuable species such as white spruce. This is accomplished through somatic embryogenesis. Crosses are made among superior trees identified from progeny tests. Clonal lines are created from a few seed from each cross. Samples of this tissue are placed into cryogenic storage while the remaining tissue is treated to produce clonal seedlings which are planted in field trials for further evaluation. As the field trials grow and develop, mixtures of these clones are deployed through our reforestation program. When data from the field trials tells us which clonal lines are the best, the poorer ones are removed from cryopreservation and discarded allowing us to focus our efforts on the better clones. Not only is growth improved but also genetic diversity in the resulting plantations is also enhanced because good individuals from poorer than average families and parents are often kept, there is greater flexibility to find diverse individuals with specific trait combinations, and more flexibility to respond to environmental change.

FOREST LEVEL IMPACTS OF TREE IMPROVEMENT

To understand the impact that silviculture, including tree improvement, can have on harvest at the forest level a simulation was run for NB Crown License # 6. A total of 275 000 m^3/yr could be sustainably harvested through to the year 2077 if there was no silviculture conducted. If silviculture was to cease now, 440 000 m^3/yr could be harvested. If the current level of silviculture continues, annual harvest increases to 625 000 m^3/yr and between the years 2030 and 2050 increases to almost 1 000 000 m^3/yr. This represents about a four fold increase in harvest volume over that of when no silviculture is conducted and tree improvement alone results in a 30% increase in available growing stock by the year 2050. When a similar analysis was conducted on our private land holding located at Black Brook, NB the result was greater than a six fold increase in harvest volumes at the end of a 75 year period due to intensive silviculture combined with commercial thinning.

ECOLOGICAL BENEFITS OF INTENSIVE SILVICULTURE

Intensively managed plantations develop physiologically faster thereby providing “mature” habitat sooner. We have found that commercially thinned stands and plantations provide key habitat features that are required for many old growth dependant species such as pine martin. Plantations established from genetically improved seedlings sequesters more carbon which helps Canada meets its Kyoto commitments. There are a number of challenges to incorporating silviculture into an ecologically balanced landscape: 1) providing stand level diversity (species, structural, and habitat diversity), 2) providing forest level diversity (age-class, covertype, and habitat objectives), 3) protecting special features and habitats, and 4) managing for multiple objectives.

CONCLUSIONS

Tree improvement is good for business, the environment, and for people!

GENETIC ARCHITECTURE OF PINE HOST INTERACTIONS WITH FUNGAL PATHOGENS

John M. Davis

School of Forest Resources and Conservation
University of Florida
Gainesville, FL, 32611-0410
USA
E-mail: jmdavis@ufl.edu

Disease-related traits are biologically interesting – and potentially very complicated – phenotypes for study by geneticists because they involve interactions between two organisms. Disease phenotypes are the visible manifestations of the interaction between two distinct genetic systems, one of the pathogen and one of the host. Thus genetic variation within either the pathogen or the host genomes can influence the outcome of the interaction, or the disease phenotype. Analysis of fusiform rust (inciting agent: *Cronartium quercuum* f.sp. *fusiforme*) and pitch canker (inciting agent: *Fusarium circinatum*) disease phenotypes in large and diverse germplasm collections of loblolly pine (*Pinus taeda* L.) have allowed estimation of genetic parameters, including heritability and genetic correlations for resistance-associated traits. These studies involving diverse germplasm coupled with field data have led to a more refined understanding of the genetic architecture of disease resistance, which in turn can guide decisions on selecting appropriate germplasm for reforestation, gene conservation, and/or breeding. Ultimately this work should permit the identification of genes that control and influence disease phenotypes, which in turn should enable a precise understanding of the biochemical mechanisms that condition disease phenotypes.

CONSERVING EVOLUTIONARY POTENTIAL: WHAT PRIORITY SHOULD BE PLACED ON PERIPHERAL POPULATIONS?

Sally Aitken[1], Bruno Fady[2] and Makiko Mimura[3]

[1] Centre for Forest Gene Conservation
Department of Forest Sciences
University of British Columbia
Vancouver, BC
V6T 1Z4
E-mail: sally.aitken@ubc.ca

[2] Institut National de la Recherche Agronomique
Unité de Recherches Forestières Méditerranéennes
Montfavet, France

[3] Gene Research Center
University of Tsukuba
Japan

There has been considerable debate over the value of peripheral populations for conservation. Evolutionary forces such as natural selection, genetic drift, and gene flow may differ in their relative strength from high-density core populations to low-density peripheral populations. Theory suggests that isolated populations at the edge of species ranges may be genetically depauperate due to small effective population sizes, repeated founder events, or isolation from gene flow. If peripheral populations are not isolated, they may be demographic sinks, swamped, and sustained by gene flow from source populations in the centre of the species range that prevents local adaptation. On the other hand, peripheral populations are often found at the limits of species' ecological tolerance, and thus may have extreme phenotypes. Research in Sitka spruce (*Picea sitchensis*) suggests that isolated peripheral populations have less genetic diversity than central populations, yet their diversity has been sufficient for local adaptation and the evolution of phenotypic extremes. However, the local adaptation of marginal populations that are not isolated appears to be somewhat restricted by gene flow. To determine whether these observed rangewide patterns of genetic variation are typical of conifers, we conducted a meta-analysis of population genetic data for 40 species of conifers in North America and Europe, and a total of 743 populations. Peripheral populations have significantly but only slightly less genetic diversity and slightly more inbreeding than central populations. Isolated populations have slightly less diversity than those at the margins of the continuous range. The diversity of central populations (as measured by average number of alleles per locus, proportion of loci that are polymorphic, expected and observed heterozygosity) is a good predictor of diversity in marginal and disjunct populations. The average inbreeding (F_{is}) of peripheral populations is not well predicted by central populations; however, disjunct populations have higher inbreeding levels, on average, than central populations. These data collectively suggest that genetic diversity will not limit the evolutionary potential of peripheral populations, and that they should be of high conservation value as they may be adapted to extreme environments.

TREE IMPROVEMENT AND SILVICULTURAL IMPACTS ON FOREST PRODUCTIVITY AND FINANCIAL VALUE TO LANDOWNERS IN THE SOUTHERN US

S.E. McKeand, B. Li, R.C. Abt and H.L. Allen

Department of Forestry and Environmental Resources
College of Natural Resources
PO Box 8002
NC State University
Raleigh, NC
27695-8002
E-mail: steve_mckeand@ncsu.edu

In the southern United States, tree improvement and silviculture are impacting today's loblolly pine plantations in unprecedented ways. When the best genetic material is planted and given the necessary resources to grow, mean annual increments of 20 $m^3 ha^{-1} yr^{-1}$ can be readily achieved on many sites. There are few other regions in the world where the use of integrated silvicultural systems and use of genetically improved planting stock is having as positive an impact on plantation productivity. Today's plantations are growing more than twice as fast as plantations of the previous rotation.

Forest managers have recognized that intensive plantation silviculture is like agronomy; both the plant and the soil need to be actively managed to optimize production. Genetic gains after 2 cycles of breeding can exceed 35% in volume production compared to unimproved loblolly pine. Based solely on growth gains, we have estimated that landowners can realize net present values of $125 USD to over $750 USD per hectare across a range of productivity and silvicultural management regimes simply by planting the best genotypes that are currently available from commercial and state forest nurseries. Landowners could pay more for the best genotypes, and the best seedlings would be well worth the additional costs.

Changes in forest ownership are impacting the way that landowners value silvicultural inputs and tree improvement. If landowners intend to establish, manage, and harvest plantations, then investment in tree improvement is a straightforward analysis. When land is "flipped" at shorter intervals and given current appraisal methods for evaluating forest stands, the answer is much more "confused". Results showing the benefits of tree improvement from various land ownership scenarios will be presented.

PROTECTING FUTURE FOREST TREE POPULATIONS THROUGH BREEDING: THE PAST, THE CURRENT AND THE FUTURE?

Alvin Yanchuk

BC Ministry of Forests and Range
Research Branch
722 Johnson St.
Victoria, BC
V8W 1N1
E-mail: alvin.yanchuk@gov.bc.ca

ABSTRACT

Tree breeders have, for close to 50 years, been selecting on heritable traits that will improve productivity of forest trees and several of these traits have focussed on pest and disease resistance. However, despite thousands of papers in the literature documenting resistances of forest trees to diseases and pests, the deployment of resistant material has been minimal, because it requires: 1) a large research effort and 'machinery' to screen many genotypes, 2) the resistance has to be silviculturally useful, and 3) an institutional commitment to obtain comfort with the resistance in the field (i.e., repeatable). What has somewhat changed over the past 10 years is not our intimate understanding of resistances (e.g., major genes, minor genes) but the fact that we may have even less knowledge of which pests and diseases we may be facing in the future. Exotic diseases and pests, and elevated activity of native diseases and pests from warming climates in Canada, suggest the problem will only get worse. In terms of research, we will require entomologists, pathologists, and molecular biologists to help us identify resistances and document more details of host and pest/disease interactions, for a broad range of resistances, or gene families (e.g., terpenoids, etc.) that may be able to respond to many unknown future threats. In terms of practice, breeders have been using mass and family selection for decades to improve resistance without an innate understanding of it; unfortunately, this has to continue as these biological details of host- pest/disease interactions remain frighteningly illusive.

INTRODUCTION

Tree breeders, forest pathologists and entomologists have now been examining and identifying trees that exhibit tolerance or resistance to pests and diseases for well over four decades. Most of these 'resistant' woody plants and trees have been identified in traditional genetics field experiments (i.e., common garden provenance or progeny tests), but of course many putatively tolerant or less susceptible trees have been found in the wild as well. An enormous body of this research has been published, which must amount to thousands of papers in scientific journals, and summarized in several books (e.g., Gerhold et al. 1966, Wagner et al. 2002). For plant and tree breeders, it makes great sense to try and increase tolerance and resistance to pests and diseases, as it is one of the most attractive and spectacular improvements a breeder can make with classical selection techniques.

Growth traits have been the major focus of most breeding programs around the world as they had to develop a thorough understanding of adaptive genetic variation and the level of genetic variations present for pre-breeding or more aggressive recurrent selection programs concentrating on productivity gains. The spectacular improvements in a few of the short rotation pine and hardwood programs in the world, have confirmed that selecting on heritable traits will improve growth potential and form, and a few have also directly focussed on pest and disease resistance. But even with a large body of research being present which clearly shows various levels of resistance of forest trees to diseases and pests, the development of resistant material for operational deployment has been limited to a few programs because it requires: 1) a large research effort and a large capability to reliably screen many genotypes, 2) the resistance has to be silviculturally useful, and 3) an institutional commitment present that will allow for confidence to be built with the resistance in the field (i.e., repeatable and durable).

Of course, the same issues discussed in 1997 at the Sainte-Foy CTIA meeting (Yanchuk 1998) are still relevant (i.e., 1) what are the types of resistance being found (i.e., mechanisms), 2) how to use them in breeding, and 3) what would be good deployment strategies with resistant material), but what has changed over the past 10 years is the fact that we may have even less knowledge of which pests and diseases we may be facing in the future. Furthermore, any real tree improvement 'response' will take 10–20 years to develop, so that is generally not an attractive short-term management option for forest managers. It is relatively clear that we can find and utilize resistance in forest trees for pests and diseases we currently face, but can we develop more generic and general resistance now to offset potential new pests and diseases? Exotic diseases and pests, and epidemic outbreaks of native diseases and pests from warming climates in Canada, suggest the problem will only get worse.

CURRENT STATUS OF RESISTANCE BREEDING PROGRAMS

As mentioned above, hundreds of research programs on woody plants are looking at and trying to understand genetic resistance; but very few have developed to the point where 'resistant' material is being operationally deployed. Table 1 represents some initial data from a literature review and survey currently being undertaken by several groups, initiated by the FAO, with the BC Ministry of Forests and Range, and future follow up work with various IUFRO groups and collaborators.

We can see that only a handful of programs are making contributions to improved productivity through resistance breeding, and these are largely with a few North American conifers under very large improvement initiatives, where millions of trees are planted annually. While this survey is still incomplete, and it seems somewhat disappointing considering the length of time and resources that have been invested in tree disease/pest interactions, several trends have emerged.

First, major genes are usually found if enough resources can be put towards finding them. But this is not always the case, so at some point the curiosity or a need to find them has to be tempered with the financial costs of identifying and evaluating them. For disease resistance, the two most impressive programs appear to be the fusiform rust (*Cronartium fusiforme*) resistance programs of loblolly (*Pinus taeda*) and slash pine (*P. elliottii*) in the southern U.S., and the white pine blister rust (*Cronartium ribicola*) resistance programs in the Inland Empire and Pacific Northwest of U.S. Single genes are present, the best example being in sugar (*P. lambertiana*) and white pine (*P. strobus*) with hypersensitive reactions of the *Cr1* and *Cr2* genes, respectively (Kinloch et al. 1999). Single genes are also present for the loblolly-fusiform system, but with a more 'complex' expression that were detected many years later only with very detailed studies (Wilcox et al. 1996).

Second, other complex resistance, usually in the form of 'bark reactions', lower levels of infection, etc., are likely due to several minor genes contributing a complex response to these. However, even if these are due to several major genes interacting with various pathotypes (i.e., isolates of single lines of the pathogen), a general response can be expected as the system will behave largely as an additive one.

Third, even with clear disease resistance being present, quantifying genetic gains from resistance breeding is difficult, as unit area yield trials are typically required. These trials usually need to be on several sites (with a range of disease or pest hazards) and old enough for the expected mortality and normal stand competition to occur. The best data seem to come from soil expectation values (SEV) for loblolly pine ranging from 6–40% and 40–90% in slash pine (Brawner et al. 1999) for fusiform resistance. Interestingly, gains in slash pine are substantially higher than in loblolly pine (due to slash pine being more susceptible), but there is a large range.

Gains from the first generations of non-major gene resistant stock in white pine (major gene resistance, of course, would be 100% in the simplest situation) range from 3–70% survival. ('SEVs' do not exist as far as I am aware for blister rust resistance). Once again, these gains may represent underestimates of what is being operationally deployed in recent years (i.e., more advanced generation material); nevertheless, it clearly shows that genetic gains are possible and important. Several programs (e.g., chestnut resistance to blight), seem to be on the verge of having novel materials to put back into ecosystems of interest; however, there will be a long period of time required before it will be known how successful this is. *Dothistroma* resistant breeds in radiata pine (*P. radiata*) have been developed, but the problem has been largely addressed with some changes to the silviculture being applied.

Major gene resistance has been well documented in pest–plant systems (e.g., Hessian Wheat fly – see Liu et al. 2005) and we should expect it as well with forest trees, but once again, this may not be too critical as long as we increase the gene frequencies of resistance alleles for mechanisms that may provide more 'general' resistances. These major gene resistances have typically been found with leaf sucking types of insects, which may be more related to a system like the green aphid resistance in Sitka spruce (*Picea sitchensis*), but detailed chemical work so far has not found any particular associations other than avfew molecular markers (Skov and Wellendorf 2000). Even though the Hessian fly system has had dozens of gene-for-gene systems identified, a detailed understanding at the physical or biochemical level is still relatively unclear, except for the interesting plant responses to larvae saliva (Puthoff et al. 2005).

Table 1. Parital list of major breeding programs in the world developing and deploying insect and pest resistant forest trees.

Genus	Species	Country		Insect /Pest problem (species/generic issue)	Sample reference(s) related to the project
Pinus	*monticola*	United States	fungus	*Cronartium ribicola* (Idaho/Oregon/BC)	Bingham et al. 1969, Kinloch et al. 1999
Pinus	*taeda*	United States	fungus	fusiform rust disease, *(Cronartium quercuum)*	Lambeth 2000
Populus	spp.	United States	disease insects	*Melampsora* spp.; *Venturia populina; Septoria populicola*	Newcombe and van Oosten 1997
		China	insects		Weilun and Wen 2005, Hu et al. 2001
		Europe	insects and diseases		van Slycken et al. 2002
Salix	spp.	United States	disease insects		Dawson et al. 2005, Larsson 2001b
		Sweden	disease insects	Leaf rust	Larsson 2001a
Pinus	*radiata*	New Zealand	fungus	*Dothistroma pini*	Carson 1990
Picea	*sitchensis*	Denmark	insect	green spruce aphid	Harding 2003
		Canada	insect	White pine weevil *(Pissodes strobi)*	Alfaro et al. 2000, Kiss and Yanchuk 1991

CLIMATE CHANGE AND SCREENING GENOTYPES

Climate change impacts on pest and disease ranges are likely to be even more complex than predicting changes to adaptive ranges of forest trees. Although huge advances are being made in predicting species-climate envelope changes (Rehfeldt et al. 2006) and population changes that will be required (e.g., Wang et al. 2006), an interesting challenge may be to overlay changes in pest or disease hazard ranges. Moreover, we have to ask ourselves what is the value of resistance breeding efforts with changing pest ranges, greater epidemic cycles, and increased exotic disease and pest introductions? Are these current disease or pest resistance mechanisms going to have any 'cross resistance' or value to other biotic challenges? Some of the best evidence that we have, and no longer just idle speculation that climate changes will greatly impact insect outbreaks, is the mountain pine beetle (MPB)(*Dendroctonus ponderosae*) epidemic in British Columbia. This outbreak is being associated with warmer winters over the last six years and although genetic resistance is present (Yanchuk et al. 2007) it is at a low frequency. Even if future planting stock was specifically improved for MPB resistance, the genetic gains would be minimal in the case of overwhelming attacks in a high infestation situation. However, a question we should be asking is, "Is the resistance being expressed by trees not killed in an outbreak situation capable of resisting other chewing and boring insects"? In other words, are the resistance mechanisms physical or chemical and how could we use this information to test or challenge selected genotypes to other potential insects? To be sure, different classes of insects are well known to trigger different types of responses in plants, some species specific, yet elicitors for defence–gene activation can be quite ubiquitous (Walling 2000).

A sobering reminder of how difficult it is to make these linkages between phenotypic variations (even with good traditional field trials with proper genetic structure) is in the work by Erkki Haukioja's lab in Finland over the last two to three decades. This work has extensively studied the detailed herbivory interaction of the autumnal moth and mountain birch. It is not possible to summarize the large body of research and results in this pest system, but after extensive study and hundreds of research papers on the topic there is still only a general understanding of the basis for resistance, largely at a population level. For instance, there is a large spectrum of compounds that change over the growing season, and the level of resistance varies by herbivore species. Moreover, changes in nutrients, water content and leaf toughness have been shown to be as important as any of the more complex chemical profiles in birch genotypes (Riipi et al. 2005). This may suggest these general types of features of resistance, although not the only resistances present, may be the ones that 1) we can afford to screen and 2) those that have some general resistance features to many other types of pests. Again, while we should not expect too much 'cross resistance' to occur, it may be important now to try and understand how much variation there is in our selected elite parent trees (making up the seed production and breeding populations) to a broader range of biotic and abiotic challenges and to try to be ahead of the game.

A reduction in the number of genotypes we can afford to work with, and should work with, of course needs to be tempered with the reality of trying to 'accommodate' more traits. This is particularly true if negative genetic correlations are present. However, it seems we have few choices but to go with a slightly broader group of our best genotypes for the growth potential and develop an understanding of their other attributes, particularly if they are showing good expressions for strong terpene profiles, resin flows, hypersensitive reactions, slow gall forming, reduced foliage feeding, etc. The supposed 'costs of resistances' have not really manifested themselves as they relate to tree breeding populations under selection (e.g., King et al. 1997), but antagonistic genetic correlations will always need to be considered at every step.

The above discussion about a reduced or relatively small set of genotypes composing a deployment population also falls well within the established numbers for acceptable risk levels being between 5–30 genotypes (Bishir and Roberds 1999, Yanchuk et al. 2006). Again, these are just general rules of thumb but they give us some comfort that we can utilize a rather small set of genotypes when establishing a plantation and not have it at any greater risk than the use of wild seed.

MOLECULAR GENETICS AND MARKERS

Genomics information is evolving at a rapid pace and many products or tools will likely be of substantial interest to breeders. For instance, we may be able to narrow down the key element working in resistance, such as a compound from resin terpenoid biosynthesis, alkaloid expressions, traumatic resin accumulation, formation of resin ducts, physical barriers such bark thickness or stone cells, etc. Whether this occurs by some association genetics (i.e., candidate genes), sequencing of thousands of ESTs, and looking for gene expression in tree defense using microarrays from resistant and susceptible genotypes, etc., or some other approaches is not clear, but it can only add to our understanding of how resistance genes and gene families may be located in the genome. One of the big challenges, however, and one of the big gaps in integrating molecular genetics into breeding programs still seems to be with making good linkages between markers, or gene expression, the phenotype expression on the trait, and then how it may affect pest or pathogen behaviour or response. This is a challenge, because it will require working with a larger number of genetic entries that can typically be handled.

SUMMARY AND CONCLUSIONS

All this leads to a somewhat new direction to consider. First, it is relatively clear that we do not require dozens of genotypes in our deployment populations to meet an acceptable level of genetic diversity. So we can, and may be forced, to evaluate a group of genotypes with good growth attributes in the first or second generations, quantify their adaptive ranges for current and future climates, and then create a portfolio of resistance scores for them for a few resistance mechanisms that may be of a very general nature. Second, we have been attempting to improve resistance to pests and diseases for decades now, and we have very little to show for it, except in a handful of the large commercial forestry species in the world. It may simply be that most of the resistances that could be developed would not be silviculturally useful, relative to other management approaches. But exotic and endemic pests and diseases are expected to increase (e.g., weevils, bark beetles, needle cast diseases, invasives) and we can expect a need for marked re-adjustment of populations across the landscape for adaptive and resistance traits – but we do not know which ones may be the targets for the future. Molecular genetics will be of interest, but there is a long way to go yet with respect to identifying the genes of interest, their gene action, their phenotypic effects on the host plant, the pest or disease. As such, molecular genetic data may be more useful for modelling purposes than selection.

Most resistances will have large variability in expression in the field, as we can expect not only genotype by environment interaction, but also unwieldy pleiotropic and epistatic effects. In the end, we will have to manage these traits at the landscape level, and population management practices and expertise will be extremely important (Namkoong et al. 2004). In terms of practice, breeders have been using mass and family selection for decades to improve resistance, without an innate understanding of it; this has to continue, as the biological details of resistance responses remain frighteningly illusive. Last but not least, the success of tree breeding for increased forest protection in the next generations of improved forest tree populations will ultimately come only in those programs that have selection and delivery systems in place at a scale that can make a difference at the landscape level, but once again, unfortunately, these can largely be counted on one or two hands.

LITERATURE CITED

Alfaro R.I.; King, J.N. 2000. Use of artificial infestations in the selection of Sitka spruce genotypes for resistance to the white pine weevil in British Columbia. Protection of World Forests from Insect Pests: Advances in Research. IUFRO World Series Vol. 11.

Bingham, R.T.; Olson, R.J.; Becker, W.A.; Marsden, M.A. 1969. Breeding blister rust resistant white pine. V. Estimates of heritability, combining ability, and genetic advance based on tester matings. Silvae Genet. 18: 23–38.

Bishir, J.; Roberds, J.H. 1999. On numbers of clones needed for managing risks in clonal forestry. For. Genet. 6: 149–155.

Brawner, J.T.; Carter, D.R.; Huber, D.A.; White, T.L. 1999. Projected gains in rotation-age volume and value from fusiform resistant slash and loblolly pines. Can. J. For. Res. 29: 737–742.

Carson, S.D. 1990. A breed of radiata pine resistant to *Dothistroma* needle blight - methods used for development and expected gains. Phytopathol. 80: 1007 (abstr.).

Dawson, W.M.; McCracken, A.R.; Carlisle, 11 April 2007. 2005. Short-rotation coppice willow mixtures and yield. Pages 195–208. *In* M.H. Pei and A.R. McCracken, eds. Rust disease of willow and poplar.

Gerhold, H.D.; Schriener, E.J.; McDermott, R.E.; Winieski, J.A. (eds.). 1966. Breeeding pest resistant trees. Pergamon Press, New York, NY. 505 p.

Harding, S.; Rouland, H.; Wellendorf, H. 2003. Consistency of resistance by the spruce green aphid in different ontogenetic stages of sitka spruce. Agric. For. Entomol. 5(2): 107.

Hu, J.J.; Tian, Y.C.; Han, Y.F.; Li, L.; Zhang, B.E. 2001. Field evaluation of insect-resistant transgenic *Populus nigra* trees. Euphytica 121: 123–127.

King, J.N.; Yanchuk, A.D.; Kiss, G.K.; Alfaro, R.I. 1997. Genetic and phenotypic relationships between weevil (*Pissodes strobi*) resistance and height growth in spruce populations of British Columbia. Can. J. For. Res. 27: 732–739.

Kinloch, B.B.; Sniezko, R.A.; Barnes, G.D.; Greathouse. T.E. 1999. A major gene for resistance to white pine blister rust in western white pine from the western Cascade Range. Phytopathol. 89: 861–867.

Kiss, G.K.; Yanchuk, A.D. 1991. Preliminary evaluation of genetic variation of weevil resistance of interior spruce in British Columbia. Can. J. For. Res. 21: 230–234.

Lambeth, C. 2000. Realized genetic gains for first generation improved loblolly pine in 45 tests in coastal North Carolina. South. J. Appl. For. 24: 140–144.

Larsson, S. 2001a. Breeding of *Salix*. Sveriges Utsadesforenings Tidskrift. 111(2): 91–97.

Larsson, S. 2001b.Commercial varieties from the Swedish willow breeding programme. Proc. Biomass and Energy Crops II, Univ. of York, Dec. 2001. Aspects Appl. Biol. 65: 193–198.

Liu, X.M.; Gill, B.S.; Chen, M.S. 2005. Hessian fly resistance gene H13 is mapped to a distal cluster of resistance genes in chromosome 6DS of wheat. Theor. Appl. Genet. 111: 243–249.

Namkoong, G.; Lewontin, R.C.; Yanchuk, A.D. 2004. Plant genetic resource management: The next investments in quantitative and qualitative genetics. Gen. Res. Crop Evol. 51: 853–862.

Newcombe, G.; van Oosten, C. 1997. Variation in resistance to *Venturia populina*, the cause of poplar leaf and shoot blight in the Pacific Northwest. Can. J. For. Res. 27: 883–889.

Puthoff, D.P.; Sardesai, N.; Subhashree, S.; Nemacheck, J.A.; Williams, C.E. 2005. Hfr-2, a wheat cytolytic toxin-like gene, is up-regulated by virulent Hessian fly larval feeding. Mol. Plant Pathol. 6: 411–423.

Rehfeldt, G.E.; Crookston, N.L.; Warwell, M.V.; Evans, J.S. 2006. Empirical analyses of plant-climate relationships for western United States. Int. J. Plant Sci. 167(6): 1123–1150.

Riipi, M.; Kause, A.; Haukioja, E.; Ossipov, V.; Ossopova, S.; Pihlaja, K. 2005. Variable responses of folivorous sawflies to leaf quality of mountain birch. Can. J. For. Res. 35: 189–198.

Skov, E.; Wellendorf, H. 2000. RAPD markers linked to major genes behind field resistance against the green spruce aphid *Elatobium abietinum* (Walker) in *Picea sitchensis* (Bong. (Carr.)). For. Genet. 7: 233–246.

van Slycken, J.; Michiels, B.; Steenackers, M. 2002. New poplar clones developed at IBW: Muur, Vesten, Oudenberg and Grimminge. Bulletin Trimestriel Centre de Populiculture du Hainaut. 2002 (4): 67–83.

Wagner, M.R.; Clancy, K.M.; Lieutier, F.; Paine, T.D. (eds.). 2002. Mechanisms and deployment of resistance in trees to insects. Kluwer Academic Press, The Netherlands. 332 p.

Walling, L.L. 2000. The myriad of plant herbivore responses. J. Plant Growth Regul. 19: 195–216.

Wang, T.; Hamann, A.; Yanchuk, A.D.; O'Neill, G.; Aitken, S.N. 2006. Use of response functions in selecting lodgepole pine populations for future climates. Global Change Biol. 12: 2404–2416.

Weilun, Y.; Wen, L. 2005. Review of tree selection and afforestation for control of Asian longhorned beetle in north China. FAO Working Paper FBS/7E, 38 p.

Wilcox, P.L.; Amerson, H.V.; Kuhlman, E.G.; Liu, B.H.; O'Malley, D.M.; Sederoff, R.R. 1966. Detection of a major gene for resistance to fusiform rust disease in loblolly pine by genomic mapping. Proc. Natl. Acad. Sci. 93: 3859–3864.

Yanchuk, A.D. 1997. Breeding for pest resistance; Towards the development of low risk strategies. Pages 37–51. *In* J. Beaulieu, and J.D. Simpson, eds. Proc. 26th Meet. Can. Tree Imp. Assoc., Part 2, 18–21 Aug. 1997, Quebec City, Quebec.

Yanchuk, A.D.; Bishir, J.; Russell, J.H.; Polsson, K.H. 2006. Variation in volume production through clonal deployment: results from a simulation model to minimize risk for both a currently known and unknown future pest. Silvae Genet. 55(1): 25–37.

Yanchuk, A.D.; Murphy, J.C.; Wallin, K.F. 2007. Preliminary evaluation of genetic variation of attack and resistance in lodgepole pine to mountain pine beetle. Tree Genet. Genom. (submitted)

CONSERVATION OF FOREST GENETIC RESOURCES IN THE UNITED STATES

Brad St.Clair[1], Sara Lipow[2], Ken Vance-Borland[3] and Randy Johnson[1]

[1] USDA Forest Service
Pacific Northwest Research Station
3200 SW Jefferson Way
Corvallis, OR 97331
E-mail: bstclair@fs.fed.us

[2] Oregon Department of Forestry
2600 State Street
Salem, OR 97310

[3] Department of Forest Science
Oregon State University
321 Richardson Hall
Corvallis, OR 97331

ABSTRACT

Conservation of genetic diversity is recognized as an important requirement of sustainable forest management. Gene conservation activities include *in situ* conservation of native stands in reserves and *ex situ* conservation in seed banks, genetic tests, seed and breeding orchards, and other plantations of known identity. We present an example from Oregon and Washington of a GIS-based "gap analysis" approach to determine the spatial distribution of protected *in situ* genetic resources. GIS coverages showing detailed distributions of eight tree species stratified into presumably unique genetic units using seed zones or ecoregions were overlaid with coverages of reserves to determine the locations of protected populations as well as gaps in protection. The gap analysis indicated that most species appear to have sufficient genetic resources conserved in *in situ* reserves. This approach may be valuable elsewhere, particularly in the eastern United States where fewer large reserves exist. Of particular note, for *ex situ* conservation, is a recent agreement between the USDA Forest Service National Seed Laboratory and the USDA Agricultural Research Service National Center for Genetic Resources Preservation to provide long-term storage of seed collections of valuable plant germplasm in their facility in Ft. Collins, Colorado. Protection from disease and insects is another important component of gene conservation.

INTRODUCTION

Conservation of genetic diversity has been recognized as an important requirement of sustainable forest management. The ability of forest trees to evolve to resist pests and adapt to changed climates depends on the genetic diversity present within a species. Genetic diversity is also essential for tree breeders in order to continue to achieve genetic improvement objectives, particularly when new traits become important, in response to changing product objectives, new disease or insect threats, or new environments. It is important that we properly manage and maintain genetic resources for future generations.

WHY CONSERVE GENETIC DIVERSITY?

Three reasons are often given for the conservation of genetic diversity: ecological, economic, and ethical (Ledig 1988).

An ecological rationale ecognizes that the diversity of life forms and ecosystem processes that shape the world are fundamentally a function of genetic diversity. Genetic diversity is the basis for evolutionary change that allows species to adapt to future biotic and abiotic environments. Gene conservation is important because we do not have a complete understanding of ecological processes; thus, we seek to save at least some of the pieces as insurance against poor or uninformed decisions in the management of our genetic resources.

An economic rationale recognizes the economic value of forests for timber and other forest products as well as social benefits. Genetic variation allows humans to select for favored characteristics to better serve our needs and desires. Genetic variation is necessary for continued genetic gain in tree breeding programs and allows us to select for new products such as wood of a specified density or grain, different pulping characteristics, or new chemical derivatives. Genetic variation allows us to select for disease and insect resistance as new pest challenges arise and to select new seed sources for moving populations to better match future climates.

The third reason for conserving genetic diversity is ethical, moral or aesthetic. An ethical or moral rationale recognizes our obligation to protect genetic diversity for future generations, partly because we cannot predict what traits may be important in the future for evolution or for genetic improvement to address new desires or challenges. An aesthetic rationale simply states that people find beauty in a world that is diverse, and genetic diversity contributes to that biological diversity.

POPULATION CLASSIFICATIONS FOR GENE CONSERVATION

Populations are the basic unit of conservation in gene conservation programs. Genetic diversity exists and is maintained within and among populations. Thus, any evaluation of gene conservation must assess the amount and distribution of diversity of genetic variation in populations as well as the population size. Populations may be distinguished by management type and by geography.

Rowland Burdon of the New Zealand Forest Research Institute presented a classification of managed forest tree populations that is useful for considering genetic conservation (Fig. 1). His classification considers the amount of genetic variation within a population (the horizontal axis) and the amount of genetic gain that may be achieved (the vertical axis). The classification helps clarify the gene conservation objectives for different management populations and the population sizes required to meet those objectives.

At the base of his classification scheme is the gene resource population. This population represents all the genetic variation that is available to a species for future generations. It includes native stands, operational plantations, genetic tests, seed and breeding orchards, and seed stores. The large genetic diversity and large population sizes of the gene resource population make it the primary place for the long-term maintenance of genetic variation. The literature suggests that population sizes in the thousands are required for the maintenance of multiple copies of rare alleles (Yanchuk 2001) or the maintenance of quantitative genetic variation in potential adaptive traits given evolutionary forces (Lande 1995, Lynch 1996).

The breeding population is the group of parents that is used to advance to the next generation in a breeding program. Because it is a more highly selected set of parents, the breeding population represents increased genetic gain over the gene resource population, but contains less genetic diversity. The objective of this population is often continued genetic gain in traits of interest. A breeding population size of 30 to 50 maintains sufficient genetic variation for continued genetic gain for five to ten generations, but other constraints involving multiple traits and restricted inbreeding would suggest sizes over 100 (White 1992, Johnson et al. 2001, Yanchuk 2001).

The production population consists of seed orchard parents or clones used to produce genetically improved planting stock for operational plantations. These parents are typically the best selections from the breeding population. This population must carry sufficient genetic variation across a landscape to buffer stands from variations in climates or pests, but must also have sufficient genetic gain to justify the expense of tree breeding. Relatively few parents are required to capture much of the variation in a population; e.g., ten parents capture 90% of the genetic variation found in a population (Johnson and Lipow 2002).

Populations may also be defined by geographic variation in alleles or quantitatively-inherited traits. For gene conservation purposes, we are particularly interested in geographic variation in adaptive traits, that often vary gradually (i.e., clinally). Common garden studies are used to explore geographic variation in quantitatively-inherited adaptive traits. For example, common garden studies of coastal Douglas-fir (*Pseudotsuga menziesii*) in western Oregon and Washington indicate that populations differ in bud-set in a predominately longitudinal direction associated with elevation and minimum annual temperatures, whereas populations differ in bud-burst in a predominately latitudinal direction associated with summer drought (Fig. 2) (St.Clair et al. 2005). Using multivariate analyses, population variation in several traits was summarized in two traits, one trait largely associated with bud-set, germination rate, and growth, and the other trait largely associated with bud-burst and stem height:diameter ratio. Geographic variation in these two multivariate traits was overlayed to create a map of populations that are similar in a variety of traits measured in the study (Fig. 3). Results from common garden studies may be used to delineate seed and breeding zones, that are simply a summary of our best available knowledge of geographic variation in adaptive traits. In the absence of knowledge from common garden studies, we might use important climate variables, ecoregions, vegetation types or other information to serve as surrogates for genetic variation to delineate populations.

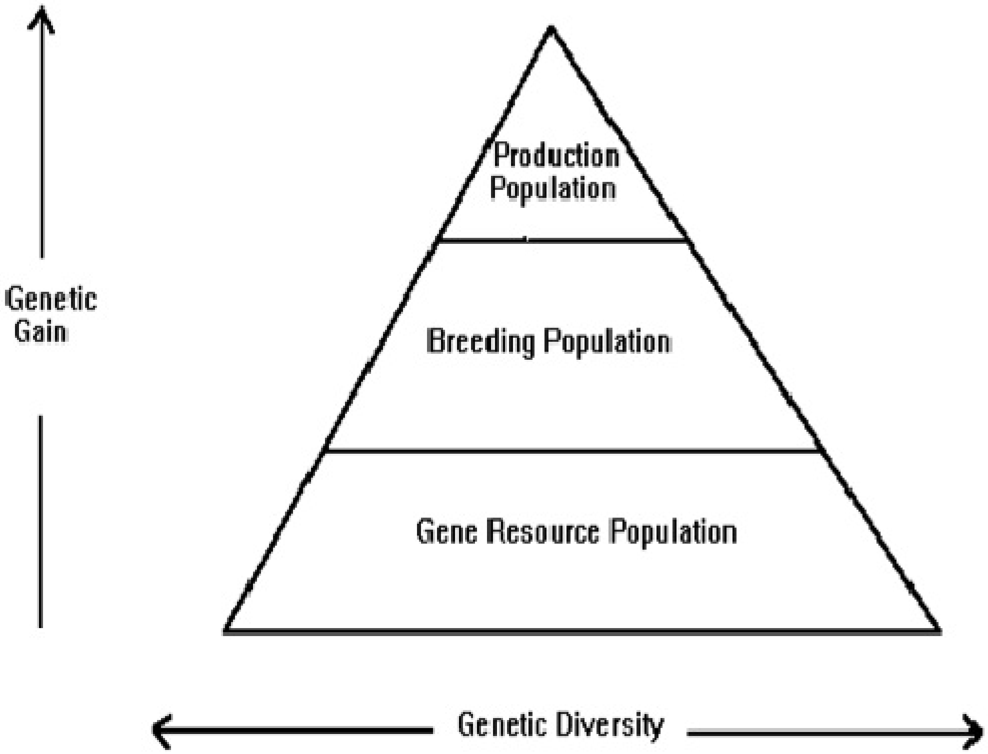

Figure 1. Conceptualization of gain versus genetic variation for a gene resource management program. (from Rowland Burdon, New Zealand Forest Research Institute)

Difficulties in delineating populations for gene conservation arise when a trait of interest is controlled by alleles at very low frequencies or when alleles can only be found in a few localized populations. Often this is the case when looking for pest resistance. One example is the MGR gene for blister rust resistance in sugar pine (*Pinus lambertiana*). Over the range of the species, the frequency of this allele is 0.022, although the frequency varies geographically from absent in the north to 0.087 in the south (Kinloch 1992). Another example is white pine weevil (*Pissodes strobi*) resistance in Sitka spruce (*Picea sitchensis*) in which resistance was found predominately in two localized British Columbia populations (Ying 1997).

GENE CONSERVATION ACTIVITIES IN THE UNITED STATES

Gene conservation activities have traditionally been classified as *in situ* and *ex situ*. *In situ* conservation is the conservation of genetic diversity in its original location, usually in protected areas with little active management, such as national parks, wilderness areas, research natural areas, and other reserves. The goal of *in situ* conservation is to protect and perpetuate the integrity of native gene pools and the natural evolutionary processes affecting those gene pools. *Ex situ* conservation is the conservation of genetic diversity at some place other than the original native habitat. *Ex situ* conservation includes collections of plant material in seed banks, tissue culture, genetic tests, seed and breeding orchards, and other plantations of known genetic identity. In the future, even DNA in genomic libraries may serve as *ex situ* collections. Breeding programs may be thought of as a type of *ex situ* conservation activity since the genetic material is removed from the original location before being planted back into the breeding zone.

Another type of activity that is not often thought of as either *in situ* or *ex situ* conservation is the use of seed zones and seed transfer guidelines for the movement of planting material to ensure adapted, productive stands. But seed zones also help to maintain some of the native genetic structure and locally-adapted gene pools, and thus serve an important gene conservation role. Seed zones and seed movement guidelines have been in use for decades for forest trees in the western United States (Kummel et al. 1944, Isaac 1949). The

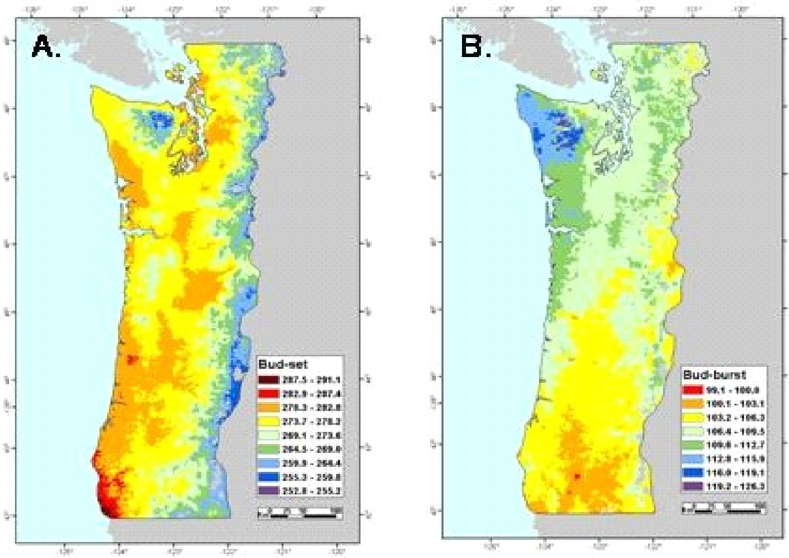

Figure 2. Geographic variation in first-year bud-set (A) and second-year bud-burst (B) in Douglas-fir from western Oregon and Washington. (from St.Clair et al. 2005)

widely-used seed zone maps for Washington and Oregon were published in 1966 and for California in 1970. Seed zones for Oregon and Washington were later revised for each species based on available knowledge of geographic patterns of genetic variation (Randall 1966, Randall and Berrang 2002). More recently, there is increased interest in seed zones for native shrubs, grasses and forbs due to increased use of these species in restoration projects (Johnson et al. 2004).

In situ conservation in the United States generally happens as a consequence of setting aside lands for other purposes. One exception is the "gene-pool reserve system" set up by the Washington State Department of Natural Resources (DNR) (Wilson 1990). The DNR set aside over 100 reserves in western Washington for the explicit purpose of the conservation of Douglas-fir genetic resources (although the genetic diversity of other species is also being protected in these reserves).

Because few formal gene conservation reserves exist for many species, a group of interested land managers in the western United States came together to fund a project to evaluate the role of current reserves in protecting genetic diversity for eight conifer species in western Oregon and Washington (Lipow et al. 2004, 2007). A "gap analysis" approach was used, similar to the approach previously used to identify gaps in species protection (Scott and Jennings 1997). Using GIS, maps of protected areas and tree distributions for each species were overlaid onto maps of seed zones or ecoregions, where seed zones or ecoregions represent genetic variation in adaptive traits. The tree distribution maps were stratified into three levels of stand density for purposes of estimating population sizes. Seed zones or ecoregions in which a species was considered poorly protected in *in situ* reserves were identified. A species was considered poorly protected if fewer than 5,000 trees or 10% of a species' population were found in reserves in each seed zone or ecoregion. The gap analysis indicated that most species appear to have sufficient genetic resources conserved in *in situ* reserves throughout their ranges. Some genetic gaps were found, however, for noble fir (*Abies procera*) in southwest Washington and for western white pine (*Pinus monticola*) and Sitka spruce in the Puget Sound. Western white pine is of particular concern due to the impact of urbanization and blister rust (*Cronartium ribicola*), and because that area of its range has not been well sampled for blister rust resistance (Fig. 4).

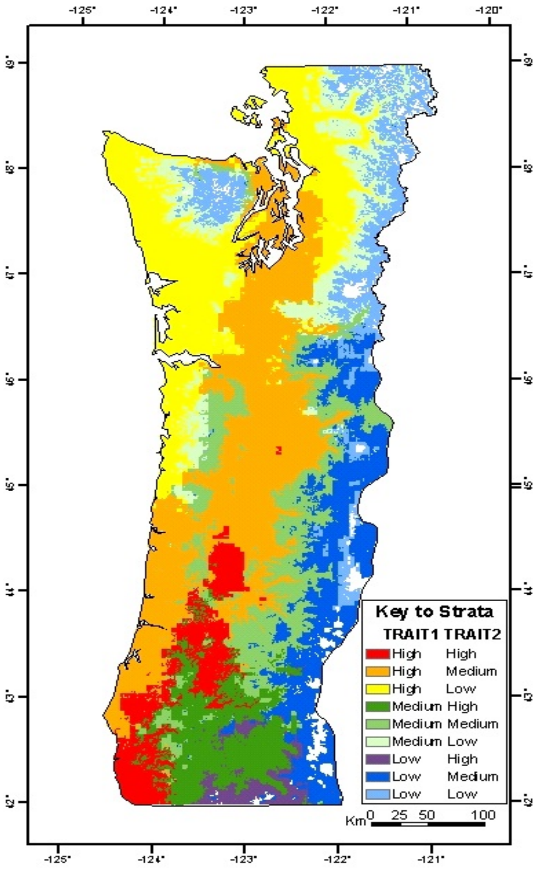

Figure 3. Map of areas of similar adaptive characteristics for Douglas-fir in western Oregon and Washington. (from St.Clair et al. 2005)

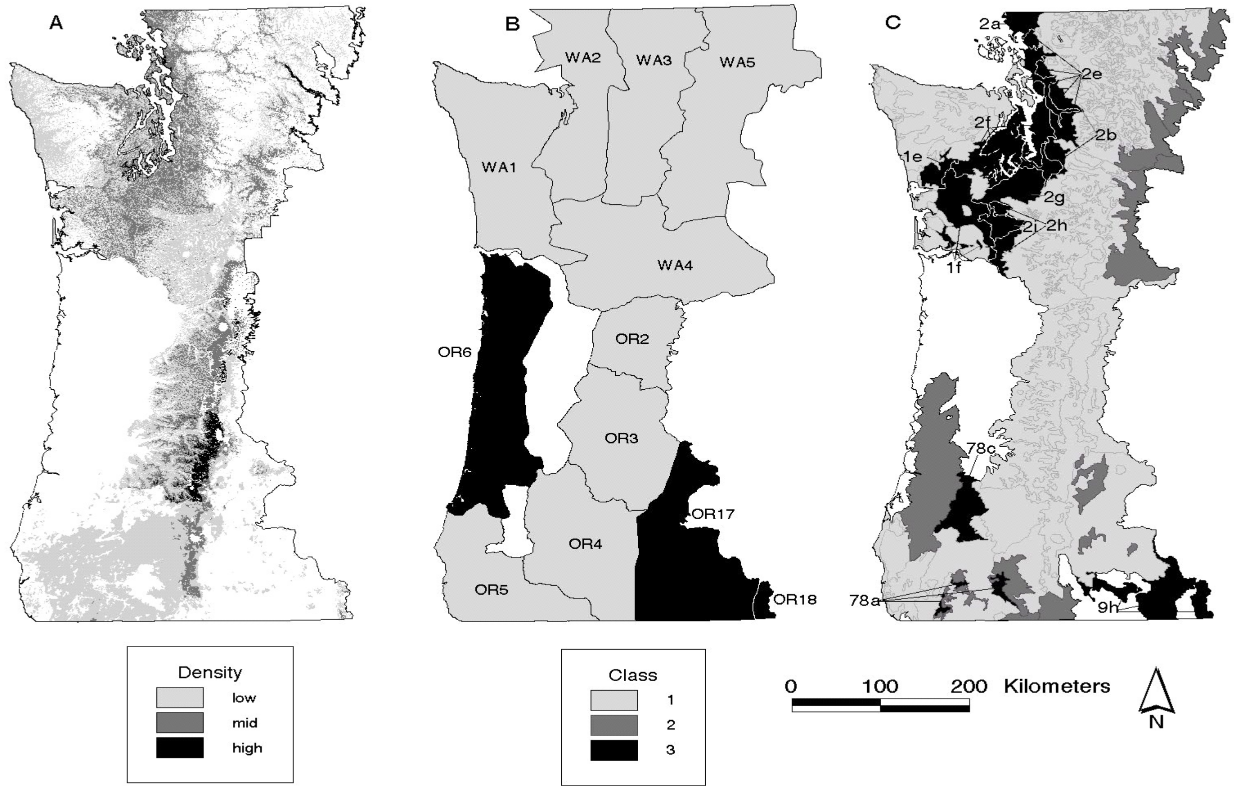

Figure 4. Distribution of western white pine (A), and results from the gap analysis for *in situ* gene conservation indicating seed zones (B) and ecoregions (C) with less than 5,000 individuals in protected areas. (from Lipow et al. 2004)

The findings from the gap analysis of sufficient protection of genetic resources for most species in most locations may not be surprising since Oregon and Washington have a high proportion of land in protected areas, particularly at higher elevations. A similar analysis was done in British Columbia with similar conclusions (Lester and Yanchuk 1996, Hamann et al. 2004). A gap analysis approach may be valuable elsewhere in the United States, particularly in the eastern United States where fewer large reserves exist. Fewer reserves may be required in the East, however, since climatic variation and the associated genetic variation in adaptive traits are generally more homogeneous.

Several organizations are actively involved in *ex situ* conservation by maintaining seed banks or *ex situ* plantations. The U.S. Forest Service maintains extensive seed collections of forest trees, many from first-generation selections in their tree improvement programs. Although the tree improvement programs have been de-emphasized in recent years, the seed banks are maintained in regional facilities (e.g., the Dorena Tree Improvement Center in Oregon). The Bureau of Land Management maintains seed stores for forest trees from their forestlands in Oregon. The Bureau of Land Management, the Agricultural Research Service, and the Forest Service's National Seed Laboratory (all federal agencies) have begun to maintain collections of native shrubs, grasses, and forbs. More recently, the Forest Service has entered into an agreement with the Agricultural Research Service for the long-term storage of up to 3,000 seeds of valuable germplasm of native plants at the National Center for Genetic Resources Preservation at Fort Collins, Colorado (http://www.nsl.fs.fed.us/nsl_ars_mou.html).

Tree improvement programs in the United States are also repositories for considerable genetic resources for species of economic interest. For example, a survey of organizations involved in Douglas-fir tree improvement indicates that over 33 000 parents are growing in over 1,000 first-generation progeny tests representing most of the range of Douglas-fir from British Columbia to California (Table 1) (Lipow et al. 2003). The genetic resources of other species in the region are represented in tree improvement programs to a lesser degree

(Lipow et al. 2002). Recognizing the value of Douglas-fir parents in progeny tests for gene conservation, members of the Northwest Tree Improvement Cooperative are thinning and maintaining a portion of the tests to preserve family identity for the future. A similar approach is being taken by the North Carolina State University – Industry Tree Improvement Program to set up genetic diversity archives to maintain unique genotypes, particularly those that may not be perpetuated in their mainline breeding populations (McKeand and Svensson 1997).

Table 1. Estimates of the numbers of parental selections included in first-generation Douglas-fir tree improvement programs throughout western Oregon and Washington, British Columbia, and northern California. (from Lipow et al. 2003)

Program	Number of first-generation breeding zones	Number of first-generation selections	Number of test plantations
Oregon and Washington			
NWTIC	72	19,421	620
USDA Forest Service [a]	14	3,152	110
USDI Bureau of Land Management [a]	9	2,219	60
Oregon Department of Forestry [a]	1	150	3
Washington Department of Natural Resources [a]	6	720	21
Weyerhaeuser Company	6	3,707	Not available
Other industry	16	1,809	47
California USDA Forest Service	9	1,800	36
British Columbia Ministry of Forests	2	650	102
Total	135	33,628	>999

[a] These organizations have independent programs in some regions, but in other regions they participate in NWTIC programs. Only the independent programs are listed here.

Tree improvement programs recognize the need to conserve genetic variation in breeding populations for purposes of continued genetic gain in advanced generations. Most breeding populations have between 200 and 400 parents, sufficient to allow continued genetic gain for several generations (White 1992, Johnson et al. 2001). For Douglas-fir tree improvement in western Oregon and Washington, several second-generation breeding programs have been initiated for different parts of the species range. Although a portion of the parents overlap between programs, each program has well over 200 unique, unrelated parents (Table 2).

Table 2. Number of first- and second-generation parents in Northwest Tree Improvement Cooperative Douglas-fir second-generation breeding programs.

Second-generation breeding program	Number of first-generation breeding zones combined into second-generation program	Number of first-generation parents	Number of second-generation parents
Washington Coast	5	1,203	294
Puget Sound	7	1,186	255
Washington Cascades	17	2,995	379
Vernonia	3	1,372	501
Trask Coast	11	2,541	444
Trask Inland	9	1,625	334
South Central Coast	6	2,048	423
North Oregon Cascades	14	3,208	394
Total	78	13,082	1,722

Another important component of gene conservation is protection of species from pests. Examples of concern over the loss of populations from disease and insects are numerous: chestnut blight (*Cryphonectria parasitica*), butternut canker (*Sirococcus clavigignenti-juglandacearum*), blister rust on white pines, pitch canker (*Fusarium moniliforme* var. *subglutinans*) on Monterey pine (*Pinus radiata*), *Phytophthora lateralis* root rot on Port Orford cedar (*Chamaecyparis lawsoniana*), emerald ash borer (*Agrilus planipennis*), and hemlock whooly adelgid (*Adelges tsugae*) to name a few. Research on and applied breeding for tolerance or resistance to pests is an important component of gene conservation work in the Forest Service, as well as an important component of work at universities, non-profits, and other organizations. Seed collections for populations at threat are also an important component. The Forest Service has seed banks for species in resistance breeding programs such as western white pine and sugar pine. Recently they have initiated seed collections of ash (*Fraxinus* spp.) in the Lake States for *ex situ* conservation to protect against population extirpation by the emerald ash borer. The Forest Service is working with CAMCORE to establish *ex situ* plantations of eastern (*Tsuga canadensis*) and Carolina hemlock (*T. caroliniana*) at risk from hemlock whooly adelgid (http://www.camcore.org/projects/hemlock.php).

CONCLUSIONS

Genetic conservation activities are being undertaken by a variety of organizations directed towards a range of native species in the United States. Although the Forest Service has always been concerned with gene conservation at the regional level and in research, they have taken a more active role recently with national-level agreements to store seed at the National Center for Genetic Resources Preservation and agreements for *ex situ* plantations of hemlock to protect against the hemlock whooly adelgid. Tree improvement programs also play an important role in gene conservation by maintaining first-generation parents and by maintaining genetic diversity in advanced generation breeding. *In situ* gene conservation is largely a result of reserves set aside for other purposes. A gap analysis was carried out in western Oregon and Washington to evaluate the effectiveness of current reserves for gene conservation purposes. Results indicated that most species are adequately protected. We recommend expanding this approach to other species in other regions.

LITERATURE CITED

Hamann, A.; Aitken, S.N.; Yanchuk, A.D. 2004. Cataloguing *in situ* protection of genetic resources for major commercial forest trees in British Columbia. For. Ecol. Manage. 197: 295–305.

Isaac, L.A. 1949. Better Douglas-fir forests from better seed. Univ. Washington Press. 64 p.

Johnson, R.; St. Clair, B.; Lipow, S. 2001. Genetic conservation in applied tree breeding programs. Pages 215–130. *In* B.A. Thielges, S.D. Sastrapradja and A. Rimbawanto, eds. *In situ* and *ex situ* Conservation of Commercial Tropical Trees. Faculty of Forestry, Gadjah Mada University, Yogyakarta, Indonesia.

Johnson, R.; Lipow, S. 2002. Compatibility of breeding for increased wood production and long-term sustainability: the genetic variation of seed orchard seed and associated risks. Pages 169–179. *In* Proc. Wood Compatibility Initiative Workshop. USDA, For. Serv., Pacific Northwest Res. Sta., Portland, OR, Gen. Tech. Rep. PNW-GTR-563.

Johnson, G.R.; Sorensen, F.C.; St.Clair, J.B.; Cronn, R.C. 2004. Pacific Northwest forest tree seed zones: a template for native plants? Native Plants J. 5: 131–140.

Kinloch, B.B. 1992. Distribution and frequency of a gene for resistance to white pine blister rust in natural populations of sugar pine. Can. J. Bot. 70: 1319–1323.

Kummel, J.F.; Rindt, C.A.; Munger, T.T. 1944. Forest planting in the Douglas fir region. USDA, For. Serv., Pacific Northwest Region, Portland, OR.

Lande, R. 1995. Mutation and conservation. Conserv. Biol. 9: 782–791.

Lynch, M. 1996. A quantitative-genetic perspective on conservation issues. Pages 471–501. *In* J.C. Avise and J.L. Hamrick, eds. Conservation Genetics: Case Histories from Nature. Chapman and Hall, New York.

Ledig, F.T. 1988. The conservation of diversity in forest trees: why and how should genes be conserved? Biosci. 38: 471–479.

Lester, D.T.; Yanchuk, A.D. 1996. A survey of the protected status of conifers in British Columbia: *In situ* gene conservation. Min. For., Res. Br., Victoria, BC, Res. Rep. No. 4.

Lipow, S.R.; St.Clair, J.B.; Johnson, G.R. 2002. *Ex situ* gene conservation for conifers in the Pacific Northwest. USDA, For. Serv., Pacific Northwest Res. Sta., Portland, OR, Gen. Tech. Rep. PNW-GTR-528, 54 p.

Lipow, S.R.; Johnson, G.R.;. St.Clair, J.B.; Jayawickrama, K.J. 2003. The role of tree improvement programs for *ex situ* gene conservation of coastal Douglas-fir in the Pacific Northwest. For. Gen. 10: 111–120.

Lipow, S.R.; Vance-Borland, K.; St.Clair, J.B.; Henderson, J.A.; McCain, C. 2004. Gap analysis of conserved genetic resources for forest trees. Conserv. Biol. 18: 412– 423.

Lipow, S.R.; Vance-Borland, K.; St.Clair, J.B.; Henderson, J.A.; McCain, C. 2007. *In situ* gene conservation of six conifers in western Washington and Oregon. Western J. Appl. For. (in press)

McKeand, S.; Svensson, J. 1997. Sustainable management of genetic resources. J. For. 95(3): 4–9.

Randall, W.K. 1996. Forest tree seed zones for Western Oregon. Oregon Dept. For., Salem, OR. 82 p.

Randall, W.K.; Berrang, P. 2002. Washington tree seed transfer zones. Washington Dept. Nat. Res., Olympia, WA. 72 p.

Scott, J.M.; Jennings, M.D. 1997. Large-area mapping of biodiversity. Ann. Missouri Bot. Garden 85: 34–47.

St.Clair J.B.; Mandel, N.L.; Vance-Borland, K.W. 2005. Genecology of Douglas-fir in western Oregon and Washington. Ann. Bot. 96: 1199–1214.

White, T. 1992. Advanced-generation breeding populations: size and structure. Pages 208–222. *In* Proc. Breeding Tropical Trees – Resolving Tropical Forest Resource Concerns Through Tree Improvement, Gene Conservation and Domestication of New Species. IUFRO Res. Grp S 2.02.08, 9–18 Oct. 1992, Cali, Columbia. CAMCORE, Raleigh, NC.

Wilson, B.C. 1990. Gene-pool reserves of Douglas-fir. For. Ecol. Manage. 35: 121–130.

Yanchuk, A.D. 2001. A quantitative framework for breeding and conservation of forest tree genetic resources in British Columbia. Can. J. For. Res. 31: 566–576.

Ying, C.C. 1997. Effects of site, provenance and site interaction in Sitka spruce in coastal British Columbia. For. Gen. 4: 99–112.

PANEL PERSPECTIVE

FOREST PRODUCTIVITY PERSPECTIVE

D.P. Fowler

It has been five decades ± a few years since the three of us (Kris, Kit, and myself) started our careers in forest genetics and tree breeding. We have seen an embryonic CTIA grow from 20 Active members to 85. We have witnessed the use of genetically improved seedlings rise from zero to almost all seedlings planted.

Increasing forest productivity, quantitatively and qualitatively, has always been the underlying objective of most tree improvement programs. The earliest efforts in tree improvement attempted to identify those provenances, populations, and hybrids that were most productive. In addition many studies were initiated to obtain information on the magnitude and distribution of genetic variation, especially for species of interest in reforestation of Crown and private lands.

Greater reliance on planting as a regeneration method and recognition that productivity could be enhanced with the use of genetically improved seedlings led to the expansion of provincial tree improvement programs as well as the formation of several provincial-industrial cooperatives.

The decades of work, not to mention the substantial investments, are now paying off. Most of the seedlings planted in Canada are products of first- and second-generation seed orchards. It is encouraging to note that the realized gains in productivity meet or exceed the predicted gains. Tuesday’s presentation by Blake Brunsdon on the J.D. Irving, Limited management strategy clearly demonstrated the significant contribution of tree improvement. It is also evident that much greater gains in productivity will be realized in the future. This point was especially well made by Steve McKeand in his paper on tree improvement in the southern US. The use of best families and clones will provide an opportunity to further increase productivity.

An important lesson to be learned from the presentations is that gains in productivity will be maximized only where the best genetic materials are planted on the best sites and nurtured using intensive management technology. It follows that by concentrating on the best sites it should be possible to increase overall forest productivity and use less intensive forestry practices on a wide array of ecologically sensitive as well as economically less productive sites.

FOREST PROTECTION PERSPECTIVE

E.K. Morgenstern

My message here is that due to climate change, measures of forest protection will become more important in the future and that research must be designed to meet that challenge. Tim Flannery's book "The Weathermakers" is the best summary of all the issues related to climate change and global warming, and Al Gore's "An Inconvenient Truth" contains excellent illustrations of these effects. Briefly, global warming leads to increased stress on organisms due to drought, loss of synchronization between phenology of plants and insect development that contributed to a balance in the past, arrival of new pests, and shrinking population sizes of plants that could imply a loss of genetic variation.

During this meeting we have heard good presentations related to this complex of issues from John Davis, Ashley Thomson, Bill Parker, Michael Stoehr, and Alvin Yanchuk.

Five years ago Ben Wang and I (Forestry Chronicle 77: 1014–1021) reviewed forest depletion, seed supply, and reforestation in Canada during the past four decades. Depletion is defined as the total loss of growing forest area due to harvesting, forest fires, insects, diseases, and natural disasters such as storms, droughts, and floods. We found that total forest depletion had increased from about 2 million ha in the preceding decades to 2.5 million ha, i.e., 1% of the total commercial forest area during the last few years of the last century.

In less than one decade depletion has increased substantially. The most recent annual report on "The State of Canada's Forests" shows that the total area of forest fires in 2004 was 3.3 million ha, exceeding the 10-year average by 32%. The area affected by insect defoliation and with beetle-killed trees rose from 5.1 million ha in 1999 to 19.2 million ha in 2003. The major insects involved during 2003 were mountain pine beetle, forest tent caterpillar, large aspen tortrix , spruce budworm, Gypsy moth, and jack pine budworm.

The interpretation of these numbers requires caution. The burned area reported now includes the total forest area and not just the area under management often considered in earlier reports. Further, defoliation does not imply mortality, and is often followed by full recovery, for example, when the forest tent caterpillar is involved. For these reasons we must wait for longer time periods before real trends are confirmed. It would not be surprising, however, if these trends reveal at least a doubling of depletion in the first decade of this century. Although depletion also includes higher levels of harvesting (which is still below the allowable cut), the larger figures for fire, insects and dieases given above are of great concern.

FOREST CONSERVATION PERSPECTIVE

C.W. Yeatman

Genetic resources and diversity among individuals, populations, and species are the essential and dynamic foundations for sustainability and productivity of all living organisms, not the least being forest trees. Recognition of types and patterns of phenotypic and adaptive genetic differences within and among tree species and their importance in utilization, management, and renewal of forests is widely recognized throughout the world today. This meeting demonstrated just how far Canadian forest agencies, both public and private, have come in integrating concepts and knowledge of genetic diversity and conservation into forest education, research, and application. Today, detailed records are created and maintained of geographic, environmental, population, and parental origin of seed collected for reforestation. Strict control is exercised over the geographic and environmental distribution of seed and planting stock. In addition, studies of molecular genetics of tree species have enhanced and deepened our understanding of relationships and diversity among individuals and populations.

Climate change has been the norm as tree species evolved and adapted genetically with migration in time and space. Most recently, post-glacial migration from southern refugia of Canadian trees induced current patterns of population diversity and adaptation to temperature, latitude, moisture, and soil. The accelerating rate of climate change calls for careful consideration of management choices to meet this challenge to established adaptive norms. Selection and testing for pre-adaptation of sample populations will be a major requirement to adjust and optimise future seed source selection and utilization.

The creation at this meeting of CON**FOR**GEN, a “Canadian Program for the Conservation of Forest Genetic Resources”, is a credit to progress in this area to date and will help ensure future improvement and security of genetic conservation of forest trees throughout Canada. It is established to be “collaborative and cooperative, with contributions from various provincial/territorial and federal government departments, industry, universities, institutes and ENGO’s”. The executive and members of the Canadian Tree Improvement Association are to be congratulated for vigorously pursuing this initiative.

I wish to thank the CTIA for the invitation and support I received to attend this meeting. It was most enjoyable and encouraging to meet the many enthusiastic and knowledgeable students, forest geneticists, genecologists, seed scientists, and forest practitioners in attendance. I extend my best wishes to all in your careers and the valuable contributions you are making to forestry in Canada.

VOLUNTEER PAPER ABSTRACTS

TREE SPECIES NATIVE TO CANADA REQUIRING *ex situ* CONSERVATION: THE ISSUES AND CHALLENGES

Beth Arsenault, Tannis Beardmore, Judy Loo, Dale Simpson
and Tracy White

Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: bearsena@nrcan.gc.ca

A survey was conducted in 2003 to identify Canadian native tree species that may be in need of gene conservation. Results showed that *ex situ* conservation was recommended for 47 of the 124 tree species, *in situ* conservation was recommended for 20 species, and 10 species and 4 varieties may need attention but insufficient knowledge is currently available. Of the species requiring *ex situ* conservation 14 produce recalcitrant seed (seed which cannot be stored in the long term), 33 produce orthodox seed (seed which can be stored in the long term), and 3 produce seed considered to be intermediate in storage behaviour. The large number of species that produce recalcitrant seeds and require *ex situ* conservation presents a challenge in developing conservation priorities. Butternut (*Juglans cinerea* L.), a species requiring *ex situ* conservation, produces a recalcitrant seed. Embryonic axes, when excised from the nut with approximately 3 mm of cotyledonary tissue, can be induced to tolerate exposure to -196°C and subsequently germinate, forming a viable seedling. These results suggest that ultra low temperature storage of embryonic axes may be a viable method for the *ex situ* conservation of other species producing recalcitrant seeds.

USDA FOREST SERVICE NATIONAL SEED LABORATORY'S NEW MISSION

Jill Barbour

USDA Forest Service
National Seed Laboratory
5675 Riggins Mill Road
Dry Branch, GA, 31020
E-mail: jbarbour@fs.fed.us

The USDA Forest Service National Tree Seed Laboratory's name has been changed to USDA Forest Service National Seed Laboratory (FSNSL). This change reflects the new mission to develop seed testing requirements for all forest plant species and establish a genetic resources conservation program. All National Forests and private land native plant species are considered for preservation and fall within the Native Plant Genetic Resources Conservation *ex situ* Plan.

Cooperative projects are being formed with public and private agencies to address the problems of propagating native plants for ecosystem restoration of grass, shrub, and forest sites. The laboratory is cooperating with the Forest Service Rocky Mountain Experiment Station and the Bureau of Land Management on a Great Basin native plant propagation research project. The objective of the great basin restoration project is to restore the native plant communities that are anticipated to be more resilient to invasive weeds and fire. Seed conditioning and testing protocols are being developed for 23 forb and 10 grass species. Results can be viewed on the laboratory website, http://www.nsl.fs.fed.us. Seeds from 36 herbaceous species native to the *Pinus palustris*, longleaf pine, ecosystem are being collected, cleaned, and tested for future nursery production and re-establishment to their native habitat. Many species' ranges have been severely restricted due to the reduction of longleaf pine acreage in the southern United States. A native plant network has been established as a means of sharing information on collection, cleaning, and propagation techniques. A website, http://nativeplants.for.uidaho.edu/network, and Native Plants Journal can be accessed to obtain information on native plant restoration.

Emphasis is shifting within the United States Department of Agriculture, USDA, to incorporate native plant species' germplasm in their preservation program. Seeds from fewer than 300 threatened native plant species are presently stored at the nation's genetic resources storage facility. To address this concern, the USDA FSNSL and the USDA Agricultural Research Service, National Center for Genetic Resources Preservation (NCGRP), formerly the National Seed Storage Laboratory, are cooperating to preserve native plant species through long-term seed storage. In 1992 the seed storage vaults were enlarged to include cryopreservation and modified to withstand natural disasters and explosions and now maintain over 450 000 accessions of genetic resources.

The FSNSL is responsible for preparing native seed collections for long-term storage. Seeds are checked for viability through X-ray analysis and seed testing to ensure seed lots are impurity free and moisture content is below 10%. Seeds are packaged in poly-foil bags, heat sealed, identified with barcode stick-on labels, and then cold stored until the NCGRP is ready to receive shipment. Packets containing 500 to 3,000 seeds are stored at -18°C at the NCGRP for as long as the seeds remain viable. Working samples can be stored at the FSNSL or other facilities for ease of distribution and testing.

Native plant seed collections receive accession numbers and become part of the National Plant Germplasm System, a public and private cooperative effort to preserve plant genetic diversity. Accession numbers include information on seedlot origin and ownership which are maintained in the Germplasm Resource Information Network (GRIN) database, accessible through the internet http://www.arc-grin.gov.

MALE REPRODUCTIVE SUCCESS AND PEDIGREE ERROR WITHIN OPEN- POLLINATED AND POLYCROSS MATING IN RED SPRUCE

T.K. Doerksen, K.M. Gardner and C.M. Herbinger

Department of Biology
Dalhousie University
1355 Oxford St.
Halifax, NS
B3H 4J1
E-mail: trevor.doerksen@gmail.com

Open pollinated and polycross mating systems are widely used in forest genetics and breeding to quickly, simply, and inexpensively generate progenies assumed related as half-sibs (coefficient of relationship, r = 0.25) from a random mating population. However, non-random mating, such as differential male reproductive success or selfing, can increase the genetic correlation and thus genetic variance and heritability are overestimated. On the other hand, pedigree errors will cause additive genetic variance and heritability to be underestimated. The objective of this study was to test for differential male reproductive success, estimate level of selfing (open pollinated), and to uncover potential sources of pedigree error (volunteers, mishandled maternal IDs, pollen foreign to mating system) in operational open pollinated and polycross progeny tests, administered by the Nova Scotia Tree Improvement Working Group, through paternity testing using microsatellite DNA markers. An ongoing objective is to test the impact of new pedigree information (assigned male and removed errors) on quantitative genetic parameters.

THE GENETIC STATUS OF EASTERN WHITE CEDAR IN THE MARITIME PROVINCES

Lisa O'Connell[1], Om Rajora[1] and Alex Mosseler[2]

[1] University of New Brunswick
Faculty of Forestry and Environmental Management
PO Box 44555
Fredericton, NB
E3B 6C2
E-mail: oconnell@unb.ca

[2] Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7

The conversion of forested land for agriculture, and other human uses, has greatly reduced and fragmented the original forests of the Maritime Provinces. Fragmentation of forests can affect the genetic composition and breeding system of natural populations. Historical records indicate that the range and number of populations of eastern white cedar (*Thuja occidentalis*) has diminished due to logging, and clearing for agriculture throughout the Maritimes. In Nova Scotia, eastern white cedar has recently been listed as an endangered species under the Nova Scotia Endangered Species Act. The distribution of extant eastern white cedar in Nova Scotia is limited to scattered populations in five western Counties. Historically the species was found in five additional counties in Nova Scotia. The primary objective of this research project is to assess the genetic status of eastern white cedar in the Maritime Provinces to direct conservation guidelines. Specifically, to assess the amount of genetic diversity within populations and genetic connectivity between populations and to identify the evolutionary origin of the populations, in order to identify populations of interest for conservation. We have used highly variable genetic markers, microsatellites, and genotyped populations from New Brunswick, Nova Scotia, Prince Edward Island, and state of Maine. Preliminary results indicate that the Nova Scotia populations of white cedar have low genetic diversity and are highly isolated from each other. Nova Scotia populations are also highly divergent from the New Brunswick and Prince Edward Island populations and are possible remnants of a separate glacial refugium. We will also be testing whether current isolated populations are newly established or are remnants of much larger populations. These data will help identify populations of interest, and direct harvesting practices and conservation guidelines for white cedar.

ENHANCING FOREST PRODUCTIVITY THROUGH MULTI-VARIETAL FORESTRY

Yill-Sung Park[1], Greg Adams[2] and Yuhui Weng[3]

[1] Natural Resources Canada
Canadian Forest Service
Fibre Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: Yill_Sung.Park@nrcan.gc.ca

[2] J D Irving, Limited
Sussex Tree Nursery
181 Aiton Road
Sussex, NB
E4G 2V5

[3] New Brunswick Department of Natural Resources
Kingsclear Forest Nursery
Island View, NB
E3E 1G3

In the past 30 years, tree improvement programs in Canada have contributed to the significant increase in forest productivity by providing genetically improved seeds. These programs typically produce 3–5% gain in height when evaluated at about 10 years of age. Our experience also indicated that the efficient capture of variability among the individuals of elite crosses could yield 4–6 times the gain available from the use of seed orchard seeds. Multi-varietal forestry (MVF), defined as the use of genetically tested tree varieties in plantation forestry, is the means of utilizing additional genetic variances contained in the breeding population. The implementation of MVF requires efficient vegetative propagation techniques, the development of high-value tree varieties, and the management of plantation genetic diversity. Owing to the recent development and refinement in conifer somatic embryogenesis, options for implementing MVF became increasingly available for several conifers, particularly spruce species. In this presentation, we discuss the advantages of MVF, technical requirements for MVF, strategies for developing tree varieties, and balancing genetic gain and diversity.

EFFECTS OF ELEVATION TRANSFER ON LOW ELEVATION SEED SOURCES OF DOUGLAS-FIR FROM COASTAL BRITISH COLUMBIA

William H. Parker[1] **and Michael Stoehr**[2]

[1] **Faculty of Forestry and the Forest Environment**
Lakehead University
955 Oliver Road
Thunder Bay, ON
P7B 5E1
E-mail: whparker@lakeheadu.ca

[2] **BC Ministry of Forests and Range**
Research Branch
PO Box 9519 Stn Prov Govt
Victoria, BC
V8W 9C2

Coastal Douglas-fir seed transfer in British Columbia is tightly restricted by elevation. Currently there is an abundance of low elevation seed being produced in B.C. seed orchards, but inadequate seed to fill the demand for higher elevation reforestation requirements. Data from the 599-01 Provenance Trial Series were utilized to help determine whether low elevation seed could be moved upwards to some degree without significantly affecting productivity. Height, diameter, and survival data recorded at periodic intervals from 6 to 30+ years for 36 seed sources from coastal British Columbia grown at 7 test sites were used to produce spatially explicit growth models. These models were related to elevation. Contour lines expressing -1, 0 and +1 LSD ($p=0.05$) growth performance intervals draped on a 25 m resolution digital elevation model indicated that some low elevation (< 700 m) coastal Douglas fir sources could be transferred upwards an additional 500 m without exceeding the 1 LSD growth interval.

SEED SOURCE PORTFOLIO SELECTIONS OF JACK PINE TO MINIMIZE RISK IN AN UNCERTAIN FUTURE CLIMATE

Kevin A. Crowe and William H. Parker

Faculty of Forestry and the Forest Environment
Lakehead University
955 Oliver Road
Thunder Bay, ON
P7B 5E1
E-mail: whparker@lakeheadu.ca

There is broad consensus among meteorologists that the earth's climate is changing and will continue to change, although there is deep uncertainty over the rate and magnitude of future change. Planned adaptation to climate change is therefore a necessity of growing importance. To date, there exists no method or decision support model to determine the most suitable seed source to use in artificial regeneration of a given site under the conditions of a changing climate. The goal of this study was to develop and implement a decision support model to select a mixture of seed sources that minimizes risk of maladaptation at a given site under a number of equally probable climate change scenarios as indicated by several global circulation models. Elements of modern portfolio theory were combined with a species range impact model (SRIM) based on genecological data from a series of jack pine provenance trials to construct the decision support model. The SRIM was used to provide estimates of how well adapted a given seed source would be to a predicted climatic condition at a given site for each climate change scenario. The first field application of the model is a south to north implementation of the seed source portfolio selections for jack pine in northwestern Ontario. Completely randomized block trials of selected and local sources are being established as demonstration plots near Fort Frances, Dryden, and Red Lake.

HYBRID POPLAR BREEDING: CASE OF THE 2004 INTRA- AND INTERSPECIFIC HYBRIDIZATION PROGRAM FOR NORTHWESTERN QUÉBEC

Pierre Périnet

Direction de la recherche forestière
Ministère des Ressources naturelles et de la Faune
2700, rue Einstein
Sainte-Foy, Québec
G1P 3W8
E-mail: pierre.perinet@mrnf.gouv.qc.ca

In 2004, a new poplar breeding program was initiated for the Abitibi-Témiscamingue region in northwestern Québec with two objectives: 1) the production of parental populations of *Populus balsamifera* and *P. maximowiczii* through intraspecific breeding and 2) the procurement of hybrid populations among the following parents: Balsam poplars (**B**) from local and Alberta provenances, and selected trees obtained from progenies of *P. maximowiczii* (**M**) and *P. deltoides* (**D**) from northern locations. Additional hybrid trees were crossed in various combinations to obtain multi-species hybrids for selection of high productivity cultivars. As expected, intraspecific breeding for BxB and MxM was successful with two thirds of the attempted crosses producing seedlings. For interspecific breeding, mean rate of success was 64% for the BxM and the MxB crosses. On the other hand, DxD crosses, with less parents involved, were much less successful with a mean rate of 38%. In general, both male and female D trees were performed less when used in several interspecific crosses (16 to 33%). Unexpectedly, the MxD crosses, with less involved combinations, were more successful than the DxM with a rate of 29 and 17%, respectively. For *P.* X*jackii*, DxB was slightly easier to cross with D as the female parent than the reciprocal cross (5% for BxD comparatively to 13% for DxB). Overall performance of male and female parents for B, M and hybrids, used in different combinations, was relatively high (40 to 85%) for this breeding program, except for three females ranging from 12 to 22%. Multi-species hybrids were also quite successful and yield a high number of seedlings per family. In May 2006, seedlings were established in three progeny tests (BxB, MxM, MxB) and as family collections for clonal selection at the Trécesson provincial nursery.

CONSERVATION AND PROPAGATION OF BEECH THROUGH SOMATIC EMBRYOGENESIS

S.E. Pond

Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: Sharon.Pond@nrcan.gc.ca

American Beech (*Fagus grandifolia* Ehrhart) is commonly found in eastern North American forests. However, due to Beech Bark Disease (an exotic insect-disease complex of *Cryptococcus fagisuga* and *Nectria coccinea* var. *faginata*) infected trees are small and have distorted trunks usable only for firewood. The disease is present in the Maritimes, much of northeastern United States and is still spreading. There is no practical chemical control of the beech scale and natural predators are not effective enough to stop the spread of the disease. Some trees show resistance to beech scale attack. Vegetative propagation of these resistant trees will help conserve the gene pool and restore disease-free beech to the forest. The first record of somatic embryogenesis in American beech will be presented and the role of somatic embryogenesis in conservation and propagation of Beech will be discussed. Initiation of somatic embryogenesis from various explants (e.g., buds, leaves of mature beech trees, and mature beech nuts) was attempted. Only the zygotic embryos produced embryogenic tissue (ET). The ET readily produced somatic embryos and was easily cryopreserved, thawed, and regrown. Work is ongoing to germinate the somatic embryos and to initiate ET from explants from mature tissue.

ASSESSING GENETIC RESISTANCE OF AMERICAN BEECH TO THE BEECH SCALE INSECT

Marianela Ramirez[1], Judy Loo[2] and Marek J. Krasowski[1]

[1] Faculty of Forestry and Environmental Management
University of New Brunswick
PO Box 44555
Fredericton, NB
E3B 6C2
E-mail: Marinela.Ramirez@nrcan.gc.ca

[2] Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7

American beech, a major component of hardwood forests in eastern North America, has been severely affected by beech bark disease (BBD). BBD development is initiated by infestation with a scale insect (*Cryptococcus fagisuga* Lind.) that attacks the bark and makes trees susceptible to infection by fungi of the genus *Nectria*. Studies have shown that some American beech trees that show no sign of the disease are resistant to the scale insect and therefore to BBD. The resistance is believed to be of genetic origin because groups of resistant trees that occur in heavily diseased stands typically consist of closely related or genetically identical individuals. We have shown that, when challenged, grafted scions from putatively resistant trees retain at least partial resistance to the scale insect one year after inoculation with scale eggs. Our results indicate that there is a range of resistance but the scale successfully reproduced only on clones grafted from known susceptible trees.

The purpose of this project was to determine the time in the life cycle of the insects when they fail to colonize or fail to thrive once they have established on putatively resistant genotypes. Previously tested three-year-old grafts from putatively resistant and known susceptible trees were retested for resistance by inoculating eggs of the scale insect on the bark of the scions. The timing of one or more resistance mechanisms was evaluated by repeating the inoculations on nine sites on the bark. Every six weeks, one inoculation site was examined and measurements of insect length and width were taken. Insects on scions from putatively resistant trees were much smaller than those developing on scions from diseased trees. Our results show that there may be two resistance mechanisms: 1) inhibition of colonization resulting in rapid death of most of the scale larvae and 2) nutritional factors, resulting in high numbers of scale colonization but many of them failing to complete their life cycle.

GEOGRAPHIC VARIATION FOR 15-YEAR SURVIVAL AND GROWTH OF TAMARACK AT SEVEN SITES IN ALBERTA

Deogratias M. Rweyongeza[1] and Leonard K. Barnhardt[2]

[1] Department of Agricultural, Food & Nutritional Science
University of Alberta
Edmonton, AB
T6G 2P5
Email: drweyong@ualberta.ca

[2] Alberta Sustainable Resource Development
Alberta Tree Improvement and Seed Centre
Smoky Lake, AB
T0A 3C0

Larix laricina (Du Roi) K. Koch (tamarack) has one of the widest natural ranges of all conifers in North American, extending from Newfoundland and Labrador across the boreal region of Canada and south into the USA with a disjunct occurrence in Alaska. Yet, the species is one of the least studied genetically. The present series of provenance trials of tamarack in Alberta consists of 25 populations of diverse origin (52°05' – 59°12' N; 111°25' – 118°45' W; 274 – 1410 m above sea level). The climatic range of these populations include -2.2 – 2.7°C mean annual temperature (MAT), 766 – 1,343 degree days above 5°C (GDD), 24 – 38.9°C difference (CI) between the warmest (TWM) and coldest month (TCM), and 402 – 633 mm of mean annual precipitation (MAP). The trials are located on 7 sites representing the main reforestation regions of Alberta.

Significant (P 0.05) variation in 15-year survival (S15) existed only at two sites where the range of provenance mean S15 was 53.3 – 89.3% (Swartz Creek) and 48.2 – 89.4% (Diamond Hills). We found that variation among provenances for 15-year height (H15) and diameter at breast height (D15) constituted 3.4 – 15.4% (H15) and 2.5 – 11.1% (D15) of the provenance phenotypic variance on individual sites and 2.1% (H15) and 1.5% (D15) across sites. However, variation was significant only on three sites where the range of provenance means for H15 was 4.69 – 6.66 m (Whitecourt), 4.80 – 6.78 m (Diamond Hills), and 3.89 – 5.38 m (Wandering River). Principal component analysis (PCA) using MAT, TWM, TCM, GDD, CI, MAP, and degree days below 0°C (NDD) separated provenances from a highly continental region in northern Alberta from those in the foothills region where climate is the least continental. PCA also showed, that based on growth variables, provenances of low growth potential originated from the highly continental region in the north, whereas those of high growth potential originated in the lower foothills and central Alberta where climate is least continental. This pattern of variation is typical of Alberta and has also been demonstrated in *Picea glauca* (Moench) Voss (white spruce) and *Picea mariana* (Mill.) BSP (black spruce).

THE REGULATION OF PNT TREES: AN OVERVIEW AND UPDATE

**Wendy Shearer[1], Isabelle Gamache[2], Anne-Christine Bonfils[2]
and Kirsten Finstad[1]**

**[1] Canadian Food Inspection Agency
Plant Products Directorate
Plant Biosafety Office
59 Camelot Drive
Ottawa, ON
K1A 0Y9**
E-mail: shearerw@inspection.gc.ca

**[2] Natural Resources Canada
Canadian Forest Service
Science and Programs Branch
580 Booth Street
Ottawa, ON
K1A 0E4**

Canada has a unique regulatory approach for biotechnology products which considers the novelty of an organism the trigger for regulatory review instead of how the product was developed. A plant with a novel trait (PNT) may be a product of recombinant DNA techniques, mutagenesis or even conventional breeding, provided that a trait has been introduced which is both new to Canadian populations of that species and has the potential to have an environmental impact.

Under the authority of the *Seeds Act* and *Regulations Part V*, the Canadian Food Inspection Agency (CFIA)–Plant Biosafety Office (PBO) grants approval for the environmental release of PNTs. This can be either a confined research field trial or unconfined environmental release. Currently the PBO is updating the confined research field trial directives as they relate to forestry trees and will be seeking input through an online consultation which is being co-developed with Natural Resources Canada, Canadian Forest Service.

RESPONSE AND TRANSFER FUNCTIONS OF JACK PINE TO PREDICT HEIGHT GROWTH ASSOCIATED WITH CLIMATE CHANGE IN ONTARIO AND THE LAKE STATES

Ashley M. Thomson[1], William H. Parker[1] and Mark R. Lesser[2]

[1] Faculty of Forestry and the Forest Environment
Lakehead University
955 Oliver Road
Thunder Bay, ON
P7B 5E1
E-mail: whparker@lakeheadu.ca

[2] University of Wyoming
1000 E. University Ave.
Laramie, WY 82071

Climate change, resulting from global warming, is expected to impact both productivity and biodiversity of forest ecosystems over the next century. Provenance tests provide valuable information about species' climatic adaptation that can be used to predict and model species' responses to environmental change. Height, diameter, and survival data from 16 tests of the Canadian Forest Service's experiment 255 range-wide jack pine provenance trial series were obtained during the summer of 2005. August minimum temperature and January maximum temperature produced the strongest and most consistent relationships between climate and height growth for response functions, while March precipitation and December minimum temperature were strong predictors for site transfer functions. Lines of present and future optimal height growth for Ontario and the Great Lakes States were determined by fitting contours to current (1971–2000) and future (2041–2070) climate grids of Ontario and the Great Lakes States. Optimal growth is currently achieved between 46 and 47° N latitude for the majority of jack pine seed sources. Future temperature increases are predicted to cause a northward shift of the optimal habitat by approximately 2° for most sources. Northern sources are currently growing at temperatures below the optimum and would benefit from transfer to warmer environments provided that other environmental factors do not become limiting. Central sources are currently close to optimum and will be negatively affected by increased temperatures in the future. Southern sources may benefit from transfer to cooler environments, as the effects of global warming may cause significant height growth loss and potential extirpation of these populations.

REALIZED GENETIC GAINS OBTAINED IN FIRST-GENERATION PROGRAMS FOR JACK PINE IN NEW BRUNSWICK, CANADA

Y.H. Weng, K. Tosh and M.S. Fullarton

New Brunswick Department of Natural Resources
Kingsclear Forest Nursery
3732 Route 102
Island View, NB
E3E 1G3
E-mail: yuhui.weng@gnb.ca

First-generation jack pine seed orchards were established in New Brunswick in the 1970's. While a 4–5% gain in height at 10 years was predicted for this approach from genetic tests, realized genetic gains in operational plantations had never been evaluated. One series of jack pine realized gain tests with a design similar to operational plantations was established using seedlots from J.D. Irving, Limited's seedling seed orchard. Three seed orchard seedlots representing different improvement stages were included: before roguing (UNROG), after 1st rogueing (1STROG), and after 2nd rogueing (2NDROG). In order for comparison, two unimproved stands, ROGER and WMUZ, were also included as a control. Individual tree data were analyzed at 5, 10, and 15 years. Realized gain for each seed lot varied with age but no consistent temporal patterns stood out. At 15 years, the realized gains were 3.8%, 3.1%, and 0.3% for height growth for 2NDROG, 1STROG, and UNROG, respectively. The corresponding realized gains for volume per hectare were 20.1%, 17.3%, and 5.9% for those same seed lots. The gains in DBH and stem straightness showed similar results to height with the 2NDROG consistently superior.

TREE SEED WORKING GROUP
WORKSHOP ABSTRACTS

APPRECIATING, QUANTIFYING AND UTILIZING FAMILY DIFFERENCES

The workshop theme is aimed at family variability and the three keywords in the title:
Appreciate – to be aware of the incredible variation present,
Quantify – to be able to express as a number, measure or quantity, and
Utilize – to put into service this family variability.

Family differences are the foundation of our tree improvement programs utilizing seed as the deployment vehicle. The theme is similar to the 2004 theme of 'Quality Assurance in the Seed Handling System", but the focus here is on the genetic aspects of quality assurance vs. the phenotypic QA in 2004. The topic is incredibly important and I'll use this introduction to put forth some questions on the topic and extend some personal opinions.

In terms of family contributions to seedlots, Do we have good measurement methods and estimates of parental contribution in our operational seedlots? How do we value diversity? How do we balance diversity and yield? How much of the initial family variability is present in our reforestation seedlings? What are the most significant points of genetic erosion in the Seed Handling System? I think these are important questions related to the efficiency of our tree improvement programs.

There is a great deal of data collected from our operational facilities (seed orchards; processing facilities, and nurseries) that never get utilized. This is the point at which real efficiency gains can be implemented directly, but there is rarely the statistical expertise to design trials or analyze operational data to improve efficiency. This expertise is often restricted to scientific research that is often at least one step removed from reality in one of the following attributes:

Scale – operational results may not mimic lab results (i.e., western white pine (*Pinus monticola*) stratification)
Genetic Representation – a well designed study is not overly useful if based on one or a few seedlots. There is just too much variation in conifers to accept this.
Funding Buzzwords – funding based on using the most current, trendy technology even if the problem is not the highest priority.

The area of extension is also not well appreciated or funded today and I think this is a serious issue. Through a better understanding of our families I think there is a great deal of untapped potential or lost efficiency in our tree improvement programs. I suggest that the use of path analysis is a valuable tool to enable us to appreciate and quantify our bottleneck steps and to move forward in utilizing our germplasm to its potential.

Dave Kolotelo
Chair, Tree Seed Working Group

25+ YEARS OF FAMILY-BLOCK PLANTING IN THE SOUTHERN US – FROM NOVELTY TO STANDARD OPERATING PROCEDURE

Steve McKeand[1], Dave Gerwig[2], Patrick Cumbie[1] and J.B. Jett[1]

[1] NC State University
Department of Forestry and Environmental Resources
College of Natural Resources
PO Box 8002
Raleigh, NC 2769-8002
E-mail: steve_mckeand@ncsu.edu

[2] MeadWestvaco Corporation
PO Box 739
Ravenel, SC 29470

Operational family-block planting with loblolly pine (*Pinus taeda* L.) was begun by Weyerhaeuser Company in the mid-1970's (Gladstone 1981) and has been one of the most significant forest management decisions made with southern pines. After more than 30 years, planting of individual open-pollinated families and more recently full-sib families and clones has become standard practice in the southern United States. In the early 2000's, 59% of the loblolly pine plantations were established as single open-pollinated (OP) family blocks (McKeand et al. 2003). About 80% of the regeneration on company lands was with OP families, and 48% of seedlings used for market sales were as OP families. Fourteen companies used family blocks for deployment of loblolly pine. On average, a company deployed 47 different families on its own land, but there was tremendous variation in the number of families deployed in a region, ranging from as few as 4 to as many as 90.

In our opinion, nothing has had a greater impact on operational genetic gain than deployment of individual families of loblolly pine to specific sites. With loblolly pine, deployment is fairly straightforward; plant the best families on the best sites to realize the most genetic gain (Duzan and Williams 1988). The best families tend to be the best on all sites within broad adaptability zones, so more wood production is realized from the combination of the best families, sites, and silvicultural practices (McKeand et al. 1997, 2006). Even with the availability of many tons of loblolly pine seed each year (Figure 1), foresters don't plant the best family everywhere, since seedlings of best genotypes are always in short supply and because of diversity concerns.

In the last 10 years, seed orchard managers have had great success in developing methods to mass produce full-sib families for operational planting (Bramlett 1997, Bridgwater et al. 1998). The gains from improved quality and yield are very impressive when both the female and male parents are selected. While production figures are not available for the South, our estimate is that approximately 40 million full-sib seedlings have been planted each of the last 3 to 5 planting seasons.

Since production costs for mass control pollination (MCP or CMP) are large, production characteristics of the parent selections can be overwhelmingly important. When orchard managers are pollinating 40 000 to 80 000 bags each spring, production efficiency is critical. While the genetic quality of the parent trees used for MCP is critical, the morphological, physiological, phenological, and yield characteristics of the trees are extremely important. Virtually everything in a seed orchard is clonal; susceptibility to insects, drought, diseases, animal predation, and even hurricane damage varies tremendously among parental selections. For an orchard manager to make MCP cost-effective, he or she must understand these differences and manage the orchard and MCP production efficiently.

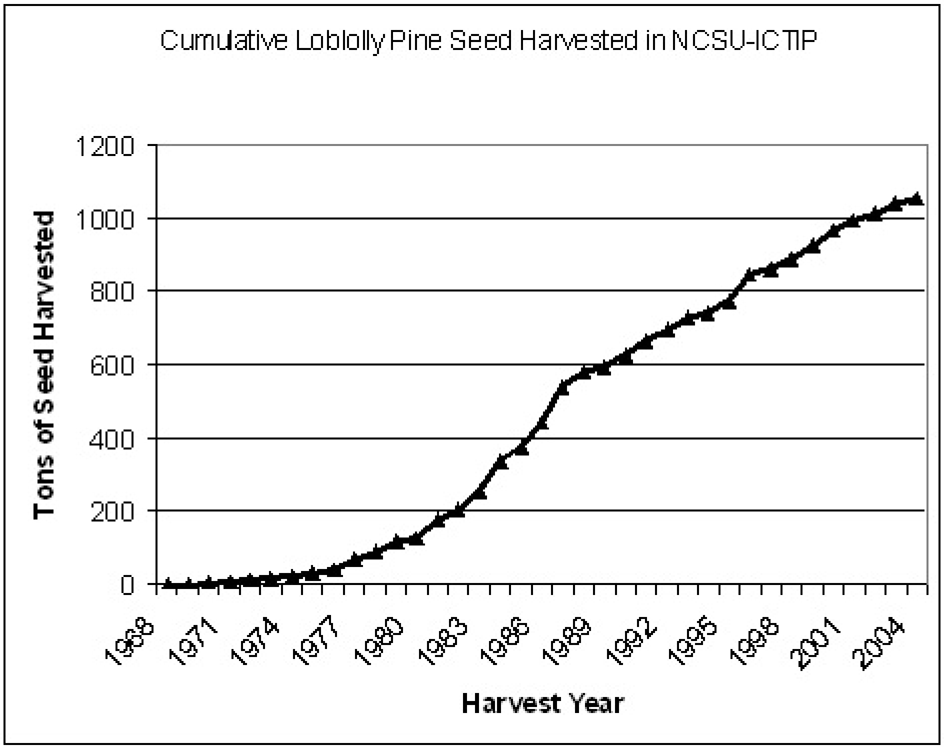

Figure 1. Cumulative production of loblolly pine seed by members of the NC State Tree Improvement Cooperative. Enough seeds have been produced to plant over 30 billion seedlings in the last 40 years.

REFERENCES

Bramlett, D.L. 1997. Southeastern conifers: Genetic gains from mass control pollination and topworking. J. For. 95(3): 15–19.

Bridgwater, F.E.; Bramlett, D.L.; Byram, T.D.; Lowe, W.J. 1998. Control mass pollination in loblolly pine to increase genetic gains. For. Chron. 74: 185–189.

Duzan, H.W. Jr.; Williams, C.G. 1988. Matching loblolly pine families to regeneration sites. South. J. Appl. For. 12: 166–169.

Gladstone, W. 1981. Customize or compromise, an alternative for loblolly. Pages 200–204. *In* Proc. 16th South. For. Tree Impr. Conf., Blacksburg, VA.

Li, B.;. McKeand, S.E. 1989. Stability of loblolly pine families in the southeastern U.S. Silvae Genet. 38: 96–101.

McKeand, S.E.; Crook, R.P.; Allen, H.L. 1997. Genotypic stability effects on predicted family responses to silvicultural treatments in loblolly pine. South. J. Appl. For. 21: 84–89.

McKeand, S.E.; Jokela, E.J.; Huber, D.A.; Byram, T.D.; Lee Allen, H.; Li, B.; Mullin, T.J. 2006. Performance of improved genotypes of loblolly pine across different soils, climates, and silvicultural inputs. For. Ecol. Manage. 227: 178–184.

PROCESSING FAMILY SEEDLOTS

Al Foley

Ministry of Natural Resources
Ontario Tree Seed Plant
PO Box 2028
Angus, ON
L0M 1BO
E-mail: al.foley@mnr.gov.on.ca

The presentation began with a discussion about the art of quality tree seed processing and a tribute to the technicians whose dedication and experience produce a quality product. The term “Small Lot” is defined to clarify it’s use at the Ontario Tree Seed Plant and normally consists of less than 5 L of cones or fruits, that has unique characteristics requiring it to be processed on its own. Particular emphasis is placed on receiving of shipments at the Seed Plant because this stage is essential to the chain of custody and most prone to errors. The processing stages of cone drying, extraction, de-winging and cleaning, testing, and storage were presented photographically. The presentation concluded with a discussion about the dilemma of data management, how information should or can be collected, and where it should be stored.

ESTIMATING PARENTAL CONTRIBUTIONS TO ORCHARD SEEDLOTS IN BRITISH COLIMBIA

J.H. Woods

Forest Genetics Council of BC
3370 Drinkwater Road
Duncan, BC
V9L 5Z2
E-mail: jwoods.fgc@shaw.ca

In British Columbia (BC), approximately 93% of the forest land is under public ownership and over 90% of the provincial harvest volume is from public lands. The "social license" to harvest timber is expressed in public land policy and programs. These include objectives for the use of genetically selected seed from seed orchards and minimum thresholds for seedlot genetic diversity.

Value from the use of select (orchard) seed is based on increased growth and/or pest resistance. This value is complex and is derived from the impact of increased growth rates on timber flow from a given geographic area. In BC, timber supply analyses are conducted every five years for all 72 management units. Incorporation in timber supply analyses of estimates of genetically-based increases in timber-volume production provides a technical basis for the adjustment of allowable annual cut (AAC) based on the use of select seed. To achieve the linkage between timber-supply analyses and the use of select seed, standard protocols are needed:
1) estimation of parent-tree breeding values (BV) in a way that is consistent across species, site indices, and geographic areas,
2) estimation of gametic contributions from individual parent trees to an orchard seedlot,
3) estimation of a seedlot's genetic worth (GW) based on BVs and gametic contributions,
4) growth models that are capable of incorporating GW and providing stand yield estimates for plantations with a range of GW values (also for multiple species and stand types), and
5) timber supply analysis methods that incorporate stand growth estimates that have utilized seedlot GWs and estimated GWs over time.

This complex series of events requires standardization of methodology in each step to ensure consistency in application and reliability of the final result. Estimates of parental contributions to orchard seedlots are one step in the series and provides data for both estimating GW and for estimating effective population size (Ne) as a surrogate measure of seedlot genetic diversity.

Protocols for estimating parental contributions to orchard seedlots are set out in a Technical Report of the BC Ministry of Forests and Range[1]. Methods are described for both male and female contributions and formulae are provided for estimating seedlot GW and Ne under a variety of circumstances. Methodology is designed for applied use in BC seed orchards.

---

[1] Woods, J. H. 2005. Methods for estimating gamete contributions to orchard seed crops and vegetative lots in British Columbia. BC Min. For. Range, Tech. Rep. 25, 17 p.

FAMILY VARIATION IN WHITE SPRUCE SEED AND SEEDLING CHARACTERISTICS

S.A. Carles[1], J. Beaulieu[2], M.S. Lamhamedi[3], F. Colas[3], D. Stowe[1] and H.A. Margolis[1]

[1] Centre d'Étude de la Forêt (CEF)
Faculté de Foresterie et de Géomatique
Pavillon Abitibi Price
Université Laval
Sainte Foy, QC
G1K 7P4

[2] Natural Resources Canada
Canadian Forest Service
Canadian Wood Fibre Centre
PO Box 10380
Sainte Foy Stn., QC
G1V 4C7
E-mail: jeanbeau@nrcan.gc.ca

[3] Direction de la recherche forestière
Ministère des Ressources naturelles et de la faune
2700 rue Einstein
Sainte Foy, QC
G1P 3W8

In Québec, about 28 million white spruce (*Picea glauca*) seedlings are planted annually. Previous studies have shown that white spruce exhibits family and clonal genetic variation in most of its phenotypic traits. Use of this variability, through selection and breeding, might contribute to improvement of seedling quality. In addition, it is generally accepted that larger seeds give rise to better performing seedlings, at least for the first few years. Could seedling performance be improved through indirect selection for seed traits? To answer this question, we must first test whether: 1) there is sufficient family variation in white spruce seed characteristics and seedling morphological traits, and 2) correlations between seed and seedlings characteristics at the family level are strong and positive.

Seeds from 75 open-pollinated families were used. Seed traits (length, width, area, volume) were measured on 400 seeds per family. Percent germination and germination value were determined for each of the 75 families under controlled conditions. Seedling traits (height, diameter, shoot and root dry mass) were measured at the end of the first growing season under standard nursery cultural practices.

Significant differences among families were found for all traits with the exception of root-collar diameter. Family explained from 39.9% (seed width) to 52.5% (seed projected area) of total seed trait variation, 88.8% of total germination value variation, and from 7.5% (root dry mass) to 19.4% (height) of total seedling morphological variation. All traits were moderately to strongly intercorrelated at the family level. Seed width was the morphological trait showing the strongest correlation with seedling morphology. Positive significant correlations were found between seed width and height (0.22), diameter (0.39), shoot dry mass (0.40), and root dry mass of seedlings. Positive significant correlations of the same order were found between other seed characteristics and the same seedling traits. Correlations between seed germination variables and seedling morphology were, however, not significant.

Whereas correlations between seed characteristics and seedling height, root collar diameter or shoot and root biomass were positive at the family level, they were not strong enough to warrant selection of the best performing families based on seed characteristics only. Results suggest that inferior families could be culled using seed characteristics, that would allow reducing field testing costs. However, seed effects might disappear after several years. This is why this study should be pursued over several years to evaluate whether family ranks change over time and to confirm the present conclusions.

BC EXPERIENCE OF PROCESSING BY FAMILY

Dave Kolotelo

Ministry of Forests and Range
Tree Seed Centre
187923 – 32nd Avenue
Surrey, BC
V3S 0L5
E-mail: Dave.Kolotelo@gov.bc.ca

A review of some of the trial results for family processing conducted on lodgepole pine (*Pinus contorta*), interior spruce, and Douglas-fir (*Pseudotsuga menziesii*) were presented. The goal of this presentation was to illustrate the variability found between families in a wide range of investigated processing activities and biological traits. The trial consisted of ten families per seed orchard in a given year (repeated over two or three years). Ten per cent of the cones from each family were combined and processed as a bulk sample while the remaining 90% was processed as individual families. A total of twenty variables was measured and a few representative results were presented

At cone tumbling, the number of unextracted filled seeds per cone is used as a variable to describe extraction efficiency. Low values of 0.1 for Douglas-fir and 0.2 for Lodgepole were obtained, but the average value was 0.7 for interior spruce. The range in interior spruce was from 0.1 to 1.1 filled seeds per cone. Seed yield varied by family, but the trend was consistent between years (i.e., for lodgepole pine all 1997 yields were higher than in 1996). Seed size also showed variability and consistency across years (no family X year interactions), but there was a large impact of development year on seed size (i.e., one spruce family varied from 429 to 598 seeds per gram across years). Seed dormancy was estimated based on stratified and soak-only test results with the following species Dormancy Index values: Interior spruce – 3%, Douglas-fir – 15%, and lodgepole pine – 21%. Family dormancy values did not always show consistent year-to-year patterns across families like seed yield and seed size.

Seed yield comparisons between average family yields and the bulk processing indicates that there appears to be family processing efficiencies for Douglas-fir and interior spruce, but not for lodgepole pine. Cost effectiveness appeared greatest in Douglas-fir due to superior growth rates and/or reduced harvest age. A sensitivity analysis indicated that Site Index of the reforestation site was the most important factor in evaluating cost effectiveness of family processing.

Some benefits of family processing include:
1) An ability to create custom seedlots based on the latest breeding value information including the introduction of new traits.
2) An ability to create custom seedlots for specific elevation bands.
3) Possibly greater seed-use efficiency through gains in processing and growing on a family basis.

TREE IMPROVEMENT DELIVERY SYSTEM: CRITICAL EVALUATION WITH EMPHASIS ON SEED AND SEEDLING PRODUCTION

Yousry A. El-Kassaby

The University of British Columbia
Department of Forest Sciences
2424 Mail Mall
Vancouver, BC
V6T 1Z4
E-mail: y.el-kassaby@ubc.ca

Successfully implementing tree improvement programs (breeding and delivery systems) requires diverse perspectives and expertise. Tree breeding activities have generally been successful capturing substantial genetic gains per unit time, effort, and cost. The systematic, methodical, and sophisticated methods used to advance and apply breeding theory, and the fact that most forest tree species are in the early stage of domestication, are key reasons for this success. Although it is an operational paradigm, delivering captured gains to planted forests builds on solid scientific foundations ranging from reproductive biology and ecology, tree physiology, seed biology, to more applied aspects including seed orchard management, seed processing and seed pre-treatment, and seedling production. The components of the delivery system are diverse and often managed horizontally. They become compartmentalized and create conditions that inadvertently counteract each other within the system, impeding the delivery of captured gains. The tree improvement delivery system is critically evaluated and its caveats are highlighted. Finally, an alternative tree improvement delivery management system is proposed. This option applies vertical management concepts to combine the benefits of expertise in different aspects of the system, providing opportunities to achieve and surpass the goals of any traditional tree improvement delivery system.

WOOD QUALITY WORKSHOP

ABSTRACTS

WOOD QUALITY AND UTILIZATION OF YOUNG PLANTATION-GROWN WHITE SPRUCE

Jean Beaulieu

Natural Resources Canada
Canadian Forest Service
Canadian Wood Fibre Centre
PO Box 10380, Stn. Sainte-Foy
Sainte-Foy, QC
G1V 4C7
E-mail: jeanbeau@nrcan.gc.ca

Breeding programs were set up in the early 1970s in Canada. Since then, seed orchards were established to produce genetically improved seed and reforestation was intensified. Among the species used in reforestation programs, white spruce (*Picea glauca* [Moench] Voss) is one of the most preferred species because of its large ecological plasticity and its high yield. Many plantations are now old enough to be commercially thinned. Moreover, in the near future, harvesting in natural stands is bound to be reduced whereas that from plantations will increase. Will wood characteristics and properties of plantation-grown trees be similar to those of trees of old-growth or second-growth stands? Over the last 20 years, as part of our research program on the genetics of white spruce, we have conducted a series of studies to assess wood properties and fibre characteristics of young plantation-grown trees. Traits assessed include wood density, tracheid length and coarseness, lumber mechanical properties, veneer mechanical properties, warp and shrinkage, and machining properties. Our studies showed that some of the traits such as wood density were under strong genetic control whereas others such as tracheid length or wood stiffness were under low to medium genetic control. Hence, most of the properties and characteristics can be improved through breeding. There was also large tree-to-tree variation in every trait, which means that vegetative propagation would be very efficient to produce better quality wood. Mechanical properties of young plantation-grown white spruce were weak due to a large proportion of juvenile wood and a large number of knots. However, they should improve by rotation age with a higher proportion of mature wood. Machining properties were generally good to excellent except for turning and mortising. On average, plantation-grown wood had warp, shrinkage, and machining properties similar to those of second-growth wood. After having spent a few decades selecting the best genotypes for growth, it is now time to turn our attention to wood and fibre characteristics and our preliminary results show that quick progress is possible.

A METHOD TO ASSESS LUMBER GRADE RECOVERY IMPROVEMENT POTENTIAL IN BLACK SPRUCE

Jeff Benjamin[1], Ying Hei Chui[2] and Tony Zhang[3]

[1] **Department of Forest Management**
University of Maine
5755 Nutting Hall
Orono, ME
04469
E-mail: Jeff_Benjamin@umenfa.maine.edu

[2] **Faculty of Forestry and Environmental Management**
University of New Brunswick
PO Box 44555
Fredericton, NB
E3B 6C2

[3] **Forintek Canada Corp.**
319 rue Franquet
Quebec, QC
G1P 4R4

A log-level lumber quality assessment method was developed to bring lumber grade considerations into forest management planning. The method is based on knot size and location at log surface, internal knot shape, log size, and visual grading rules for dimension lumber. A theoretical exercise was initially undertaken to examine influence of horizontal knot angle (or branch azimuth) and knot size on lumber grade recovery. Assuming a cylindrical log shape, difference in horizontal knot angle between successive knots decreased with increasing log size if product specifications were held constant and increased with increasing product width if log size remained constant. A log transformed linear regression model was developed to predict minimum angle between successive knots, with respect to log size, that would produce at least one piece of lumber at a desired grade, by product, from the centre cant using either an edge or centreline knot pattern.

The number of logs for which improvements in lumber grade could be made if consideration is given to knot size and location around the stem prior to processing were then assessed in three ways. The first assessment determined which grades of lumber could be produced by “default” through a comparison of the largest knot per log and minimum product and grade knot size limits. This is an “all-or-nothing” assessment in that even though some products, those processed closest to the pith, may still meet minimum grade requirements, the default assessment is concerned with all products from a given log. Potential to improve lumber grade based on an edge knot pattern was determined by comparing the largest angle difference between successive knots with minimum knot angle determined from the edge knot model. Potential to improve lumber grade based on centreline knot pattern was determined by comparing knot angle differences between three consecutive knots using the centreline knot model.

INCORPORATING WOOD DENSITY IN BLACK SPRUCE AND JACK PINE BREEDING PROGRAMS IN ONTARIO FOR MAXIMUM FIBRE YIELD PRODUCTION

Paul Charrette[1], Tony Zhang[2] and Pengxin Lu[3]

[1] Superior-Woods Tree Improvement Association
Faculty of Forestry and the Forest Environment
Lakehead University
955 Oliver Road
Thunder Bay, ON
P7B 5E1
E-mail: paul.charrette@lakeheadu.ca

[2] Forintek Canada Corp.
319 rue Franquet
Sainte-Foy, QC
G1P 4R4

[3] Ontario Forest Research Institute
Ministry of Natural Resources
1235 Queen Street East
Sault Ste Marie, ON
P6A 2E5

An operational-level evaluation of growth traits and wood density, including a new selection trait, dry fibre weight, was conducted in a black spruce (*Picea mariana*) and a jack pine (*Pinus banksiana*) tree improvement program in Northwestern Ontario. Estimates of genetic variation, heritability, and age-age correlation of wood density, growth traits (height, DBH, and volume), and dry fibre weight at different ages were made. In addition, genetic gains were estimated for different selection scenarios. For black spruce, a negative but weak genetic correlation between wood density and growth traits was found, resulting in no loss of genetic gain in dry fibre weight production due to selection based on growth traits, such as height and DBH. For jack pine, genetic correlations between wood density and growth traits were negative and moderately strong, especially between DBH and wood density, indicating that faster-growing trees are genetically associated with lower wood density. If the primary objective of a jack pine tree improvement program is to increase wood production for solid wood products this study then suggests that wood density be considered.

VARIATION OF WOOD AND FIBER QUALITY ATTRIBUTES IN *Pinus banksiana* GROWN IN INTENSIVELY MANAGED BOREAL STANDS

Ahmed Koubaa

Université du Québec en Abitibi-Témiscamingue
445, boul. de l'Université
Rouyn-Noranda, QC
J9X 5E4
E-mail: ahmed.koubaa@uqat.ca

Variation in wood anatomical, physical, and chemical properties of jack pine (*Pinus banksiana*) grown in five different natural stands in the boreal forest was studied. In each stand, three commercial thinning intensities were applied from 1998 to 2000: heavy, moderate, and control. Factors studied included site, tree, thinning intensity, and longitudinal and radial positions in the tree. The effects of these factors on lignin content, extractive content, fiber length and diameter, sapwood, and heartwood proportions were examined. Results indicated that site and within-tree variation are the most important factors of the wood properties studied. Variation with thinning intensity, although significant, is weak compared to environmental and physiological variation.

IMPACT OF WHITE PINE WEEVIL DAMAGE ON LUMBER RECOVERY AND LUMBER QUALITY CHARACTERISTICS IN NORWAY SPRUCE PLANTATIONS IN QUÉBEC

Marie-Josée Mottet[1], Gaëtan Daoust[2] and Tony Zhang[3]

[1] Ministère des Ressources naturelles et de la Faune
Direction de la recherche forestière
2700 rue Einstein
Sainte-Foy, QC
G1P 3W8
E-mail: marie-josee.mottet@mrnf.gouv.qc.ca

[2] Natural Resources Canada
Canadian Forest Service
Laurentian Forestry Centre
PO Box 10380, Stn. Sainte-Foy
Sainte-Foy, QC
G1V 4C7

[3] Forintek Canada Corp.
319 rue Franquet
Sainte-Foy, QC
G1P 4R4

This study quantified the impact of stem deformations caused by white pine weevil on lumber recovery and lumber quality characteristics in Norway spruce (*Picea abies* [L.] Karst.). Through a commercial thinning operation, 148 32- to 34-year-old sample trees were taken from three plantations which were attacked by the white pine weevil (*Pissodes strobi* [Peck]). The sample trees, with diameters at breast height ranging from 14–23 cm, were grouped into three quality classes according to the number of major stem deformations caused by the weevil. The effects of stem deformations on lumber volume recovery and lumber quality characteristics were quantified.

The study showed that deformations led to a loss of less than 5% in the total merchantable volume over the rotation. Stem deformations did not significantly affect the lumber properties of Norway spruce on medium to high quality sites. For the three Norway spruce plantations, the mean modulus of elasticity (MOE) of the lumber varied from 8510 to 9357 MPa, the mean modulus of rupture (MOR) ranged from 360 to 425 MPa, and the mean wood density varied from 324 to 343 kg·m^{-3}. For comparison purposes, the same measurements were taken on lumber from 38 trees in a white spruce (*P. glauca* [Moench] Voss) plantation that was unaffected by the weevil, but comparable to one of the three Norway spruce plantations studied. Norway spruce stems, including those with deformations, were found to yield a higher merchantable volume (12.5%) and the monetary value of the lumber was 26% higher than that of white spruce. These differences are largely attributable to a less pronounced stem taper in Norway spruce. Lumber properties of Norway spruce were 34% superior to those of white spruce for MOE, 20% for MOR, and 8% for wood density. The smaller knots in Norway spruce explain part of the differences. On the other hand, visual grading of this type of wood reveals little differences in lumber grade yield and bending properties.

EFFECT OF GENETIC AND ENVIRONMENTAL FACTORS ON RADIAL GROWTH OF DIVERSE POPULATIONS OF *Pinus banskiana* IN SOUTHERN ONTARIO, CANADA

Y. Savva, B. Denneler, A. Koubaa, F. Tremblay and Y. Bergeron

Université du Québec en Abitibi-Témiscamingue
445, boul. de l'Université
Rouyn-Noranda, QC
J9X 5E4
E-mail: julia.savva@uqat.ca

Understanding the role of genetic and environment effects on long-term tree growth is essential in predicting tree response to climate change. This study is part of a range-wide jack pine (*Pinus banksiana*) provenance study of 99 seed sources collected from native stands throughout the geographic range of the species and planted in 1966 at sites in the United States and Canada. This study was conducted with 22 jack pine provenances planted in contrasting common-garden environments in Petawawa, Canada.

Environmental factors mainly affected long-term radial growth of jack pine provenances rather than genetic factors related to provenance origin. First principal component extracted from ring-width chronologies explained 76% of the variance held in common by the provenances. Cluster analysis distinguished the provenances into five clusters depending upon their geographical origin. Ring width increased with increasing growing season degree-days and decreasing latitude of provenance origin. Sensitivity of ring width to interannual climate variations was high for the northern populations compared to the southern populations. Climatic transfer functions and dendroclimatolgical techniques have been applied to reveal the main climatic predictors of tree growth of diverse jack pine populations in Petawawa, Canada.

MAPPING ENVIRONMENTAL VARIATION IN WOOD DENSITY IN DOUGLAS-FIR

Michael Stoehr

BC Ministry of Forests and Range
Research Branch
722 Johnson St.
Victoria, BC
V8W 1N1
E-mail: Michael.Stoehr@gov.bc.ca

In order to map climatic factors that drive wood density (WD) in coastal Douglas-fir (*Pseudotsuga menziesii)* plantations, two sets (Series) of 10 full-sib families were evaluated on 22 sites each. WD was determined for 12 seedlings per family per site using the maximum moisture method on increment cores, taken at breast height. Only the inner 8 rings were evaluated on each sample. Family means in WD ranged from 0.398 to 0.454 and from 0.414 to 0.457 for Series 1 and 2, respectively. Correspondingly, site means ranged from 0.378 to 0.474 and 0.403 to 0.460. Site by family interactions were absent. Correlating site mean WD with various climate and geographical variables showed that WD was most closely correlated with “Continentality” (TD), the difference between the mean temperature of the warmest month minus the mean temperature of the coldest month at each test site. Climate variables were obtained using the Climate BC software application of Wang and Hamann. Exploratory regression analysis revealed a polynomial relationship ($WD=0.0215\ TD-0.0005TD^2+0.2$) with a $R^2=0.39$. Therefore, higher WD can be found on sites with hot summers and cold winters, i.e., further away from the Pacific coast.

VALUE-ADDED FOREST PRODUCTS – AN APPROACH TO OPTIMISE MANAGEMENT AND CONSERVE FOREST RESOURCES IN AFRICA

R. Venkatasamy

Department of Wood Science
Moi University
Kenya
E-mail: venkatasamyr@yahoo.com

The urgency to curtail deforestation in Africa has been of national and international concern in recent years. Population growth in most African countries has been rapid over the past 30 years, resulting in increased demands for land for food production, and wood for the manufacturing industries, shelter, and energy. In Kenya, forests, which used to form about 3.4% of the total land cover, now stand at less than 2%. Harvesting has been regular and replanting reduced. The consumption of wood per capita fell from 1.2 to 0.9 m^3 within a short period of 5 years, between 1995 and 2000, production falling by 46% in 1997 alone. This is the general trend in many African countries. Apart from demands for more land, the lack of a policy on wood utilisation has also contributed to excessive pressures on forests. Mis-utilisation, non-utilisation, under-utilisation, and ineffective preservative treatment have resulted in unnecessary waste. Wastage is high at all stages of processing, with no efforts to develop products that mainly utilise waste. The lack of a grading system results in high-grade timber being utilised for low-grade products. A sound policy aimed at intensifying forest management and optimising utilisation, reducing waste, encouraging waste utilisation and, especially, ensuring effective chemical treatment to significantly extend service lives of timbers, will certainly reduce pressures on forests and help in conserving existing resources.

NEW SOLUTIONS FOR RAPID, COMPREHENSIVE WOOD AND FIBER ANALYSES

K.L. Woo, G. Sherson, A. Goodison and P.A. Watson

Pulp and Paper Research Institute of Canada
3800 Wesbrook Mall
Vancouver, BC
V6S 2L9
E-mail: kwoo@paprican.ca

Environment, genetics, and silvicultural modifications all influence fundamental wood and fibre properties within a stem. With our changing resource base, it is becoming increasingly important to understand and assess wood quality characteristics in order to identify value-added opportunities. Traditional analytical techniques are time-consuming and costly to measure statistically valid sample sets that reflect within-tree, between-tree, within-stand, and stand-to-stand variability. A renaissance in development of optical based technologies for wood quality assessment is underway and has enabled researchers to more accurately reflect the opportunities for more efficient utilization of our current forest resources and to include wood and fibre quality parameters in future resource development. Paprican, in collaboration with the University of Northern British Columbia, the University of Victoria, and CSIRO-Ensis has established the EvaluTree™ laboratory that has brought together a unique suite of state-of-the-art high throughput wood and fibre analysis technologies. Many of these technologies have been applied in support of research programs in tree breeding, the impact of silvicultural techniques, and the impact of genetics on wood quality. This presentation will discuss a selection of data generated at high resolution using confocal microscopy, environmental scanning electron microscopy, and SilviScan. In addition, recent work using optical spectroscopy techniques for high throughput laboratory and in-field analysis of wood physical properties will be presented.

POSTER ABSTRACTS

ASSOCIATION MAPPING FOR WOOD CANDIDATE GENES IN WHITE SPRUCE

Jean Beaulieu[1,3,4], Paul Watson[2,4], Nathalie Isabel[1,3,4], Jean Bousquet[3,4],
Patrick Lenz[3,4] and John Mackay[3,4]

[1] Natural Resources Canada
Canadian Forest Service
Laurentian Forestry Centre
PO Box 3800
Sainte-Foy, QC
G1V 4C7
E-mail: beaulieu@nrcan.gc.ca

[2] Pulp and Paper Research Institute of Canada
3800 Wesbrook Mall
Vancouver, BC
V6S 2L9

[3] Chaire de recherche du Canada en génomique forestière et environnementale
and
[4] *ARBOREA* Project
Université Laval
Sainte-Foy, QC
G1K 7P4

White spruce is one of the most economically important tree species in Canada. Study of its wood properties is essential to help enhance the economic output of the Canadian forest product industry. The discovery of genes that are linked to these properties can be used to develop molecular tools for more efficient selection of high performance trees. These selection tools can be applied to breeding programs and lead to greater gains per unit of time to benefit industry more rapidly. In this project we propose to identify favourable alleles for 500+ such candidate genes in mature white spruce. For each candidate gene, primers are designed to sequence and identify a number of common single nucleotide polymorphisms (SNPs). All genotyping arrays are developed for high-throughput genotyping. A 495-tree discovery population has been assembled with three siblings per family. Phenotyping will be carried out using Paprican's Evalutree, which encompasses a unique suite of technologies, including the SilviScan from CSIRO. We aim to detect associations between polymorphisms in candidate genes and phenotypic variation by using Quantitative Transmission/Disequilibrium Testing (TDT), a family-based association test. A second population of 200 trees will also be used for the validation of the associations revealed by TDT. These populations will also be used to estimate genetic variance components for wood properties and crown architecture, and assess correlations between these traits. This research is part of *ARBOREA* II, a large-scale project funded by Genome Canada, Genome Québec, and the Canadian Biotechnology Strategy which aims to develop molecular breeding tools for softwood trees.

HOW ARE THE CHANGING CLIMATE PATTERNS IN BRITISH COLUMBIA IMPACTING RADIAL GROWTH IN LODGEPOLE PINE?

Sierra Curtis-McLane

The University of British Columbia
Department of Forest Sciences
Vancouver, BC
V6T 1Z4
E-mail: sierracm@interchange.ubc.ca

The unprecedented rate of climate change that occurred during the twentieth century is projected to continue throughout and beyond the fossil fuel era, provoking concerns regarding how plant species are and will continue to respond to new climatic conditions. This study will evaluate ring width indices for *Pinus contorta* var. *latifolia* (lodgepole pine) throughout its range in British Columbia in order to examine correlations between growth and climate trends over the last three decades. Genetic responses of lodgepole pine to changing climate variables will be analyzed based on radial increment data for 6 populations planted 35 years ago in 15 environmentally disparate common gardens throughout the province. These analyses will be used to make predictions regarding a potential shift in the growth rates, competitive ability, and ultimately the range distribution of lodgepole pine under future climate change scenarios.

UNDERSTANDING SEED BIOLOGY FOR IMPROVING UTILIZATION: LODGEPOLE PINE

Y.A. El-Kassaby[1], D. Reid[2] and D. Kolotelo[2]

[1] The University of British Columbia
Department of Forest Sciences
2424 Main Mall
Vancouver, BC
V6T 1Z4
E-mail: y.el-kassaby@ubc.ca

[2] BC Ministry of Forests and Range
Tree Improvement Branch
7380 Puckle Road
Saanichton, BC
V8M 1W4

[2] BC Ministry of Forests and Range
Tree Seed Centre
1879 - 32 Avenue
Surrey, BC
V4P 1M5

Germination behaviour of seed from 18 lodgepole pine (*Pinus contorta* var. *latifolia*) (Pli) clones collected over two years was assessed to evaluate the extent of variation among clones and between years. For each year, individual clone seed was tested using standard germination protocols following International Seed Testing Association (ISTA) rules that consisted of control (unstratified) and one stratification treatment (4 weeks pre-chilling). Germination capacity (GC: % of total germination), germination speed (R_{50}’: number of days required for 50% of the germinating seed to germinate; indicative of emergence promptness), and seed dormancy (effectiveness of the stratification treatment on breaking dormancy; expressed as dormancy index (DI)) were evaluated. Stratification effect was overwhelming and the role of clones, years, and their interaction were assessed on unstratified and stratified tests separately. These analyses indicated that the year was a non-significant term, but that clone was significant. This indicates that clone (genetic background) is the main factor controlling germination behaviour, thus allowing a generalization of clonal performance over years. Operationally, germination behaviour after stratification is the main interest and non- and significant differences were observed for GC and R_{50}’, respectively. The results demonstrated the effectiveness of stratification on minimizing clonal dormancy differences resulting in the production of higher GC; however, R_{50}’ differences persisted. The impact of stratification treatment length (1 to 5 weeks) was further investigated on composite seedlots from each collection year separately and the results of 5 weeks stratification produced a 2% improvement in GC (increase) coupled with an improvement in R_{50}’ (decrease). The DI showed a steady increase with length of stratification demonstrating the effectiveness of increased stratification in maximizing germination. Extending stratification by one week resulted in improvement to the recommended ISTA prescription for this species. When the slight increase of 2% GC was applied to the provincial 2006 sowing request total for lodgepole pine (133.7 million seedlings), it was estimated that an additional 7,000 ha could be planted. Thus, the magnitude of this 2% GC increase is very significant when Pli seed, especially high genetic gain seed orchard seed, is in short supply.

STORAGE OF BEECH (*Fagus grandifolia*) POLLEN

K. Forbes,[1] T.Beardmore[1], J. Loo[1], M. Krasowski[2] and M. Ramirez[2]

[1] Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: Kathleen.Forbes@nrcan.gc.ca

[2] University of New Brunswick
Faculty of Forestry and Environmental Management
PO Box 44555
Fredericton, NB
E3B 6C2

Beech pollen was collected from 2 locations in New Brunswick in 2005, from one tree putatively resistant to beech bark disease (beech scale insect - *Cryptococcus fagisuga* Lind. + fungi - primarily *Nectria coccinea* var. *faginata*) and one diseased tree at each location. Pollen was stored at one of 4 temperatures (4°C, -20°C, -80°C, and -196°C) in cryo-vials for 1 month, 6 months, and 1 year. Pollen germination was tested after the different storage durations and varied among individual trees. Germination was not correlated with apparent tree health. At one location (DT), fresh pollen from putatively resistant tree (DT-2) had higher germination than that from a diseased tree (DT-1). However, this was not the same for pollen from the second location (JC). Apart from DT-2, all other pollen germinated better after long ultra-low temperature storage than after storage at 4°C and -20°C for even shorter durations. Storage at ultra-low (-80°C and -196°C or just -196°C) temperatures has been shown to enhance pollen viability in some species. Pollen morphology was also examined in relation to viability. Results suggest that ultra-low temperature storage may be better for preserving pollen germplasm than storage at higher temperatures.

ONLINE CONSULTATION ON FEDERAL REGULATIONS FOR CONFINED FIELD TRIALS OF PLANTS WITH NOVEL TRAITS THAT ARE FOREST TREES

Isabelle Gamache[1], Wendy Shearer[2], Kirsten Finstad[2] and Anne-Christine Bonfils[1]

[1] Natural Resources Canada
Canadian Forest Service
Science and Programs Branch
580 Booth Street
Ottawa, ON
K1A 0E4
E-mail: Isabelle.Gamache@nrcan.gc.ca

[2] Canadian Food Inspection Agency
Plant Products Directorate
Plant Biosafety Office
59 Camelot Drive
Ottawa, ON
K1A 0Y9

The introduction of novel traits into forest trees may be desirable to improve the productivity of tree plantations and their ability to withstand environmental threats. In Canada, the introduction of a novel trait to a plant triggers regulations for environmental release. Confined research field trials constitute the first level of environmental release of plants with novel traits (PNTs); they provide an opportunity to evaluate field performance, gather data on environmental safety, or conduct fundamental research on materials that are not targeted for commercial release. The Canadian Food Inspection Agency's (CFIA) Directive 2000-07 *Conducting Confined Research Field Trials of Plants with Novel Traits in Canada* is being updated to address the unique regulatory challenges posed by PNTs that are forest trees compared to agricultural crop species. The CFIA and the Canadian Forest Service (CFS) have jointly prepared a draft amendment to Directive 2000-07, integrating comments from meetings held by the CFS since 1998 with provincial authorities and scientific experts on federal regulations relating to PNTs that are forest trees. An online consultation is being held to solicit feedback on this draft amendment from tree improvement experts of the academic, federal, provincial/territorial, and private forest sectors. Between July 24 and September 29 2006, participants are invited to review the draft amendment and the species-specific terms and conditions for poplar (*Populus* spp.) and spruce (*Picea* spp.) and propose changes to ensure that adequate and realistic confinement measures are taken. The Internet address of the consultation will be disclosed at the Canadian Tree Improvement Association meeting. Comments received through this consultation will be integrated into an improved version of the Directive.

THE ACCUMULATION OF ANTHOCYANINS IN JUVENILE *Pinus contorta* Dougl. var. *latifolia* SEEDLINGS: ARE PHENOTYPIC DIFFERENCES AMONG PROVENANCES DUE TO AN ADAPTATION TO LOCAL ENVIRONMENTS?

Erin T. Hamanishi and Sally N. Aitken

The University of British Columbia
Department of Forest Sciences
Vancouver, BC
V6T 1Z4
E-mail: erintaya@interchange.ubc.ca

Purpling of lodgepole pine (*Pinus contorta* Dougl. var. *latifolia*) seedling foliage, observed at the onset of cooler temperatures, was found to be a result of anthocyanin accumulation. The objective of this study was to determine if anthocyanin accumulation varied among provenances and with temperature. Seedlings were chosen from three provenances (Northern B.C., Prince George, and Nelson) and were grown in two growth chambers with different temperature regimes (MAT 4°C and 10°C). Four anthocyanins were characterized (t_R = 41, 45, 48, and 51) using reverse phase HPLC. Only the anthocyanin with t_R = 51 was found to be significantly different among the provenances and differences between the two temperature regimes were found to be significant for all four anthocyanins. Cold hardiness was calculated using an electrolyte leakage method at a test temperature of -10°C. Differences among provenances and temperature regimes were significantly different. Anthocyanin accumulation in juvenile lodgepole pine seedlings appears to be influenced by its current environment and its genetics.

POPULATION GENETICS OF PACIFIC DOGWOOD (*Cornus nuttallii*)

Karolyn R. Keir and Sally N. Aitken

The University of British Columbia
Department of Forest Sciences
Vancouver, BC
V6T 1Z4
E-mail: karolynk@interchange.ubc.ca

Pacific dogwood (*Cornus nuttallii*) is a beautiful deciduous tree found in forests along the Pacific Coast from southwestern British Columbia to southern California and disjunctly in Northern Idaho. This tree is insect pollinated while seeds are animal dispersed. Threats to Pacific dogwood include loss of habitat from human development and an introduced fungus (*Discula* spp.), which causes a potentially fatal disease, anthracnose. At present, there is very little known about the population genetics of *C. nuttallii*. I propose to fill some of these knowledge gaps and in doing so, aid in the development of an effective conservation strategy, if necessary, to maintain healthy populations of this tree. Foliage and seeds will be collected from 20 populations throughout this species' native range. Using microsatellite and chloroplast DNA (cpDNA) markers, I hope to determine the genetic diversity, population structure, and mating system for these populations. I plan to investigate the effect location, level of anthracnose infection, insect pollination, and animal dispersal will have on these genetic parameters. Furthermore, I plan to use maternally inherited cpDNA to determine the post-glacial migration strategy of this species. These data can be useful in setting guidelines for seed collections, species restoration, and determining the effects climate change will have on these genetic parameters.

REPRODUCTIVE BARRIERS AND HYBRIDITY IN TWO SPRUCES, *Picea rubens* AND *Picea mariana*, SYMPATRIC IN EASTERN NORTH AMERICA

John E. Major[1], Alex Mosseler[1], Kurt H. Johnsen[2],
Om P. Rajora[3], Debby C. Barsi[1] and Moira Campbell[1]

[1] Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: John.Major@nrcan.gc.ca

[2] USDA Forest Service
3041 Cornwallis Road
Research Triangle Park
NC, 27709, USA

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

Hybridization between red spruce (*Picea rubens* Sarg.) and black spruce (*P. mariana* (Mill.) BSP), respectively late- and early successional species, has resulted in identification and management problems. We investigated the nature and magnitude of reproductive and life-cycle success barriers in controlled intra- and interspecific crosses of red and black spruce. We quantified a number of reproductive, germination, phenological, and performance traits, and examined traits by parental pedigree and hybrid index. Species' pollen had no effect on number of aborted or non-pollinated ovules. Controlled intraspecific crosses had, on average, 6.6 times more filled seeds than interspecific crosses. Cone and seed morphometric traits were species specific, with seed traits showing negative hybridization effects on both species. Germination, cotyledon number, and seedling height had significant species-specific traits, with hybrids showing an additive or slightly negative heterosis. Severe, negative heterosis appears to be of limited importance as an isolating barrier between red and black spruce. Reproductive phenology was remarkably similar among species and hybrid progenies when grown in common garden experiments. Crossability barriers are clearly paramount in maintaining the separation of the species. Ecological separation based on ecophysiological differences (e.g., shade tolerance) also represents an important pre-zygotic barrier for minimizing the negative effects of hybridization (e.g., post-zygotic inviability) on reproductive fitness.

GENETIC VARIATION AND CONTROL OF CHLOROPLAST PIGMENT CONTENT IN *Picea rubens*, *Picea mariana*, AND THEIR HYBRIDS UNDER AMBIENT AND ELEVATED CO_2 ENVIRONMENTS

John E. Major, Debby C. Barsi, Alex Mosseler and Moira Campbell

Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: John.Major@nrcan.gc.ca

Traits related to light-energy processing have significant ecological implications for plant fitness. Our objective was to examine and compare chloroplast pigment content traits from a red spruce (RS) (*Picea rubens* Sarg.) – black spruce (BS) (*P. mariana* (Mill.) BSP) genetic complex under ambient and elevated CO_2 conditions. We used two genetic experiments: 1) a comparative species provenance experiment from across the near-northern part of the RS range, and 2) an intra- and interspecific controlled-cross hybrid experiment. Results from the provenance experiment showed total chlorophyll content (*a* and *b*) was, on average, 15% higher under ambient than elevated CO_2 ($P < 0.001$). Under ambient CO_2, BS populations had, on average, 11% higher total chlorophyll and carotenoid content than RS populations ($P < 0.001$). There were significant species, CO_2, and species x CO_2 interaction effects, where chlorophyll content decreased on average 7% and 26% for BS and RS, respectively. Results from the hybrid experiment showed hybrid index 25 (25% RS) had the highest total chlorophyll content, and hybrid indices 75 and 100 had among the lowest. Initial analysis of the hybrid experiment supported a more additive model of inheritance; however, parental analysis showed a significant and predominant male effect for chlorophyll content. Crosses with BS males had 10.6 and 17.6% higher total chlorophyll content than crosses with hybrid and RS males under ambient and elevated CO_2 environments, respectively. Our results show a strong genetic control of chlorophyll content and that these traits have a positive correlation with productivity within and across species. A significant positive correlation between chlorophyll content and nitrogen assimilation rate was also found ($r = 0.872$). Results indicate that RS would most probably be at a competitive disadvantage in a higher CO_2 environment.

GENETIC GAINS OF 2ND GENERATION *Larix decidua* AND *L. kaempferi* THAT FORM THE NEW QUÉBEC SEED ORCHARD OF HYBRID LARCH

Martin Perron

Ministère des Ressources naturelles et de la Faune
Direction de la recherche forestière
2700, rue Einstein
Québec, QC
G1P 3W8
E-mail: Martin.Perron@mrnf.gouv.qc.ca

After 35 years of breeding larch, the MRNF has passed an important milestone for implementing intensive silviculture in Québec. In 2005, the 40 best larch parents (20 *Larix decidua* Mill. [EL] and 20 *L. kaempferi* [Lamb.] Carrière [JL]) were identified among over 40 000 candidate trees. Those selected trees were grafted during the winter of 2006 and will be used for interspecific controlled crosses to produce the new improved variety of Québec 2nd generation hybrid larch (*L.* x *marschlinsii* Coaz. [HL]). Estimates of genetic gains for stem straightness (SS) and total height (TH) were made independently for each of the parent species. The 20 EL all have an acceptable SS (straight or slightly crooked). Considering the heritability of this characteristic, 93% of their progeny should achieve an acceptable SS at roughly age 12, while it should reached for 62% of the progeny of the 20 JL at age 9. It should be pointed out that such an improvement in SS also increases wood quality. As for the projected genetic gain in TH, the 20 EL should present an increase of 8% at age 12 (954 vs. 884 cm) compared to the weighted average of the three tests having served to make the selection. This is why the gain in MV for a spacing of 2 x 3 m should reach 14%, both at 30 and 45 years, compared with the average MV of the three tests. For the 20 JL, these gains should reach 4% (750 vs. 720 cm) for TH at 9 years and 7% for MV (30 and 45 years). A supply of improved seedlings will be available for the short-rotation cultivation of HL in Québec. It goes without saying that the MRNF is reaping the rewards from 35 years of breeding larch.

WHITE SPRUCE IN QUÉBEC: A MULTI-DISCIPLINARY APPROACH TO ENHANCING FOREST PRODUCTIVITY

Laurence Tremblay[1,2], Mohammed S. Lamhamedi[1], Fabienne Colas[1], Denise Tousignant[1], André Rainville[1], Guy Prégent[1], Jean-Yves Guay[2], Michel Rioux[2] and Jean Beaulieu[3]

[1] Ministère des Ressources naturelles et de la Faune
Direction de la recherche forestière
2700, rue Einstein
Québec, QC
G1P 3W8
E-mail: Laurence.Tremblay@mrnf.gouv.qc.ca

[2] Ministère des Ressources naturelles et de la Faune
Direction de la production des semences et des plants
Pépinière forestière de Saint-Modeste
410 rue Principale
Saint-Modeste, QC
G0L 3W0

[3] Natural Resources Canada
Canadian Forest Service
Fibre Centre
PO Box 10380
Sainte-Foy, QC
G1V 4C7

Among the genetic improvement programs for coniferous species in Québec, the one for white spruce (*Picea glauca* [Moench] Voss) is the most advanced. Presently, in the province, there are 17 first-generation and two second-generation seed orchards, established in the early 1980's and 1999, respectively. Due to its superior growth and wood quality, white spruce is sought after by the wood products industry. It is the third most important reforestation species. Approximately 25 million white spruce seedlings are planted annually. More than 85% of these seedlings are grown from genetically improved seeds. Among them, almost two million plants are mass-propagated from rooted cuttings originating from stockplants of the most successful recent controlled crosses.

In 2002, the Ministère des Ressources naturelles et de la Faune du Québec began to produce seedlings by somatic embryogenesis at an operational scale. Because of its superior qualities, white spruce was the first species selected for this program aimed at propagating the best clones.

The provincial government has the responsibility for producing both tree seeds and seedlings. This creates a unique opportunity for rapid transfer of research advances to the operational scale. By capitalizing on the knowledge gained from the genetic improvement program for white spruce (rigorous selection process for the best parent trees), nursery cultural practices (genetic variability, irrigation, fertilization, frost tolerance, etc.), and tree seedling production through rooted cuttings and somatic embryogenesis (development of rooting enclosures, different rooting and culture scenarios, somatic embryos production, etc.) Québec is in a position to increase tree plantation performance through the development of a clonal forestry program.

SURVIVAL AND ROOTING OF CANADA YEW (*Taxus canadensis*) STEM CUTTINGS TREATED WITH CONCENTRATED IBA SOLUTION

L. Webster[1], M. Krasowski[1], R. Smith[2] and S. Cameron[3]

[1] University of New Brunswick
Faculty of Forestry and Environmental Management
PO Box 44555
Fredericton, NB
E3B 6C2
E-mail: p166h@unb.ca

[2] VarFor Ltd.
12 Chateau Drive
McLeod Hill, NB
E3A 5X2

[3] Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Center
PO Box 4000
Fredericton, NB
E3B 5P7

The anti-cancer drug paclitaxel is extracted from the bark and foliage of different species of yew (*Taxus* spp.). Since the early 1990s, when paclitaxel was first marketed, woodland yew species around the world have been decimated by unsustainable harvesting practices. Canada yew (*Taxus canadensis* Marsh.) is native to eastern Canada and the northeastern United States. In response to an increasing demand for Canada yew biomass, and to take some of the harvesting pressure off of woodland stocks, a domestication program to develop Canada yew as a nursery field crop was started in 1997 at the Canadian Forest Service, Fredericton, NB. In propagation studies to produce stock for field planting it was found that there is genetic variation among clones in the ease of rooting cuttings. In the study described here, a nursery trial was initiated to evaluate the use of concentrated indole-3-butyric acid (IBA) solution dips for improving rooting success of recalcitrant (poor rooting) clones. Cuttings from two good and four poor rooting clones were dipped for ten seconds in a control (0 ppm), 10 000 ppm or 20 000 ppm IBA solution. Rooting success is being evaluated by survival and root dry weight. Survival was similar between most clones for the control treatment despite the previous distinction of clone type. Survival rates were highest for all clones in the 10 000 ppm treatment. The 20 000 ppm treatment decreased survival from the 10 000 ppm treatment but was above the control for all but two clones (one good and one poor rooter). Foliage from the last two years was sampled from ortets for nutrient analyses. For N, P, K, and Mg there were significant differences among all clones but not correlated with good or poor rooting clone types. Calcium was the exception being the only nutrient where a significant difference was found, with higher levels in clones originally assigned as poor rooting.

BLACK ASH PROPAGATION METHODS

L.D. Yeates and B.I. Daigle

Natural Resources Canada
Canadian Forest Service
Atlantic Forestry Centre
PO Box 4000
Fredericton, NB
E3B 5P7
E-mail: Laurie.Yeates@nrcan.gc.ca

Black ash seed from New Brunswick requires more extensive treatment to break dormancy than the 90 day warm/90 day cold treatment that is currently prescribed. Black ash seed was subjected to varying durations of warm/cold and cold/warm/cold treatments to evaluate its germination requirements. Results indicated that black ash seed requires a longer period of stratification and that an initial cold treatment produced better results than the traditional warm/cold. Greater than 90% germination was obtained with a 90 day cold/90 day warm/180 day cold treatment. Seedlings grown in Jiffy cells performed better than those grown in multipots. Black ash can be successfully grafted which may provide a means to establish seed orchards.

ATTENDEES OF THE
30th CTIA/ACAA MEETING

Greg Adams
J.D. Irving, Limited
181 Aiton Road
Sussex East, NB
E4G 2V5

Sally Aitken
Department of Forest Science
University of British Columbia
3041-2424 Main Mall
Vancouver, BC
V6S 1Z7

Beth Arsenault
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 5P7

Jill Barbour
USDA Forest Service
National Seed Laboratory
5675 Riggins Mill Road
Dry Branch, GA
31020

Leonard Barnhardt
Sustainable Resource Development
Alberta Tree Improvement & Seed Centre
P.O. Box 750
Smoky Lake, AB
T0A 3C0

Debby Barsi
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 5P7

Tannis Beardmore
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3A 5P7

Jean Beaulieu
Natural Resources Canada
P.O. Box 10380
Sainte-Foy, QC
G1V 4C7

Robert Bettle
Department of Natural Resources
Kingsclear Forest Nursery
3732 Route 102
Island View, NB
E3E 1G3

Kathleen Brosemer
Forest Genetics Ontario
510 Queen St. East, Suite 24
Sault Ste. Marie, ON
P6A 2A1

Blake Brunsdon
J.D. Irving, Limited
300 Union Street
Saint John, NB
E2L 4M3

Mike Butler
Natural Resources
P.O. Box 2000
Charlottetown, PEI
C1A 7N8

Craig Carr
Department of Natural Resources
3732 Route 102
Island View, NB
E3E 1G3

Paul Charrette
Forest Genetics Ontario
Lakehead University
955 Oliver Road
Thunder Bay, ON
P7B 5E1

Sierra Curtis-McLane
University of British Columbia
6201 Cecil Green Park Road
Vancouver, BC
V6T 1Z1

Bernard Daigle
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 5P7

Bruce Dancik
University of Alberta
Devonian Botanic Garden
Edmonton, AB
T6G 2E1

Gaëtan Daoust
Natural Resources Canada
C.P. 10380
Sainte-Foy, QC
G1V 4C7

John Davis
School of Forest Resources and Conservation
University of Florida
P.O. Box 110410
Gainesville, FL
32611

Steve D'Eon
Natural Resources Canada
Petawawa Research Forest
P.O. Box 2000
Chalk River, ON
K0J 1J0

Trevor Doerksen
Department of Biology
Dalhousie University
1355 Oxford Street
Halifax, NS
B3H 4J1

Eric Earle
Department of Natural Resources
P.O. Box 2006
Corner Brook, NL
A2H 6J8

Yousry El-Kassaby
Department of Forest Science
University of British Columbia
2424 Main Mall
Vancouver, BC
V6T 1Z4

Gordon Falk
Manitoba Conservation – Forestry Branch
Box 27, Grp. 8, R. R. 2
Dugald, MB
R0E 0K0

Steve Fawcett
Department of Natural Resources
3732 Route 102
Island View, NB
E3E 1G3

Al Foley
Ministry of Natural Resources
Ontario Tree Seed Plant
141 King Street
P.O. Box 2028
Angus, ON
L0M 1B0

Don Fowler
2785 Woodstock Road
Fredericton, NB
E3C 1R1

Howard Frame
Department of Natural Resources
P.O. Box 68
Truro, NS
B2N 5B8

Michele Fullarton
Department of Natural Resources
3732 Route 102
Island View, NB
E3E 1G3

Isabelle Gamache
Natural Resources Canada
580 Booth Street, 12th floor
Ottawa, Ontario
K1A 0E4

Peter Goodine
Department of Natural Resources
3732 Route 102
Island View, NB
E3E 1G3

Erin Hamanishi
University of British Columbia
11038 Bond Blvd.
Vancouver, BC
V4E 1M7

Andreas Hamann
University of Alberta
739 General Services Bldg.
Edmonton, AB
T6G 2H1

Sally John
Isabella Point Forestry Ltd.
331 Roland Road
Salt Spring Island, BC
V8K 1V1

Cheryl Johnston-Schuetz
University of Northern British Columbia
3333 University Way
Prince George, BC
V2N 4Z9

Karolyn Keir
Department of Forest Sciences
University of British Columbia
2424 Main Mall
Vancouver, BC
V6T 1Z4

Stan Kempton
Bowater Mersey Paper Company Ltd.
P.O. Box 1150
Liverpool, NS
B0T 1K0

David Kolotelo
Ministry of Forests and Range
Tree Seed Centre
187923-32nd Avenue
Surrey, BC
V3S 0L5

Jarkko Koskela
International Plant Genetic Resources Institute
Via dei tre Denari 472 – Maccarese
Fiumicino
Italy 00057

Hartmut Kunze
J.D. Irving, Limited
169 Aiton Road
Sussex East, NB
E4G 2V5

Michée Lemieux
Department of Natural Resources
Route 19, 15039
Inverness, NS
B0E 1N0

Barry Linehan
Department of Natural Resources
Wooddale Provincial Tree Nursery
P.O. Box 616
Grandfalls-Windsor, NL
A2A 2K2

Judy Loo
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 6J6

Tom Matheson
Neenah Paper Co. of Canada
P.O. Box 220
Debert, NS
B0M 1G0

Shelagh McCartan
Forest Research
Alice Holt Lodge
Wrecclesham
Farnham, Surrey
United Kingdom

Steve McKeand
NC State University Tree Improvement Cooperative
P.O. Box 8002
Raleigh, NC
27695-8002

Kris Morgenstern
323 Sandy Beach Road
Pembroke, ON
K8A 6W8

Marie-Josée Mottet
Ministry of Natural Resources
2700 Einstein
Québec, QC
G1P 3W8

Mary Myers
Natural Resources
P.O. Box 2000
Charlottetown, PEI
C1A 7N8

Lisa O’Connell
University of New Brunswick
Tweedale Centre
1350 Regent St.
Fredericton, NB
E3C 2G6

Conor O’Reilly
UCD School of Biology and Environmental Science
Agriculture and Food Science Centre
University College, Dublin
Ireland

Donna Palamarek
Sustainable Resource Development
Alberta Tree Improvement & Seed Centre
P.O. Box 750
Smoky Lake, AB
T0A 3C0

Yill-Sung Park
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 5P7

William Parker
Faculty of Forestry and the Forest Environment
Lakehead University
955 Oliver Road
Thunder Bay, ON
P7B 5E1

Martin Perron
Ministry of Natural Resources
2700, rue Einstein
Sainte-Foy, QC
G1P 3W8

Pierre Perinet
Direction de la recherche forestière
2700, rue Einstein
Sainte-Foy, QC
G1P 3W8

Sharon Pond
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 5P7

André Rainville
Ministry of Natural Resources
2700, rue Einstein
Ste-Foy, QC
G1P 3W8

Om Rajora
Faculty of Forestry and Environmental Management
University of New Brunswick
P.O. Box 44555
Fredericton, NB
E3B 6C2

Marianela Ramirez
Faculty of Forestry and Environmental Management
University of New Brunswick
P.O. Box 44555
Fredericton, NB
E3B 6C2

David Reid
Ministry of Forests and Range
7380 Puckle Road
Saanichton, BC
V8M 1W4

Deogratias Rweyongeza
Department of Agricultural, Food & Nutritional Science
University of Alberta
Edmonton, AB
T6G 2P5

Yuliya Savva
University of Quebec
445, boul. de l’Université
Rouyn-Noranda, QC
J9X 5E4

Natacha Sénéchal
Université de Moncton
Campus d’Edmundston
421, rue Victoria app. E
Edmundston, N.-B.
E3V 2K6

Wendy Shearer
Canadian Food Inspection Agency
59 Camelot Drive
Ottawa, ON
K1A 0Y9

Gail Sherson
Paprican
3800 Wesbrook Mall
Vancouver, BC
V6S 2L9

Dale Simpson
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 5P7

Brad St. Clair
USDA Forest Service
3200 SW Jefferson Way
Corvallis, OR
97331

Dave Steeves
Department of Natural Resources
P.O. Box 68
Truro, NS
B2N 5B8

Michael Stoehr
Ministry of Forests and Range
722 Johnson Place
Victoria, BC
V8W 9C2

Francis Tang
Ministry of Natural Resources
1235 Queen Street E.
Sault Ste. Marie, ON
P6A 2E5

Ashley Thomson
Faculty of Forestry and the Forest Environment
Lakehead University
955 Oliver Road
Thunder Bay, ON
P7B 5E1

Kathy Tosh
Department of Natural Resources
3732 Route 102
Island View, NB
E3E 1G3

Ben Wang
Natural Resources Canada
Petawawa Research Forest
P.O. Box 2000
Chalk River, ON
K0J 1J0

Laurie Webster
Faculty of Forestry and Environmental Management
University of New Brunswick
Fredericton, NB
E3B 6C2

Yuhui Weng
Department of Natural Resources
3732 Route 102
Island View, NB
E3E 1G3

Kathy Woo
Paprican
3800 Wesbrook Mall
Vancouver, BC
V6S 2L9

Jack Woods
Forest Genetics Council of BC
3370 Drinkwater Road
Duncan, BC
V9L 5Z2

Alvin Yanchuk
Ministry of Forests and Range
Research Branch
722 Johnson St.
Victoria, BC
V8V 1N1

Laurie Yeates
Natural Resources Canada
P.O. Box 4000
Fredericton, NB
E3B 5P7

Kit Yeatman
98 Glendale Avenue
P.O. Box 721
Deep River, ON
K0J 1P0

S. Y. Zhang
Forintek Canada Corp.
319, rue Franquet
Sainte-Foy, QC
G1P 4R4

PHOTOS

Invited speakers and panelists. Front row, left to right: Steve McKeand, Kris Morgenstern, Bruce Dancik, Sally Aitken, Brad St.Clair. Back row: John Davis, Blake Brunsdon, 'Kit' Yeatman, Alvin Yanchuk, Don Fowler.

CTIA sponsored students; left to right: Ashley Thomson (Lakehead U), Cheryl Johnson-Schuetz (UNBC), Laurie Webster (UNB), Erin Hamanishi (UBC), Natasha Sénéchal (U de M).

Dave Reid models the latest “west Coast” line of field clothing to Sally Aitken, Laurie Webster, Tannis Beardmore, Wendy Shearer, Debi Barsi and Kathleen Brosemer.

‘3 hats to none’! Gordon Falk discusses the need to wear a hat with Jean Beaulieu while Mike Butler and Mike Stoehr compare notes.

Howard Frame and Steve McKeand are amazed by Jack Woods' orange peeling ability.

Kathy Tosh prays that nobody will move a motion to change the name of CTIA while Dale Simpson records the minutes of the business meeting.

Marianela Ramirez (UNB) receives the Carl Heimburger Award from Kathy Tosh and Yill Sung Park for best student oral presentation.

Erin Hamanishi (UBC) and Karolyn Keir (UBC) receive the Gene Namkoong Award from Kathy Tosh and Yill Sung Park for best student posters.

The 'BC Boys' at home in a tamarack seed orchard; Jack Woods, Dave Reid, and Dave Kolotelo.

Laurie Webster and Marianela Ramirez enjoying the field tour.

“My tractor is faster than yours!” Bill Butler, Michele Fullarton, David Carmichael and Tom Matheson discuss the rules before the race.

Yousry El-Kassaby shows us how to enjoy lobster with pizzaz. (Is it really better than BC salmon?)