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

Climate Change and Forest Genetics

Changements climatiques et génétiques

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

CTIA Agenda – 29th Biennial Meeting

The Grand Okanagan Lakefront Resort
July 26- 29, 2004

Sunday, July 25

1600-1800	Registration

Monday, July 26

0730 – all day	Registration
0830 - 1500	IUFRO 7.01.04 Resistance Breeding Workshop
0830 – 1230	Tree Seed Working Group Workshop
1330 – 1700	NWSOMA and BCSOA Workshop and NWSOMA Business Meeting
1830 – 2130	Reception (No Host Bar)
1830 – 1900	WFGA Business Meeting
1900	National Survey of Forest Genetic Resources Management Processes and Practices

Tuesday, July 27

0730 - ongoing	**Registration**
0730	**Breakfast** (provided)
0820	**Welcoming Address** *Dale Draper*
	INVITED SPEAKERS' SESSION
0840	**The Science of Climate Change** *Andrew Weaver*
0930	**Refreshments and Posters**
1000	**Impacts of Historical Climate Change on Species and Populations Shifts** *Steve Jackson*
1050	**Stretch Break and Posters**
1110	**Climate Change: Impacts and Adaptations for Forestry** *Dave Spittlehouse*
1200	**Lunch** (provided)
	VOLUNTEER SPEAKERS' – CONCURRENT SESSION A
1300	**Survey of Gene Conservation Requirements for Forest Tree and Shrub Species in Canada** *Dale Simpson*
1320	**Potential Impact of Climate Change on Ecosystems, Species Distributions, and Genetic Resource Management in BC** *Andreas Hamann*
1340	**Reconstructing a Past Climate using Current Multi-species' Climate Spaces** *Bob Westfall*
1400	**Stretch break**
	VOLUNTEER SPEAKERS' – CONCURRENT SESSION B
1300	**Selection, Gene Flow, and Adaptation in Sitka Spruce: Life on the Edge** *Makiko Mimura*
1320	**Towards the development of a composite genetic map in white spruce** *Stéphanie Beauseigle*

1340	**Ecological Genetics of Whitebark Pine** *Andy Bower*
1400	**Stretch break**
	VOLUNTEER SPEAKERS' SESSION
1410	**Global Warming and the 'Chilling Requirement' of some Confers** *Denis Lavender*
1430	**Modelling Frost Risk in Norway Spruce** *Mats Hannerz*
1450	**Effect of Thermal Climatic Changes on Volume Grown Response in Sitka Spruce** *Jodie Krakowski*
1510	Refreshments and posters
1530	**Climate Models and Genetic Applications for Lodgepole Pine in British Columbia** *Tongli Wang*
1550	**Brave New Breeding Zones** *Greg O'Neill*
1610	**White Spruce Limestone Ecotypes: Do They Really Exist?** *Mark Lesser*
1800	**Winery dinner and tour – Summerhill winery**. Bus transportation provided

Wednesday, July 28

0700	**Breakfast** (provided)
0800 – 1700	**Field trip to Skimikin and Vernon** (box lunch provided)
1800	**No host bar**
1900	**BBQ at The Grand Okanagan Lakefront Resort**

Thursday, July 29

	Breakfast (on your own)
	INVITED SPEAKERS' SESSIONS
0830	**Impacts of Climate Change on Populations and Species Distributions** *Isabelle Chuine*
0920	**Refreshments and posters**
0950	**Biome, Species, and Population Responses to Climate and Climate-Change: a Comparison of Siberia with North America** *Jerry Rehfeldt and Nadja Tchebakova*
1110	**Stretch break**
	VOLUNTEER SPEAKERS' SESSION
1120	**Effects of Genotype and Silviculture on Western Hemlock Diameter Growth and Wood Density** *Charlie Cartwright*
1140	**Genetic Variation in Black Cottonwood (*Populus trichocarpa*)** *Cheng Ying*
1200	**Lunch** (on your own)
1300	**Techniques and Preliminary Results from Four Generations of Selfing Western Redcedar** *John Russell*
1320	**Selfing Results in Inbreeding Depression of Growth but not of Gas Exchange**

John Major

1340 **Climate-Change Response Strategies Among Three Co-occurring, Ecologically Distinct Northern Coniferous Tree Species**
Scott Green

1400 **Stretch break**

1410 **Comparison of Seed Transfer Function and Focal Point Seed Zone Approaches Regarding Present and Future Climates**
Bill Parker

1430 **Applications of Seed Transfer Expert Systems in Reforestation and Restoration**
Mary Frances Mahalovich

1450 **Holocene Climate Change and its Impact on Genetic Structures**
Bob Westfall

1510 **Refreshments and posters**

1530 **Initiation of Stem Infection in Western White Pine by Blister Rust**
Rich Hunt

1550 **Genetic Variation in Tolerance to Swiss Needle Cast in Coastal Douglas-fir**
Randy Johnson

1610 **Dothistroma Needle Blight of Lodgepole Pine in Northwest British Columbia**
Alex Woods

1630 **CTIA business meeting**

CTIA conference closes

1800 **BC Tree Seed Dealers Meeting**
Coyote Waterfront Bar & Grill, 1352 Water St. (near the hotel).

The science of climate change

Andrew Weaver
School of Earth and Ocean Sciences, University of Victoria, BC

Central to the findings of the Intergovernmental Panel on Climate Change (IPCC) third assessment report, released in Shanghai in January 2001, was the statement: "There is now new and stronger evidence that most of the warming observed over the last 50 years is attributable to human activities." This represents a significant strengthening of the analogous statement issued by the IPCC in 1996: "The balance of evidence suggests a discernible human influence on global climate" In this talk the scientific evidence leading up to these IPCC statements is reviewed. A historical perspective of the Earth's climate over the last 400,000 years is presented, as is the science of global warming over the last 200 years. The range of projections of climate change over the next century is also summarized giving particular emphasis to projections concerning Canada. The issue of public confusion arising from the media portrayal of the science and its entry into the political arena discussed. Finally, recent research is presented that demonstrates that the area burned by forest fires in Canada has increased over the past four decades, at the same time as summer season temperatures have warmed. Output from a coupled climate model is used to demonstrate that this warming is attributable to human emissions of greenhouse gases and sulfate aerosol. We further show that human-induced climate change has had a detectable influence on the area burned by forest fires in Canada over recent decades.

Impacts of past climate change on species distributions of woody plants in North America

Steven Jackson
University of Wyoming

The modern distributions and genetic structure of North American tree species represent, in part, legacies of climate changes of the past 25,000 years and more. Development of extensive networks of pollen and plant-macrofossil records from lakes, wetlands, and woodrat-middens across North America are revealing the magnitude and complexity of climate-change effects. Climate changes since the last glacial maximum have affected the geographic distributions of every tree species on the continent. However, not all species have been affected in the same way. In fact, a broad spectrum of responses is observed in the fossil record. Species responses have ranged from complete geographic displacements to relatively minor shifts along local habitat gradients. Many species that were widespread and dominant during the last glacial maximum continue to be widespread and dominant today, although in different locations. However, other dominant, widespread species of the past are now highly restricted (and in one case, extinct), while several minor glacial-age species have expanded to become dominant over wide regions today. Several species, rare today and rare during the last glacial maximum, were regionally dominant during the late-glacial transition. Some species have even contracted their ranges southward since the last glacial period. The diversity of responses observed in the fossil record can be explained by the diversity of ecological niches represented by tree species, together with the complex and multivariate nature of climate change. Many of the unexpected distributional changes (e.g., southward migration during a glacial-to-interglacial transition) and peculiar species assemblages (e.g., forests of spruce, elm, ash, and hornbeam) observed in the fossil record are attributable to past climates that have no counterparts in the modern world. A major challenge for the future is to determine whether we can develop capability to predict responses to ongoing and future climate change. This task is not as straightforward as it might seem; future climates are likely to have no modern analogs, and may be as different from those of the 20th Century as were climates of 11,000 years ago. It is thus essential to integrate our understanding of past responses from the fossil record with knowledge of modern ecology and genetics to identify the critical climate controls of abundance and distribution.

Climate change; impacts and adaptations for forestry

Dr. Dave Spittlehouse
British Columbia Ministry of Forests, Victoria, British Columbia

Adaptation to climate change
Climate change adaptation strategies should be based on the application of vulnerability assessments or risk management concepts. A planning framework for facilitating adaptation in forestry must address biophysical and socio-economic impacts and will include policy and institutional considerations. The framework requires us to analyse the situation and assess current and future vulnerabilities of forests to climate change. We can then develop risk management strategies that include actions needed now as well as future actions required when climate change has an unacceptable impact on forests. Adaptation needs to reduce current vulnerability, speed recovery after disturbance, and reduce vulnerability to further climate change. The adaptation plan should include monitoring the state of the forest to detect change. An example of using this framework in forest management to adapt to change will be presented. Many forest ecosystems and species will have to adapt autonomously because management can only influence the timing and direction of forest adaptation at selected locations. In general, society will have to adjust to however forests adapt.

Impacts of climate change on populations and species distributions

Dr. Isabelle Chuine
Centre for Evolution and Functional Ecology, France

Concern about climate change is increasing because ecological as well as socio-economic impacts are more and more perceptible. Reported ecological consequences of global warming mainly concern changes in the phenology and the distribution of the flora and fauna (see for Review Parmesan and Yohe 2003). In this talk I will present advances in species distribution modelling and provide predictions about species distribution changes for a couple of forest trees and compare them to past changes.

Biome, species, and population responses to climate and to climate-change in Siberia and western North America

Gerald Rehfeldt, USDA, Forest Service
Nadezda Tchebakova, and Elena Parfenova, Russian Academy of Science

Our work is governed by the principle that climate is the primary factor controlling the distribution of plants. This climate-plant relationship was recognized long ago (e. g., Plesheev in 1797 and Humboldt in 1807) but even today is poorly understood (Woodward 1987). As an aid, we use the thin plate splines of Hutchinson to develop climate surfaces from which the effects climate and climate-change on the distribution of biomes, species, or climatypes (climatic ecotypes) can be mapped.

Bioclimatic models relating the distribution of vegetation zones to climate have been developed for central Siberia. According to these models, the greenhouse gas scenario of the Hadley Centre should result ultimately in a complete redistribution of vegetation zones over the plains and tablelands of Siberia by the end of this century. Northern vegetation types (tundra, forest-tundra, and northern taiga) which are dominant in the contemporary climate should be replaced by southern types such as the southern taiga and subtaiga, forest-steppe, and steppe move northward. Of these southern types, neither of the latter two currently occur north of 56°. Dark-needled taiga concomitantly should move eastwards following the retreat of permafrost.

Species distributions also have been mapped for *Pinus sylvestris* and *Larix* spp. of Siberia using the three-variate climatic envelope of Box (1999) and for *Picea engelmannii* of western USA using 17 climate variables and a combination of the climatic envelope and a discriminant function of 10 species. Once mapped, distributions can be recast according to climate-change scenarios of the GCM’s. For *P. engelmannii* in the region south of 51°N, the 2100 distribution is projected to be 12% of the contemporary. In Siberia, the areal extent of lands potentially suitable for *P. sylvestris* and *Larix* spp. should increase markedly by 2100, although actual distributions will depend on rates of change in permafrost.

As controlled experiments in climate-change, long-term provenance tests are helping to unravel plant-climate relationships. Analyses show that for *P. sylvestris* and *Larix* spp. of Siberia and for *P. engelmannii* of USA, accommodating unmitigated global warming will require a wholesale redistribution of genotypes across the landscape to maintain growth and productivity. Yet, effects of a warming climate should be much more positive for the Siberian species than for *P. engelmannii*, even though the climate is expected to warm 6-8 ºC in Siberia but only 2-3 ºC in western USA. This difference in response results because the distribution of genotypes is controlled not by climate alone, but by an interaction between adaptation to climate and competition. While genotypes occur where they can be competitively exclusive, most nonetheless have been competitively excluded from their climatic optima. Most populations, therefore, exist in climates that are colder than the optimal for their growth, productivity, and survival, with the discrepancy between the inhabited and the optimal climate increasing with the severity of the climate.

In south-central Siberia, *P. sylvestris* and *Larix* spp. inhabit climates that are among the coldest within their respective distributions. Populations tend to exist far from their climatic optima, and effects of a warming climate should be highly positive as cold tolerant populations are replaced by those of higher growth potential. Some climatypes should disappear; others should arise; but the areal extent of all should change. *P. sylvestris* genotypes projected to be the best suited for the climate of 2100 in the mountains of southern Krasnoyarsk Territory exist today in the Altai Republic and southern Ural Mountains, regions which today are 700-1200 km distant. By contrast, in USA, *P. engelmannii* inhabits the mildest climates within its distribution; populations therefore should exist near or at their climatic optima. Consequently, effects of a warming climate should be highly negative with extirpation commonplace as the contemporary climatypes are pushed upwards and northwards.

Conclusions: (1) when converted to variables of known physiological impact (e. g., degree-days), a change of a few degrees in mean annual temperature is projected to have dramatic effects on the vegetation at all levels of organization, from the biome to the species and population; (2) accommodating global warming will require a redistribution of genotypes within species to maintain adaptedness; (3) the culprit is not so much the amount of change as the speed; (4) maintaining forest growth and productivity in the face of global warming will require the participation of mankind in the evolutionary process; and (5) buy today for your grandkids or great grandkids estates in the soon-to-be equitable Siberian or Yukonian climates.

Towards the development of a composite genetic map in white spruce

Stéphanie Beauseigle[1], Betty Pelgas[1], Isabelle Gosselin[1], Manuel Lamothe[2], Jean Bousquet[1] and Nathalie Isabel[1, 2]
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Comparative mapping is an alternative method for non-model species to better understand their genome organization and highlight homeologous chromosomic segments involved in adaptative and economical traits. Recently (Pelgas *et al.* 2004, Mol. Breed.), we have developed over a hundred of multiallelic ESTP anchor markers for comparative mapping between *Picea mariana* (Mill.) B.S.P. and *P. glauca* (Moench) Voss, two evolutionary distant species in the genus *Picea*. Among these, more than 50 ESTP markers were identified as potential candidate genes involved in abiotic stresses and/or wood formation, and polymorphisms (either SNPs or indels) were detected for all of them. All ESTP markers were used in combination with AFLPs and microsatellite markers to generate a composite map for *P. glauca*. Two crosses were selected with one parent in common to maximize the number of segregating ESTPs. Up to now, four individual linkage maps have been constructed from these crosses, with a length ranging from 2045 cM to 2801 cM and a marker density of about 8.4 cM. The use of two pedigrees in *P. glauca* resulted in 25% additional anchor markers useful for interspecific comparison with *P. mariana*.

Ecological genetics of whitebark pine

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

Effects of genotype and silviculture on western hemlock diameter growth and wood density

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Wood quality is clearly responsive to genetics, with most traits having high heritabilities relative to growth traits. It is also apparent that site has a strong influence. It follows from this that silvicultural treatments might have an effect, and it is possible that there could be interactions between genotypes and silvicultural treatments. 70 open-pollinated hemlock families in a progeny trial were thinned to two densities, and aspects of cell morphology measured for the growth ring of the year before treatment, the year of treatment and the year after. Similarly, on a separate site in the same series, the families were fertilized with either 300 or 600 kg/ha. In both studies the treatments resulted in improved growth, yet wood density was not diminished as might be anticipated. Family by treatment interactions were statistically significant in both investigations, however this result is rendered hard to interpret because the treatment by family by year (growth ring) effect was not. Several possible explanations and some details of the results are rendered.

Climate-change response strategies among three co-occurring, ecologically distinct northern coniferous tree species

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

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

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

Potential impact of climate change on ecosystems, species distributions, and genetic resource management in British Columbia

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

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

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

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

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

Modelling frost risk in Norway spruce

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

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

Initiation of stem infection in Western white pine by blister rust

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

Genetic variation in tolerance to Swiss needle cast in Coastal Douglas-fir

Randy Johnson[1], Fatih Temel[2], Keith Jayawickrama[3]
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[3]Oregon State University

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

Effect of thermal climatic changes on volume growth response in Sitka spruce

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

Keywords: thermal climate change; volume response; provenance trial; Sitka spruce, *Picea sitchensis*

Global warming and the "Chilling Requirement" of some conifers

Denis P. Lavender, Professor Emeritus of Forest Sciences
Oregon State University and University of British Columbia

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

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

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

A third study of Douglas-fir seedlings grown under natural conditions in the Corvallis area but with mean temperatures raised three and one half degrees Centigrade demonstrated reduced bud break and poor growth.

Accordingly, if the mean temperature of elevations below three hundred metres in the Willamette-Puget Sound-Gulf of Georgia Trench were to rise about 4 degrees Centigrade between November and February we could expect to lose Douglas-fir and associates.

White spruce limestone ecotypes: Do they really exist?

Lesser, M.R.[1], M. Cherry[2], W.H. Parker[1], 2004.

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

Keywords: white spruce, limestone ecotypes, edaphic ecotypes, bedrock classification, provenance test

Applications of seed transfer expert systems in reforestation and restoration

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

Selfing results in inbreeding depression of growth but not of gas exchange

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

Keywords: carbon isotope discrimination, inbreeding, photosynthesis, *Picea mariana*, stomatal conductance

Selection, gene flow, and adaptation in Sitka spruce: life on the edge

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

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

Brave new breeding zones

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

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

Comparison of seed transfer function and focal point seed zone approaches regarding present and future climates.

Parker, W.H.[1], M. Cherry[2] and M.R. Lesser[1], 2004.
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The Cauchy function was used to model height growth of white spruce (*Picea glauca* (Moench) Voss) based on data from a 25 year-old range-wide provenance test series. Transfer functions were produced for 3 test site locations from eastern Ontario based on late summer temperatures, and predicted height of all sources at each test site was mapped. Data from a recently established greenhouse and 5 common garden trials was used to generate focal point seed zones for the same locations. Results for present-day (1961-1990) climate normals were compared with those determined for a future climate scenario (GCM1 2040-2069). Seed transfers for best present-day growth based on the Cauchy models are differentially compatible with predicted climate change depending on latitude. The use of focal point seed zone models forecast into the future provides an additional and more robust means to evaluate the adaptive suitability of potential seed transfers.

Keywords: white spruce, *Picea glauca*, adaptive variation, transfer functions, focal point seed zones, climate change

Techniques and preliminary results from four generations of selfing Western redcedar

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

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

Survey of gene conservation requirements for forest tree and shrub species in Canada

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

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

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

Climate models and genetic applications for lodgepole pine in British Coulmbia

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and Greg A. O'Neill(2)
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Maps of interpolated climate normals have recently become essential tools for many types of forestry research, such as studying genetic adaptation of trees to local environments, modeling species ranges shifts, or forest productivity under climate change scenarios. In this paper we evaluate two widely used climate models (i.e., polynomial functions of Rehfeldt and others (1999) and the PRISM climate model) for British Columbia, and improved the PRISM model through an elevation adjustment for temperature variables. Both models accurately predicted temperature variables; however, the PRISM model had a greater ability to predict local variation in precipitation.

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

Holocene climate change and its impact on genetic structures

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

Reconstructing a past climate using current multi-species' climate spaces

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We present an analysis of a ghost forest on Whitewing Mt at 3000 m in the eastern Sierra Nevada, southeast of Yosemite NP. Killed by a volcanic eruption about 650 years ago, the deadwood on Whitewing dates by standard tree-ring analysis to 800-1330 CE, a period known as the Medieval Warm Anomaly. Individual stems have been identified as *Pinus albicualis*, *P. monticola, P. jeffreyi*, *P. contorta*, *P. lambertiana*, and *Tsuga mertensiana*. With the exception of *P. albicualis*, which is currently in krummholz form at this elevation, the other species are 200 m or more lower in elevation. One, *P. lambertiana*, is west of the Sierran crest and 600 m lower in elevation. Assuming that climatic conditions on Whitewing during this period were mutually compatible with all species, we reconstruct this climate by the intersection of the current climatic spaces of these species. We did this by first generating individual species' ranges in the Sierran ecoregions through selecting vegetation GIS polygons from the California Gap Analysis database (UCSB) that contain the individual species. Climatic spaces for each species were generated by the GIS intersection of its polygons with 4 km gridded polygons from the PRISM climatic estimates (OSU); this was done for annual, January, and July maximum and minimum temperature, and precipitation, merged together for each species. Climatic intersections of the species were generated from the misclassified polygons of a discriminant analysis of species by the climatic data. The average data from these misclassified polygons suggest that the climate on Whitewing during the existence of this forest community was 230 mm, 1°C, and 3°C greater than present in precipitation, and maximum and minimum temperature, respectively.

Dothistroma needle blight of lodgepole pine in Northwest British Columbia

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

Genetic variation in black cottonwood, *Populus trichocarpa*

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Genecology study of black cottonwood was initiated in the mid-1990s. Cuttings were collected from over 1000 trees throughout the major drainage along the coast of British Columbia, and Washington and Oregon, USA. Two common-garden tests were established in 1999 at two contrasting sites, Surrey Nursery (south coast) and Terrace (north coast). About 900 clones were tested. Stem elongation were measured every two weeks from April till elongation ceased and bud flushing were assessed at weekly interval from late February till leaflet fully extended in 2001 and 2002. The north coast test suffered extensive damage caused by the moose. Our data collection emphasised on the south coast test. Our data analyses focus on parameter estimates from fitting growth curves and vegetative cycles, and their variation associated with drainage, stands (provenance) within drainage, and trees within stands. Preliminary results indicate an ecotypic pattern of geographic variation with a division along Skeena and Nass Drainage. Substantial variation exists also among and within stands.

Is British Columbia’s silviculture policy framework adequate for responding to climate change?

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

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

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

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

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

Ex situ conservation strategy for butternut (*Juglans cinerea* L.)

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Butternut (*Juglans cinerea* L.) survival is threatened in North American by the fungus *Sirococcus clavigignenti-juglandacearum*. To date, control for this fungal disease does not exist and long-term seed storage, as a means to assure survival of the species, is not a viable option.   For these reasons, there is a requirement to develop *ex situ* conservation strategies for butternut. One such strategy involves developing storage using embryonic axes from seed collected from non-infected butternut. Embryonic axes, when excised from the nut with approximately 3 mm of cotyledonary tissue, will tolerate exposure to B196^{0}C and subsequently germinate, forming a viable seedling. Water content of 4.8% appears to be a threshold below which some of the axes will germinate following cryopreservation. These results suggest that ultra low temperature storage of embryonic axes may be a viable method for butternut *ex situ* conservation.The use of other *ex situ* conservation methods such as the cryopreservation of apical and lateral buds, and somatic embryogenesis will be discussed.

Genetic structure and mating system of Arbutus (*Arbutus menziesii*)

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

Effects of fragmentation on genetic structure and inbreeding in Bigleaf maple populations

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

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

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

Genetic gain and gene diversity under thinning scenarios in a seedling seed orchard of *Quercus accutissima*

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

GIS-based seed zones for white spruce in Ontario.

Parker, W.H. and M.R. Lesser, 2004.
Lakehead University, Thunder Bay, ON

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

Keywords: white spruce, *Picea glauca*, focal point seed zone, provenance test, adaptive variation.

Microsatellite analysis of genetic effects of domestication in lodgepole pine

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

Inter- vs. intra-provenance crosses in *Pinus monticola*: early plantation results, with recommendations for seed transfer in British Columbia

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

Key Words: Heterosis, genotype-environment interaction, seed orchards, seed zones

Reproductive and genetic characteristics of rare, disjunct Pitch Pine populations at the Northern limits of its range in Canada

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

Key words: allozymes, genetic diversity, inbreeding, *Pinus rigida*, reproductive fitness.

Gene Resource Information Management in British Columbia –Building a Resource Information Strategy for Genetic Resource Mapping, Land-based Strategic and Operational Planning and Effectiveness Monitoring

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

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

Keywords: gene resource information management, GR resource information strategy, GRM-based seed planning zones, forest-tree genetic resource mapping

Vegetative propagation of *Fagus grandifolia* Ehrh. (American beech) resistant to beech bark disease

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

Defining black spruce growth optima in Ontario: present and future

Parker, W.H., C.L. Riddell and M.R. Lesser, 2004.
Lakehead University, Thunder Bay, ON

Height data from 19 range-wide black spruce (Picea mariana [Mill.] B.S.P.) provenance trials were regressed against monthly minimum and maximum temperatures and monthly precipitation using the Cauchy function. **Response functions** were developed for individual **populations** to predict the climate value that will maximize performance for each source. **Transfer functions** were developed for individual **test sites** to predict climate values of populations that maximize performance at each of the test locations. Mid-spring and mid-to late-winter temperature data generally yielded the best fitting response and transfer functions. For each population/climate variable combination, a grid was developed to map predicted height growth of that population at all points within the region. Likewise, for each test site/climate variable combination, a grid was developed to predict height growth of all potential seed sources planted at that test site. Contours indicating maximal height growth for present and predicted 2040--69 climate variables were added to these grids. Excluding the southern part of its range, black spruce seed sources produce better growth when moved south and should achieve better growth under warmer predicted future temperature regimes provided that other factors are not limiting. The incorporation of more southerly seed sources into today's northerly reforestation efforts will result in more rapidly growing trees today, and will also yield trees better adapted to predicted future temperatures.

Keywords: black spruce, *Picea mariana*, provenance test, adaptive variation, climate change, response function, transfer function, maximum growth.

Response functions of lodgepole pine to temperature and CO_2

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This project-in-progress is a short-term growth chamber experiment to establish norms of reaction to temperature and carbon dioxide. Seedlings of ten populations of lodgepole pine are being subjected to four temperature regimes and two CO_2 levels (ambient and elevated). Each population is represented by open-pollinated families, B+ seedlots, control-pollinated families and seed orchard seedlots. The four temperature regimes correspond to the growing season of 4 locations with mean annual temperatures (MAT) of 1, 4, 7 and 10 degrees C. Two of these regimes, MAT 4 and 10, receive both ambient and elevated CO_2 concentrations. Daylength is the same for all chambers, but varies from week to week as the season progresses. Water and nutrients are provided in excess. Height is measured periodically, while dry mass, allocation, photosynthetic rate and water-use efficiency will be measured at the end of the season. Genotypes will be compared in order to determine which populations perform best in future climate scenarios and if there is rank change of genotypes among the scenarios. Differences between natural populations and improved seedlots, if any, will be identified. Gas exchange measurements will reveal whether photosynthetic acclimation to enriched CO_2 (downscaling) occurs. The underlying aim is to understand the physiological basis of these response functions, and to determine if norms of reaction in growth chambers resemble those found in long-term field trials in different climates, such as the large-scale Illingworth lodgepole pine trials in B.C.

Climate change and forestry in Sweden- a literature review

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The scope of the study was to review the relevant literature regarding the impact of climate change on forestry in Sweden, to synthesise the current knowledge, to draw conclusions on likely effects of climate change and to identify the need for new research and knowledge.

We have limited the study to the effects at a short and medium time span (20-100 years). We have focused on the impact on the trees, both direct and indirect through the climatic impact on soils, herbivores, insects, pests and diseases. We have made sharp delimitations to other aspects of forests and climate change.

This literature review has revealed major shortcomings in our knowledge about impacts that climate change will have on the forest ecosystems. Not only the nature and magnitude of a climate change is uncertain, but even more its potential effects on the structure and processes of the forest ecosystems.

However, the most likely effects of climate change can be predicted. They generally include an increase in potential biomass production, possibilities to grow new species commercially and increased risk for damages of several kind. It seems that climate change offers new opportunities to forestry in Sweden. At the same time the risks for calamities increases. This calls for demanding new approaches to forest- as well as risk-management.

Future research on the effects of climate change on forestry and forest ecosystems has to take account of a broad spectrum of scientific fields, but most important are probably the need for a multidisciplinary scientific approach.

Intraspecific responses to climate in *Pinus albicaulis*

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Provenance tests of 42 populations of *Pinus albicaulis* originating from inland northwestern United States revealed genetic differentiation for growth potential and phenology in relation to climate. The provenance tests were established at Priest River Experimental Forest, Idaho in 2000 using 2 year old seedlings. Patterns of shoot elongation were recorded beginning in the second growing season. Hutchinson's thin plate splines were used to make point predictions for climate at each provenance. These climate predictions were then used to describe genetic variation. Genetic variation was significantly correlated with climate effects derived from temperature. Correlations were strongest for degree days > 5ºC and timing of last spring frost. The relationship between growth potential and degree days > 5ºC was negative. The analyses suggests that genetic differentiation for growth potential and phenology is controlled by the relative mildness of climate in relation to temperature.

Poplar leaf rust caused by *Melampsora* species in Korea

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The severity of poplar leaf rust caused by *Melampsora* species on 15 poplar clones was investigated to select resistance clones to the pathogens and to see whether the pathogens exhibit specificity toward the poplar clones. Cuttings of 15 poplar clones were planted at a nursery bed in Suwon, Korea, in March of 2003. Three rusted leaves per clone were collected from each of the 15 clones, and 10 urediniospores per leaf were observed with both scanning electron microscopy(SEM) and light microscopy(LM). Rust severity was rated on September 2 and 27 and October 20, 2003, using the Schreiner scale(0-100).

Urediniospores from all clones except 72-30, 72-31, Bong-wha 1, and Hyunsasi 3 were oval and tended to be clavate to broadly ellipsoid. Both apices and bases were mostly rounded, but the wall surface of the urediniospore was echinulate except for a smooth patch on the apex. However, urediniospores from the rest of 4 clones had the uniform echinulation. The size of the spores from two groups was also different from each other. The former(11 clones) measured 24-46 X 13-23 µm, and the latter(4 clones) measured 20-29 X 13-20 µm. On September 2, 2003, the first rust severity rating date, only two clones, 97-17 and Eco 28, rated a Schreiner score of 100. However, by October 20, 2003, a total of 12 clones rated 100. Bong-wha 1, Dorskamp, and Hyunsasi 3 were only lightly rusted (all 20 on October 20, 2003). All of the leaf rust samples taken from the 11 clones were identified as *M. larici-populina*; however, samples from the 4 clones were not exactly identified. It seems that they belong to the difficult species complex on *Populus* section *Populus.*