



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 expertise or resources to do so if they were obligated.

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

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

This poster and discussion will be used in refining the topic for a Master'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 America by the fungus *Sirococcus clavigignenti-juglandacearum*. To date, control for this fungal disease does not exist and long-term seed storage, as a means to assure survival of the species, is not a viable option. For these reasons, there is a requirement to develop *ex situ* conservation strategies for butternut. One such strategy involves developing storage using embryonic axes from seed collected from non-infected butternut. Embryonic axes, when excised from the nut with approximately 3 mm of cotyledonary tissue, will tolerate exposure to B196°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 classes based on their frequencies (high: $P > 0.75$, intermediate $0.25 \leq P < 0.75$, low: $0.01 \leq P < 0.25$, and rare: $P < 0.01$). The majority of alleles fall into the low and rare frequency classes. 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 CO₂

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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 CO₂ 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 CO₂ 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 CO₂ (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 Ilingworth 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 > 5°C and timing of last spring frost. The relationship between growth potential and degree days > 5°C 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*.