



Towards the development of a composite genetic map in white spruce

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Comparative mapping is an alternative method for non-model species to better understand their genome organization and highlight homeologous chromosomal 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

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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 lose a large portion of their suitable habitat (e.g. *Abies lasiocarpa*, *Picea glauca*, *P. engelmannii*, *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

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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 find family differences in the amount of fungus in needles, we propose that Douglas-fir exhibits tolerance, the ability to continue growth in the presence of the disease, as opposed to resistance, i.e. actively resisting the fungus. The tolerance mechanism is not completely understood, but some aspect appears to be associated with the tree's ability to shed unproductive needles. Although provenance variation has been shown for SNC tolerance, there is very little association between the climate of a seed source location and its tolerance level when examined within a seed zone. Breeding programs are actively underway to develop SNC tolerance and seed resulting from our most recent orchards should be appropriate for use in areas with moderate SNC symptoms.



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

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The potential impacts of anticipated temperature increases due to climate change within the next century were 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 5°C. The actual impacts will be tempered by moisture availability, which current models can predict with only low certainty. Summer drought will likely be more prevalent, resulting in lower gains than predicted based on temperature alone.

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

Global warming and the “Chilling Requirement” of some conifers

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The existence of a “chilling requirement” of some perennial, woody temperate zone plants has been recognized for over a century and has limited the areas suitable for establishment of non-indigenous trees. More recently, with the possibility of a general global warming, it may result in dramatically reduced survival and growth of both native and introduced plants. The term “chilling requirement” refers to the requirement of vegetative buds of some trees to be exposed for a period of at least several weeks to temperatures of about 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. Cherry², W.H. Parker¹, 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 CO₂ 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 CO₂ 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. Cherry² and M.R. Lesser¹, 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. This allowed us to evaluate the frequency with which a given species was given a rating. Species were often assigned different ratings in different jurisdictions depending on their status for a particular province or territory. To simplify summarizing the survey, we only considered the highest rating value which is indicative of the worst case scenario for that species.

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

The results of the survey provide a basis for identifying gene conservation priorities for tree and shrub species in Canada but there are other considerations such as: 1) geographic distribution of species is important for setting priorities for conservation work and supporting



research, 2) determining the need to work on species with populations threatened in part of its range but under no threat throughout the remainder of the range, 3) prioritizing efforts on threatened outlying populations of species with known information on economic, ecological, and genetic parameters vs. those where these parameters are unknown, and 4) difficulties in taxonomic identification of some species and varieties.

Climate models and genetic applications for lodgepole pine in British Columbia

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Maps of interpolated climate normals have recently become essential tools for many types of forestry research, such as studying genetic adaptation of trees to local environments, modeling species 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

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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; García-Ramos and Rodríguez 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.