

An ecogeographic framework for in situ conservation of forest trees in British Columbia

Andreas Hamann, Pia Smets, Alvin D. Yanchuk, and Sally N. Aitken

Abstract: We present a comprehensive approach to carry out community-wide assessments of in situ conservation of forest trees based on basic botanical and ecological data. This is a first step, resulting in a consistent framework to set priorities for collection and inclusion of species-specific biological and genetic information. We use botanical sample data to generate high-resolution distribution maps as a basis for a gap analysis of how well each species is represented in protected areas. To account for adaptive genetic variation of tree species we stratify populations by ecological zones that represent different macroclimates. In a detailed example for Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco), we show that under certain conditions this approach can pinpoint gaps at the level of genetically differentiated populations without actually using genetic data. In a comprehensive case study, evaluating the outcome of a major protected area expansion between 1991 and 2001 for British Columbia, we demonstrate how extensive results from a community-wide GIS analysis can be summarized and presented for decision-making. We provide methods to identify and efficiently cope with in situ conservation gaps, where lack of data or low protected area coverage requires additional conservation efforts or collection of better data.

Résumé : Les auteurs proposent une approche d'ensemble afin de réaliser, à l'échelle de la communauté, les évaluations concernant la conservation in situ des arbres forestiers à partir de données botaniques et écologiques de base. Cette approche est une première étape devant constituer un cadre cohérent afin de décider des priorités pour la collecte et l'inclusion d'informations génétiques et biologiques spécifiques à chaque espèce selon les besoins. Les auteurs ont utilisé des données d'échantillonnage botanique afin de produire des cartes à haute résolution de la distribution des espèces. Ces cartes sont à la base de l'analyse de carence qui permet d'évaluer le niveau de représentation de chaque espèce au sein des aires protégées. Afin de tenir compte de la variation génétique liée à l'adaptation chez les arbres forestiers, les auteurs ont stratifié les populations par zones écologiques représentatives de différents macroclimats. Utilisant un exemple détaillé avec le douglas (*Pseudotsuga menziesii* (Mirb.) Franco), les auteurs démontrent que cette approche peut, dans certaines conditions, identifier des carences au niveau de populations génétiquement différenciées, sans effectivement recourir aux données génétiques. Lors d'une étude de cas complète ayant pour but d'évaluer les résultats d'une expansion majeure des aires protégées en Colombie-Britannique entre 1991 et 2001, les auteurs démontrent comment la masse de résultats découlant d'une analyse par SIRS à l'échelle de la communauté peut être résumée et présentée pour faciliter la prise de décision. Les auteurs présentent des méthodes pour identifier et faire face efficacement aux carences de la conservation in situ, là où le manque de données ou la faible attention accordée aux aires protégées requièrent des efforts additionnels de conservation ou la collecte de meilleures données.

[Traduit par la Rédaction]

Introduction

Because of its topographic range and coastal position, British Columbia contains a wide range of climatic conditions that include boreal, sub-boreal, humid-maritime, temperate-continental, and semiarid environments (Demarchi 1993). As a consequence, the land base supports unusually high species richness and ecosystem diversity for a temperate region. Forest ecosystems include boreal and sub-boreal forests in the north, coastal temperate rainforest, dry forests on

the east side of the Coast Mountains and on the central interior plateau, a unique second "inland rainforest" along the interior mountain ranges west of the Rocky Mountains, and high-elevation forest ecosystems throughout much of the province. According to the *State of the Forest Report* (B.C. Ministry of Forests 2005), the total potentially forested area in British Columbia is approximately 60×10^6 ha, with approximately one-third of this area currently economically usable. This resource currently provides nearly half of Canada's pulp and wood products, and adequate protection

Received 1 March 2005. Accepted 14 July 2005. Published on the NRC Research Press Web site at <http://cjfr.nrc.ca> on 4 November 2005.

A. Hamann,^{1,2} P. Smets, and S.N. Aitken. Centre for Forest Gene Conservation, Department of Forest Sciences, The University of British Columbia, Vancouver, BC V5Y 2X8, Canada.

A.D. Yanchuk. B.C. Ministry of Forests, Research Branch, 722 Johnson St, 3rd Floor, Victoria, BC V8W 1N1, Canada.

¹Corresponding author (e-mail: andreas.hamann@ualberta.ca).

²Present address: Department of Renewable Resources, University of Alberta, Edmonton, AB T6G 2H1, Canada.

of this forest resource at the ecosystem, species, and genetic level is not only desirable to sustain biological diversity but is also economically imperative.

A common approach for assessing the level of protection, redundancy of protected areas, and need for additional in situ reserves is to collect good census information on population size and distribution for species of concern. Based on such survey data, species can be ranked to set priorities for data collection and conservation (Dinerstein et al. 1995; Jenkins 1996). Provided that landscape classification variables or zonation can be interpreted in terms of biotic or abiotic habitat conditions, they can be efficient means for quantification of biological diversity in concert with inventory records (Ferrier and Smith 1990). GIS can be used for spatial modeling of population distribution and frequencies (Davies et al. 1990; Ferrier and Smith 1990; Pressey et al. 2000). These extrapolations from census data can ultimately be used for gap analysis, reserve evaluation, and optimized selection of additional reserves for species that are underprotected (Davis 1995; Pressey et al. 1996; Stoms et al. 1998; Lipow et al. 2004).

There are approximately 50 native tree species in British Columbia (depending on whether tall shrubs and outlying populations are included). An analysis of the in situ protection status at the species level, however, is not sufficient. Populations of a species often occur over a wide variety of ecosystems, sometimes showing disjunct distributions. Provenance studies show that such populations can be genetically differentiated and adapted to local climatic conditions of their source location. Loss of genetic diversity within a species may compromise the potential to adapt to new environmental conditions and also reduces the utility of a genetic resource for commercial tree breeding programs. Such a loss might take place unnoticed even in common species that appear to be in no danger (Ledig 1993). An efficient method to protect genetic diversity in many species is through a network of in situ genetic reserve forests (Ledig 1986; Koski 1996; Turok 1997).

Information regarding genetic variation in quantitative and adaptive traits is available for 10 commercially important conifer species for selected regions, and we have previously evaluated whether these genetic resources are adequately protected in situ (Hamann et al. 2004). In this study we extend this approach to all tree species and all regions of British Columbia. However, since genetic data are not available for minor tree species, we must assume that genetic differentiation has tracked geographic and climatic landscape patterns for this analysis. This is a reasonable assumption for British Columbia, since there is little indication that small-scale genetic adaptation of populations to edaphic or other localized, nonclimatic environmental conditions has taken place since the last glaciation (Critchfield 1984; Ledig et al. 1998; Yanchuk and Lester 1996). By comparing this approach (using delineations based on geography and climate) with our previous approach (delineations based on genetic data) we want to investigate whether an ecogeographic approach to genetic conservation can be effective, meaning that spatial coverage for landscape-level units will automatically capture underlying genetic variation as well.

In a comprehensive case study evaluating the outcome of a major protected area expansion between 1991 and 2001 for

British Columbia, we demonstrate how extensive results from a community-wide analysis of 49 species can be summarized and presented for decision-making. During this period, the protected area coverage has been doubled under a major provincial program (Land Use Coordination Office 1992). We evaluate whether this initiative improved the in situ conservation status of forest genetic resources where it was needed or whether this expansion mostly resulted in an increase of already redundant protected area coverage with respect to forest genetic resources. Finally, we provide methods to efficiently cope with in situ conservation gaps. Key genetic reserve forests are identified for efficient ex situ sampling or ground truthing to determine the conservation status of species that do not meet conservation criteria.

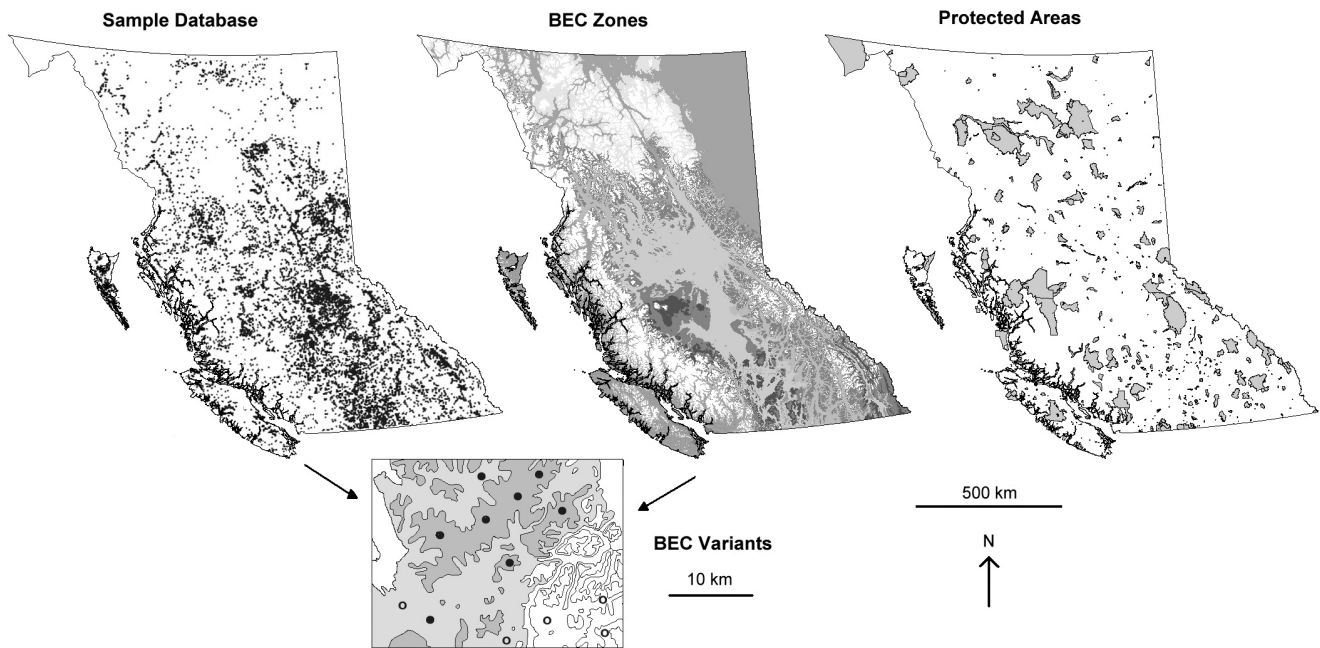
Methods

Maps of species ranges and frequencies

For modeling species distribution and frequency, we use a detailed botanical sample database (B.C. Ministry of Forests 2001) and a high-resolution spatial coverage of the hierarchical Biogeoclimatic Ecological Classification (BEC) system (Meidinger and Pojar 1991). The sample data of the provincial ecology program consist of 34 000 sample plots 0.04 ha in size that have been established throughout the province. Plot data include a full botanical inventory including a species frequency measure (percent ground cover). The ecological classification system subdivides the land base into 14 zones, 97 subzones, and 152 variants. BEC variants are often continuous landscape units that typically cover 0.5%–1% of the province. Only a few variants of the interior plateau and the prairies are much larger, and some montane variants are much smaller as well as noncontinuous (around mountain tops). We use release version 4 of this spatial data set, which has a useful resolution down to a scale of 1 : 250 000. This data set is publicly available online through the B.C. Ministry of Sustainable Resource Management (<http://srmwww.gov.bc.ca/gis/arcftp.html>).

The species distribution maps we generated are extrapolations from sample data to the spatial coverage of ecological zones at the BEC variant level or, in a few cases, at the BEC subzone level if less than five samples were available for a BEC variant (Fig. 1). Even at the zone level the classification closely follows species ranges and is therefore a good basis for spatial extrapolation of species frequencies. We first calculated the average percent ground cover (including zero cover samples) of each species in each BEC variant and added these data to the BEC spatial coverage (e.g., Fig. 1, bottom). The resulting raw frequency maps were then manually refined by inspecting an overlay of sample plot locations that indicated the presence or absence for each species. First, we applied a somewhat arbitrary frequency threshold to define the species range limit. Polygons with low predicted species frequencies (less than one-hundredth of the average species frequency) and containing no or few samples of a species were eliminated. Second, because a species may not fully occupy suitable habitat as a result of topographic barriers or other factors limiting its distribution, large polygons (usually with a wide north–south range) were truncated if the species samples only occurred in a portion of the polygon.

Fig. 1. Data used for modeling species frequency and gap analysis are 34 000 botanical inventory plots, the Biogeoclimatic Ecological Classification (BEC) system, and a spatial layer of protected areas. Rangemaps were derived by calculating the average frequency of a species for each BEC variant. In the example detail, a filled circle indicates species presence, an open circle a species absence at a sample plot, and the shading an expected species frequency. A gap analysis of protected areas was then carried out at the BEC zone level.



These steps were necessary because every ecological zonation is to some degree artificial and any delineation is to some degree inaccurate. Species occurrences outside our range maps could be considered “artificial fringe populations” (due to delineation errors) or “true outlier populations” (isolated occurrences of species). We decided to exclude these populations from further analysis because the “artificial fringe populations” are not likely to be genetically differentiated because of gene flow from nearby high-frequency populations, and the majority of “true outlier populations” would not be detected through our sample-based approach. When viewed at a resolution of 1 : 1 000 000 or lower, the resulting species range maps are virtually identical to distribution maps based on forest inventory data that are available for a few major forest species. However, unlike distribution maps that delineate individual stands of a few hectares, our range maps delineate the potential habitat of a species with an expected frequency.

Gap analysis of in situ protection

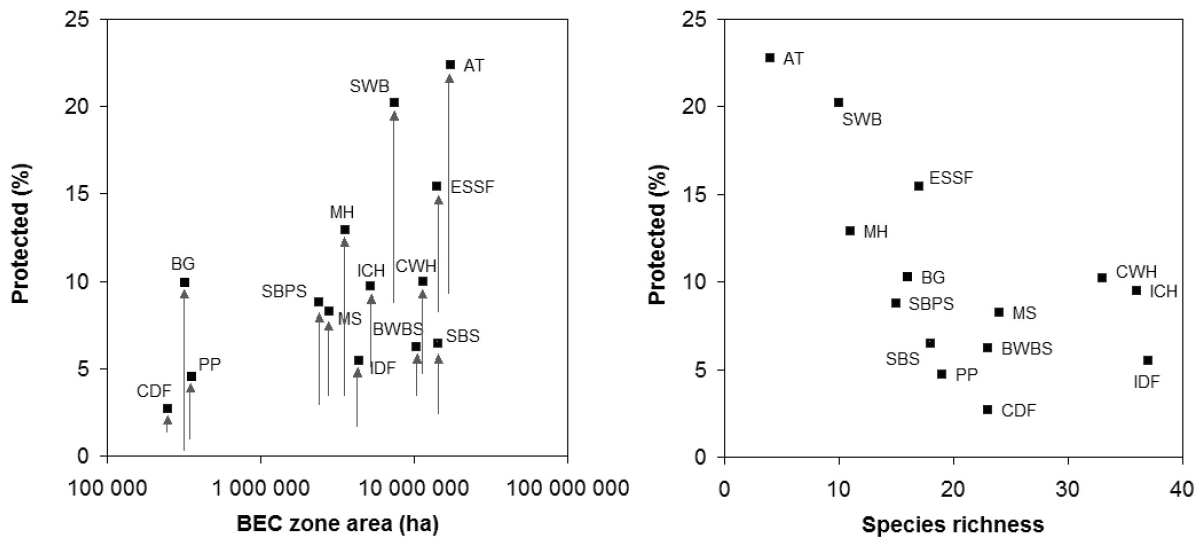
A gap analysis was performed by overlaying the protected area spatial layer with each species distribution map. Subsequently, the size of protected areas, the number of protected areas, and the species frequency in each reserve was calculated for each ecological zone in which the species occurred. Note that while we model species frequencies at the “BEC variant” level, we perform the gap analysis at the “BEC zone” level because genetic differentiation would not usually be expected at finer spatial scales in tree species because of gene flow. Consequently, we define the term “population” as the individuals of a species in a “BEC zone”, making the implicit assumption that these populations are genetically dif-

ferentiated and should receive an appropriate level of in situ protection.

For a protected area to be included in this analysis it cannot be subjected to any type of resource extraction or human manipulation such as logging, mining, oil or gas extraction, urbanization, or conversion to agriculture. Protected areas must also be permanent to be included in this analysis, being formally designated under legislation. This includes national parks, ecological reserves, class A and C provincial parks, recreation areas, and protected areas that fall under the Environment and Land Use Act, following the guidelines of the International Union for the Conservation of Nature (IUCN 1998). Over 800 protected areas covering approximately 11% of the provincial land base met these conditions and were evaluated in this study. About half of those reserves were less than 100 ha in size, 250 reserves ranged from 100 to 1000 ha, and the remaining 150 exceeded 1000 ha (Hamann et al. 2004). The GIS coverage is publicly available online through the B.C. Ministry of Sustainable Resource Management (<http://srmwww.gov.bc.ca/gis/arcftp.html>).

Since some reserves contain large water bodies, we used a GIS coverage of water features to remove these nonforested areas from the analysis. It is important to note that no further adjustments of nonforested areas were made, for example, because of urbanization, logging, or other human disturbance. The species range and frequency maps therefore indicate the expected species distribution in its natural state and are not equivalent to an actual forest inventory. For this analysis we must assume that protected areas actually contain natural forest with the expected species composition. While this is a reasonable assumption for most reserves, the interpolated species range and frequency outside reserves is only

Fig. 2. Conservation status of ecosystems plotted as a function of total area in British Columbia (left) and species richness (right). Arrows indicate the change from 1991 to 2001. Biogeoclimatic zone names are as follows: AT, Alpine Tundra; BG, Bunch Grass; BWBS, Boreal White and Black Spruce; CDF, Coastal Douglas-fir; CWH, Coastal Western Hemlock; ESSF, Engelmann Spruce – Subalpine Fir; ICH, Interior Cedar–Hemlock; IDF, Interior Douglas-fir; MH, Mountain Hemlock; MS, Mountain Spruce; PP, Ponderosa Pine; SBPS, Sub-Boreal Pine–Spruce; SBS, Sub-Boreal Spruce; SWB, Spruce–Willow–Birch.



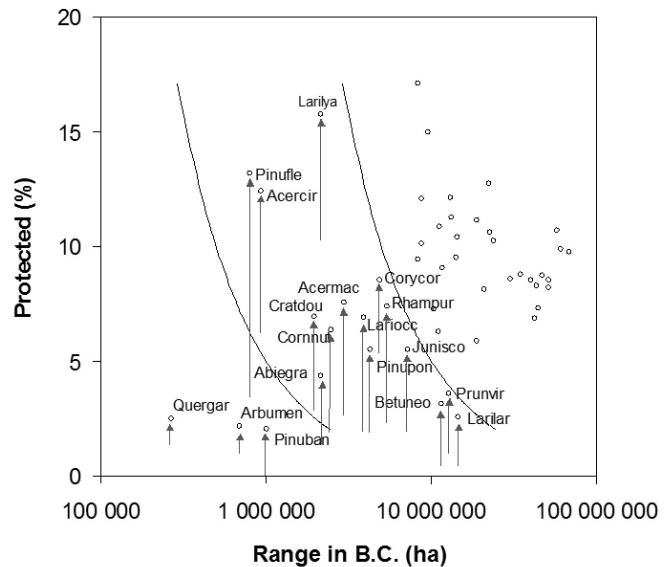
given as a reference and may not reflect the actual forest cover.

Importance of genetic reserves

To qualify as a genetic reserve, a protected area should be large enough to ensure adequate genetic variability and functioning of mating systems of tree species. The population size needed depends on several factors and will usually exceed a census population size of 5000 individuals to allow an effective population size (N_e) of at least 1000 individuals (Aitken 2000; Yanchuk 2001). Our botanical inventory data, however, only provide percent ground cover for each species and not the number of individuals. Using forest inventory data that are available for major commercial conifer species, it is possible to convert an expected cumulative ground cover (with an error estimate) into a probability of a reserve exceeding 5000 mature equivalent individuals (Hamann et al. 2004). For commercial conifers, a cumulative ground cover of 10 ha will likely contain this census population size (for example a 200 ha reserve that contains a species with an average ground cover of 5%). For other species this conversion factor may be different, and we therefore also identified reserves that contained >0, >2.5, >5, and >50 ha of cumulative cover.

Key genetic reserve forests areas should contain populations that are not under extensive protection elsewhere and preferably protect several species simultaneously. Accordingly, we calculated a score for each reserve by giving an importance value of one unit to a reserve for each population that is represented with a cumulative cover of 10 ha or more. To account for redundancy, the value of one unit for each population was divided by the total number of reserves in which the population is adequately represented. For example, for a reserve–ecosystem combination that contained species A, B, and C, where species A was only represented in this location, species B was found in two other reserves,

Fig. 3. Conservation status of tree species plotted as a function of their range in British Columbia (B.C.). Arrows indicate changes from 1991 to 2001. Points that fall on the same curve have equal total protected area coverage. Abbreviations are based on the first four letters of the genus and the first three letters of the species name.



and species C was found in five other reserves the score is $1/1 + 1/3 + 1/6 = 1.5$. It should be noted that this scoring implies a certain value for the degree of redundancy, for the number of populations in a reserve, and for the value of redundancy relative to the number of populations it contains.

Results and discussion

For forest trees in British Columbia and elsewhere, protection at the species level is usually not sufficient. Popula-

tions of a species often occur over a wide ecological amplitude and are physiologically or even morphologically differentiated. Populations conserved in situ should be representative of this genetic diversity within a species. Collecting comprehensive data of genetic differentiation in quantitative traits or genetic markers is expensive and time consuming and can only be carried out for selected species, and even then only for particularly valuable populations. How can we prioritize in collecting additional census information, biological data on a species' resilience to biotic and abiotic stresses, and reproductive capacity? When are additional conservation efforts or estimation of genetic parameters such as minimum viable population size or genetic differentiation necessary? In the first case study, a community-wide ecogeographic gap analysis for tree species by ecosystems in British Columbia, we demonstrate how prioritization of conservation efforts, data collection, and biological or genetic research can be carried out efficiently. In the second, more detailed example, we investigate whether an ecogeographic approach can serve as a substitute for genetic data under certain conditions.

Evaluating in situ conservation efforts in British Columbia

The outcome of a major protected area expansion between 1991 and 2001, doubling the protected area coverage for British Columbia, may be summarized only by landscape units or species for a general overview. A breakdown by BEC zones reveals that not all ecosystems are equally well represented in protected areas. Unfortunately, ecosystems that are relatively rare in British Columbia and ecosystems that have a high tree species richness tend to be under-protected (Fig. 2). On the positive side, important improvements between 1991 and 2001 in the protection status of some rare or species-rich ecosystems should be noted, for example, in the Bunchgrass (BG), Ponderosa Pine (PP), and Interior Douglas-fir (IDF) zones.

A breakdown of in situ protection by tree species as a function of species range in British Columbia reveals a similar trend. Species that are restricted to small areas also tend to have the smallest portion of their range protected. Examples are Garry oak (*Quercus garryana* Dougl.; abbreviated Quergar in Fig. 3) and arbutus (*Arbutus menziesii* Pursh.; Arbutum). However, there are a number of species with larger ranges that also have a low percentage of their range protected (lower right corner of Fig. 3). Several species significantly benefited from the expansion of protected areas between 1991 and 2001 (Fig. 3, arrows). Jack pine (*Pinus banksiana* Lamb.; Pinuban), is an example of a species that only has a small portion of its total range present in north-eastern British Columbia. Nevertheless, for administrative reasons it was specifically targeted through conservation efforts, which brought much of this and the associated species tamarack (*Larix laricina* (Du Roi) K. Koch; Larilar) and Alaska paper birch (*Betula neoalaskana* Sarg.; Betuneo) under protection in British Columbia. Infrequent species in the southern coastal area of British Columbia have also benefited from new protected areas, such as vine maple (*Acer circinatum* Pursh.; Acercir), bigleaf maple (*Acer macrophyllum* Pursh.; Acermac), Pacific dogwood (*Cornus nuttallii*

Aud. ex T. & G.; Cornnut), and the coastal populations of grand fir (*Abies grandis* (Dougl. ex D. Don) Lindl.; Abiegra).

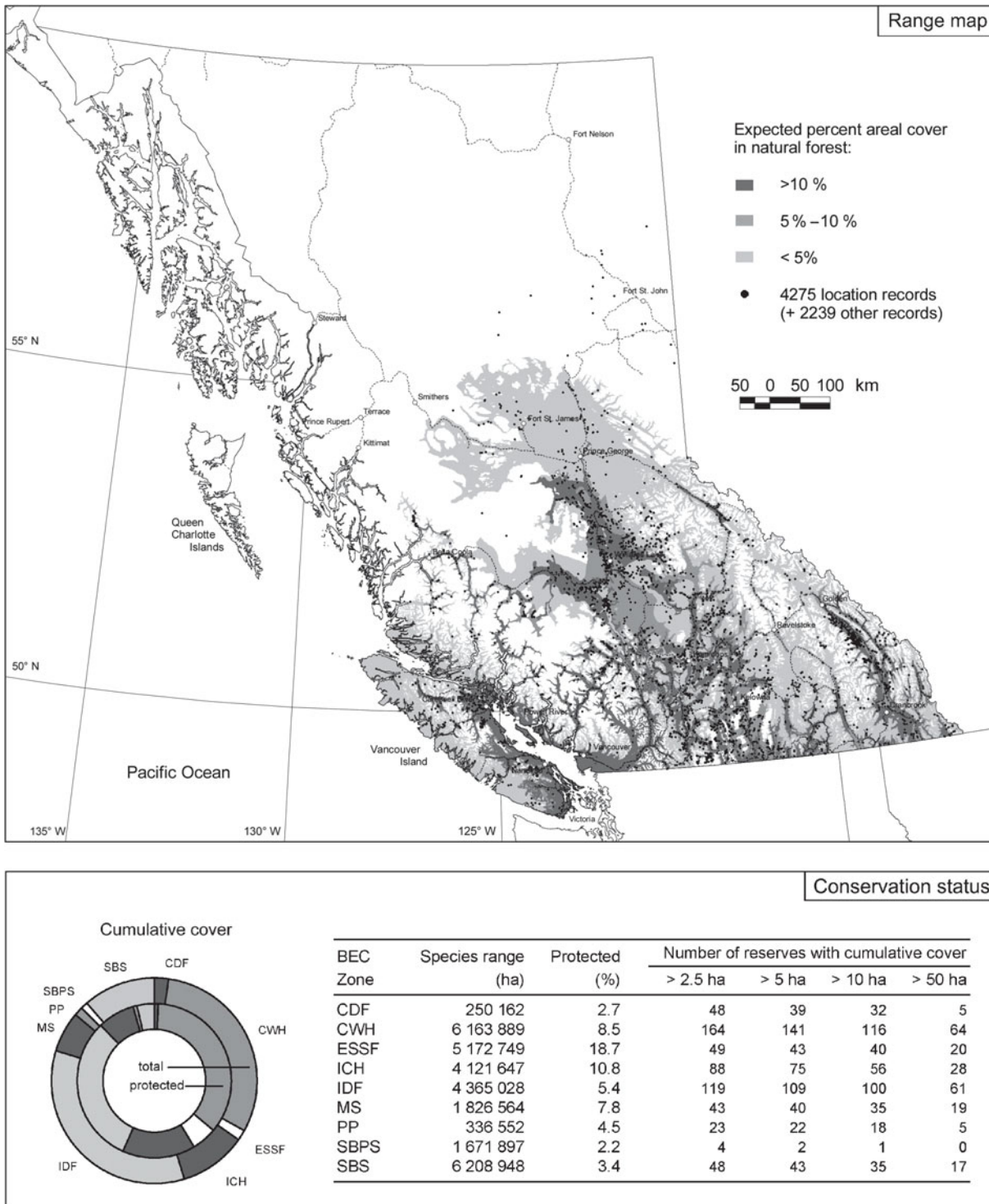
Ecogeographic stratification for Douglas-fir populations

We use Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco) as an example for population stratification by ecological zones as a representation of genetic resources. Equivalent statistics for all other species are available online.³ Douglas-fir occurs in nine ecological zones (Fig. 4). Zones that either have a small total protected area coverage or that are proportionally underrepresented are the Coastal Douglas-fir (CDF), Ponderosa Pine (PP), Sub-Boreal Pine–Spruce (SBPS), and the Sub-Boreal Spruce (SBS) BEC zones. This doughnut chart in combination with statistics on frequency and number of reserves visualizes two aspects of a potential lack of protection: (1) an absolute lack of reserve coverage and (2) a lack of reserve coverage in proportion to the total natural population size in a BEC zone. For a community-wide perspective, the 10 proportionately least protected populations of all species are listed in Table 1. The SBPS – Douglas-fir population ranks second overall, suggesting that Douglas-fir has a notable lack of protection in the SBPS zone by community-wide standards.

Douglas-fir is a useful example because it has one of the very few major conservation gaps previously identified for commercial tree species populations using delineations based on genetic data (Hamann et al. 2004). The population for the ecological zone SBPS identified previously covers a large area (300 000 ha), mostly east and west of Williams Lake, which is only covered by a few very small reserves (Table 1, “Nunsti” etc.). This area corresponds to the seed planning unit Fd-CT-a (approximately 60% overlap) of the genetic analysis, pinpointing the same gap. Thus, the analysis appears to be quite robust against moderate changes in the geographic delineation of populations. It also suggests that the use of ecological or macroclimatic zones to approximate patterns of genetic differentiation due to local adaptation can be a reasonable approach if no genetic data are available. There are, however, several important limitations that need to be considered: (1) the approach works best for populations that belong to geographically widespread species and makes the assumption of clinal patterns of genetic variation that represent adaptation to macroclimatic conditions; (2) species and populations that are not frequent enough to be reliably and representatively recorded by this sample-based approach are inevitably excluded from this analysis. This applies to small outlying populations and ecological fringe populations, although they may harbor valuable genotypes because of genetic isolation and high selection pressure; (3) spatial patterns of genetic diversity that are due to migration history rather than consisting of adaptive variation to current conditions are not covered through this approach. Similarly, inferred coverage of genotypes representing adaptations to macroclimate may not be fully realized because of adaptational lag; (4) finally, species with restricted distribution or population differentiation corresponding to very fine scales (e.g., particular soils, riparian areas) are not sufficiently evaluated by this broad ecogeographic approach. It should be noted that this analysis is a

³<http://www.genetics.forestry.ubc.ca/cfgc/in-situ-stats.html>.

Fig. 4. Example synopsis of the in situ conservation status for Douglas-fir populations in British Columbia. GIS data and summaries for all tree species are available at <http://www.genetics.forestry.ubc.ca/cfgc/in-situ-stats.html>.



first step, resulting in a consistent framework to set priorities for additional conservation efforts, biological and genetic information, or additional census data. In the next section, we outline how such prioritization may be carried out efficiently.

Ground truthing and evaluation of protected areas

In our previous study (Hamann et al. 2004) the benchmark of sufficient protection of genetic resources in seed zones

was set as the 95% confidence of tree populations being represented with an effective population size of at least 1000 individuals (or a census population size of at least 5000 mature individuals) in at least three spatially separated reserves. Only a few seed planning units did not meet this requirement. However, a lack of in situ protection identified by this type of analysis does not necessarily signify that these populations are not adequately covered. It means that

Table 1. The 10 populations of all species with the least percentage of cumulative cover in protected areas.

Species (BEC zone) ^a	Protected area		Protected areas sorted by decreasing importance
	(%)	(ha)	
<i>Pinus monticola</i> (MS)	0.0	0	(No park with a cumulative cover >2.5 ha)
<i>Pseudotsuga menziesii</i> (SBPS)	0.2	39	Nunsti, Big Creek, Nazko Lake, White Pelican
<i>Salix lucida</i> (IDF)	0.9	10	Premier Lake, Kikomun Creek, Kootenay, Columbia Lake
<i>Pinus flexilis</i> (IDF)	1.0	1	(No park with a cumulative cover >2.5 ha)
<i>Acer macrophyllum</i> (IDF)	1.1	6	Birkenhead Lake, Nahatlatch
<i>Prunus virginiana</i> (BWBS)	1.3	117	Peace – Moberly, Gwillim Lake, Peace River – Bodreau, Bearhole Lake, Bearhole Lake, Milligan Hills, Chinchaga Lakes, Peace River Corridor – Peace River I, Butler Ridge, Beatton-Doig Canyon and Beatton River, Pine River Breaks, Sukunka Falls, Beatton, Clayhurst
<i>Prunus pensylvanica</i> (BWBS)	1.5	3	Peace – Moberly
<i>Abies grandis</i> (ICH)	1.5	39	West Arm, Champion Lakes, Syringa, Pilot Bay, Lockhart Creek, Kootenay Lake, Valhalla, Kokanee Creek, King George VI
<i>Alnus viridus</i> (SBPS)	1.8	301	Entiako, Tweedsmuir North, Entiako, Kluskoil Lake, Tweedsmuir (South), Nazko Lake, Nunsti, White Pelican, Narcosli Lake
<i>Corylus cornuta</i> (SBS)	1.8	195	Fraser River, Schoolhouse Lake Park, Fort George Canyon, Ten Mile Lake, Pinnacles, Cinema Bog, Cottonwood River

Note: The full table and data for all 226 species–ecosystem combinations can be obtained online at <http://www.genetics.forestry.ubc.ca/cfgc/in-situ-stats.html>.

^aBWBS, Boreal White and Black Spruce; ICH, Interior Cedar–Hemlock; IDF, Interior Douglas-fir; MS, Mountain Spruce; SBPS, Sub-Boreal Pine–Spruce; SBS, Sub-Boreal Spruce.

Table 2. Examples of protected areas in British Columbia with their importance rank as a genetic reserve (1, most important; 839, least important) and populations of tree species that they contain.

Park name	Rank	Populations in park ^a
Adams Lake	346	ICH: Abielas 3, Alnuvir 3, Betupap 6, Pinucon 7, Pseumen 19, Thujpli 29, Tsughet 27 IDF: Betupap 3, Pinucon 4, Pseumen 20, Thujpli 7
Akamina-Kishinena	120	ESSF: Abielas 1137, Acergla 31, Alnuvir 50, Larilya 212, Lariocc 6, Piceeng 947, Pinualb 107, Pinucon 516, Pseumen 112, Salisco 23
Alexandra Bridge	524	IDF: Pseumen 14, Thujpli 6
Aleza Lake	497	SBS: Abielas 21, Alnuinc 5, Picegla 4, Pinucon 10
Alice Lake	334	CWH: Abieama 5, Acercir 26, Acermac 14, Alnurub 21, Picesit 6, Popubal 13, Pseumen 102, Salisit 3, Thujpli 97, Tsughet 113
Andy Bailey	634	BWBS: Picegla 3, Picemar 6
Anne Vallee	496	CWH: Abieama 8, Chamnoo 7, Picesit 18, Pinucon 10, Thujpli 14, Tsughet 29
Ansty Hunakwa	122	ESSF: Abielas 20, Alnuvir 3, Piceeng 13, Pinucon 3 ICH: Abielas 111, Acergla 57, Alnuinc 22, Alnuvir 98, Betupap 179, Corycor 27, Piceeng 44, Pinucon 218, Pinumon 39, Popubal 13, Poputre 48, Pseumen 595, Salibeb 3, Salisco 53, Salisit 13, Taxubre 38, Thujpli 1026, Tsughet 1031
Antoine-Fred	54	ESSF: Abielas 402, Alnuinc 11, Alnuvir 7, Piceeng 190, Pinualb 89, Pinucon 127, Pseumen 8 IDF: Acergla 8, Alnuinc 10, Alnuvir 9, Betuocc 7, Betupap 3, Junisco 6, Piceeng 29, Pinucon 118, Pinupon 13, Popubal 12, Poputre 31, Pseumen 622, Salibeb 11, Salisco 25 MS: Abielas 58, Alnuinc 7, Alnuvir 16, Piceeng 41, Pinucon 250, Pseumen 75, Salisco 3 PP: Acergla 4, Betuocc 3, Pinupon 21, Pseumen 18
Apex Mountain	604	ESSF: Abielas 62, Piceeng 41, Pinualb 3, Pinucon 42

Note: The full table and data for all 839 protected areas can be obtained online from <http://www.genetics.forestry.ubc.ca/cfgc/in-situ-stats.html>.

^aCodes for biogeoclimatic zones are as follows: BWBS, Boreal White and Black Spruce; CWH, Coastal Western Hemlock; ESSF, Engelmann Spruce – Subalpine Fir; ICH, Interior Cedar–Hemlock; IDF, Interior Douglas-fir; MS, Mountain Spruce; PP, Ponderosa Pine; SBPS, Sub-Boreal Pine–Spruce; SBS, Sub-Boreal Spruce; SWB, Spruce–Willow–Birch. Following the zone name, the expected cumulative cover (ha) for each species is listed. Species abbreviations are as based on the first four letters of the genus and the first three letters of the species name.

with the currently available data, a lack of protection cannot be excluded without visiting the reserves and confirming the population presence and size of selected species in protected areas.

According to (the extended) Table 1, the list of populations that require ground truthing is quite long when the same criteria are applied to noncommercial tree species. Most of these populations are found in the proportionally underprotected ecological zones IDF, CDF, ICH, SBPS, and BWBS. Ground truthing a few carefully selected reserves in each of these zones could clarify the conservation status of these species quite efficiently. In Table 2 (extended table available online) we provide a list of parks with the populations they are predicted to contain. A high rank indicates that a protected area covers one or several populations that are not well protected in other reserves. This list is also available in a database format that can be queried using GIS or any database software (e.g., find protected areas that contain species A, B, and C in zone X with at least Y ha of cumulative cover).

In our analysis we use cumulative cover to quantify species abundance because this is the native format of the survey databases. For gene conservation purposes, census population size of mature-equivalent individuals, or estimates of reproductively effective population size (N_e), would be a better measure. For common canopy tree species, such as commercially important conifers, a cumulative ground cover of 10 ha will likely represent a census population size larger than 5000 individuals (Hamann et al. 2004). For small trees and tall shrubs, which may have a higher number of mature-equivalent stems per hectare, the required cumulative cover will be smaller. Since there are no detailed forest inventory data available for minor tree species, we determined for each species the number of reserves that contain >2.5, >5, >10, and >50 ha of cumulative cover (Fig. 4). The resource manager who is interested in the redundancy of protected area coverage for a minor tree species must either make an educated guess as to what cumulative cover is equivalent to a sufficient population size, or collect additional inventory data.

If we define sufficient protected area coverage of a population as at least 10 ha of cumulative ground cover in a reserve-ecosystem combination, all but one commercially important conifer population and 90% of minor tree species populations are now covered by at least one reserve. Eighty percent of all populations are adequately covered by at least three reserves. All zone-species combinations are now covered by multiple protected areas (although they may contain less than 10 ha of expected cumulative cover). Ground truthing may reveal adequate protected area coverage of most populations, but it is not safe to infer this from currently available sample data alone. The statistics provided in this analysis may be used to efficiently clarify the conservation status of a few relatively rare tree species (e.g., pacific yew, black hawthorn, cascara, beaked hazelnut, cherry species, and some willows) in particular zones that are proportionally not well protected (CDF, IDF, ICH, SBPS, and BWBS).

Acknowledgements

This study was conducted under the auspices of the Forest Genetics Council of British Columbia and was funded

through Forest Renewal British Columbia and the Forest Investment Account of British Columbia (grant holder: S.N. Aitken). We thank Del Meidinger for providing data from the provincial ecology program. Help in planning this study by Leslie McAuley and Ron Planden and review of species range maps by Andy McKinnon is gratefully acknowledged.

References

- Aitken, S.N. 2000. Conserving adaptive variation in forest ecosystems. *J. Sustain. For.* **10**: 1–12.
- B.C. Ministry of Forests. 2001. Mensuration data from the provincial ecology program. B.C. Minist. For. Work. Pap. 62.
- B.C. Ministry of Forests. 2005. The state of British Columbia's forests 2004 [online]. B.C. Ministry of Forests, Victoria, B.C. Available from <http://www.for.gov.bc.ca/hfp/sof/> [accessed 2 April 2005].
- Critchfield, W.B. 1984. Impact of the Pleistocene on the genetic structure of North American conifers. *In* Proceedings of the Eighth North American Forest Biology Workshop, Logan, Utah, 30 July – 1 August 1984. *Edited by* R.M. Lanner. Utah State University, Logan, Utah. pp. 70–118.
- Davies, F.D., Stoms, D.M., Estes, J.E., Scepán, J., and Scott, M.J. 1990. An information systems approach to the preservation of biological diversity. *Int. J. Geogr. Info. Syst.* **4**: 55–78.
- Davis, F.W. 1995. Information systems for conservation research, policy, and planning. *Bioscience*, **12**(Suppl.): S36–S42.
- Demarchi, D.A. 1993. Ecoregions in British Columbia: third approximation. B.C. Environment, Wildlife Branch, Victoria, B.C.
- Dinerstein, E., Wikramanayake, E.D., and Forney, M. 1995. Conserving the reservoirs and remnants of tropical moist forest in the Indo-Pacific region. *In* Ecology, conservation and management of southeast Asian rainforests. *Edited by* R.B. Primack and T.E. Lovejoy. Yale University Press, New Haven, Conn. pp. 140–175.
- Ferrier, S., and Smith, A.P. 1990. Using geographical information systems for biological survey design, analysis and extrapolation. *Aust. Biol.* **3**: 105–116.
- Hamann, A., Aitken, S.N., and Yanchuk, A.D. 2004. Cataloguing in situ protection of genetic resources for major commercial forest trees in British Columbia. *In* Dynamics and conservation of genetic diversity in forest ecology. *For. Ecol. Manage.* **197**: 293–303.
- IUCN. 1998. 1997 United Nations list of protected areas. Prepared by WCMC and WCPA. International Union for the Conservation of Nature, Gland, Switzerland.
- Jenkins, R.E. 1996. Natural heritage data center network: managing information for managing biodiversity. *In* Biodiversity in managed landscapes. Oxford University Press, New York. pp. 176–192.
- Koski, V. 1996. Treatment of gene reserve forests. *In* Assessment of Biodiversity for Improved Forest Management: Proceedings of the International Workshop, Koli, Finland, 12–17 June 1995. *Edited by* P. Bachmann, K. Kuusela, and J. Uuttera. European Forestry Institute, Joensuu, Finland. pp. 49–52.
- Land Use Coordination Office. 1992. Protected areas strategies. Land Use Coordination Office, Victoria, B.C.
- Ledig, F.T. 1986. Conservation strategies for forest gene resources. *For. Ecol. Manage.* **14**: 77–90.
- Ledig, F.T. 1993. Urgent global need to stem losses in U.S. forest tree genetic resources. *Diversity*, **9**: 77–80.
- Ledig, F.T., Vargas-Hernandez, J.J., and Johnsen, K.H. 1998. The conservation of forest genetic resources: case histories from Canada, Mexico, and the United States. *J. For.* **96**: 32–41.

- Lipow, S.R., Vance-Borland, K., St. Clair, J.B., Henderson, J., and McCain, C. 2004. Gap analysis of conserved genetic resources for forest trees. *Conserv. Biol.* **18**: 412–423.
- Meidinger, D., and Pojar, J. 1991. *Ecosystems of British Columbia*. B.C. Ministry of Forests, Victoria, B.C.
- Pressey, R.L., Ferrier, S., Hager, T.C., Woods, C.A., Tully, S.L., and Weinman, K.M. 1996. How well protected are the forests of north-eastern New South Wales? Analyses of forest environments in relation to formal protection measures, land tenure, and vulnerability to clearing. *For. Ecol. Manage.* **85**: 311–333.
- Pressey, R.L., Hager, T.C., Ryan, K.M., Schwarz, J., Wall, S., Ferrier, S., and Creaser, P.M. 2000. Using abiotic data for conservation assessments over extensive regions: quantitative methods applied across New South Wales, Australia. *Biol. Conserv.* **96**: 55–82.
- Stoms, D.M., Borchert, M.I., Moritz, M.A., Davis, F.W., and Church, R.L. 1998. A systematic process for selecting representative research natural areas. *Nat. Areas J.* **18**: 338–349.
- Turok, J. 1997. International collaboration on the conservation of forest genetic resources in Europe. *IUFRO World Ser.* **6**: 149–158.
- Yanchuk, A.D. 2001. A quantitative framework for breeding and conservation of forest tree genetic resources in British Columbia. *Can. J. For. Res.* **31**: 566–576.
- Yanchuk, A.D., and Lester, D.T. 1996. Setting priorities for conservation of the conifer genetic resources of British Columbia. *For. Chron.* **72**: 406–415.