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Forest Ecology and Management 197 (2004) 295–305

Forest Ecology  
and  
Management

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# Cataloguing *in situ* protection of genetic resources for major commercial forest trees in British Columbia

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## Abstract

Loss of genetic diversity can be due to a variety of causes and might take place unnoticed even in widespread and frequent species. *In situ* reserves can be a very efficient method of protecting genetic diversity in tree species if they are sufficiently large to sustain adequate populations and spatially well distributed to protect populations adapted to a range of environmental conditions. We use a geographical information system (GIS) based approach to assess the level of *in situ* protection based on forest inventory data. Recently revised maps of seed planning units used for management of genetic resources for 11 major commercial conifer species reflect geographic variation as observed in genetic tests. On this basis we investigate how well populations are represented in protected areas. Due to a systematic expansion of protected areas in the 1990s, it appears that conifer genetic resources are now well represented in protected areas. In this study we identify the remaining gaps for *in situ* protection and discuss implications for genetic resource management. Further, we evaluate protected areas for their importance with respect to gene conservation, and determine whether ground truthing is necessary to confirm that populations in protected areas are sufficiently large.

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**Keywords:** Gene conservation; Conifers; Gap analysis; GIS; British Columbia

## 1. Introduction

Loss of genetic diversity in species reduces the potential for adaptation to new environmental conditions and the potential for selection and breeding for new objectives. Such a loss can be due to a variety of causes and 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 regional or international network of genetic reserve forests (Koski, 1996;

Ledig, 1986; Turok, 1997). In addition, monitoring, active management, and integration of *ex situ* programs may be needed to supplement the *in situ* reserve system (Ledig et al., 1998). Nevertheless, a network of *in situ* reserves is essential for any forest gene conservation program targeting the natural distribution of a species that aims at being comprehensive and cost efficient.

A common approach for assessing the level of protection, redundancy of protected areas, and the need for additional *in situ* reserves is to collect good census information on population size and distribution for the 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,

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1996). In addition, geographic information systems (GIS) can be used for spatial modelling of population distribution and frequencies (Davies et al., 1990; Ferrier and Smith, 1990; Pressey et al., 2000). These extrapolations from census data can then be used for gap analysis, reserve evaluation, and reserve selection (Davis, 1995; Pressey et al., 1996).

While this type of spatial gap analysis has previously been used to assess the conservation status of endangered species, it has only recently been applied in a gene conservation context (Lipow et al., 2004). The reason is that detailed maps associating genetic variation for a species with geography are not usually available. However, for major commercial conifer species in British Columbia, genetic data on geographic differentiation are available from extensive provenance and progeny trials. Digital maps of seed planning zones (SPZs) that reflect this genetic differentiation, have been developed at a scale of 1:250,000 (BC Ministry of Forests, 1998). Recently, seed planning units (SPUs) were also digitally mapped to reflect genetic differentiation over elevation gradients within SPZs (BC Ministry of Forests, 2003). These delineations are widely used in practical genetic resource management. Here we assume SPUs contain distinct commercially valuable genetic resources, although they might not be ideal delineations to capture all types of genetic diversity. Further, we define a population as individuals of a species that occur in an SPU.

This survey complements previous work by Lester and Yanchuk (1996)<sup>1</sup> and Yanchuk and Lester (1996) with a quantitative analysis of the *in situ* gene conservation status of commercial conifers. We utilise available information from various ecological and forest inventory databases that are maintained by the British Columbia provincial government to estimate population sizes of tree species in protected areas. Based on this information we evaluate current protected areas individually for their value as genetic reserves. To qualify as a primary genetic reserve, a protected area should contain populations that are not covered elsewhere, and it should also be large enough to ensure adequate genetic variability, maintenance of local adaptation and functioning of mating systems of

tree species. The population size needed depends on several factors and will usually exceed 5000 individuals (Aitken, 2000). A reserve larger than 250 ha will almost certainly contain this census population size for conifers in British Columbia (Yanchuk and Lester, 1996). However, we calculate the probability for reserves of all sizes to exceed 5000 individuals, and then use this data to assess if ground truthing is necessary and determine how it can be carried out most efficiently.

Approximately 4.5 million hectares of protected areas were initially established in British Columbia, mainly in the 1940s, with the objective to set aside areas for recreation and tourism. This number remained more or less stable with only occasional additions for half a century, until a major provincial initiative more than doubled the number of reserves and land cover between 1991 and 2001. The focus of this recent expansion was to achieve satisfactory representation of biological diversity, unique natural environments, and different ecosystems in protected areas (Land Use Coordination Office, 1992). It is often argued that such a “coarse filter” or “landscape level” approach to conservation will also protect the underlying genetic diversity of species. In this paper we will also investigate the degree to which this initiative improved the *in situ* conservation status of conifer genetic resources in British Columbia.

## 2. Methods

### 2.1. Spatial data and GIS analysis

The first part of this analysis is based on spatial coverage data of protected areas, seed planning units (SPU), water features, and a hierarchical biogeoclimatic ecological classification (BEC) system. These data sets are publicly available on-line through the BC Ministry of Sustainable Resource Management of British Columbia (Information Management Branch, 2002) and the Tree Improvement Branch (BC Ministry of Forests, 2002).

For a protected area to be included in this analysis it must be excluded from any type of resource extraction or human manipulation such as logging, mining, oil or gas extraction, urbanisation or conversion to agriculture. Protection of areas must also be permanent, being

<sup>1</sup>Note that all cited Ministry of Forests and Ministry of Sustainable Resource Management publications are available on-line at <http://www.for.gov.bc.ca/HFD/library/>.

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 IUCN (International Union for the Conservation of Nature, 1998). Over 800 protected areas covering approximately 11% of the provincial land base met these conditions and were evaluated in this study (Fig. 1).

As a spatial representation of genetic variation we used the seed planning units for 11 commercially important conifers in British Columbia. These are derived from seed zones, which are geographic areas across which individuals of a species are adapted to similar environmental conditions. Seed zones were originally used to ensure that reforestation stock is

planted within the same general area and climate in which seed was collected from wild stands. Based on genetic information from extensive provenance testing for most of these species, these zones have been revised and combined into the current seed planning zones and seed planning units. These zones are used to control the use for reforestation of seed produced in seed orchards from phenotypically selected and tested trees originating from natural stands in the local SPU. SPUs are high and low elevation bands within seed planning zones (Fig. 1). Sometimes they contain an “overlap” elevation band where seed sources from both high and low bands may be used. SPUs are species-specific and their names consist of three components, a provincial species code (e.g. Fd, for Douglas fir), a regional code (e.g. PG, for Prince George)

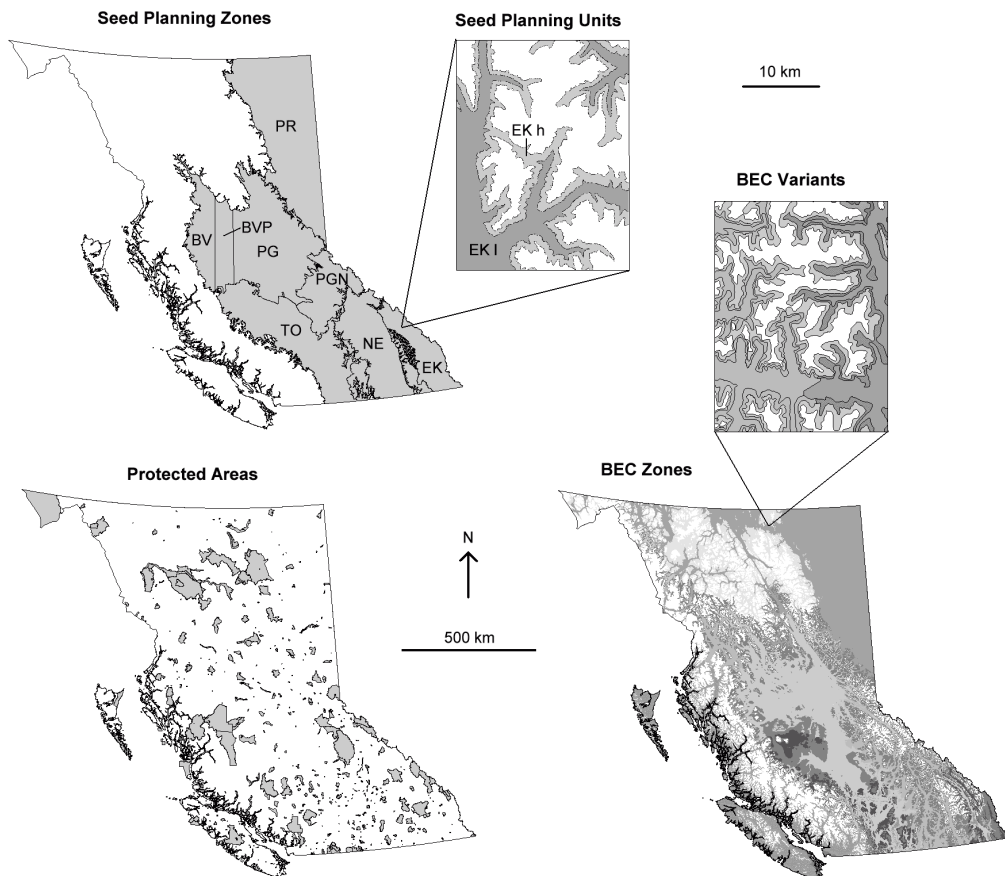


Fig. 1. Examples of GIS data sets used in this analysis. Seed planning zones for interior spruce are shown in the upper left, with the enlargement showing seed planning units consisting of two elevational bands (h, high; l, low). This layer was intersected with protected areas (lower left) for a gap analysis. Species frequency modelling is based on the hierarchical biogeoclimatic ecological classification (BEC) system.

and an elevation band (h, high; l, low, o, overlap). There may also be regional overlap zones indicated by three letter codes (e.g. BVP and PGN in Fig. 1) where seed from two adjacent zones may be used.

A standard gap analysis was performed by intersecting the protected area spatial layer with the SPU layer for each species. Subsequently, the proportion of protected areas, and the number of reserves larger than 250 ha, was determined for each SPU. For estimating population sizes, the union of the protected area and SPU layer was further intersected with BEC zone and water feature layers.

## 2.2. Inventory data and estimation of population size

The BC Ministry of Forests maintains a detailed Timber Supply Area (TSA) database that contains information on forest cover, stand age, species composition, and other attributes for most forest stands in the province. This database has been assembled from interpretations of aerial photographs and is updated weekly as stands are logged, replanted, and resurveyed. The inventory covers approximately 90% of the province but cannot be used directly for this analysis because protected areas are not included unless they have recently been established. Instead, we use a detailed botanical sample database of the provincial ecology program (BC Ministry of Forests, 2001), consisting of 34,000 sample plots 0.04 ha in size, which includes an area measure (percent cover for each species) and for selected samples also includes data from two prism plots that were used to determine the number of stems (>10 cm dbh) per hectare for each species. We then use the TSA database only to make adjustments for the portion of the land base that are naturally non-forested.

Species frequencies were calculated for variants of the Biogeoclimatic Ecological Classification (BEC) system (Meidinger and Pojar, 1991). This hierarchical system subdivides the landbase into 14 zones, 97 subzones and 152 variants. Even at the zone level species ranges are concordant with BEC classification, indicating the latter is a good basis for spatial computations of species frequencies. The population size in each protected area was estimated using factors for converting cumulative cover to stems per hectare. We only used stems per hectare data from mature stands (100 years and older), and only considered individuals

with a dbh >30 cm. When this factor is applied to cumulative cover data for successional stands the resulting number represents a “mature equivalent” census population size of reproducing individuals. This conversion factor was calculated separately for each BEC zone with an error estimate. The expected number of “mature equivalent” individuals in a protected area was then determined by multiplying the total cumulative cover of a species in each BEC variant of a protected area with this conversion factor for stems per hectare. Standard deviations were estimated for all mean values calculated from sample data, allowing for estimation of the standard deviation for number of mature equivalent individuals using standard rules for multiplication and addition of variances. Finally, we used the probability function of the normal distribution to determine the probability of a protected area containing at least 5000 individuals.

One limitation of this estimation procedure is its underlying assumption that individuals of a species are randomly distributed within their range. Because of landscape features, random historic events, or metapopulation dynamics, a species may not be present in a particular reserve that contains appropriate habitat. To account for possible non-random distributions we also assessed the probability of a species being entirely absent in a protected area by calculating the probability of its absence in an inventory plot. This results in a conservative underestimate of the probability of a species being represented in a protected area because sample plots are much smaller than protected areas. However, for relatively common species this underestimate may not be large.

## 2.3. Evaluation of protected areas

To qualify as a high priority genetic reserve, a protected area should contain populations that are not well protected elsewhere, and preferably protect several species simultaneously. For all 800 reserves included in this analysis, we calculated a score that reflected these values by giving a value of one unit to a reserve for each species that had an expected population size of 5000 individuals or more in this reserve. Then the value for each species was divided by the number of times it was also represented in another reserve (plus unity in the denominator). For example, for a reserve that contained species A, B, and C, where

species A was only represented in this location, species B was found in one other reserve and species C was found in nine other reserves the score would be  $1/1 + 1/2 + 1/10 = 1.6$ .

We also evaluated reserves for the need for ground truthing using a similar procedure. If ground truthing is necessary to confirm that a species is adequately protected, one should first visit the reserves that have the highest probability of containing the species, and one should start with species that are least protected. Therefore we only included populations in the ranking procedure that were not adequately protected, and then divided the probability of the reserve of containing a population size 5000 individuals or more by the number of times the species may also be found in other locations (i.e. expected population size of 5000 individuals) in other reserves (plus unity in the denominator). For example, for a reserve that contained species A and B, where species A was only represented in this location with a probability 0.68 and species B with a probability of 0.82 in this reserve and occurs in one other reserve, the score would be  $0.68/1 + 0.82 = 1.09$ . If a species has a probability below 0.5 of having 5000 individuals, it is not included in the denominator.

### 3. Results and discussion

Of a total land base of 94 million hectares in British Columbia, protected areas cover approximately 10 million hectares (11%). Approximately 800 protected areas are included in this study. However, about half of those are less than 100 ha in size. There are about 250 medium sized reserves (100–1000 ha) and another 150 protected areas are large (up to 100,000 ha). Another 17 protected areas exceed this number with sizes of up to 1 million hectares. These very large reserves account for approximately one third of the total protected area.

#### 3.1. Representation of species and populations in protected areas

At the species level, all but two species are represented in protected areas at the expected level of approximately 11% (Fig. 2). The coastal species yellow-cedar (Yc, *Chamaecyparis nootkatensis* (D.

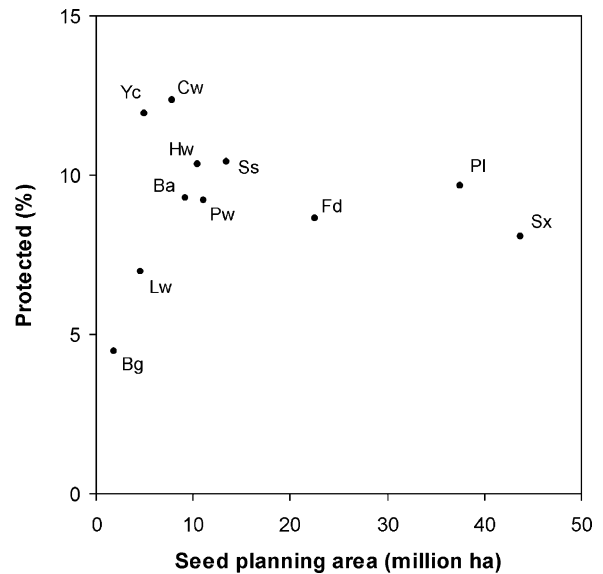


Fig. 2. Proportional representation of 11 major commercial conifer species in protected areas as a function of the seed planning unit size. Only the portion of the species range that falls into seed planning zones has been analysed. Refer to Fig. 3 for species codes.

Don) Spach), western redcedar (Cw, *Thuja plicata* Donn ex D. Don), western hemlock (Hw, *Tsuga heterophylla* (Raf.) Sarg.), amabilis fir (Ba, *Abies amabilis* (Dougl. ex Loud.) Dougl. ex Forbes) and Sitka spruce (Ss, *Picea sitchensis* (Bong.) Carr. and Sxs, *P. sitchensis* × *glauca* Little) have the highest level of *in situ* protection. These species have natural ranges covering the entire coast of British Columbia which is generally well represented in protected areas. However, grand fir (Bg, *Abies grandis* (Dougl. ex D. Don) Lindl.) with a very small distribution in drier areas of the most southwestern portion of the coast shows less than half the expected level of protection compared to provincial averages. This region is heavily populated and lacks protected areas. Widespread species that have the majority of their range in the interior of British Columbia such as interior spruce (Sx, including *Picea glauca* (Moench) Voss, *P. engelmannii* Parry ex Engelmann, and hybrids), lodgepole pine (Code PI, *Pinus contorta* var. *latifolia* Engelmann ex S. Watson), and Douglas-fir (Fd, *Pseudotsuga menziesii* var. *menziesii* (Mirbel) Franko and *P. menziesii* var. *glauca* (Beissner) Franko), and with a smaller, more southern range western white pine (Pw, *Pinus monticola* Dougl. ex D. Don) show a level



of protection slightly lower than the expected 11%. The only species covered in this study with a range exclusively in the southern interior portion of British Columbia, western larch (Code Lw, *Larix occidentalis* Nutt.), exhibits the second lowest level of protection.

Fig. 3 provides a comprehensive summary of the *in situ* conservation status at the population (i.e. seed planning unit, SPU) level. These charts are drawn to scale, so that the area of a slice of a pie chart (extrapolated to the center of the circle) is proportional to the total size of the SPU. The inner circle indicates the relative representation in protected areas with the number of protected areas >250 ha indicated by the inner legend. In order to interpret the more complicated diagrams start at the 12 o'clock position and follow the legends clockwise or counter-clockwise using the shading as an aid. For example, the first SPU (BV h) in the first diagram shows interior spruce (Sx) is very well represented by three large protected areas (approximately three to four times the expected area for this species). Another example for a similar sized SPU is the first unit (CT a) in the diagram for Douglas-fir (Fd) below. This seed planning unit is considerably under-represented in protected areas for its size although it contains three protected areas >250 ha. Under the assumption that a single protected area >250 ha contains a sufficiently large population size of a particular species to maintain genetic diversity, no SPU lacks protection entirely (regional and elevational overlap zones excluded). However, a number of SPUs are represented by only a few protected areas, and because of non-random spatial distribution of a species, temporal stochasticity of population size, or disturbance dynamics, a single protected area may not be an adequate genetic reserve forest by chance.

In order to better assess the status and redundancy of *in situ* protection of genetic resources in SPUs, we add information from forest inventory data to the spatial analysis. Population densities vary among both species and regions but typically range from 50 to 100 mature-equivalent stems/ha with a dbh >30 cm for all but four species: western hemlock and amabilis fir usually have densities of 100–200 stems/ha and grand fir and white pine have approximately 20 stems/ha. Therefore, the minimum size of protected areas that can be expected to contain at least 5000 mature-equivalent individuals varies among species and regions from approximately 25 to 250 ha. Although

these estimates are statistically precise with standard errors often approaching zero because of the large sample size, the coefficients of variation are quite large (usually between 0.6 and 0.8) reflecting the natural variation in population density for these species. In addition, the probability of a species being present in a reserve (based on presence in sample plots) varies from around 0.15 for the less frequent species western larch, grand fir, and white pine to around 0.75 for the most common one, western hemlock. The status of *in situ* protection based on these estimates for each individual population in each reserve is summarised in Table 1, where we calculated the overall probability of each SPU being adequately covered by at least one, three, five or ten reserves. Depending on the level of protection desired, not all populations of all species may be adequately covered. If the desired level of protection is, for example, at least three protected areas per population with a confidence level of 95% that each reserve contains at least 5000 individuals, then 15 populations of western larch, Douglas-fir, lodgepole pine, grand fir, and interior spruce require further investigation (Table 1).

Table 1

Seed planning units that have the least degree of *in situ* representation, ranked by the probability of containing at least one, three, five, or ten reserves with more than 5000 mature-equivalent individuals (contact the authors for a full listing)

SPU	Rank	Probability			
		1	3	5	10
PI NS h	1	0.41	0	0	0
Sx BV h	2	0.63	0.06	0	0
Fdi CT a	3	0.67	0.08	<0.01	0
Sx PR h	4	0.88	0.35	0.03	0
Lw EK a	5	0.90	0.39	0.06	<0.01
Lw NE h	6	0.93	0.51	0.12	<0.01
Sxs NS a	7	0.95	0.54	0.10	0
PI PR h	8	0.96	0.56	0.13	<0.01
PI EK h	9	0.98	0.63	0.20	<0.01
PI NS l	10	0.98	0.69	0.23	<0.01
Bg M l	11	0.98	0.75	0.34	<0.01
PI BV h	12	0.99	0.76	0.32	<0.01
PI EK l	13	>0.99	0.88	0.53	0.01
Pw KQ a	14	0.99	0.89	0.58	0.03
Sx BV l	15	>0.99	0.92	0.60	0.01
⋮	⋮	⋮	⋮	⋮	⋮
PI TO h	25	>0.99	0.99	0.89	0.17
⋮	⋮	⋮	⋮	⋮	⋮
Fd M l	50	>0.99	>0.99	>0.99	>0.99

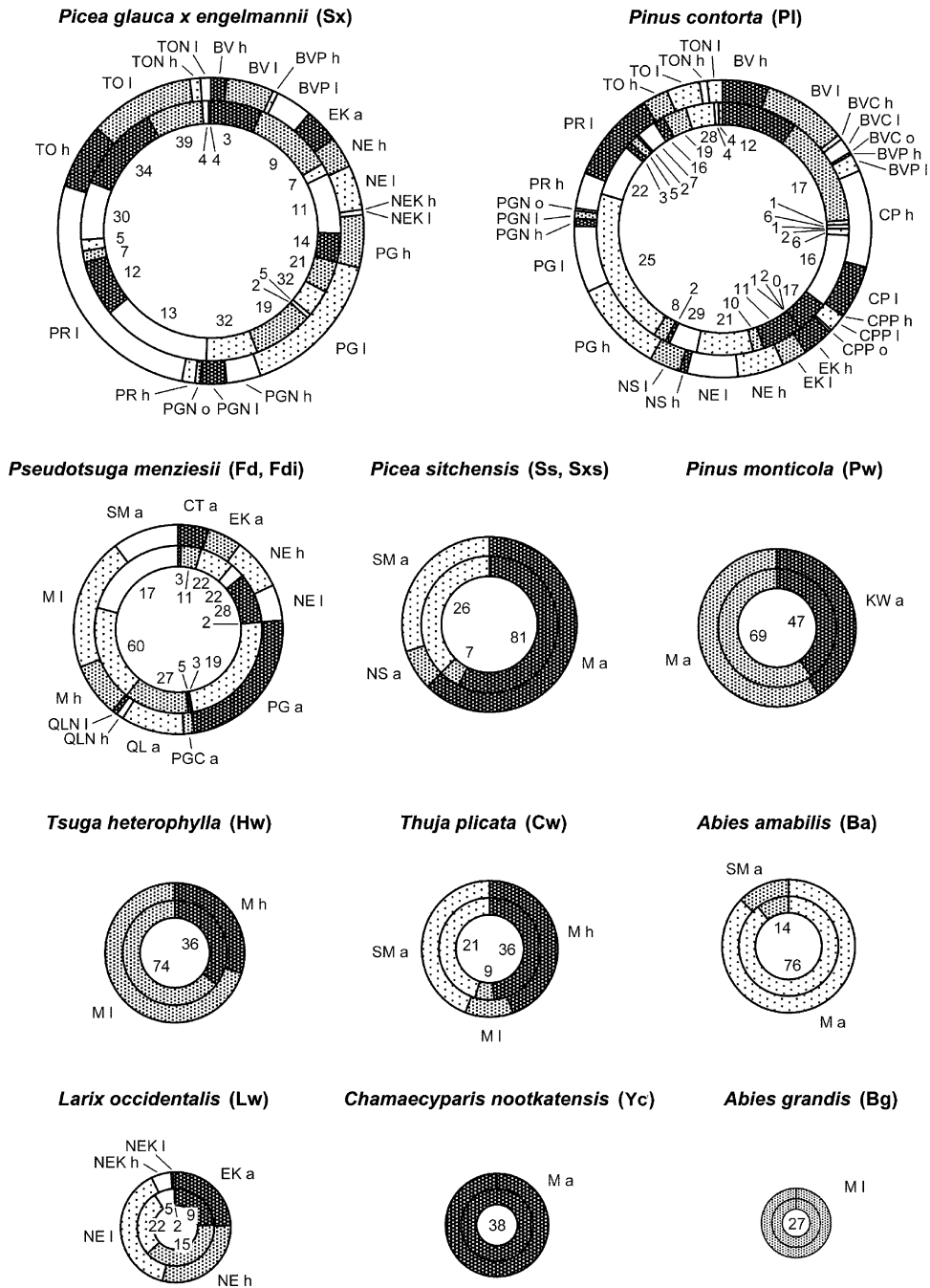


Fig. 3. Representation of conifer populations in protected areas. The outer circle is equivalent to the total size of seed planning units (circles are drawn to scale; SPU codes are indicated by the legend). The inner circle shows the proportional representation of protected areas (the number of protected areas >250 ha is indicated by the legend). To match total and protected areas, start at the 12 o'clock position and follow legends clockwise or counter-clockwise using the shading as an aid.

### 3.2. Evaluation of protected areas and ground truthing

The large differences in current *in situ* protection status that we observed among different SPUs implies that individual reserves are not equally important from a gene conservation perspective. In Table 2 we ranked reserves based on the number of populations they cover and their redundancy. The most important reserves are predictably the very large protected areas, 10,000 to 1 million hectares in size, which typically include a wide range of ecosystems. The top 25 reserves rank high because they contain at least one population that is not (or not often) covered elsewhere. They are followed by approximately 100 reserves that provide adequate protection for many species, but also have a high level of redundancy (e.g. Sugarbowl in Table 2). The remaining protected areas are usually small, redundant reserves that cover only a few populations adequately (e.g. Eagle River and Dionisio Point in Table 2). It should be noted that our scoring method implies a certain value for the degree of redundancy, for the number of populations in a reserve, and the value of redundancy relative to the

number of populations. The formula could be modified with coefficients and constants to alter these weights.

The potential lack of *in situ* protection that we identified in Table 1 does not necessarily imply that these populations are not adequately covered. It means that with the available data, a lack of protection cannot be excluded at a level of  $P < 0.05$  without visiting the reserves and confirming the presence of the populations or compiling this information from existing reserve inventories, if available. Using a similar ranking procedure as above, but only for the least protected SPUs listed in Table 1, we can generate a list of reserves where ground truthing should be carried out to clarify the population size and status of protection in these cases (Table 3). Protected areas are listed in the order of the highest to lowest probability of containing at least 5000 individuals. The complete Tables 1 and 2 can be obtained from the authors. These listings give the forest manager more flexibility in deciding the level of redundancy required (e.g. one reserve for small seed planning units and five for larger ones) and the possibility to find all potential reserves for all SPUs.

Table 2

Examples of protected areas in the order of importance from a gene conservation perspective, reflecting number of populations covered and redundancy of populations in other reserves (contact the authors for a full listing)

Rank	Protected area name	Area (ha)	Score <sup>a</sup>	Seed planning units covered in the reserve
1	Tweedsmuir	990448	0.74	Ba SM a, Cw M 1, Cw SM a, Fd SM a, PI BV h, PI BV 1, Sx BV h, Sx BV 1, Sx BVP h, Sx BVP 1, Sxs SM a, Sx TO h, Sx TO 1
2	Swan Lake–Kispiox	62360	0.69	PI NS h, PI NS 1, Sxs NS a
3	Glacier National Park	135828	0.55	Fdi EK a, Fdi NE h, Fdi NE 1, Lw EK a, Lw NEK h, PI EK h, PI EK 1, PI NE h, PI NE 1, Pw KQ a, Sx EK a, Sx NE h, Sx NE 1
4	Purcell Wilderness Cons.	198071	0.53	PI EK h, Sx EK a, Fdi EK a, Fdi NE h, Fdi NE 1, Lw EK a, Lw NE h, Lw NE 1, PI EK h, PI EK 1, PI NE h, PI NE 1, Pw KQ a, Sx EK a, Sx NE h
5	Sustut	75687	0.50	PI BV h, PI BV 1, PI BVC h, PI BVC 1, PI BVC o, PI CP h, PI CP 1, Sx BV h, Sx BV 1
⋮	⋮	⋮	⋮	⋮
10	Kakwa	170893	0.36	Fdi PG a, PI PG h, PI PG 1, PI PR h, Sx PG h, Sx PG 1, Sx PGN h, Sx PR h, Sx PR 1
⋮	⋮	⋮	⋮	⋮
50	Sugarbowl	20319	0.20	Fdi PG a, Fdi QL a, PI CP 1, PI PG h, PI PG 1, Sx PG h, Sx PG 1
⋮	⋮	⋮	⋮	⋮
250	Eagle River	396	0.07	Fdi NE 1, Lw NE 1, PI NE 1, Sx NE 1
⋮	⋮	⋮	⋮	⋮
500	Dionisio Point	151	0.02	Ba M a, Fd M 1, Hw M 1

<sup>a</sup> Sum of the number of populations covered divided by their respective redundancy in other protected areas.



Table 3  
Reserves where ground truthing should be carried out to confirm that they contain at least 5000 mature-equivalent individuals

Seed planning unit	Protected areas (in order of most to least likely to be adequate)
PI NS h	Damdochax, Swan Lake, Kispiox River
Sx BV h	Sustut, Tweedsmuir, Babine Mountains
Fdi CT a	Taweel, Emar Lakes, Schoolhouse Lake Park, Green Lake, Ruth Lake
Sx PR h	Kakwa, Graham Laurier, Wapiti Lake, Butler Ridge, Gwillim Lake, Pink Mountain, Northern Rocky Mountains
Lw EK a	Purcell Wilderness Conservancy, Glacier National Park, Height of the Rockies, Kootenay, Yoho, Ram Creek, Akamina-Kishinena, Columbia Lake, Mount Fernie, Premier Lake, Whiteswan Lake, Windermere Lake, Crowsnest, Elk Valley, Norbury Lake, Cummins Lakes
Lw NE h	Purcell Wilderness Conservancy, Gladstone, Silver Star, Granby, Lockhart Creek, Kalamalka Lake, Graystokes, Goat Range, Greenbush-Caribou, Lew Creek, Monashee, Syringa, Valhalla, West Arm, Kokanee Glacier, Englishman River, Kingfisher Creek, Stagleap

Only the least protected seed planning units are included (refer to electronic Appendix 1 for a full list).

### 3.3. Changes of *in situ* conservation status between 1991 and 2001

A comparison of the current *in situ* protection status of genetic resources with their status 10 years ago reveals that the complete coverage of all populations and all species that we have today is

largely the result of a major initiative to achieve satisfactory representation of biological diversity, unique natural environments, and different ecosystems in protected areas over the last decade (Land Use Coordination Office, 1992). This “coarse filter” or “landscape level” approach to conservation appears to be effective to protect the underlying genetic diversity of species as far as it is revealed in provenance tests and reflected in SPUs. No population currently lacks protection entirely, whereas in 1991 genetic resources in one SPU were not protected areas at all. The 10 least protected seed planning units (excluding the one without protection), had an increase of protected area by a factor of 22 since 1991 (Fig. 4, lower left). In contrast, the level of protection increased by a factor of only 1.5 for the 10 most protected SPUs since 1991 (Fig. 4, upper right), while the total protected area has doubled. Using another statistic to evaluate this change: of the 50 protected areas that are most important from a gene conservation perspective (Table 2), only 11 existed prior to 1991. It should be noted that protection of genetic resources was not a direct objective when delineating protected areas. However, because representation of different ecosystem types was considered in the selection of new reserves, and both genetic and ecological differentiation occurs predominantly along climatic gradients, protection of genetic resources improved significantly with the additional protected areas. For other values, the result of this initiative may be even more noteworthy.

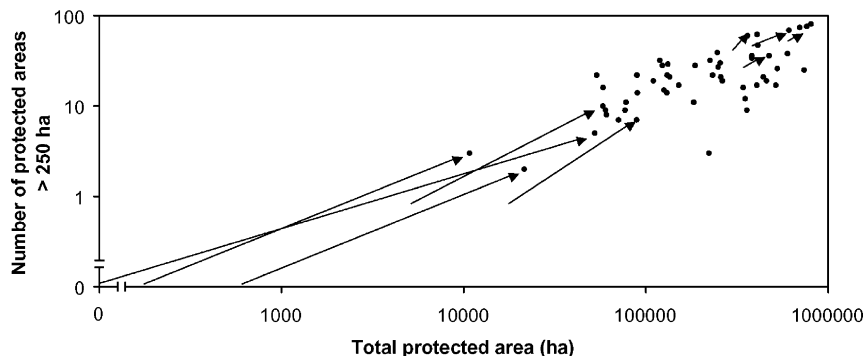


Fig. 4. Change of the status of *in situ* protection of conifer populations from 1991 to 2001. Circles represent the 2001 status for 11 species in each seed planning unit (overlap zones excluded). Arrows indicate the change from 1991 for the five least protected (lower left), and some well protected (upper right) populations.

#### 4. Conclusions

Due to a systematic expansion of protected areas in British Columbia in the 1990s, it appears that conifer genetic resources are now well represented in protected areas. The landscape level approach to conservation of this initiative appears to have covered the underlying genetic diversity of species as far as it is revealed in genetic tests and reflected in seed planning units. We identified four species where gaps cannot be excluded using current data: most populations of western larch, and some populations of Douglas-fir, lodgepole pine, and interior spruce. In particular, the seed planning units Fd CT a, Lw NE a, and Lw EK h need attention because although they are large in size they may not be adequately protected. We present new methodology to clarify conservation status of populations and prioritise reserves for ground truthing. Genetic resources of two other species, grand fir and white pine appear to be reasonably well represented in protected areas although they are relatively infrequent and their range coincides with heavily populated areas. It should be noted, however, that some populations, such as the interior distribution of grand fir, are not covered in this analysis because in this region the species is not under intensive forest management. The conclusions of this study apply to genetic resources of species that are of current commercial interest and for which genetic data is available. A similar investigation covering all populations of all 50 tree species native to British Columbia using ecological classification instead of seed planning zones is underway.

#### Acknowledgements

This study was conducted under the auspices of the Forest Genetics Council of BC and funded through Forest Renewal BC and the Forest Investment Account of BC. We thank Del Meidinger for providing data from the provincial ecology program and Alf Kivari for extracting information from the forest inventory planning database. Help in planning this study, provision of GIS data, and review of the manuscript by Leslie McAuley and Ron Planden is gratefully acknowledged.

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