Indigenous-Tree Genetic Conservation in British Columbia

A Plan Prepared by the Genetic Conservation

Technical Advisory Committee

for the Forest Genetic Council

of British Columbia

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with review and input by GCTAC members

Definition of Genetic Conservation
The conservation of forest-tree genetic resources is the combination of actions and policies that maintain the genetic structure and diversity of tree species and support the continued evolutionary potential and availability of a broad genetic resource to provide environmental services and economic value for present and future generations.

FGC

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1.0 Introduction

The genetic resource of forest trees is a fundamental element of all forest values, and the conservation of their genetic diversity supports continued adaptation, evolution and use for economic purposes.

For this reason, the Strategic Plan[1] of the Forest Genetics Council of BC (FGC) states that the conservation and management of the genetic pool of forest tree species is fundamental to all activities concerned with the use of forests, including ecological services and the long-term viability of a commercial forest industry.

At the request of the Forest Genetics Council of BC, the Genetic Conservation Technical Advisory Committee (GCTAC) has prepared this report outlining the knowledge needs, structural elements, and resourcing required for a comprehensive forest-tree genetic conservation program in British Columbia.

2.0 Background

2.1 GCTAC Mandate

At it's March 14th, 2007 meeting, the FGC approved the following mandate for the GCTAC:

- provide guidance and recommendations to the FGC on genetic conservation issues for indigenous forest trees, including conservation issues associated with climate change
- Lead the development of genetic conservation strategies and programs
- Provide business planning direction to the UBC Centre for Forest Genetic Conservation (CFGC) and review reports
- Recommend genetic conservation project budgets to the FGC, including the CFGC annual budget.
- Bring together a wide range of expertise to address genetic conservation issues
- Develop applied genetic conservation measures
- Provide leadership in the promotion of scientific discourse, extension, and education on genetic conservation issues

Note: These mandate points have been modified by the committee from those provided by Council to increase clarity. There have been no intentional additions or deletions.

2.2 FGC request for a genetic conservation plan

At its December 13, 2006 meeting, the FGC asked the GCTAC to develop a plan that would address the following points:

- clearly define genetic conservation
- clearly articulate conservation objectives
- suggest a performance measure(s) for genetic conservation
- re-define the structure and delivery of the genetic conservation program, including responsibilities

[1] *FGC Strategic Plan 2004-2008*

2.3 Existing provincial genetic conservation programs

2.3.1 UBC Center for Forest Genetic Conservation

The UBC Center for Forest Genetic Conservation was initiated in 2000 by the FGC, with input from UBC and MFR staff. The original mandate for the CFGC was two-fold; to develop and maintain a catalogue of the *in situ* and *ex situ* genetic resource for indigenous forest tree species, and to undertake research on conservation strategies and issues. Since this time, the Center has developed a comprehensive gap analysis and catalogue of the genetic resource for all 49 tree species indigenous to British Columbia, added substantially to the knowledge base for conservation strategies, and undertaken research on conservation issues for seven indigenous species. This work has greatly advanced the knowledge base and strategic approach to genetic conservation, given focus to conservation efforts, and provided the information needed to confidently proceed with other program components directed at increasing timber supply through the use of select seed, with confidence that the conservation status of key commercial species is not threatened.

2.3.2 Ministry of Forests and Range

MFR genetic conservation efforts began with a preliminary gap analysis (Yanchuk and Lester 1996) that led to more comprehensive cataloguing work by the CFGC. The MFR has also provided extensive technical support for all facets of existing conservation efforts, a very substantial amount of genecology research that provides the basis for the portion of conservation cataloguing that is based on seed planning units for economically important species, *ex* situ seed collections, and development of conservation frameworks and management plans for key *inter situ*[2] populations. In addition, MFR staff have been instrumental in their contributions to strategy development.

Under the Forest and Range Practices Act (FRPA), the Chief Forester of the MFR has established standards governing the use of tree seed for Crown land reforestation. These standards include minimum genetic diversity requirements for seedlots and vegetative lots collected from wild stands and tested parent trees. ..

The Forest and Range Evaluation Program (FREP) assesses the effectiveness of various forest management activities and policies in achieving stewardship of the eleven resource values identified in FRPA. These values include Timber and Biodiversity. Indicators for tree species and genetic diversity are being developed under the Timber value. Stand and landscape level diversity are being assessed under the Biodiversity value. Therefore, the genetic diversity of indigenous tree species is a subset of these broader MFR initiatives.

2.3.3 Other agencies

The BC Ministry of Environment (MOE) has within it's mandate the preservation of biological diversity and representative ecosystems. The existing network of parks and ecological reserves are designed to conserve a comprehensive sample of native ecosystems, and to restrict resource consumption within these areas. The MOE maintains lists and rankings of species at risk (red and blue listed).

The Conservation Data Centre (CDC) is part of the Environmental Stewardship Division of the MOE and NatureServe, an international organization of cooperating

[2] *Inter-situ* genetic conservation resources refers to breeding and genecology populations established in progeny tests, provenance tests, and clonebanks.

Conservation Data Centres and Natural Heritage Programs. The CDC's mandate is to systematically collect and disseminate information on plants, animals and ecosystems (ecological communities) at risk in British Columbia.

Key point

Specific genetic conservation activities are not currently carried out by any government agencies or conservation organizations.

The mandate of the MOE includes the hierarchical preservation of landscapes, ecosystems, and species. The preservation of genetic diversity within species is contained within this broad mandate, and, although not specifically mentioned, is captured through the preservation of representative ecosystems. Therefore, the genetic conservation of indigenous forest tree species is a subset of the broader conservation objectives of the MOE. Specific conservation activities and cataloguing of genetic diversity of tree species is not undertaken by the MOE or any other provincial government agency.

Non-governmental organizations such as The Nature Trust of British Columbia and The Land Conservancy acquire private land through purchase or donation, and hold this land in a natural state for conservation purposes. There are no activities directly related to the genetic conservation of forest tree species, but these lands are reserve areas that effectively conserve genetic resources in a similar manner to parks and ecological reserves.

Federal programs also contribute to provincial genetic conservation objectives. The Federal government's Species at Risk Act (SARA) is intended to protect and recover endangered and threatened species and species of concern. Parks Canada also has a mandate to protect natural environments representative of Canada's natural heritage, and manages five National Parks within BC. Parks Canada is currently giving consideration to listing whitebark pine as a species of concern.

The federal government reports out on national progress in sustainable forest management using the (CCFM) Canadian Criteria and Indicators Framework for Sustainable Forest Management. The status of *in situ* and *ex situ* conservation efforts for native tree species within each ecozone is a core indicator of genetic diversity within this framework. The MFR contributes information to this report.

3.0 Scope and definition

3.1 Definition of genetic conservation

The following definition is specific to indigenous forest tree species in British Columbia within the context of this report. It is intended to serve as a basis for program development and monitoring.

The conservation of forest-tree genetic resources is the combination of actions and policies that maintain the genetic structure and diversity of tree species and support the continued evolutionary potential and availability of a broad genetic resource to provide environmental services and economic value for present and future generations

3.2 Species

It is recommended that a provincial genetic conservation program cover all indigenous British Columbia trees, including 23 coniferous and 26 broadleaved species (Appendix 1). The Forest Genetics Council of BC's Tree Improvement Program only supports tree improvement activities for commercial tree species in geographic areas in which they are economically important. However, the genetic conservation program should, at a minimum, catalogue protection for all 49 tree species for the following reasons:

Key point

This recommendation covers all 49 tree species indigenous to British Columbia.

- some species that are not economically important at present may become much more important in British Columbia given climate change (e.g., those species with their northern range limit in southern BC; and many broadleaves; see Hamann and Wang 2006);
- some boreal and subboreal species may become much less important economically over time;
- the environmental services provided by BC's forests are not only provided by those tree species of current economic importance; e.g., many broadleaves are of more critical importance in providing food and habitat for bird species than commercially important conifers;
- new forest products may be developed based on fiber or chemical resources from tree species currently considered economically unimportant (e.g., Pacific yew, *Taxus brevifolia,* and discovery of Taxol); and
- there is no other group or agency in the province addressing genetic conservation issues related to indigenous tree species.

Ten indigenous conifer species are utilized in breeding programs and four more are under provenance testing. The nine remaining conifers are rare, have minimal commercial value, or have a small portion of their range in BC. Of the broadleaved species, only *Alnus rubra, Acer macrophyllum* and *Populus tremuloides* are used on a scalt that approaches commercial forestry, although others play a key role in ecological restoration work. A few broadleaved species are represented in provenance trails, but our understanding of intraspecific variation and population dynamics in broadleaved species is limited compared to our knowledge of the primary commercial indigenous conifers.

3.3 Geographic area

This report covers all forested land in British Columbia.

3.4 Technical depth

The focus of genetic conservation efforts recommended in this report will be on understanding, cataloguing, and conserving genetic variation within species as one of four components of biodiversity (species, ecosystem and landscape being the other three). In addition, the development of efficient strategies for conservation will be a research focus to ensure science-based actions and effective use of resources.

Advances in biotechnology will provide tools that increase the efficiency of conservation research, and improve our understanding of population behavior and population genetics. These technologies will be incorporated as needed and when they offer techniques that have value in this conservation program.

3.5 Genetic restoration activities

Activities to restore key *in situ* populations are expected to become necessary from time to time. An outcome of the program described in this report will be the identification of restoration needs and the development of efficient strategies for implementing restoration work. However, it is not intended that this program would directly undertake significant restoration work, including activities such as large-scale planting of key genotypes or silvicultural activities (such as burning to encourage natural regeneration). The planning and development of restoration activities may be part of this program, however.

4.0 Key elements of a genetic conservation program

Key point

Scientific knowledge of species genecology and population genetics can be used to determine the number and distribution of *in situ* reserves or *ex situ* collections needed to capture most of the adaptive or selectively neutral variation present in a species

Key point

The number of populations that need to be conserved to effectively capture and perpetuate current levels of genetic diversity in a species depends on the degree of genetic differentiation of populations.

4.1 Technical elements[3]

4.1.1 Science-based knowledge of genetic diversity patterns

The amount of intraspecific genetic variation a species contains, and the distribution of that variation among and within populations, varies as a result of a myriad of factors including glacial and post-glacial history, population size and density, degree of local adaptation, dispersal capability of seeds and pollen, and mating system. Scientific knowledge of species genecology and population genetics can be used to determine the number and distribution of *in situ* reserves or *ex situ* collections needed to capture most of the adaptive or selectively neutral variation present in a species.

4.1.2 Population and quantitative genetics theory on efficient strategies

The fields of population and quantitative genetics have provided robust theories on the maintenance of adaptive and selectively neutral genetic diversity within finite populations based on population size, gains in genetic variants (alleles) due to mutation, losses of alleles due to the random process of genetic drift or the directional process of selection, and the roles of gene flow and selection in the maintenance of variation within populations. From these theories, the effective population size that will maintain genetic diversity for polygenic adaptive traits indefinitely (i.e., over many generations in isolation from other populations) can be estimated.

The number of populations that need to be conserved to effectively capture and perpetuate current levels of genetic diversity in a species depends on the degree of genetic differentiation of populations, that is, the degree of genetic redundancy or gene flow between populations (Crandall et al. 2000). This principle, through the use of population and quantitative genetics, can guide decisions on efficient conservation strategies for individual species.

4.1.3 Genetic resource catalogue and indicators

The genetic theories and principals outlined in 4.1.2 above have been used to develop conservation thresholds for maintaining the genetic diversity of tree species in BC. These thresholds have been used to develop a catalogue of the genetic resources of the 49 indigenous trees species, with the goal of having at least three *in situ* conservation populations with census sizes of mature individuals (or their equivalent in more, younger trees occupying the same amount of habitat) of at least 5,000 individuals per seed planning unit (SPU) or per BEC zone (Hamann et al. 2004, 2005). Where insufficient conservation populations exist, a gap is identified.

This approach assumes that SPUs and BEC zones provide a spatial reference for environmental variation that is likely to correspond to population differences in adaptation to climate. SPU boundaries are in some cases based on species-specific provenance data, thus likely provide a reasonable indication of the geographic scale across which adaptive differentiation is biologically significant. Multiple *in situ* reserves per SPU or BEC zone provide redundancy against catastrophic loss of populations, and *ex situ* seed collections provide insurance against loss of *in situ* resources, as well as providing an important mechanism of conserving genetic material where additional *in situ* protection is unlikely to develop in the short term under the provincial Protected Areas Strategy.

[3] See Appendix 2 for a more detailed technical discussion.

4.2 Records, resourcing, and administrative continuity

4.2.1 Why continuity matters

Key Point

Genetic conservation will build in value and complexity over time, requiring program continuity to build staff expertise

The size and complexity of the genetic resource requires cataloguing and ongoing conservation activities that operate in synchrony with other land-management programs. Actions and records associated with genetic conservation will build in value and complexity over time, and will require continuity to develop and hold expertise and staff. An ongoing conservation program will facilitate linkages to other genetic resource management activities, and to operations such as timber supply planning, provincial and national parks, ecological reserves, and forest management and harvesting. In the absence of continuity, staff expertise will not develop, conservation activities will be sporadic, and efforts will be driven by individuals promoting localized projects and protection of charismatic species, rather than by a broader and more efficient organized strategy with well-defined priorities.

4.2.2 Linkage to other data bases

Forest operations are increasingly reliant upon and linked to databases and complex information management systems. Genetic conservation databases and programs should be connected to systems such as SPAR[4], SeedMap, forest inventories, and other data bases such as that maintained by the Conservation Data Centre. These linkages will allow the effort and resources to be leveraged against other programs, and will better support forest management operations.

A high priority must be given to linkages with existing data systems, and to genetic-conservation information retrieval through these systems. For example, SeedMap could have a layer available that would show reserve areas that contain genetic resources as summarized in the catalogue process.

In addition, linkage to the national conservation initiative, CONFORGEN, and to the conservation data base CAFGRIS are important connections to broader pan-Canadian programs. Although CONFORGEN is in an early development stage, it is expected that the organization will eventually be responsible for providing data to the Canadian Council of Forest Ministers (CCFM) Canadian Criteria and Indicators Framework.

4.2.3 Human-resource development and maintenance

The highly technical nature of genetic conservation requires human resources with skills ranging from population and conservation genetics to forest operations, data-base management, and geographic information systems. Individuals with these skills are not readily available, requiring development over time, program stability to allow effective staff recruitment, and the building of expertise.

Human resource development is best accomplished through a combination of undergraduate and graduate training, and progressive work at the research and operational level. The CFGC provides high quality opportunities for graduate-level training at UBC in forest conservation genetics. Students trained through the Centre will contribute through their research, and will provide a pool of skilled individuals who can carry their experience to positions in government and industry within BC.

[4] Seed Planning and Registration System

5.0 Linkage to provincial government objectives and Chief Forester vision

5.1 Great goals

Key point

Forest tree genetic conservation is an element of the Provincial Chief Forester's stewardship vision

The Forest Genetics Council advises the Provincial Chief Forester on programs and policies related to forest genetic resource management. The Chief Forester, and the FGC are also influenced by higher level government goals, as shown in figure 1, and summarized below:

> ***BC Government Goal:***
> *To lead the world in sustainable environmental management, with the best air and water quality, and the best fisheries management, bar none.*

This has led to a set of objectives, legislation and programs to meet this goal, including;

> ***Ministry for Forests and Range Mission:***
> *To protect, manage, and conserve forest and range values through a high performing organization.*
>
> ***Chief Forester's Stewardship Vision:***
> *British Columbia is widely respected as a leader in the management of natural forest and range landscapes to maintain diverse values and an array of products that are valued in the marketplace.*

Within this vision the primary objective is "Exemplary stewardship of forest resources", and the following four strategies are aimed at achieving this objective.

- Collaboratively evaluate, improve, and manage the forest policy framework
- Adapt forest stewardship policy and practices to changing social and environmental conditions
- Apply up-to-date and accurate forest information, and best research and analysis to inform decision-makers and the public
- Develop and implement programs to restore, maintain and enhance forest resource values.

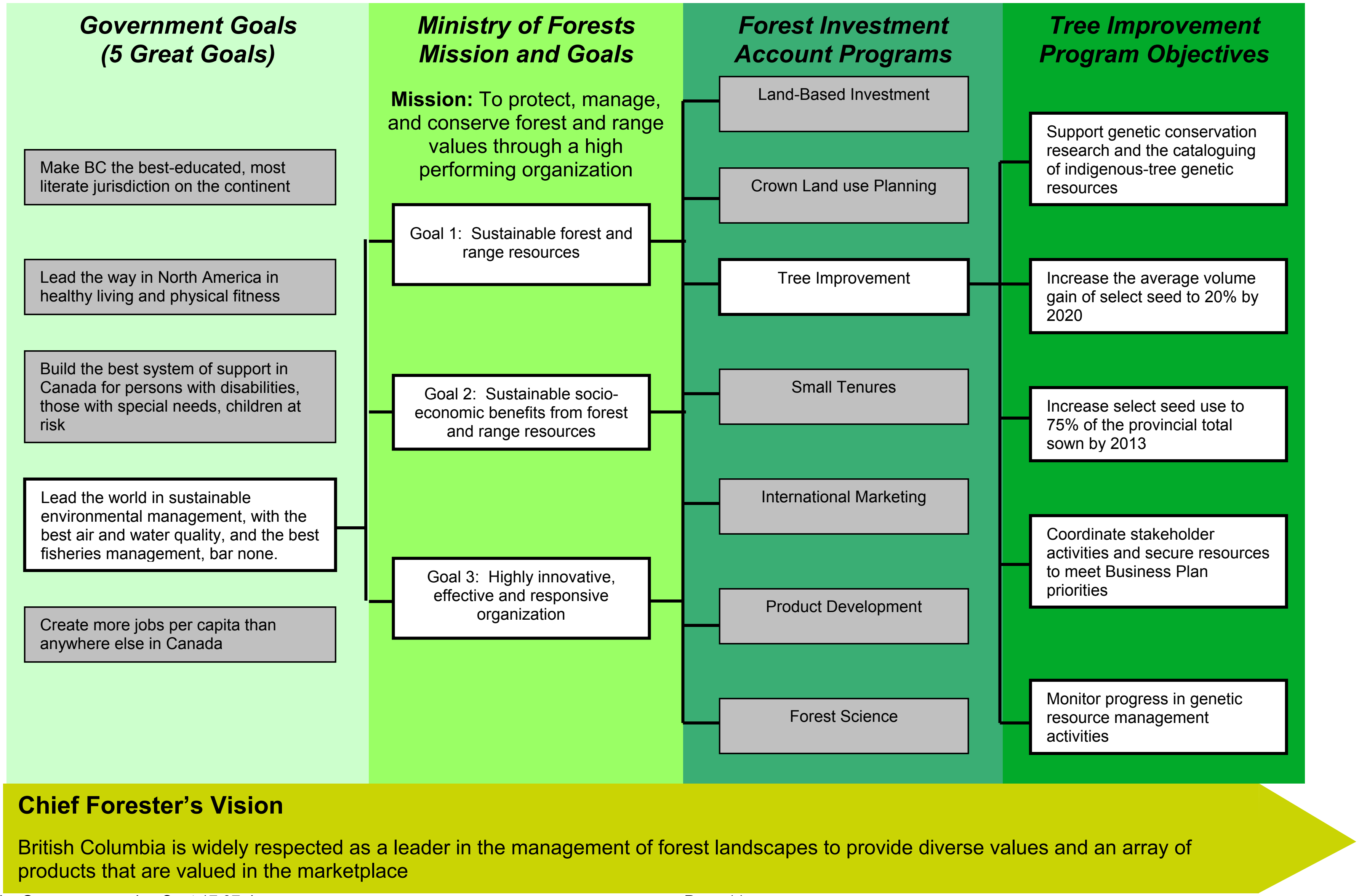
All of these strategies include genetic resource management as a Chief Forester responsibility.

The Chief Forester Stewardship Vision contains three components a) Policy and Strategic Planning; b) Operational Planning & Management; and c) Knowledge Monitoring and Reporting. The Elements, Current Emphasis and Gaps/Opportunities of these three components in relation to genetic conservation issues are presented in Table 1.

Table 1. The elements, current emphasis and gaps/opportunities of the Chief Forester's stewardship vision in relation to genetic conservation.

	Elements	Current Emphasis	Gaps / Opportunities
Policy & Strategic Planning	▪ Forest practices legislation ▪ Forest Resource analysis ▪ Land use planning ▪ Genetic resources and seed strategies	▪ Future Forests Ecosystem initiative ▪ Climate change strategies ▪ National initiatives (i.e. Can. Council of Forest Ministers)	▪ Gene resource management strategy
Operational Planning & Management	▪ FGC-led program ▪ MFR policy development ▪ MFR and industry seed orchards	▪ Cataloguing of indigenous BC tree species	▪ Climate change adaptation strategies and practices ▪ Coordinated extension, training and continuing education
Knowledge Monitoring & Reporting	▪ Resources inventory ▪ Criteria and indicators framework ▪ State of the forest Reporting	▪ Capture outstanding land base information ▪ Operational implementation of FREP (Forest Resource Evaluation Program)	▪ Incorporate long-term installations into validation monitoring

Figure 1: Relationship of Forest Genetics Council objectives to higher level provincial government programs and goals.



6.0 Current genetic conservation efforts

6.1 Research

Research relevant to the conservation of forest genetic diversity is conducted by many organizations including;

- the UBC Centre for Forest Genetic Conservtion (see research areas below),
- the Research Branch of the MFR (genecology, quantitative genetics, breeding, genetics of resistance to pests and pathogens, response to climate change),
- the Provincial Tree Seed Centre of the MFR (seed and seed storage-related research),
- other principal investigators at the University of British Columbia (population genetics, genomics, tree improvement-related, genetic diversity of seedlots), the University of Northern British Columbia (genecology, population differentiation at high elevations and northern treeline), and
- the Canadian Forestry Service (national genetic conservation strategy, *ex situ* storage of orthodox and recalcitrant species, genetics of resistance to pests and pathogens).

While there are many organizations involved in relevant research, this section will focus on the activities of the CFGC and the MFR funded through the FGC's Genetic Conservation Program.

Key point

The UBC CFGC conducts conservation research in:
1. methodology and standards,
2. distribution of genetic variation
3. impact of climate change, and
4. adaptive traits

The CFGC has conducted research in several areas since its initiation in 2000. The first is to continue the development of methodology and to develop standards for *in situ* conservation (Yanchuk and Lester 1996, Hamann et al. 2004, 2005). The second is to explore factors determining the distribution of genetic variation and rare alleles across species ranges, to evaluate genetic diversity in central versus peripheral, and continuous versus disjunct (isolated) populations, and to incorporate these findings into strategies for genetic conservation (Gapare and Aitken 2005, Gapare et al. 2005, Gapare et al. in press, Mimura and Aitken 2007a and 2007b).

The third research area that has been and continues to be a major focus of genetic conservation research for the CFGC is the potential impact of climate change for forest tree populations, and possible mitigation strategies in terms of population management. The model ClimateBC was developed by the CFGC to facilitate this research and is now being used for a wide range of other research and operational applications (Hamann and Wang 2005, Wang et al. 2006a). Projects have also been completed or are underway characterizing intraspecific variation in population response to temperature (Wang et al. 2006b, P. Smets, unpublished data). The future persistence of species in protected areas has also been evaluated based on bioclimatic envelope modeling (Hamann and Aitken, manuscript in prep.).

The fourth area involves generating knowledge about patterns of variation for both adaptive traits and genetic markers for 'special interest' species (see Category 2 under 5.1.3 above) that are under threat due to pests or pathogens, or habitat loss. Much of the research in this area has been conducted on whitebark pine genecology, population genetics, and mating system (*Pinus albicaulis*, Krakowski et al. 2003, Bower and Aitken 2006, 2007, and manuscripts in progress), but common gardens have also been established for Garry oak (*Quercus garryana*) and Pacific dogwood (*Cornus nuttallii*), and genetic marker studies are underway or planned for these species.

Some individuals in the CFGC are participating in a large project called Conifer Forest Health funded by Genome Canada and Genome BC (not funded by the FGC Genetic Conservation subprogram) to determine the genetic architecture of traits related to local adaptation to climate at a genomic level, i.e., what genes are involved, and to what extent do they vary in nucleotide sequence among phenotypically divergent populations. While none of this research is funded through the Forest Genetics Council programs, it will ultimately shed considerable light on the concepts of genetic exchangeability of populations and the ability of populations to adapt rapidly to climate change.

In the future, research area 1) above is likely to decline considerably as a research priority (once the technical report is completed this fiscal year), although it will remain important at an operational level. The other research areas described should continue to be active. There is a need to review and re-evaluate directions in research and to identify and prioritize new areas that warrant attention. A few examples of potential future areas of research include, but are by no means restricted to:

Key point

Forest management practices such as planting have the potential to be tool to facilitate the migration of genetic material in response to climate change.

1) **Landscape genetics**; We do not have a good understanding of the genetic dynamics at a landscape level among plantations, protected areas, and non-harvested parts of the forest matrix such as wildlife tree patches and riparian buffers. Questions such as whether planted forests could provide a source of pollen for 'facilitated gene flow' and resources for adaptation to new climates to natural populations require investigation. Landscape genetics may shed additional light on issues of *in situ* conservation and facilitated migration. Also, the potential to utilize forest management practices such as planting as a means of facilitating gene flow to accommodate climate change and maintain the natural adaptation of forest tree species needs additional research.
2) **Empirical testing of bioclimatic models, facilitated migration, and the role of genetics in adaptation to climate change;** In the area of climate change research, we have bioclimatic-envelope models that predict how the climates associated with species may change (Hamann and Wang 2006) but there is little empirical data about if and how species will move across wild or managed landscapes. Can we test or evaluate such models empirically? Can we establish experiments evaluating the potential for facilitated migration to expand species ranges?
3) **Conservation genomics;** As increasing numbers of genomic tools become available, how can these be better used to understand the dynamics of local adaptation?

6.2 *In situ* conservation

The network of conservation areas under the Protected Areas Strategy of BC covers 13% of the province, and provides the backbone for the conservation of forest genetic resources. These *in situ* reserves have been evaluated for the degree to which they capture representative populations of conifers in breeding programs by SPU (Hamann et al. 2004) and for all 49 tree species by BEC unit (Hamann et al. 2005). Details underpinning these published data and other information are being integrated into a large technical report on the extent of conservation of forest genetic resources in British Columbia. While most tree species are protected at levels well above the thresholds required for adequate *in situ* conservation, some gaps exist, particularly for species in the more highly populated areas of the province. Mechanisms need to be developed for addressing gaps in conservation, and for integrating information on conservation on private lands and in new provincial and federal protected areas not included in these analyses. Better linkages are needed with provincial and federal agencies and environmental non-governmental organizations (ENGO) engaged with the Protected Areas Strategy.

6.3 *Ex situ* conservation

Ex situ genetic conservation is the establishment of seed banks or clone banks for the purpose of maintaining a source of genetic diversity, and provide excellent insurance against catastrophic losses to *in situ* populations, as well as being an efficient mechanism of filling gaps in *in situ* reserves. The *ex situ* genetic resources of forest trees in BC are in the process of being evaluated and integrated into the overall conservation status of species by SPU or BEC zone, along with *in situ* and *ex situ* data. *Ex situ* collections exist at the Provincial Tree Seed Centre, and undocumented collections may reside with individual MFR Research Branch scientists. At this time, *ex situ* collections are primarily for commercially important conifers, and are problematic for recalcitrant[5] or intermediately recalcitrant species.

6.4 *Inter situ* conservation

Inter situ genetic resources comprise trees in provenance and progeny tests of known genetic origin and relatedness (Yanchuk 2001). In BC, there are >1000 field sites containing genetic tests established by the BC Ministry of Forests, but documentation and health of these tests is variable. Data are being summarized on the scope of genetic materials in these tests for integration with *in situ* and *ex situ* data. *Inter situ* genetic resources offer a third leg for 'dynamic' genetic conservation (Ericksson et al. 1993), as they provide more uniform environments with large populations to more easily identify new genotypes with unique or important traits, e.g., genotypes resistant to pests or pathogens. However, *inter situ* installations also require critical evaluation in terms of potential longevity of trials, anthropogenic selection pressures, documentation of materials, general health, development to rejuvenate populations, and possible maladaptation scenarios for climate change, as well as the extent to which they fill existing gaps identified in *in situ* protection.

6.5 Intra specific genetic diversity standards for reforestation

Standards for genetic diversity of seedlots and clonal lots for reforestation are based on effective population size thresholds developed by the BC MFR Research Branch (Yanchuk et al. 2006) and administered by Tree Improvement Branch. The intent of these standards is to ensure a minimum level of genetic diversity in operational seedlots and plantations to limit the risk of plantation loss due to pest or environmental vectors that might impact a small population subset and thus effectively eliminate enough of a plantation population to render it incapable of providing the wood value or environmental services intended. The theoretical basis for these standards should be revisited from time to time, as technology and our understanding of genetic structure and diversity advances.

[5] Recalcitrant: species with seed that cannot be dried to a low moisture content, and stored for multiple years at sub-freezing temperatures. Example, Garry oak.

7.0 Missing elements

7.1 Current programs and activities

Since 2001, the genetic conservation program under the leadership of the FGC has focused on research and genetic-resource cataloguing through the Centre for Forest Genetic Conservation (CFGC) at the University of British Columbia. The CFGC has a mandate from the FGC to:

- study population genetic structure of forest trees
- assess the current degree of genetic conservation (*in situ* and *ex situ*), and the need for additional protection, and
- evaluate the current degree of maintenance of genetic diversity in breeding and deployment populations of improved varieties to meet current and future environmental challenges.

Key point

The UBC CFGC has greatly advanced the scientific foundation for conservation, but operational conservation activities are outside it's mandate.

The CFGC is very active in meeting its mandate and has performed research in four key areas: 1) cataloguing genetic resources, 2) advancing knowledge on genetic conservation strategies, 3) predicting climate change impacts on BC tree species and evaluating genetic management strategies, and 4) investigating various aspects of special interest species with major knowledge gaps.

The CFGC has greatly improved the scientific foundation for forest-tree genetic conservation, but operational genetic conservation activities are not part of the CFGC mandate. Operational needs underlie the request from the FGC to the GCTAC for a comprehensive plan to develop a well rounded genetic-conservation program. A framework was constructed to identify the operational gaps in genetic conservation, and is presented in Table 2.

Key point

Genetic conservation should be a multistakeholder activity, but coordination among agencies will require the focus of a dedicated individual

Genetic conservation of indigenous trees would be most efficiently undertaken as a multi-stakeholder activity involving the Ministry of Forests and Range, Ministry of Environment (Class A, B, C parks, conservancies, recreation areas, and ecological reserves); Parks Canada, local governments, and environmental non-governmental organizations (ENGO's). Conservation of indigenous tree species is a common goal of these groups, but communication between the groups is minimal. If we are to efficiently advance this program then co-ordination of an indigenous genetic conservation plan must be implemented across many organizations. The Ministry of Forests and Range, Stewardship division is the appropriate leader of this cross-organizational initiative, but the culture of most groups is not one of cross-pollination, so a concerted effort by a dedicated individual is needed. The importance and complexity of this cross-organizational initiative should not be underestimated.

The CFGC cataloguing project has greatly advanced the ability to predict appropriate habitat for a particular species. In some cases, this is easily confirmed, but in other instances ground-truthing is required to confirm the presence and/or frequency of some species. This is recognized as a gap in the existing program and resources are required in the form of personnel and a budget to increase the accuracy of the information. An initial assessment of ground truthing requirements was presented in Hamman et al. (2004-Table 3) to confirm that certain protected areas contain at least 5000 mature-equivalent individuals of each species for which they serve as *in situ* reserves.

There is also a need for a mechanism to fund seed collections for *ex situ* conservation, especially in species for which collections do not exist. The FGC has allocated funds to invest in *ex situ* genetic conservation seed collections for whitebark pine, limber pine and subalpine larch this fiscal year up to a total of $30 000. Future investments will be guided through gaps identified in the cataloguing project at the CFGC.

7.2 Gaps in current programs

Programs for forest-tree genetic conservation in British Columbia have advanced a great deal over the past 5 years, and are considered leaders in Canada. However, the following elements are needed to develop a fully comprehensive set of activities that will meet a genetic conservation and stewardship mandate as discussed in section 5 of this report.

Gap 1. Operational maintenance of the genetic conservation catalogue:

Development of a genetic conservation catalogue and gap analysis was a task given to the UBC CFGC due to the technical complexity and need for substantial research and development. Methodologies are now largely developed, and a comprehensive analysis is being finalized by CFGC staff. Maintenance of the databases associated with the catalogue, and ground truthing areas where data require verification or representative populations are potentially at risk, will require ongoing work that is more operational than research-oriented. This ongoing work would be more appropriately housed within the MFR, with technical support from the CFGC.

Gap 2. Formalized collaborations with other agencies and conservation organizations:

Conservation of the genetic resource of indigenous forest trees is a function and responsibility of initiatives beyond the MFR and the FGC. Agencies like the Ministry of Environment, National and Provincial parks, and ENGO land trusts share this interest, and offer different elements of a comprehensive conservation program. Collaborations with these agencies and organizations need to be further developed and formalized. An example might be an agreement with the Ministry of Environment and Parks Canada to allow access to genetic materials for genetic conservation purposes. The staff time and effort needed to develop and maintain these collaborations should not be underestimated. The benefits of such collaborations are considerable, and will leverage conservation investments well beyond those made by the MFR or by FGC-directed Forest Investment Account funds.

Gap 3. Coordinated *in situ* actions:

In situ conservation activities are currently *ad hoc*, and take a coarse-filter approach. Reserves are largely established for reasons other than conservation of forest tree species (parks, ecosystem preservation, maintenance of habitat for threatened animal and plant species). The conservation catalogue developed by the CFGC indicates relatively few needs for additional *in situ* conservation areas, but some apparent gaps require ground truthing for confirmation as modelling of species distributions based on extrapolations from botanical plot data may result in significant error in population estimates. A focused multi-agency effort to clearly identify gaps and find solutions to these gaps is needed. Solutions may include the development of additional *in situ* reserves, targeted *ex situ* collections to fill gaps, or including certain provisions in forest management objectives in specific areas[6] . Conservation lands held by land trusts and non-provincial parks may fill important gaps in some geographic areas, and the current development of unified spatial databases across these conservation lands could be highly informative in evaluating these gaps.

***Gap 4. Ex situ* conservation actions:**

Ex situ conservation of forest trees largely consists of the storage of seed under controlled environmental conditions as a means of preserving the genetic resource. Limited conservation collections currently exist at the Provincial Tree Seed Centre, but there is a need to link collection needs more formally to a completed and ground-truthed conservation catalogue. Current efforts are somewhat ad hoc, and driven by subjective perceptions of need. *Ex situ* seed storage will only work for species with orthodox seed that stores well (i.e. conifers, *Alnus*), and will not work for the recalcitrant seeds of some species of *Acer* and *Quercus garryana*.

***Gap 5. Inter situ* conservation actions :**

Inter situ conservation includes breeding populations, provenance samples in field tests, and progeny test populations. Seed orchards are a subset of breeding populations, and neither orchards nor plantations from orchard seed are not considered to be a significant *inter situ* conservation source. At the present time, there are 977 progeny and provenance test sites established in BC, as well as genetic archives containing selected parent trees. The historical development of breeding programs has resulted in individual programs establishing data records in ways that are expedient for each program, but differ among programs. As a result, the development of a comprehensive progeny and provenance test data base that can be included in the conservation catalogue and gap analysis, and regularly updated, will require considerable effort. This work has been initiated by MFR Research Branch staff, and will need to be completed, maintained, and merged into the conservation catalogue.

Gap 6. Merging conservation data with other provincial forestry information systems:

Increasingly, information systems are central to forest management and planning. To effectively develop and maintain a conservation program, information must be made available to other information systems in a way that will allow managers to understand and consider conservation needs. Although these needs are not thought to be critical for the majority of species and geographic areas in BC, in cases where they are critical, it is very important that needs are made known to local managers through the information systems they commonly use, and through appropriate extension.

[6] Forest management objectives could range from leaving certain representative stands, to silviculture techniques such as variable retention cutting to leave representative samples of the wild population of trees.

8.0 Recommended objectives, activities, performance measures, and responsibilities

8.1 Performance measures

Performance measures for a conservation program must reflect needs, scientific and technical limitations, and budgetary realities. In addition, measures must be quantifiable to allow the setting of measurable goals and objectives and assessments against these goals and objectives. To this end, the following measures are proposed:

Performance measure 1:

Develop a matrix of indigenous tree species (Appendix 1) and biogeoclimatic zones and identify matrix cells where a species exists in it's natural range (active cells). Performance measure #1 would be the percentage of active cells in this matrix that have adequately conserved natural genetic diversity. Adequate conservation would relate to predetermined and accepted criteria and standards.

Performance measure 2:

Understanding the natural patterns of distribution for a species genetic diversity is key to efficient and effective conservation of this diversity. At the present time, a great deal is known of these patterns for the primary commercial tree species, but little is known for most other species. Performance measure #2 will quantify the percentage of indigenous tree species listed in Appendix 1 that have met a predetermined technical standard for knowledge of the patterns of genetic diversity.

8.2 Goals and objectives

Recommended goals and objectives for a genetic conservation program must be measurable and quantifiable to allow the tracking of progress. The following goal allows linkage to the performance measures listed in section 8.1:

Conservation Program Goal

To adequately conserve the genetic diversity of key populations of all forest tree species indigenous to British Columbia by 2025, through a combination of *in situ, ex situ* and *inter situ* conservation populations and activities.

The following objectives link to the performance measures listed above, and could be reported on an annual basis to track progress. Both of these objectives may be adjusted from time to time to reflect expected levels of progress. As technical development is still needed, actual quantities and years are not suggested here.

Objective #1

To adequately conserve *x*%of indigenous tree species/zones by (*year* y).

Objective #2

To develop information on the natural patterns of genetic diversity for *x*% of indigenous tree species by (*year* y).

8.3 Activities and responsibilities

> **Key point**
>
> A genetic conservation program must recognize the broad spectrum of objectives and roles associated with forest land management in BC.

Activities associated with a comprehensive genetic conservation program must recognize the broad spectrum of objectives and roles associated with forest land management and conservation activities in British Columbia, and must support the goal and objectives set out for the program as a whole. Some of these objectives are shared among agencies, while others are agency-specific. Efficient conservation efforts will recognize the various roles of all parties involved, and coordinate activities for efficiency and synergistic delivery.

Table 2 outlines the types of work associated with a comprehensive conservation program, and lists contributions by organization. Forest industry is not included in this table, as its members are expected to participate through meeting their obligations under forest management plans, under policy requirements set out for Crown land, and through participation and representation on the FGC and associated committees.

> **Key point**
>
> Implementation will require a skilled individual capable of initiating and coordinating activities.

Key to implementation of the responsibility matrix in table 2 will be a skilled individual capable of initiating and coordinating activities. Also key is the conservation catalogue that will identify gaps and help all agencies focus their efforts on the gaps.

Table 2. Activities required for a comprehensive genetic conservation program. Central to all activities are gaps identified through the genetic conservation catalogue. It is assumed that the Forest Genetics Council and the Gene Conservation TAC will coordinate activities, facilitate communication, and prepare annual business plans for Forest Investment Account investments in genetic conservation.

Work needed	Gap (see sec. 7.2)	UBC CFGC	MFR Operational	MFR Research	Ministry of Environment and others
Conservation catalogue	1	• Develop methods and strategies • Complete baseline assessment report	• Maintain catalogue and data bases	• Provide technical support	• Contribute information • Participate in oversight
Inter-agency collaborations	2	• Participate	• Initiate and Lead	• Participate	• Participate
Operational *in situ* conservation	3	• Develop methods and strategies	• Develop policy • Conduct ground truthing • Coordinate with operations • Integrate inventory & databases	• Provide technical support • Support gap analyses and ground truthing	• Provide technical support • Provide inventory and data • Interface with provincial and national parks • Integrate data from land trusts
Operational *ex situ* conservation	4	• Develop methods and strategies	• Develop and maintain seed inventory and collection	• Provide technical support • Manage *ex situ* collections in breeding programs	• Provide park support (MOE, Nat. Parks) • Permit *ex situ* collections (Parks, ENGO land trusts)
Operational *inter situ* conservation	5	• Develop methods and strategies	• Manage seed orchards	• Provide breeding and provenance data support • Mgt. And development of inter situ populations	
Amount and distribution of genetic variation	Ongoing	• Research genetic diversity patterns	• Develop policy	• Provide technical support • Genecology research/seed zones	
Conservation strategies	Ongoing	• Research methods	• Develop policy • Monitor compliance	• Provide technical support • Conduct research	
Climate change and conservation	Ongoing	• Research methods	• Develop policy • Coordinate with other activities	• Provide technical support • Conduct research	• Participate
Pest interactions		• Research	• Develop policy	• Provide technical support • Conduct research	
Extension	All	• Communicate CFGC activities and results	• Extend Information for forestry professionals • Communicate to public	• Extend results to research community • Support other communications	• Communicate relevant information as needed for individual organizations
Monitoring and reporting	All	• Report on research	• Report on performance indicators • Records and reporting	• Report on research • Provide technical support	• Participate

* Pest interactions with climate change is also a topic identified through the Future Forest Ecosystems Initiative and the Forest Science Program

9.0 Resource needs

This section addresses only those resources that would be allocated through the Forest Genetics Council process and Forest Investment Account funding, or those allocations that would be recommended by the FGC to the Provincial Chief Forester. Resource recommendations to other agencies, and assumptions about resource contributions from other agencies are considered beyond the scope of this plan.

Resource needs are summarized in Table 3, and are linked to activities listed in Table 2. Many resources are currently in place for a comprehensive genetic conservation program. The primary needs are capacity to coordinate activities, the development of conservation and management plans for key populations, links to existing databases, develop policy, and maintain the conservation catalogue through periodic updating of information and ground truthing.

9.1 Human resources

In addition to current staff capacity found in the MFR Tree Improvement and Research Branches, and at the UBC CFGC, it is proposed that one full time professional position be created in the Tree Improvement Branch. The focus of this position would be to do the following:

- Maintain an updated genetic conservation catalogue (transfer of the catalogue developed by the CFGC to the MFR) (Gap #1),
- Coordinate the integration of *ex situ* and *inter situ* information in the conservation catalogue (Gap #1),
- Lead ground truthing of gaps identified in the catalogue (Gap #1),
- Initiate and coordinate a multi-agency effort to fill conservation gaps identified in the catalogue (Gap #2),
- Work with the FGC Extension TAC and GCTAC to develop extension materials related to conservation,
- Assist with conservation policy development,
- Work with other MFR staff in the TIB and other branches to integrate appropriate genetic conservation data into other land-management databases (Gap 1),
- Report on conservation performance measures to the Chief Forester and to the FGC.

9.2 Funding resources

Funding recommendations presented in Table 3 refer only to FIA Tree Improvement Program funds directed by the FGC. Existing conservation work supported by the FGC is included if it supports work needed under this plan. It is anticipated that this budgetary need will be ongoing, although there will be some flexibility year to year. It must be noted that implementation of this plan will require a long-term budgetary commitment for a professional full-time employee.

Table 3. Recommended FIA Tree Improvement Funding allocations to genetic conservation by project and agency ($ x 1000) for years after 2008/09. Year 1 will be less due to part-years salary costs.

	Agency		
Type of work	**MFR Research**	**MFR Operational**	**UBC CFGC**
PROJECT SUPPORT			
Conservation catalogue	0	10	40
Ground truthing	0	40	0
***Inter situ* management**	40		
***Ex situ* seed collection**	0	30	0
Multi-agency coordination	0	0	0
Extension	0	10	10
Policy development	0	0	0
Database coordination and development	0	20	10
Research on conservation strategies	10	0	50
Research on species diversity and needs	20	0	60
Integration of climate change and conservation strategies	20	10	50
SALARY SUPPORT	0	135**	0 *
AGENCY TOTALS	**90**	**255**	**220**
TOTAL BUDGET			**$565**

* part of project support

** loaded salary cost; refinement needed

Table 4. Recommended Forest Investment Account, Tree Improvement Program budget; 2008 to 2013 ($ x 1000).

	Year				
Group and activity	**2008/09**	**2009/10**	**2010/11**	**2011/12**	**2012/13**
UBC Centre for Forest Genetic Conservation	220	220	220	220	220
MFR – Operational	185*	255	235	215	215
MFR – Research	90	90	90	90	90
Total	**$495**	**$565**	**$545**	**$525**	**$525**

* part-year salary costs

Other funding resources may be leveraged through other agencies, initiatives such as CONFORGEN (which is seeking support through the Canadian Council of Forest Ministers). In-kind and project collaborations can also provide substantial support to these initiatives through assistance with efforts such as ground truthing, provision of data for inventories, and local collections of seed.

9.3 Procuring resources

The primary intent of this report is to develop a framework for a comprehensive genetic conservation program, and to propose funding allocations of FIA Tree Improvement Program funds for FGC discussion and consideration.

Procuring other resources must be a priority of the overall program and considered in the context of program needs and collaborations.

10.0 Action recommendations and timeline

10.1 Steps to implementation

Steps needed to implement actions described are set out in Table 4. Excluded from this table are activities of the UBC Centre for Forest Genetic Conservation, as these are currently ongoing, and managed through an annual business planning process.

Table 5. Implementation steps for a FGC-led provincial genetic conservation program for indigenous forest tree species

Type of work	Activity leader(s)	Start	Finish
Conservation Staff Recruitment			
Completion and approval of a genetic conservation plan	GCTAC / FGC	Jan. 2007	March, 2008
Conservation budget prepared for FGC	GCTAC	Jan. 2008	March, 2008
Budget approval for 2008/09	FGC		March, 2008
Program and budget recommendation to the Provincial Chief Forester and the MFR	FGC		March 2008
MFR review and discussion with FGC	MFR – TIB	March 2008	June 2008
Development of job description; internal approvals; MFR staff recruitment	MFR – TIB	June 2008	Jan. 2009
Development of a specific program of work	MFR conservation lead and GCTAC	Feb 2009	ongoing
Operational conservation activities that can be started within the next year			
Ex situ seed collections	MFR – TIB	Aug., 2007	ongoing
Inter situ data records	MFR – Res Br.; CFGC	Aug. 2007	ongoing
Priority ground truthing of the CFGC gap analysis	CFGC, MFR Res. Br.	April, 2008	ongoing

11.0 Literature Cited

Aitken, S.N. 2000. Conserving adaptive variation in forest ecosystems. Journal of Sustainable Forestry 10: 1-12.

Bower, A.D. and S.N. Aitken. 2006. Genetics of cold hardiness in whitebark pine. Can. J. For. Res. 36: 1842-1850.

Bower, A.D. and S.N. Aitken. 2007. Mating system and inbreeding depression in whitebark Pine (*Pinus albicaulis* Engelm.). Tree Genetics and Genomes. Published online DOI 10.1007/s11295-007-0082-4.

Crandall, K.A., O.R.P. Bininda-Emonds, G.M. Mace and R.K. Wayne. 2000. Considering evolutionary processes in conservation biology. TREE 15: 290-295.

Ericksson, G., Namkoong, G. and J.H. Roberds. 1993. Dynamic gene conservation for uncertain futures. Forest Ecology and Management. 62:15-37

Gapare, W.J., A.D. Yanchuk and S.N. Aitken. In press. Optimal sampling strategies for capture of genetic diversity differ between core and peripheral populations of *Picea sitchensis* (Bong.) Carr. Conservation Genetics. Accepted April 2007.

Gapare, W.J. and S.N. Aitken. 2005. Strong spatial genetic structure in peripheral but not core populations of Sitka spruce (*Picea sitchensis* (Bong.) Carr.). Molecular Ecology 14: 2659-2667.

Gapare, W. J., S.N. Aitken and C.E. Ritland. 2005. Genetic diversity of core and peripheral Sitka spruce (*Picea sitchensis* (Bong.) Carr) populations: implications for conservation of widespread species. Biological Conservation 123: 113-123.

Hamann, A. and T. Wang. 2005. Models of climatic normals for genecology and climate change studies in British Columbia. Agricultural and Forest Meteorology 128: 211-221.

Hamann, A. and T. Wang. 2006. Potential effects of climate change on ecosystem and tree species distribution in British Columbia. Ecology 87: 2773-2786.

Hamann, A., S. N. Aitken, A. D. Yanchuk. 2004. Cataloguing *in situ* protection of genetic resources for major commercial forest trees in British Columbia. For. Ecol. Mgmt. 197(1-3): 295-305.

Hamann, A., P. Smets, A.D. Yanchuk and S.N. Aitken. 2005. An ecogeographic framework for *in situ* conservation of forest trees in British Columbia. Can. J. For. Res. 35: 2553-2561.

Howe, G.T., S.N. Aitken, D.B. Neale, K.D. Jermstad, N.C. Wheeler and T.H.H. Chen. 2003. From genotype to phenotype: Unraveling the complexities of cold adaptation in forest trees. Canadian Journal of Botany. 81: 1247-1266.

Krakowski, J., S.N. Aitken and Y. El-Kassaby. 2003. Genetics and conservation of whitebark pine. Conservation Genetics 4: 581-593.

Lande, R. 1995. Mutation and conservation. Conservation Biology 9: 782-791.

Lynch, M. 1996. A quantitative-genetic perspective on conservation issues. In J.C. Avise and J. L. Hamrick (Eds.), Conservation Genetics: Case Studies from Nature. Chapman & Hall, New York, pp. 471-501.

Lynch, M. and R. Lande. 1993. Evolution and extinction in response to environmental change. In P.M. Kareiva, J.G. Kingsolver, and R.B. Huey (Eds.), Biotic Interactions and Global Change. Sinauer Associates, Inc. pp. 234-250.

MFR – Ministry of Forests and Range. 2007. Biodiversity. FPRA Resource Values. Forest and Range Evaluation Program. Accessed on-line at: http://www.for.gov.bc.ca/hfp/frep/values/biodiversity.htm

Mimura, M. and S.N. Aitken. 2007a. Increased selfing and decreased effective pollen donor number in peripheral relative to central populations in *Picea sitchensis* (Pinaceae). American Journal of Botany. 94(6):.

Mimura, M. and S.N. Aitken. 2007b. Adaptive gradients and isolation by distance with postglacial migration in *Picea sitchensis*. Heredity. Published online in *Heredity* http://www.nature.com/doifinder/10.1038/sj.hdy.6800987 on 09/05/07 doi: 10.1038/sj.hdy.6800987

Wang, T.L., A. Hamann, A. Yanchuk, G.A. O'Neill and S.N. Aitken. 2006a. Use of response functions in selecting lodgepole pine populations for future climates. Global Change Biology 12: 1-13.

Wang, T., A. Hamann, D. Spittlehouse and S.N. Aitken. 2006b. Development of scale-free climate data for western Canada for use in resource management. International Journal of Climatology 26: 383-397.

Yanchuk, A.D. 2001. A quantitative framework for breeding and conservation of forest tree genetic resources. Can. J. For. Res. 31: 566-576.

Yanchuk, A.D., Bishir, J., Russell, J.H. and K.R. Polsson. 2006. Variation and volume production through clonal deployment: results from a simulation model to minimize risk for both a currently known and unknown future pest. Silvae Genetica. 55:25-37.

Yanchuk, A.D. and D.T. Lester. 1996. Setting priorities for conservation of the conifer genetic resources of British Columbia. Forestry Chronicle 72: 406-415.

Appendix 1 – Indigenous tree species

Tree species indigenous to British Columbia that are considered to be within the scope of this genetic conservation plan.

Code	Scientific name	Authority	Common name	Breeding Program	Provenance testing
Conifers					
ABIEAMA	*Abies amabilis*	(Dougl. ex Loud.) Dougl. ex	amabilis fir		x
ABIEGRA	*Abies grandis*	(Dougl. ex D. Don) Lindl.	grand fir		x
ABIELAS	*Abies lasiocarpa*	(Hook.) Nutt.	subalpine fir		x
CHAMNOO	*Chamaecyparis nootkatensis*	(D. Don) Spach	yellow-cedar	x	x
JUNISCO	*Juniperus scopulorum*	Sarg.	Rocky Mountain juniper		
LARILAR	*Larix laricina*	(Du Roi) K. Koch	tamarack		
LARILYA	*Larix lyallii*	Parl.	subalpine larch		
LARIOCC	*Larix occidentalis*	Nutt.	western larch	x	x
PICEENG	*Picea engelmannii*	Parry ex Engelm.	Engelmann spruce	x	x
PICEGLA	*Picea glauca*	(Moench) Voss	white spruce	x	x
PICEMAR	*Picea mariana*	(P. Mill.) B.S.P.	black spruce		
PICESIT	*Picea sitchensis*	(Bong.) Carr.	Sitka spruce	x	x
PINUALB	*Pinus albicaulis*	Engelm.	whitebark pine		
PINUBAN	*Pinus banksiana*	Lamb.	jack pine		
PINUCON	*Pinus contorta*	Dougl. ex Loud.	lodgepole pine	x	x
PINUFLE	*Pinus flexilis*	James	limber pine		
PINUMON	*Pinus monticola*	Dougl. ex D. Don	western white pine	x	x
PINUPON	*Pinus ponderosa*	Dougl. ex P.& C. Lawson	ponderosa pine		x
PSEUMEN	*Pseudotsuga menziesii*	(Mirbel) Franco	Douglas-fir	x	x
TAXUBRE	*Taxus brevifolia*	Nutt.	western yew		
THUJPLI	*Thuja plicata*	Donn ex D. Don	western redcedar	x	x
TSUGHET	*Tsuga heterophylla*	(Raf.) Sarg.	western hemlock	x	x
TSUGMER	*Tsuga mertensiana*	(Bong.) Carr.	mountain hemlock		
Broadleaves					
ACERCIR	*Acer circinatum*	Pursh	vine maple		
ACERGLA	*Acer glabrum*	Torr.	Douglas maple		
ACERMAC	*Acer macrophyllum*	Pursh	bigleaf maple		x
ALNUINC	*Alnus incana*	(L.) Moench	speckled/mountain		
ALNURUB	*Alnus rubra*	Bong.	red alder		x
ALNUVIR	*Alnus viridis*	(Vill.) Lam. & DC.	Sitka alder		
ARBUMEN	*Arbutus menziesii*	Pursh	arbutus		
BETUNEO	*Betula neoalaskana*	Sarg.	Alaska paper birch		
BETUOCC	*Betula occidentalis*	Hook.	water birch		
BETUPAP	*Betula papyrifera*	Marsh.	paper birch		x
CORNNUT	*Cornus nuttallii*	Aud. ex T. & G.	western flowering		
CORYCOR	*Corylus cornuta*	Marsh.	beaked hazel		
CRATDOU	*Crataegus douglasii*	Lindl.	black hawthorn		
MALUFUS	*Malus fusca*	(Raf.) Schneid.	Pacific crab apple		
POPUBAL	*Populus balsamifera*	L.	balsam poplar		
POPUTRE	*Populus tremuloides*	Michx.	trembling aspen		
PRUNEMA	*Prunus emarginata*	(Dougl.) Walp.	bitter cherry		
PRUNPEN	*Prunus pensylvanica*	L. f.	pin cherry		
PRUNVIR	*Prunus virginiana*	L.	choke cherry		
QUERGAR	*Quercus garryana*	Dougl.	Garry oak		
RHAMPUR	*Rhamnus purshiana*	DC.	cascara		
SALIBEB	*Salix bebbiana*	Sarg.	Bebb's willow		
SALIDIS	*Salix discolor*	Muhlenb.	pussy willow		
SALILUC	*Salix lucida*	Muhl.	shining willow		
SALISCO	*Salix scouleriana*	J. Barratt ex Hook.	Scouler's willow		
SALISIT	*Salix sitchensis*	Sanson ex Bong.	Sitka willow		

Appendix 2 –Technical summary of the key elements of a genetic conservation program

This summary is an expansion of Section 4.1 of this report.

A. Science-based knowledge of genetic diversity patterns

The amount of intraspecific genetic variation a species contains, and the distribution of that variation among and within populations, varies as a result of a myriad of factors including glacial and post-glacial history, population size and density, degree of local adaptation, dispersal capability of seeds and pollen, and mating system. Scientific knowledge of species genecology and population genetics can be used to determine the number and distribution of *in situ* reserves or *ex situ* collections needed to capture most of the adaptive or selectively neutral standing variation present in a species.

Common garden experiments provide knowledge of population variation in quantitative traits reflecting adaptation to local environments, while genetic marker studies provide information on genetic relatedness of populations, rates of gene flow among populations, patterns of postglacial recolonization, levels of genetic diversity at species range centers versus range peripheries, and levels of inbreeding. Each of these approaches contributes to science-based conservation strategies. Just as seed transfer guidelines for reforestation are based on species-specific knowledge, where available, genetic conservation strategies should also be based on the unique diversity patterns of individual species.

Information on genetic diversity comes generally from two types of studies: Genetic markers provide information on genetic diversity for a set of genes or DNA sequences thought to be selectively neutral, that is, not related to phenotypes or reflecting local adaptation. Such markers can be used to compare overall genetic diversity levels and patterns among species, and provide indirect information about population size, history and levels of gene flow, and inbreeding. Common garden experiments such as provenance trials provide information on phenotypic traits such as growth, timing of bud break or bud set, cold hardiness, or pest resistance that reflect adaptation to local environments. Genetic markers at this time cannot be used to understand local adaptation or define seed transfer rules; nor can phenotypic traits be used to infer levels of gene flow, etc.

Species-specific information on patterns of genetic variation is lacking for the majority of BC's 49 indigenous tree species, and the quantity and quality of information available is roughly proportional to the recent economic value of harvests and size of breeding programs for each species. Well-established provenance trials exist for most of the major economically important conifers with breeding programs, as well as for a few commercially important broadleaves such as *Alnus rubra* and *Acer macrophyllum.* Short-term seedling genecological experiments have also been conducted or are underway for non-commercially important species including *Pinus albicaulis, Cornus nuttallii and Quercus garryana. .* Genetic marker studies have been conducted for most of the commercially important conifers and a few broadleaves.

With knowledge of genetic diversity in some of BC's indigenous tree species and from other temperate and boreal trees, we can start to make some cautious generalizations about intraspecific patterns of variation. Lodgepole pine (*Pinus contorta*) and Sitka spruce (*Picea sitchensis*) have emerged as models for the study of conifer population genetics, and lessons learned from these species can be extended to some degree to other widespread, wind-pollinated and wind-dispersed tree species.The well-developed and widely accepted Biogeoclimatic Ecological Classification (BEC) system provides detailed mapping of patterns of environmental variation that can be used as an indicator of probability of differential adaptation to local environments, that is, the extent to which two populations of a species are 'ecologically exchangeable" (Crandall et al. 2000). It should be noted; however, that species can differ dramatically in their degree of local adaptation, for example, lodgepole pine (*Pinus contorta*) is an adaptive specialist meaning it shows steep clinal patterns with climate variables , while western white pine (*Pinus monticola*) and western redcedar (*Thuja plicata*) are adaptive generalists meaning genotypes are broadly adapted to a wide range of climatic conditions. The same genetic conservation strategy will generally not be efficient when applied to both adaptive specialists and generalists.

B. Population and quantitative genetics theory on efficient strategies

The fields of population and quantitative genetics have provided robust theories on the maintenance of adaptive and selectively neutral genetic diversity within finite populations based on population size, gains in genetic variants (alleles) due to mutation, losses of alleles due to the random process of genetic drift or the directional process of selection, and the roles of gene flow and selection in the maintenance of variation within populations. From these theories, the effective population size that will maintain genetic diversity for polygenic adaptive traits indefinitely (i.e., over many generations in isolation from other populations) can be estimated. Effective population size (N_e) is the size of a genetically idealized population where every individual contributes equal numbers of offspring to the next generation, thus the actual population (census) size N needed to obtain the same genetic dynamics as a given N_e is typically two to ten times larger than N_e. The estimated threshold N_e above which current levels of genetic diversity will be maintained indefinitely , depending on the assumptions of the models used, generally varies from 1,000 to 5,000 individuals (Aitken 2000, Lande 1995, Lynch 1996). Genetic modeling has also provided clear evidence of the importance of genetic diversity as well as generation length in determining whether wild populations will be able to adapt to projected rates of climate change (e.g., Lynch and Lande 1994).

Key point

The number of populations that need to be conserved to effectively capture and perpetuate current levels of genetic diversity in a species depends on the degree of genetic differentiation of populations.

The number of populations that need to be conserved to effectively capture and perpetuate current levels of genetic diversity in a species depends on the degree of genetic differentiation of populations, that is, the degree of genetic redundancy or 'genetic exchangeability' of populations (Crandall et al. 2000). This principle, through the use of population and quantitative genetics, can guide decisions on efficient conservation strategies for individual species. Genetic marker data and common garden experiments produce very different answers for the same population, with generally a much higher degree of population differentiation estimated, and thus lower degree of genetic exchangeability inferred, when traits controlled by many genes involved in adaptation to local climate are assessed (e.g., Howe et al. 2003). What this means from an operational genetic conservation standpoint is that we cannot rely on genetic marker data to adequately reflect among-population adaptive variation.

Ex situ collections do not typically have an opportunity to evolve while in storage, as most collections for species with orthodox seed are freezer-stored (although genotypes may vary in storage longevity). These are not usually stored, regenerated and recollected ex situ over multiple generations as is the case with some short-lived or agricultural crop species. These collections can be used to re-establish or supplement in situ or inter situ populations, thus will spend only part of one generation in storage. If unrelated seeds are stored, they will capture a proportion of the variation in the population sampled corresponding to 1 - (1/2N) where N is the number of seed parents sampled. Thus sampling one seed from each of 50 unrelated seed parents will capture 99% of the variation from a population. Most ex situ collections consist of many more seeds than this, but from a finite number of parents.

C. Genetic resource catalogue and indicators

The genetic theories and principals outlined in 5.1.2 above have been used to develop conservation thresholds for maintaining the genetic diversity of tree species in BC. These thresholds have been used to develop a catalogue of the genetic resources of the 49 indigenous trees species, with the goal of having at least three *in situ* conservation populations with census sizes of mature individuals (or their equivalent in more, younger trees occupying the same amount of habitat) of at least 5,000 individuals per seed planning unit (SPU) or per BEC zone (Hamann et al. 2004, 2006). Where insufficient conservation populations exist, a gap is identified.

This approach assumes that SPUs and BEC zones provide a spatial reference for environmental variation that is likely to correspond to population differences in adaptation to climate. SPU boundaries are in some cases based on species-specific provenance data, thus likely provide a reasonable indication of the geographic scale across which adaptive differentiation is biologically significant. Multiple *in situ* reserves per SPU or BEC zone provide redundancy against catastrophic loss of populations, and *ex situ* seed collections provide insurance against loss of *in situ* resources, as well as providing an important mechanism of conserving genetic material where additional *in situ* protection is unlikely to develop in the short term under the provincial Protected Areas Strategy.