

Ex situ conservation plan for forest genetic resources in Alberta



Agriculture and Forestry, Government of Alberta

April 2018

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ISBN 978-1-4601-3879-3

URL <https://open.alberta.ca/publications/9781460138793>

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Species distribution range map shapefiles were developed by E. Little, USDA Forest Service, accessed through Data Basin <https://databasin.org/galleries/5e449f3c91304f498a96299a9d5460a3#expand=12211> except range map shapefiles for whitebark pine and limber pine which were developed by Adam Collingwood, Parks Canada, accessed through the Whitebark Pine Ecosystem Foundation <http://whitebarkfound.org/resources/help-update-range-maps/>

Cover photos by Lindsay Robb (left) and Katherine Spencer (left)

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Executive Summary

Genetic diversity is a key element of biodiversity. It provides the raw material for adaptation to changing environmental and demographic conditions. The amount and patterns of genetic variation within each species reflects demographic and environmental influences on evolutionary processes. Conserving the genetic diversity within and among populations of Alberta's native tree species has been an important part of Alberta genetics and tree improvement programs since their inception in 1975. This plan describes the guiding principles, procedures, policies and types of ex situ gene conservation in Alberta, and the status and priorities of activities.

Gene conservation uses two main approaches: in situ and ex situ. In situ conservation consists of maintaining wild tree populations of native species functioning in their natural habitats, subject to natural evolutionary and demographic processes. In Alberta, in situ conservation is guided by the *Gene Conservation Plan for Native Tree Species of Alberta* (ASRD 2009b). Ex situ conservation consists of conserving genetic variation outside the natural habitat of the species or population, and includes seed banks, clone banks, arboreta, botanical gardens, and research field plantings. Seed banks represent most of the ex situ conservation program in Alberta. Ex situ conservation is also an important conservation tool for rare and endangered species and populations where the habitat is under threat. The Alberta program is currently focused on trees, having grown with the mandate of the Alberta Tree Improvement and Seed Centre. Both endangered tree species in Alberta, whitebark pine and limber pine, have active genetic conservation programs to support species recovery.

Ex situ genetic conservation is addressed in the *Alberta Forest Management Planning Standard* and *Alberta Forest Genetic Resource and Conservation Management Standard*, both of which are enabled under the *Timber Management Regulation* of the *Forests Act*. The genetic conservation program contributes to Alberta's commitment to sustainable forest management under the *Canadian Council of Forest Ministers Criteria and Indicators Framework* and the *Canadian Biodiversity Strategy*, a key part of Canada's commitment to the *United Nations Convention on Biological Diversity*.

The ex situ conservation program in Alberta aims to represent populations of all native trees amenable to medium to long-term seed storage. Gaps are identified by geographic and ecological regions, and plans to fill these gaps based on each species' biology and other criteria are described. Where populations of species are very common, easily accessible, and not under threat, and whose seed is not amenable to long term storage, ex situ conservation is a low priority. Seed banking is the most cost-effective and widely used option, but where species have seed that cannot be stored long term without significant viability loss, clone banking and planted trials may offer alternatives, although the cost of establishing and maintaining these installations limits the number of genotypes and populations represented.

Acknowledgement

Leonard Barnhardt and Narinder Dhir envisioned this plan. Donna Palamarek, Lindsay Robb, and Lori Siemens provided detailed information on seed collections and facilities. Reviews were provided by Andy Benowicz, Lindsay Robb, and Erica Samis. Aaron McGill and Tammy Decosta helped with mapping. Jodie Krakowski developed the document and maps.

List of Acronyms

Acronym	Definition
AAF	Alberta Agriculture and Forestry
ABMI	Alberta Biodiversity Monitoring Institute
AFGRC	Alberta Forest Genetic Resources Council
ASRD	Alberta Sustainable Resource Development, now AAF
ATISC	Alberta Tree Improvement and Seed Centre
AWLPRT	Alberta Whitebark and Limber Pine Recovery Team
CAFGRIS	Canadian Forest Genetic Resource Information System
CONFORGEN	Canadian Program for Conservation of Forest Genetic Resources
CPP	Controlled Parentage Program
ESRD	Environment and Sustainable Resource Development (formerly ASRD)
FGRMS	Forest Genetic Resource Management and Conservation Standards
GoA	Government of Alberta
ISTA	International Seed Testing Association
IUFRO	International Union of Forest Research Organizations
USDA	Alberta Agriculture and Forestry
WF	Alberta Biodiversity Monitoring Institute

Species Codes

Species name	Common name	Inventory Code
<i>Abies balsamea</i>	balsam fir	Fb
<i>Abies lasiocarpa</i>	subalpine fir	Fa
<i>Betula papyrifera</i>	paper birch	Bw
<i>Juniperus scopulorum</i>	Rocky Mountain juniper	Jrm
<i>Larix laricina</i>	tamarack	Lt
<i>Larix lyallii</i>	subalpine larch	La
<i>Larix occidentalis</i>	western larch	Lw
<i>Picea engelmannii</i>	Engelmann spruce	Se
<i>Picea glauca</i>	white spruce	Sw
<i>P. engelmannii</i> x <i>P. glauca</i>	interior spruce	Se x Sw
<i>Picea mariana</i>	black spruce	Sb
<i>Pinus albicaulis</i>	whitebark pine	Pa
<i>Pinus banksiana</i>	jack pine	Pj
<i>Pinus contorta</i> var. <i>contorta</i>	lodgepole pine	Pl
<i>P. contorta</i> x <i>P. banksiana</i>	lodgepole x jack pine hybrid	Pl x Pj
<i>Pinus monticola</i>	western white pine	Pw
<i>Populus balsamifera</i>	balsam poplar	Pb
<i>Populus deltoides</i>	plains (eastern) cottonwood	Pdox
<i>Populus tremuloides</i>	trembling aspen	Aw
<i>Prunus virginiana</i>	Choke cherry	Pv
<i>Pseudotsuga menziesii</i> var. <i>glauca</i>	Douglas-fir	Fd

Introduction

This report complements the *Gene Conservation Plan for Native Trees of Alberta* (ASRD 2009b) developed by agency experts to provide an in situ gene conservation framework for the province. This report documents the rationale, objectives, scientific principles, methodology, and prioritization for ex situ gene conservation from natural and managed forests.

There are two broad categories of gene conservation: in situ and ex situ. In situ conservation consists of maintaining wild tree populations of native species in their natural habitats along with associated plants, fungi, pollinators, and pathogens, and maintaining these under the influence of natural evolutionary processes. Ex situ conservation consists of conserving genetic variation outside the natural habitat of the species and populations being conserved. Ex situ is an important conservation tool for rare and endangered species and their representative populations, and aids conservation of valuable genetic stock in tree improvement and plant breeding programs (ASRD 2009a; Lipow et al. 2002, 2003; Krakowski et al. 2009). Some authors consider inter situ as an intermediate approach (Blixt 1994), where material is collected from disparate areas within which a metapopulation is known to be adapted, and stored as a living archive, such as a progeny trial established within the breeding zone from which the parent trees originate (Krakowski et al. 2009). This may be considered distinct from in situ in that the individuals are moved and collected as an archive, but they are subject to natural selection processes within habitats to which they are adapted. Alberta categorizes such material as in situ to streamline reporting, and because this intermediate category is not widely recognized.

Ex situ gene conservation of forest genetic resources in Alberta started in 1976, soon after the start of the genetics and tree improvement program. In its first year, the program collected and stored 735 single tree and bulk seed collections from 10 native tree species (Dhir and Vincent 1978). Early work was based in rented greenhouse and laboratory space at the federal Canadian Forest Service Northern Forestry Centre, Edmonton. In 1979 the Genetic Centre facility at Pine Ridge Forest Nursery (now ATISC, the Alberta Tree Improvement and Seed Centre) was established and the program has been centred there ever since.

Gene conservation is an integral part of conservation of biodiversity. Genetic diversity is the amount or number of genetic variants within a population or species. The total amount of genetic variation and its distribution among and between populations characterize diversity and the potential to adapt. Four evolutionary mechanisms affect genetic diversity and its distribution: mutation increases diversity, migration decreases differentiation between populations, natural selection changes the frequency of alleles, and genetic drift reduces diversity. Patterns of diversity shed light on how past events such as glaciation have influenced current distributions of populations and adaptation, and provide information on how future events such as effects of environmental change. Loss of genetic variation hinders adaptive change in populations of a species and reduces their ability to persist over the long run. Genes of native trees, and all native organisms, are a heritage resource in Alberta (ASRD 2009b).

Plan Objectives

Ex situ gene conservation is an integral part of the provincial gene conservation plan to maintain both biological and genetic diversity that contribute to sustainable forest management and conservation. The provincial in situ gene conservation plan (ASRD 2009b:32) states: “*a separate ex situ conservation plan will be developed to address the role of operational and conservation seed, linkages to the in situ program, special conservation needs and implementation ...*”

This plan has four main objectives:

1. Describe species and materials requiring ex situ conservation, and the conservation objectives for each;
2. Quantify ex situ conservation requirements for each species and category;
3. Assess current status, gaps, and priorities of current resources in ex situ conservation;
4. Describe an approach for prioritizing and implementing the plan.

There are two main purposes for the provincial ex situ collections:

1. To supplement in situ conservation.
2. A source of research seed for studies on traits including physiology and population genetics.
 - a. bulk collections can be used to assess the amount and distribution of quantitative and adaptive genetic diversity within and among populations;
 - b. single tree collections can be used to assess population level diversity as well as detailed questions regarding spatial structure of diversity within populations and identifying unique individuals.
 - c. Depending on the sampling method, other physiological and adaptive traits may be tested.

Ex situ collections have been used as a source of restoration material elsewhere where in situ populations are extirpated or at risk of extirpation, but this is not a main objective of the Alberta conservation samples due to the relatively small sample size for collections given the capacity to document, process, and store collections across the province, and the widespread and/or locally abundant distribution of Alberta native trees and shrubs which are not at risk of local extirpation. Seed collection for operational restoration is considered a separate mandate.

Jurisdictional Commitments and Agreements

Alberta supports the Canadian commitment to the 1992 *United Nations Convention on Biological Diversity*¹ which includes the sub-program *Global Strategy for Plant Conservation*² (2002, revised 2010) through its agreement to contribute to the *Canadian Biodiversity Strategy* (Minister of Supply and Services Canada 1995; Alberta Environmental Protection 1998). Several guiding policy documents commit the province to developing, using and reporting on principles of sustainable forest management and maintaining biodiversity, although genetic diversity is rarely an explicit indicator (Canadian Council of Forest Ministers 1995; Alberta Environmental Protection 1998). Alberta has a well-established biodiversity monitoring network (ABMI, Alberta Biodiversity Monitoring Institute³) focused on indicators and thresholds at the species to landscape levels. As part of the current regional planning process, the province is developing watershed, subregional and regional biodiversity indicators and targets (e.g., Government of Alberta 2012).

Although these programs may acknowledge genetic diversity as a core component of biodiversity, the structure of the assessments and reporting implicitly assumes that genetic diversity is captured at the scale used for species and regional assessments. This may not be adequate where there is cryptic variation, or genetic patterns that may differ based on drivers other than ecological factors – such as pest and disease resistance, which are often due to rare alleles and must be specifically targeted for conservation, as a coarse filter approach will not protect adequate numbers of individuals with those traits (Petit et al. 1998; Yanchuk 2001).

Alberta participates in CONFORGEN⁴ (Canadian Program for Conservation of Forest Genetic Resources) which was established in 2006 to coordinate national efforts in forest gene conservation. It is led by the Canadian Forest Service with partners from other federal and provincial departments. CONFORGEN promotes conservation of genetic resources of native tree species and synthesizes provincial reporting to Natural Resources Canada on the status of genetic resources in Canada in the periodic *Report on the State of Canada's Forest Genetic Resources* (Natural Resources Canada 2012) and compiles the data in CAFGRIS (Canadian Forest Genetic Resource Information System). Data is periodically submitted to

¹ www.cbd.int/doc/legal/cbd-en.pdf

² www.cbd.int/gspc/strategy.shtml

³ <http://www.abmi.ca/abmi/home/home.jsp>; terrestrial monitoring protocols
http://www.abmi.ca/FileDownloadServlet?filename=10001_ABMI_2010-04-20_Terrestrial_Field_Protocols.pdf

⁴ <http://www.conforgen.ca/>

international agencies to meet biodiversity reporting requirements such as those specified under the *United Nations Convention on Biodiversity*.

Ex situ gene conservation standards, compliance and reporting requirements are addressed in the *Alberta Forest Management Planning Standard* (ASRD 2006) and *Alberta Forest Genetic Resource Management and Conservation Standards* (FGRMS). FGRMS states the province may retain 5% or 30,000 seeds of a wild seedlot collected from public land with viability test data submitted for registration by a seed owner, or 10% of the seedlot or 60,000 seeds without viability data for ex situ conservation. The province is held to the same standards for its own programs.

Current Status of Ex Situ Genetic Conservation in Alberta

The scope of the provincial forest genetic resource conservation and management program includes 28 native tree species (ASRD 2009b). Interest has been increasing in woody shrubs and other species for reclamation of disturbed sites, but there is no formal gene conservation program in place to date for plants other than trees. Both endangered tree species in Alberta (whitebark pine and limber pine) have active genetic conservation programs as components of their recovery strategies. The province has no endangered or threatened shrub species, but 31 are listed as S1⁵, S1S2, S2, or S2S3 (based on the Alberta Conservation Information Management System ranks using NatureServe Criteria⁶). Alberta status listings largely reflect species at their range limits in Alberta which have more extensive ranges in adjacent jurisdictions (36 taxa are listed in ACIMS of which 28 are recognized in NatureServe). Table 1 describes categories of ex situ conservation in the Alberta program.

Table 1. Categories of ex situ conservation of forest genetic resources in Alberta

Type	Description
Wild seed collections	All native tree species and selected woody shrub species with seed amenable to storage to maintain viability for at least 5 years
Germplasm collections of selected genetic stock	Seed, research or provenance selections of known origin outside of a research trial; may include pollen, cryogenically stored material such as embryos or in vitro samples (not currently in Alberta program)
Seedlings and vegetative materials of representative or unique native tree and shrub wild populations	Includes: arboreta, botanical gardens, clone banks, progeny and provenance trials, seed orchards, other research trials with genetic value, genetic demonstration plantings
Extra-provincial ex situ resources	Alberta tree samples or seeds provided through exchanges or cooperative agreements in other jurisdictions

⁵S indicates subnational (provincial) rank, where S1 has five or fewer occurrences or highly vulnerable to extirpation, S2 is known from 20 or fewer occurrences or vulnerable to extirpation, and S3 is known from 100 or fewer occurrences or somewhat vulnerable to extirpation; S1S2 or S2S2 reflects data or uncertainty intermediate between the two classes.

⁶ <http://www.albertaparks.ca/albertaparksca/management-land-use/alberta-conservation-information-management-system-acims/tracking-watch-lists/species-conservation-ranks/> [accessed August 3 2017]

Wild seed collections

The conservation seed archive is at ATISC in Smoky Lake. Seed is stored in a secure facility according to International Seed Testing Agency (ISTA) protocols at -20°C. Limited lower temperature storage is available, but there are no cryopreservation facilities. Data on each accession is maintained in a database housed on agency servers.

ATISC seed inventory is divided into bulk and single genotype accessions. Accessions with over 100 viable seeds are summarized here. Seeds of uncertain location origin, non-wild sources (e.g. seed orchards), and bulk collections with fewer than the regulatory minimum thresholds for diversity are excluded from the following summaries. Lipow et al. (2002) emphasize the value for genetic programs of archiving single-tree collections due to the additional genetic data that can be obtained through family selection and testing. This report also includes bulk collections as a resource that provides useful population genetic data at the provenance level.

Bulk accessions include 18 native tree species, including 2 native hybrids, and 3 native shrub species, and several species native to other jurisdictions. There are 478 collections from Alberta, 43 from nine other provinces and territories, and accessions from Russia, Sweden, and the U.S.A. In total there are 521 accessions totaling over 25 kg of seed, over 3 million seeds (Figure 1, Table 2).

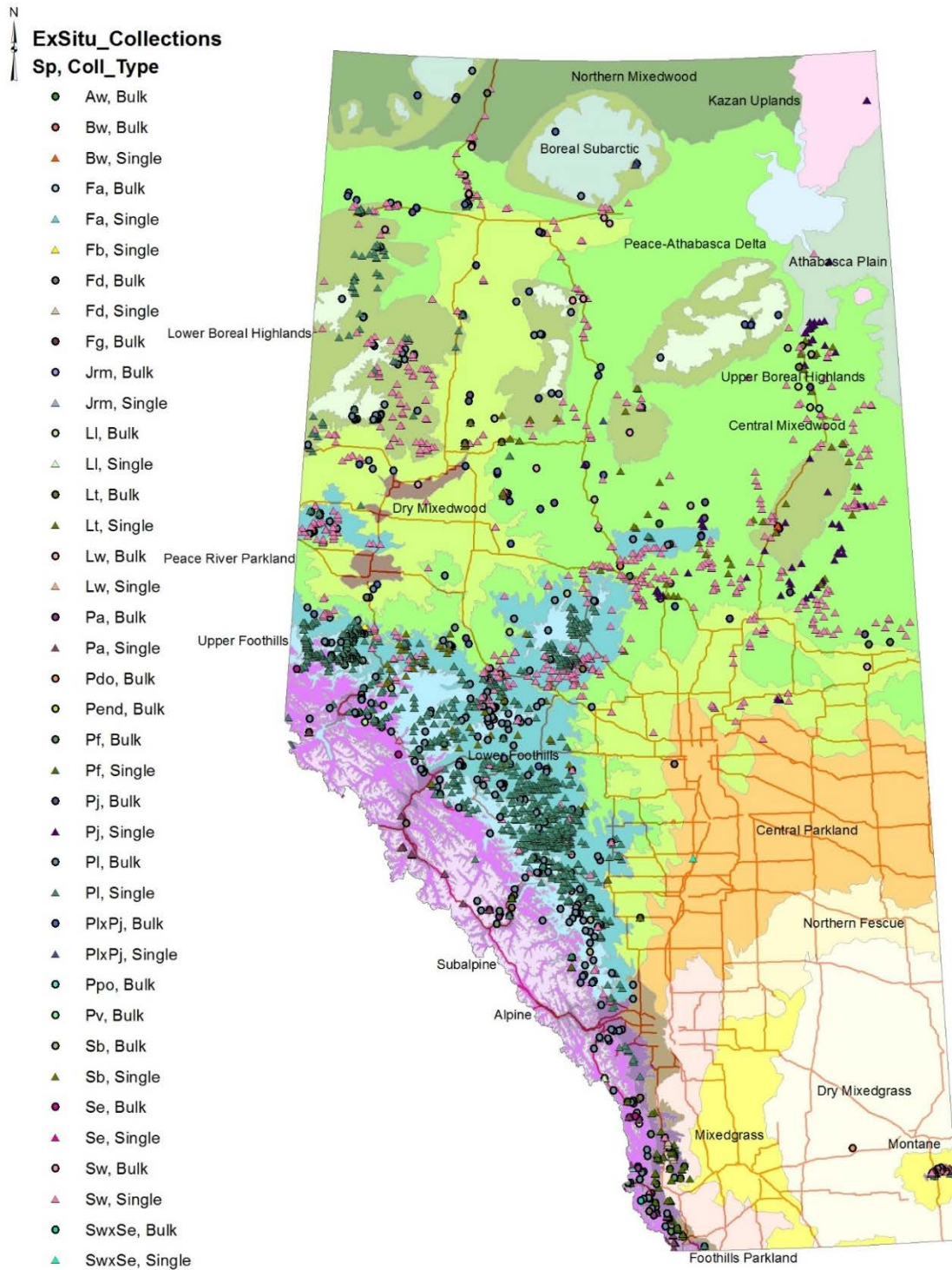


Figure A2. 1. Map of stream 1 (wild) seed collections showing Alberta's natural subregions

Table 2. Inventory of native bulk wild tree seed held at Alberta Tree Improvement and Seed Centre (June 2017)

Jurisdiction	Species	Accessions	Seeds (g)	Seeds (No.)
Alberta		478	22,667	2,650,869
	<i>Abies lasiocarpa</i>	1	18	1,548
	<i>Betula papyrifera</i>	2	6	41,727
	<i>Corylus cornuta</i>	2	4	993
	<i>Juniperus scopulorum</i>	1	96	8,465
	<i>Larix laricina</i>	14	106	71,082
	<i>Larix lyallii</i>	5	60	13,403
	<i>Picea engelmannii</i>	4	62	32,692
	<i>Picea glauca</i>	30	385	107,019
	<i>Picea mariana</i>	19	209	180,152
	<i>Picea glauca</i> x <i>P. engelmannii</i>	4	85	39,213
	<i>Pinus albicaulis</i>	16	3,036	59,551
	<i>Pinus banksiana</i>	15	366	101,916
	<i>Pinus contorta</i> var. <i>latifolia</i>	288	5,925	1,582,198
	<i>Pinus flexilis</i>	29	10,945	121,182
	<i>Pinus contorta</i> x <i>P. banksiana</i>	34	591	173,604
	<i>Populus deltoides</i>	1	21	34,928
	<i>Populus tremuloides</i>	3	4	39,695
	<i>Prunus virginiana</i>	1	354	3,803
	<i>Pseudotsuga menziesii</i> var. <i>glauca</i>	7	321	33,811
	<i>Symphoricarpos albus</i>	1	5	1,273

Jurisdiction	Species	Accessions	Seeds (g)	Seeds (No.)
	<i>Viburnum edule</i>	1	67	2,616
	<i>Populus tremuloides</i>	3	4	39,695
BC	5 species ^a	11	1,399	63,104
Manitoba	2 species ^b	7	70	22,116
New Brunswick	<i>Picea glauca</i>	1	7	4,030
NWT	<i>Picea glauca</i>	2	52	24,220
Ontario	2 species ^c	7	20	7,491
PEI	<i>Picea glauca</i>	1	3	1,149
Quebec	<i>Picea glauca</i>	7	29	12,810
Saskatchewan	<i>Picea glauca</i>	4	13	6,070
Yukon	2 species ^d	3	6	2,159
Russia	<i>Pinus sibirica</i>	1	114	505
Sweden	2 species ^e	4	28	3,007
USA	<i>Picea glauca</i>	1	4	1,630
BC	5 species ^a	11	1,399	63,104

^a*Pseudotsuga menziesii* var. *glauca*, *Abies grandis*, *Larix occidentalis*, *Pinus albicaulis*, *Pinus ponderosa*

^b*Pinus resinosa*, *Picea glauca*

^c*Pinus strobus*, *Picea glauca*

^d*P. contorta* var. *latifolia*, *Picea glauca*

^e*Pinus sylvestris*, *Picea abies*

Single tree collections total 4,546 accessions comprising nearly 150 kg of seed, which is nearly 35 million seeds (Table 3, Figure 1). Alberta accessions represent 16 native tree species and 2 hybrids, and no shrub species. Details of collections meeting minimum seed viability and sample sizes described in Section 5 are in Appendix 1 and selected maps are in Appendix 2.

Table 3. Inventory of Alberta native single wild tree seed held at Alberta Tree Improvement and Seed Centre (June 2017)

Jurisdiction	Species	Accessions	Seeds (g)	Seeds (No.)
Alberta		4,446	140,877	32,460,536
	<i>Abies balsamea</i>	1	201	21,507
	<i>Abies lasiocarpa</i>	30	2,990	291,694
	<i>Betula papyrifera</i>	1	17	101,479
	<i>Juniperus scopulorum</i>	1	72	6,839
	<i>Larix laricina</i>	89	787	451,350
	<i>Larix lyallii</i>	4	27	4,817
	<i>Picea engelmannii</i>	10	1,095	437,677
	<i>Picea glauca</i>	1,130	45,172	21,122,582
	<i>Picea mariana</i>	157	545	489,186
	<i>Picea glauca</i> x <i>P. engelmannii</i>	11	402	152,138
	<i>Pinus albicaulis</i>	346	24,094	215,899
	<i>Pinus banksiana</i>	129	2,149	599,024
	<i>Pinus contorta</i> var. <i>latifolia</i>	288	5,925	1,582,198
	<i>Pinus flexilis</i>	470	33,224	431,523
	<i>Pinus contorta</i> x <i>P. banksiana</i>	65	651	222,211
	<i>Prunus pensylvanica</i>	1	5	127
	<i>Prunus virginiana</i>	1	17	289
	<i>Pseudotsuga menziesii</i> var. <i>glauca</i>	29	1,594	184,146
BC	3 species ^a	78	1,676	26,719
Nova Scotia	<i>Picea glauca</i>	2	6	2,289

Jurisdiction	Species	Accessions	Seeds (g)	Seeds (No.)
Ontario	3 species ^b	15	47	15,306
Quebec	<i>Picea glauca</i>	1	2	967
Saskatchewan	<i>Picea glauca</i>	3	333	131,587
Finland	<i>Larix sibirica</i>	1	37	29,254

^a*Larix occidentalis*, *Pinus albicaulis*, *Picea glauca* x *P. engelmannii*

^b*Pinus resinosa*, *Pinus strobus*, *Picea glauca*

Germplasm collections of improved genetic stock

FGRMS provides for provincial acquisition and storage of seed orchard or stream 2 seed for ex situ conservation. These acquisitions represent a comprehensive collection of commercial conifer seed focused on timber producing areas and species (Table 4).

Table 4. Inventory of stream 2 (seed orchard) seed held in conservation collections at Alberta Tree Improvement and Seed Centre (January 2016)

Type	Accessions				Accessions				Accessions			
	Pj	PI	Sw	Total	Pj	PI	Sw	Total	Pj	PI	Sw	Total
Bulk	5	25	63	93	88	149	1,230	1,387	41	581	2,952	3,573
Single	26	310	697	1,033	76	237	2,199	2,513	322	2,526	6,780	9,629
Total	6	335	760	1,126	85	386	3,429	3,900	363	3,107	9,732	13,202

Nearly 2,000 genets of eight native species and their hybrids are established in 11 clone banks in Alberta, primarily at ATISC (Table 5, Appendix 3). All have multiple ramets and are regularly maintained and augmented. Some represent selections from tree improvement programs, while others are a representative genetic archive of population genetic resources.

Table 5. Clone banks listed by breeding region (includes some un-tested selected material)

Species	CPP region	Genotypes	Ramets	Project
PI	A/B1	3	12	G206A,B
PI	B1	109	337	G206A,B,C
PI	B1/B2	4	16	G206A
PI	B2	165	465	G206A,B,C
PI	C	158	430	G206C
PI	J	85	219	G206A,B,C
PI	K1	182	520	G206A,B,C
PI	no ID or outside CPP region	186	604	G206A,B,C
Pj	P1	11	29	G349
Pj x PI	hybrid zone	50	144	G349
Sw	D1	6	24	G218B
Sw	D	47	188	G218A,B
Sw	E	97	385	G218A,B
Sw	E1	57	207	G218B
Sw	E2	35	142	G218B
Sw	G1	151	604	G218A,B
Sw	G2	80	321	G218A,B
Sw	H	68	271	G218A,B
Sw	I	134	533	G218A,B
Sw	no ID or outside CPP region	65	257	G218A,B
Sw x Se	hybrid zone	61	224	G218B,C

Species	CPP region	Genotypes	Ramets	Project
Sb	L1	18	53	G323
Sb	L2	38	113	G323
Sb	L3	48	147	G323
Lw	M	40	68	G269, G312A, G323
Lw	no ID or outside CPP region	21	66	G312A, G323
Lt	NA	10	30	G323
Fd	F1	39	80	G268
Fd	no ID or outside CPP region	26	69	G312A
Sb	L3	48	147	G323
Lw	M	40	68	G269, G312A, G323
Lw	no ID or outside CPP region	21	66	G312A, G323
Lt	NA	10	30	G323
Fd	F1	39	80	G268
Fd	no ID or outside CPP region	26	69	G312A

Seed orchards, both for improved growth and for seed production of unimproved material, are listed in Table 6. Improved selections for height growth are currently represented in orchards for white spruce (CPP regions D, D1, E, G1, G2, H, I) and lodgepole pine (CPP regions A, B1, B2, C, K1, J), with other orchards either producing unimproved material or with trials below the minimum age for height gain approval.

Progeny trials contain material that may be also in clone banks and seed orchards. The province has an extensive network of test sites for various species (Table 7), and industry cooperators are partners in several programs (Table 6). Some trials are established solely by industry in support of their tree improvement programs. The Province has been developing agreements regarding ownership and use of forest genetic resources in regional tree improvement programs. Figure 2 shows provincial trial locations.

Table 6. Seed orchards listed by CPP region and project number

Location	Species, CPP region, description, project number: G###						
(owner / partner)	Sw	Sb	Pl	Pj	Fd	Lw	Lt
ATISC (GoA)	D1 G205 seedling E G259 E1 G334 E2 G313 H G242	L1 G275 L3 G338					G274
Grande Prairie (Huallen Seed Orchard Co.)	G1 G351 I G333	L2 G326	B1 G147 seedling B1 G804 clonal B2 G303				
Presslee (Hinton Wood Products-WF)		L1 G806 seedling	A G801				
North Star (GoA, Manning Diversified-WF)	G2 G318		J G319				
Linaria (Millar Western)		L1 G802 seedling & clonal					
Wandering River (GoA)				P1 G331			
Jumpingpound (GoA)					F1 G286		
Whitecourt (Blue Ridge Lumber- WF)	D G291		C G284 seedling				
Brooks (GoA, Sundre Forest Products-WF)			K1 G278		F1 G286	M G245B	

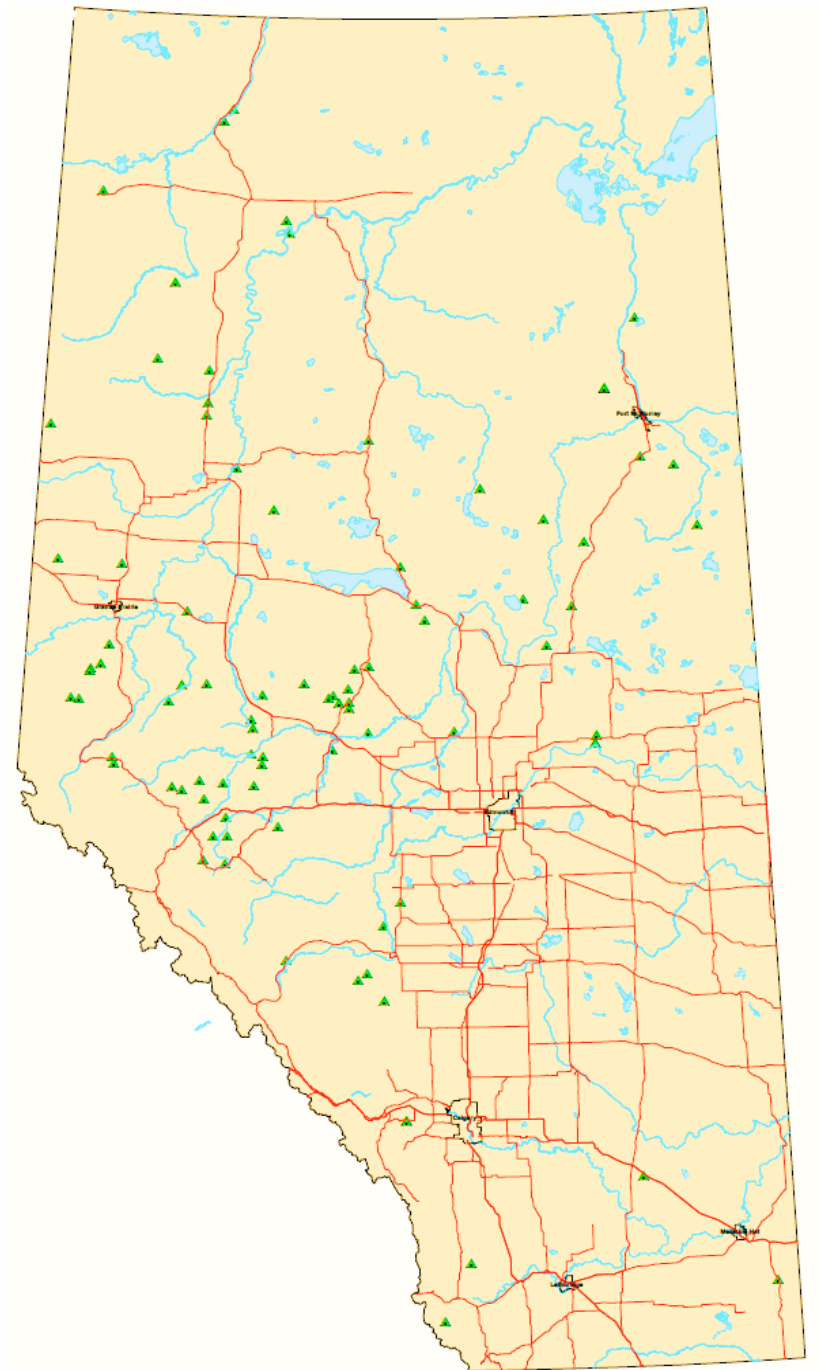


Figure A2. 2. Map of genetic installations: test sites, seed orchards, clone banks

Table 7. Progeny trials listed by CPP region (number of test sites)

Location	Aw	Aw/poplar complex	Sb	Sw	PI	Pj	Fd
ATISC		1		G (1)	B1 (1), Cypress Hills sources (1)	P1 (1)	1
Calgary area				Various incl. D1/G2 (1)	K1 (2), Cypress Hills sources (1)		F1 (3)
Calling Lake			L3 (1)	E (3), E1 (1), Cypress Hills sources (1)			
Chinchaga				H (1)			
Cypress Hills				Cypress Hills sources (1)	Cypress Hills sources (1)		
Drayton Valley				I (1), G1 (1)			
Edson/Hinton				I (2)	A (7)	B2 (1)	
Fort MacMurray			L3 (2)	E/E1 (6), E1 (2)		P1 (3)	
Grande Prairie				D (1), G (1)	B1 (4), B2 (1)		
Hay River			L1/ L2 (2)	G2 (1), H (1)	J (2)		
Lac La Biche				D (1)			
Manning				G2 (6), Various incl. D1/G2 (1)	J (2)		
Peace River				G (1), G2 (1), Various incl. D1/G2 (1)			
Pembina River				I (1)			
Red Earth				H (1)			
Slave Lake				D (7), G2 (1)	1 multiple sources, J (1) (multiple sources)		
Sturgeon Lake				G1 (1)	B1 (2)		
Wapiti River					B2 (1)		
Waskahegan			L1/L2 (1)	G1 (1)			

Location	Aw	Aw/poplar complex	Sb	Sw	PI	Pj	Fd
Whitecourt	1			I (1)	B1 (1), J (1), C (4), Cypress Hills sources (1)		
Yellowhead					B2 (2)		

Seedlings and vegetative materials from wild populations

Approximately 420,000 trees are established in 229 research and ex situ conservation plantings throughout Alberta, primarily in provenance trials (Table 8), but also in some progeny trials (Table 7) and clone banks (Table 5). The primary objective of provenance trials is genecology, but these installations also are important for ex situ conservation. Further work is planned to establish grafted clone banks of selected putatively and tested rust resistant whitebark and limber pine genotypes. Clone banks of these selections, established in regional blocks, may also serve as seed orchards, pending disease resistance screening results.

Table 8. Provenance trials of native species, and number of test sites

Species	ATISC	Other location
<i>Betula papyrifera</i>	1	1
<i>Fraxinus pennsylvanica</i>	1	
<i>Larix laricina</i>	1	6
<i>Picea engelmannii</i>		1
<i>Picea glauca</i>	1	26
<i>Picea glauca</i> x <i>P. engelmannii</i>		1
<i>Picea mariana</i>	3	9
<i>Pinus contorta</i> var. <i>latifolia</i>		2 (1 only region K)
<i>Pinus flexilis</i>		1
<i>Pseudotsuga menziesii</i> var. <i>glauca</i>		5

Extra-provincial ex situ resources

Extra-provincial resources are collections of Alberta material in research trials and archives in other jurisdictions.

Alberta has germplasm tested in numerous IUFRO trials. Lodgepole pine provenance trials (IUFRO series 70/71) were established in the mid-1980s with two Alberta sources (Swan Hills, Hawk Hills) out of 178 provenances tested across Yukon, BC, Finland and Sweden (Lindgren et al. 1994; Fries et al. 2000). Provenance trials established in the early 1980s on two sites in B.C. included three Alberta sources. This series tested lodgepole, jack pine, and their hybrids to assess traits including tolerance to stalactiform blister rust, western gall rust, needle cast, and sequoia pitch moth (Wu et al. 1996) in 53 provenances represented by 778 open-pollinated families.

There are several lodgepole pine provenance tests and progeny trials in British Columbia established under an interprovincial agreement, including the well-known Illingworth trial series with five Alberta populations out of the 140 range-wide populations tested across 60 sites, but only the test at Prince George Tree Improvement Station one has retained family identities. This test series has yielded numerous publications on adaptive patterns (e.g., Rehfeldt et al. 1999; O'Neill et al. 2008; Wang et al. 2010; Berland 2013; Montwé et al. 2016). These trials have been decimated by the recent mountain pine beetle outbreak, but numerous sites remain and data collection and analysis continues.

The Canadian Forest Service established a series of range-wide black spruce provenance trials between 1973 and 1977. A total of 218 sources, including several from Alberta, are tested across 34 sites, including one in Alberta (Morgenstern and Mullin 1990).

Isaak-Renton (2013) documented results from Douglas-fir provenance trials established by IUFRO across Europe. Two Alberta sources (Kananaskis, Strong IR) were planted at test sites in Germany in 1977, but were not at other test sites.

A range-wide white spruce provenance trial series established at 16 Ontario sites between 1978 and 1985 (plus additional sites in other provinces; data not available) tested 245 sources, including 10 from Alberta (Lu et al. 2014).

Alberta has shared whitebark and limber pine seeds with the USDA Forest Service facilities at Coeur D'Alene Idaho and Dorena Oregon for disease resistance screening. This data has contributed to provincial, national, and range-wide data sets on disease resistance and provenance variation. In 2015 and 2016 seeds from 20 putatively resistant whitebark pine trees were sent to the BC Ministry of Forests, Lands and Natural Resource Operations facility Kalamalka Research Station for screening by ATISC and Parks Canada. A limber pine

provenance trial was established at two sites in 2016 including one in Alberta and one in Colorado. A total of 145 families from 30 provenances along a Rocky Mountain transect were included, with 7 provenances and 29 families from Alberta.

Alberta has also contributed material to academic studies that have generated DNA libraries. The University of British Columbia-led AdapTree project included approximately 100 bulk Alberta sources each of white spruce and lodgepole pine in its applied genomics studies, yielding phenotypic as well as genotypic data on adaptive portfolios of wild trees (e.g., Liepe et al. 2016), and has also used Alberta material held in cryopreservation, in probe libraries, and on microarray chips. The TRIA (Turning Risk Into Action) project at University of Alberta has also used material provided by Alberta to delineate lodgepole and jack pine ranges and introgression zones, and assess susceptibility to mountain pine beetle (e.g., Cullingham et al. 2013). This genomics project retains DNA microarray chips and probe libraries and some cryopreserved material. Collaborations with academic partners are ongoing to support basic research and to develop and utilize emerging tools and analytical approaches that may not be available in house to support forest genetic resource management in the province.

Collection Criteria and Sample Sizes for Ex Situ Conservation

Common and abundant species

Genotypic considerations

Quantitative population genetic criteria inform “how much is enough”. The biology and genetics of our conifers is well studied, and many non-commercial tree species in Alberta, or closely related species, have data available on the amount and distribution of genetic diversity. Alberta commercial conifers are outcrossing monoecious species, with inbreeding coefficients (Wright’s F) of 0.1 or less, with moderate levels of genetic diversity population differentiation (F_{ST} , G_{ST} , ϕ_{ST} or other comparable statistics), indicating that 90-95% of total population diversity is within populations, and between 5 and 10% is found between populations (e.g., Hamrick and Godt 1989; Yang and Yeh 1992; Nybom 2004). Thus for temperate and boreal forest trees, sampling even a single population captures most of the genetic diversity in native populations, but would not discriminate or capture alleles that are responsible for differentiation between populations.

The literature on this topic generally recommends for ex situ conservation to not focus on rare alleles (those with frequency <0.05) as their fitness effects are usually neutral or negative, they contribute negligible amounts to population genetic diversity indices such as expected heterozygosity, and only rarely would capturing rare alleles justify the exponential increase in sampling effort (Marshall and Brown 1975; Brown and Briggs 1991; Neel and Cummings 2003). One example where rare allele sampling may be warranted is disease resistance, which should use a targeted or stratified phenotypic sampling approach to increase the likelihood of sampling those low frequency alleles.

Yanchuk (2001) quantified in situ population sizes needed to capture a threshold number of copies of dominant and recessive alleles at varying frequencies: to capture five copies of a common (frequency >0.05) allele about 2000 individuals are needed for a recessive allele and 89 for a dominant allele; to capture 20 copies, about 5500 individuals are needed for a recessive allele and 275 for a dominant allele. Yang and Yeh (1992) took a similar approach modelling genetic diversity impacts over multiple generations in finite population sizes, and estimated ex situ collection sizes needed to conserve alleles at various frequencies using different models: from 15 to 80 individuals were needed to capture at least one copy of all common alleles. Brown and Hardner (2000) use a neutral allele model, consistent with most genotypic markers and assumptions underlying estimates of population genetic statistics, to quantify the logarithmic relationship between sample size, allelic richness (average number of alleles per locus), and

population size. At low to moderate levels of polymorphism a sample of 20 to 25 individuals captures nearly all the allelic richness found in 200 individuals; only at the highest diversity levels are 50 samples needed to capture more than half of the allelic richness. Neel and Cummings (2003) estimate sampling at least five populations captures 90-95% of all common alleles, based on rare and endemic annual plant data (which would contain higher heterozygosity and more private alleles than occur in Alberta's widespread forest tree species), so this number would be extremely conservative for Alberta's forest gene conservation objectives.

The literature contains ample discussion on sampling effects, particularly when populations are small, peripheral or isolated (Lesica and Allendorf 1995; Lynch 1996; Petit et al. 1998; Gram and Sork 1999; Gapare et al. 2008). Nearly all ATISC collections represent common, widespread or locally abundant species, including some peripheral populations, and should capture nearly all common alleles in a representative distribution.

For outcrossing forest conifers, Brown and Hardner (2000) recommend vegetative material from 30 plants, or seed from at least 15 trees per population for ex situ conservation which is consistent with CONFORGEN guidelines (CONFORGEN 2014). Brown and Marshall (1995) recommend as a general guideline for a 95% likelihood of capturing all alleles with greater than 5% frequency in an entire species: at least 50 propagules collected from 50 individuals each from 50 populations. This sample size would account for effects such as relatedness, viability decay over time, etc. Lipow et al. (2002) recommend 100 seeds per tree, from 30 unrelated parents per population. The recommendations of Brown and Marshall (1995) are regarded as an upper sample size limit using un-stratified or completely randomized sampling. Prior biological, distribution, and genetic knowledge more efficiently and effectively captures genetic diversity using a stratified approach with a much smaller sample (Brown and Marshall 1995; Guerrant Jr. et al. 2014). Other research or restoration projects would require additional seed collections according to specific project design needs as this sampling approach and sample size would only satisfy gene conservation or population genetic diversity objectives.

Adaptive considerations

Clinal differences in adaptive traits among populations often evolve along environmental gradients. Most neutral and adaptive genetic patterns studied have weak or nonexistent correlations. Based on these factors, Alberta supports a stratified species-wide sampling approach with 20 to 50 individuals from each of 20 to 50 populations (species wide, reduced for provincial sampling), with the number of propagules depending on the rarity of the species (Guerrant Jr. et al. 2004; ANPC 2006). Johnson et al. (2004) recommend using seed zones for native plant species that correspond with ecological zones which tend to capture the majority of adaptive and genotypic differentiation (Bower et al. 2014). Most forest species indigenous to Alberta are relatively common and abundant within their native habitats. Studies on population

adaptive differences using Alberta material have stratified populations into natural subregions (e.g., Liepe et al. 2016), which are reasonable population units for sampling.

Sampling criteria

Single tree collections

Single tree collections provide the best value in terms of genetic data and utility of the data and germplasm (Lipow et al. 2002). To represent a population, collect a minimum of 100 seeds per tree, from by a minimum of 30 trees (Brown and Marshall 1995; Brown and Hardner 2000), and consider collecting more in case of viability or germination problems. For most Alberta native trees, collecting 1000 or more seeds per individual does not take much more time or effort to collect and process, and provides far more options for testing and research to supplement the genetic archive. Not all current collections meet these criteria (Appendix 1A, 1B), but collections can be supplemented, and future conservation seed collections will strive to do so.

Bulk collections

When it is not possible to sample from individual trees, a bulk population sample may be warranted, but the value of the individual tree data is lost. To capture ecological diversity and to hedge against degradation or accident, three bulk population samples containing 1000 seeds from each of 20 to 50 parents, with data on the amount of seed collected from each parent tree and some geographic and phenotypic data on each parent tree, is a minimum population sample that would serve both long term gene archiving as well as provide material for population genetic research projects. Given typical dispersal and life history characteristics of most forest trees, this would require sampling of trees at least 50 m to 100 m apart in a stand, and maintaining a distance of at least 20 km (preferably 30-50 km) between sampled stands to ensure each collection represents a single genetic population.

No previous data on genetic patterns

Where previous genetic data on population variability is totally lacking for a species or related species with similar habitat and distribution, more extensive sampling is required to establish a baseline. Because not all samples can be grown, amplified, or have material successfully extracted for genotyping, one must strike a balance between sampling sites and sampling individuals. Sample approximately 100 propagules per individual, with an objective of producing 30-50 useable genotypes and/or phenotypes per population. Do not sample more than 50 individuals each or 50 populations per species, rather cover as much spatial and ecological variation as possible. A common target for statistical robustness, genotypic and/or adaptive data is to collect data from 30 or more individuals per population – collecting samples from more individuals is recommended because not every one might yield useable results. If a species'

distribution is restricted or homogeneous then sampling fewer populations stratified according to ecological and geographic distribution, and taking life history characteristics into account, should capture most of the variability (Krakowski 2010).

Sampling summary

If no previous genetic information on population differentiation exists

- 100 propagules or more from 50 individuals each from 50 populations covering the geographic distribution of the species OR an adequate number to cover the geographic and ecological distribution within a smaller area such as a province or seed zone – allows delineation of genetic populations and quantification of baseline parameters of the amount and distribution of genetic diversity.

If previous genetic information on population differentiation exists

- Single tree collections representing a population: For common (i.e., commercial) species that have long-lived seeds with high viability, collect at least 30 single-tree samples at least 50-100 m apart with over 100 seeds each. Recommend collecting more seeds per tree, and from more individuals if available. Ensures long term ex situ conservation of known or likely population diversity, and allows for testing. Total at least 3,000 seeds.
- Bulk collections representing a population: sample at least three stands within the population (where the extent of “populations” are known or can be reasonably inferred, e.g. a seed zone) comprised of at least 1000 seeds from each of 20 to 50 individuals at least 50-100 m apart. At least 20,000 to 50,000 seeds from at least three stands, minimum 60,000 to 150,000 seeds per population.

Non-standard species: rare, patchy, clonal, dioecious

Some species have biology or distribution characteristics requiring modified collection criteria. These require adjustments to the number of seeds per collection, the number and distribution of individuals per population, and the number and distribution of populations according to their biology and genetics.

Rare species or patchy distribution with small populations

For extremely rare or patchy species, the impact of collecting seed on the persistence of the population must be considered. Menges et al. (2004) advise: collecting 10% of seeds 10% of the time has little to no impact on very small populations, while collecting 50% or more of seeds, every other year or every year is detrimental. If populations are as low as ten individuals and the

collection is for conservation and/or restoration of a declining species, all seed may be collected for a given year, but not every year. The Alberta Native Plant Council guidelines also have recommendations addressing rare plant collections and documentation (ANPC 2006).

For species with very patchy distributions, adjust the number of collections to representatively sample the distribution of habitat types and ecological subregions, and consider both disjunct and contiguous populations. Sample from at least three populations per natural subregion as per advice in section 5.1, and include the full spectrum of habitat types to capture maximum genetic variation.

Population fecundity varies across years

If individuals within a population have extreme inter-annual variation in fecundity, multiple visits to collect over several years is required, ensuring sampled individuals are tagged to prevent repeat collections which would bias population genetic diversity assays. Where entire populations have simultaneous masting followed by one or more years of little or no seed production, be prepared to collect the sample during a mast year as low seed production years tend to have very disproportionate parental contributions, poor seed viability, and does not merit the effort for collecting.

Clonal species

Clonal species present a special challenge. Where clonal boundaries are obvious, try to select from the requisite number of individuals per population. However, individual genotypes may not always be visually apparent (e.g., Ally 2008; Gardner 2013). In these cases, consult the literature for an estimate of clonal size. If information is not available, use visual differences such as foliage shape, colour, stem form or phenology for a conservative estimate of clonal distribution.

Dioecious species

Collecting seeds from dioecious species only samples the female cohort. This may result in a biased sample if there are genetic differences between male and female individuals; this is only likely to cause issues if the collection is specifically used to assay population gene expression on reproductive traits, as male and female shrubs and trees of Alberta tend to differ little in other traits (Obeso 2002, but see Nielsen et al. 2010). Studies have identified genotypic, gene expression, and some adaptive differences between plant sexes (Juvany and Munné-Bosch 2015) but collecting only seeds should not detrimentally affect ex situ conservation because the embryos contain the male genotype. Collecting ramets from male trees, or pollen, can provide an ex situ sample that will conserve the germplasm over the long term. Storage and processing capacity such as 20°C to -80°C freezers, rootstock, grafting and clone beds, might be limiting

factors so plans should be clear before proceeding to ensure success, and whether collecting only seeds will meet objectives.

Summary

- Common species with no previous genetic information: at least 100 propagules from 50 individuals each from 50 populations covering the species' distribution of the species, or from at least 50 individuals to sample the study area
- Common species with existing genetic information: preferred sample is over 100 seeds from each of at least 30 individuals at least 50-100 m apart (single-tree); alternatively, collect bulk samples from at least 1000 seeds from each of 20 to 50 individuals at least 50-100 m apart in at least three stands per population.
- Rare species: Collections may need to be repeated over multiple years to sample adequate diversity within a population without harming the population. For populations with over 10 individuals, sample less than half the seeds produced, for up to 50 individuals per population. For populations with fewer than 10 individuals, ensure sampling will not harm the population and collect every second or third year. (Currently this does not apply to any species in ATISC collections). Also consult Alberta Native Plant Council rare plant collection guidelines (ANPC 2006) regarding best practices, permits, and voucher specimens.
- Patchy distributions: 1000 seeds from each of 20 to 50 individuals per population, at least three widely spaced populations per habitat type (e.g. Natural Subregion and/or distinct edaphic combination), and represent all habitats.
- Seed production varies across years: 1000 seeds from each of 20 to 50 individuals per population, at least three widely spaced populations per habitat type – repeat visits during mast years.
- Clonal species: 1000 seeds or five ramets from each of 20 to 50 individuals per population, at least three widely spaced populations per habitat type, and represent all habitats.
- Dioecious species: special efforts to collect, process and store pollen or grafted scion must be made to sample males if that is an objective; adequate diversity within the species or population can still be captured by sampling female individuals.

Prioritizing Ex Situ Conservation

Filling ex situ program gaps

Prioritization of conservation efforts is necessary to maximize effectiveness relative to costs. For most species, the most cost-effective category of ex situ conservation is wild seed collections and storage. Even with facilities already on site, factoring in the costs of collection, processing and storage drives the cost per sample from tens to hundreds, and sometimes thousands of dollars. Storage space is limited so collections should be high quality, and have enough seeds from a properly designed collection to meet conservation objectives and some surplus to support research. Species that retain good viability for at least five years under normal collection conditions are candidates for seed collection. Ageing seedlots of species with a storage life of several decades, e.g. *Picea* species, may require recollection over the longer term but are a lower priority than filling current gaps.

Collections are planned to acquire a broad geographic sample of native species that are not in provincial storage, as well as a broader sample of species that have few samples. Gaps will be filled initially based on seed crop and resource availability, then targeting remaining gaps. The two endangered pine species which will be targeted during next years. Species with known short-lived seeds in cold storage such as *Betula* and *Salix* species will not be conserved via seed storage if wild populations are secure and genetic diversity is not a concern; ex situ conservation for these species may be supplemented with vegetative archives if an opportunity exists. The lowest priority is to recollect older species-ecoregion combinations that are declining in viability due to age.

The recent mountain pine beetle epidemic spurred geographically targeted seed collections of lodgepole pine in areas of high mortality. An annual seed collection program is administered by the Forest Resource Improvement Association of Alberta. Industry leads collections in their operating areas, and the Province collects seed from areas with little or no commercial forestry. Seed is being collected both as a reserve for restoration, and a portion is retained for long-term conservation and research at ATISC.

Setting priorities

Alberta's two endangered tree species, limber and whitebark pine, have been assigned high priority for seed collections: currently the breadth of distribution and habitat types is well represented, but there is a significant gap in accessions of selected individuals with phenotypic resistance to white pine blister rust that is a critical foundation of the recovery strategies for these species (AWLPRT 2014a,b). Starting in 2015, this has been the focus of ex situ collections for

these two species. Given their remote locations, the need to protect cones from predation by caging and then revisit each tree for collection during the same year, the cost is disproportionately high to collect these species compared to all others in the province.

A summary of ex situ gene conservation objectives reflecting an update of the conservation criteria in the Gene Conservation Plan for Native Trees of Alberta (Government of Alberta 2009b) is in Table 9. A summary of all collections meeting these criteria is in Appendix 1A and 1B, with selected maps in Appendix 2.

Table 10 summarizes ex situ conservation categories applicable to each species and natural subregion. This list, combined with Table 9, was used to prioritize ex situ conservation activities by comparing current seed and clone bank inventories (Tables 2, 3, 5, Appendix 1A) and identifying gaps.

Tree species priorities

Many ex situ seed collections at ATISC reflect accessible populations of abundant and widespread species. Current seed inventory and viability data, housed in a database called GSIMS (Gene Conservation Seed Information Management System), has been overlain with species distributions and seed zones to identify gaps and set future priorities; this exercise will be periodically repeated to revise priorities every five years.

Limber pine and whitebark pine are the only native tree or shrub Species At Risk listed as of August 2017 under the Alberta *Wildlife Act* or federal *Species At Risk Act*. Ex situ conservation of these species is a high priority due to their rapid decline. Mature, large five-needle pine trees are extremely valuable for several reasons: they take centuries to replace due to their slow growth, they are the main seed source for a population, and heritable resistance to white pine blister rust found in rare individuals is the key for restoration. While these species are well protected in situ, passive conservation has proven ineffective to halt or reverse the decline of these species. Ex situ conservation, combined with proactive management actions, are required for successful recovery and restoration (AWLPRT 2014a,b). Populations of these species are prioritized based on health status and threats, for ex situ collection of putatively rust resistant individuals that are being screened for resistance.

Other special cases include species whose ranges peripherally extend into Alberta's jurisdiction, but are well protected and secure within Alberta, or contiguous and secure in the rest of their ranges. These species include western hemlock, western redcedar, western larch, subalpine larch, and western yew. It may be expedient to collect ex situ samples of Alberta populations but conservation urgency is low. Western white pine has experienced dramatic range-wide declines due to white pine blister rust but is not classified as at-risk, although it is classified as S2 in

Alberta, limited to a very small disjunct population with limited viability, but it is globally secure. All jurisdictions adjacent to Alberta with western white pine have successful blister rust resistance tree improvement and operational restoration programs. Given the plasticity of western white pine, rust resistant seed sources from adjacent areas are considered well adapted, and reduce the conservation urgency for Alberta sources to low.

Shrub species priorities

Woody shrubs may be included in future ex situ collections where optimal seed collection and long-term storage protocols, or clone bank space and resources, are available. There is no systematic genetic conservation plan at this time for native shrubs, but their 2016 addition to the provincial FGRMS warrants their inclusion in the next iteration of this plan.

Table 9. Species abundance^a and priority ranking^b for native tree species. Priority 1 and 2 collections are bold.

Natural Region	Boreal								Shield	Foothills		Rocky Mountain			Parkland				Grassland			
Natural Subregion	CM	NM	DM	PAD	LBH	UBH	AP	BSA	KU	LF	UF	M	SA	A	PRP	CP	FP	NF	FF	MG	DMG	
Alaska birch	U 4	U 4	U 4	U 4	O 4	U 4	U 4	U 4	O 4													
alpine larch													U 4	U 4								
balsam fir	O 4	U 4	U 4	U 4	O 4		U 4			U 4	U 4				U 4							
balsam poplar	A 5	C 5	C 5	O 4	C 5	U 4	U 4	U 4	U 4	C 5	O 4	U 4	U 4		U 4	U 4	U 4	U 4	U 4			
black spruce	C 1	A 1	O 1	O 3	C 1	A 1	C 1	A 1	C 1	C 1	A 1	U 3	U 3		U 3	U 3		U 3				
Douglas-fir												O 4	U 4				U 4		U 4			
Engelmann spruce											O 4	U 4	A 5	U 4								
jack pine	C 1	O 3	O 3		U 3		A 1		O 3	U 3					U 3	U 3						
limber pine										R 1	U 1	U 1	U 1	U 1								
lodgepole pine					O 3	A 1		O 3		A 1	A 1	A 1	A 3	U 3								
Manitoba maple																U 4	U 4			U 4	U 4	
narrow-leaf cottonwood										U 4									U 4	O 4		
peach-leaved willow																				U 4	U 4	
Rocky Mountain juniper												U 4	U 4									U 4
Scouler's willow	U 4		U 4	U 4						U 4		U 4										
subalpine fir					U 4	U 4				U 4	O 4		C 5	U 4								U 4

Natural Region	Boreal								Shield	Foothills		Rocky Mountain			Parkland				Grassland			
Natural Subregion	CM	NM	DM	PAD	LBH	UBH	AP	BSA	KU	LF	UF	M	SA	A	PRP	CP	FP	NF	FF	MG	DMG	
tamarack	C 4	C 4	O 4	U 4	C 4	O 4	U 4	U 4	U 4	C 4	O 4				U 4	U 4						
trembling aspen	A 5	C 5	A 5	O 4	A 5	U 4	U 4	U 4	U 4	A 5	O 4	C 5			A 4	A 4	A 4	U 4	U 4	U 4	U 4	
water birch	U 4		U 4							U 4	U 4	U 4				U 4	U 4	U 4	U 4	U 4	O 4	
western hemlock												R 1										
western larch												R 1	R 1									
western redcedar												R 1	R 1									
western white pine												R 1										
western yew												R 2										
western/plains cottonwood																				U 4	U 4	
white birch	O 4	O 4	O 4	O 4	C 5	U 4	U 4	U 4	U 4	O 4	U 4	U 4			U 4	O 4				U 4		
white spruce	A 1	A 1	C 1	A 1	A 1	A 1	U 3	O 3	U 3	A 1	O 3	C 1			U 3	U 3	U 3					
whitebark pine													O 1	C 1								

^aA: abundant - a major component of stands throughout the subregion

C: common - either frequent with a patchy distribution or as a minor but significant component of stands throughout the subregion

O: occasional - occurs in occasional localized patches, as a minor component in stands throughout the subregion, or as a significant species in part of the subzone

U: uncommon - a minor presence within a subregion either as occasional individuals or isolated small populations

R: rare - occurs in limited numbers and distribution

NOTE: species are not listed for a subregion when they have a limited presence in the ecotone with a zone where the species is more common
^bpriority ranking (high 1 to low 5). See Section 6.1.

Table 10. Ex situ conservation categories^a by natural subregion

NATURAL REGION	BOREAL								SHIELD	FOOTHILLS		ROCKY MOUNTAIN			PARKLAND				GRASSLAND			
NATURAL SUBREGION	CM	NM	DM	PAD	LBH	UBH	AP	BSA	KU	LF	UF	M	SA	A	PRP	CP	FP	NF	FF	MG	DMG	
Alaska birch	1	1	1	1	1	1	1	1	1													
alpine larch													1	1								
balsam fir	1	1	1	1	1		1			1	1				1							
balsam poplar	1	1	1	1	1	1	1	1	1	1	1	1	1		1	1	1	1	1			
black spruce	1, 3	1	1, 3	1	1	1	1	1	1	1	1	1	1		1	1		1				
Douglas-fir												1, 3	1				1, 3		1			
Engelmann spruce											1	1, 3	1, 3	1, 3								
jack pine	1, 3	1	1		1		1		1	1					1	1						
limber pine										1, 2	1, 2	1, 2	1, 2	1, 2								
lodgepole pine					1, 3	1, 3		1		1, 3	1, 3	1	1	1								
Manitoba maple																1	1			1	1	
narrow-leaf cottonwood										2									2	2		
peach-leaved willow																				2	2	
Rocky Mountain juniper												1	1									1
Scouler's willow	2		2	2						2		2										

NATURAL REGION	BOREAL								SHIELD	FOOTHILLS			ROCKY MOUNTAIN			PARKLAND				GRASSLAND		
NATURAL SUBREGION	CM	NM	DM	PAD	LBH	UBH	AP	BSA	KU	LF	UF	M	SA	A	PRP	CP	FP	NF	FF	MG	DMG	
subalpine fir					1	1				1	1		1	1								1
tamarack	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3				1	1						
trembling aspen	2	2	2	2	2	2	2	2	2	2	2	2			2	2	2	2	2	2	2	2
water birch	1		1							1	1	1				1	1	1	1	1	1	1
western hemlock												1										
western larch												1, 3	1									
western redcedar												1	1									
western white pine												1										
western yew												1										
western/plains cottonwood																					2	2
white birch	1	1	1	1	1	1	1	1	1	1	1	1			1	1					1	
white spruce	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3	1, 3			1	1	1					
whitebark pine													1, 2	1, 2								

^a1: wild stand seed collections, 2: germplasm collections of improved genetic stock, 3: seedlings and vegetative materials from wild populations

Regional priorities

Alberta's landscape has six natural regions, 21 natural subregions and is divided into 90 seed zones (Natural Regions Committee 2006; ASRD 2009a). Superimposed on the ecological regions and subregions are breeding regions for species where species specific tree improvement programs are in place. For example white spruce tree improvement programs currently delineate nine breeding or CPP (controlled parentage program) regions. Tree improvement programs are in place or under development for eight species (white spruce, black spruce, lodgepole pine, jack pine, Douglas-fir, western larch, balsam poplar, and trembling aspen).

For the purposes of gene conservation all regions are considered equally important with additional emphasis on regions where genetic deployment of tree improvement materials is starting to occur and there is a designated CPP region. Guidance in this regard can be derived from Table 2 of the *Alberta Forest Gene Conservation Plan* where each species is discussed regarding emphasis on gene conservation according to regional geography.

To capitalize on known adaptive patterns of Alberta species and to provide potential supplementary genetic resources, species whose ranges overlap adjacent jurisdictions are of interest to the province. Adaptation studies have shown that select material from US jurisdictions may perform well in Alberta, particularly given anticipated climate change, and material from other prairie provinces and British Columbia may also provide valuable genetic resources. This is especially the case for tested parent trees to potentially include in breeding programs and, for endangered species, tested rust resistant trees. These been low priorities and will continue to be low priority for now, but should seed be available from seed zones that projections predict are likely to be compatible with Alberta deployment zones currently or in the future, then Alberta would seek to include this material in ex situ collections.

Monitoring and Implementation

The program and species priority list will be reviewed every five years to account for advances in conservation science, equipment availability, land use planning, and provincial priorities. Seed and clone bank inventory will be reviewed every three to five years to evaluate whether gaps are being filled, or collections with low viability need to be replaced. Clone banking needs for species with seeds that do not store well in a seed bank will also be assessed. Annual lists of ATISC ex situ seed inventory species-seed zone combinations that exceed the requirements will be provided to forest companies identifying collections for which seed contributions are not required.

As seed orchards advance and some genotypes are eliminated through roguing, the representation of material in clone banks, seed banks, and progeny trials should maintain adequate representation to conserve population diversity ex situ, as required by FGRMS. There is no need to retain copies of every clone ever selected or tested for the sake of gene conservation because, as described above, the existing production and testing populations will meet conservation objectives.

The opportunity to expand seed collections to conserve other species should be considered when the strategic direction and objectives of Forest Management Branch are reviewed. Alberta has hundreds of plant species at risk, but only a handful of woody perennials. All others are non-vascular plants, annual plants, and herbaceous perennials and forbs. The seeds are often miniscule and would not take up much space, but proper collection protocols may not exist, identification can be tricky, and processing could be extremely labour intensive. There are currently no other provincial programs or facilities that would conserve seeds of native species at risk. Extension is needed to ensure proper collection procedures and timing and possibly processing, but volunteer groups have expressed interest in contributing native seeds for conservation, and there has been considerable interest in a native seed bank or organization for western Canada (R. Moody, Keefer Ecological Services, pers. comm.; T. White, Tipi Mountain Native Plants, pers. comm.; D. Pigott, Yellow Point Propagation, pers. comm.).

Representing the Forest Management Branch, the provincial tree seed centre has the opportunity to expand its existing collaboration with the National Tree Seed Centre in New Brunswick and the Tree Seed Centre in British Columbia. This agency is a valuable national resource that stores seed and germplasm of native trees of Canada, and provides them at no cost for research projects. Sharing the considerable expertise between agencies in seed biology, processing, and storage, as well as research and extension opportunities, benefits all parties.

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Appendix 1A: Wild seed collections of indigenous species by natural subregion

Species	Natural Subregion	Bulk*	Single*
Aw	Central Mixedwood	<u>3</u>	
Bw	Central Mixedwood	1	
Bw	Lower Boreal Highlands	1	1
Fa	Montane	1	10
Fa	Subalpine	0	20
Fb	Lower Foothills	0	1
Fd	Central Parkland	1	
Fd	Montane	<u>4</u>	29
Fd	Subalpine	1	
Jrm	Montane	1	1
Ll	Alpine	0	2
Ll	Subalpine	<u>4</u>	2
Lt	Central Mixedwood	<u>5</u>	<u>38</u>
Lt	Dry Mixedwood	<u>6</u>	<u>50</u>
Lt	Lower Foothills	1	1
Lt	Northern Mixedwood	1	
Lt	Upper Foothills	1	
Pa	Alpine	2	<u>46</u>
Pa	Montane	1	2

Species	Natural Subregion	Bulk*	Single*
Pa	Subalpine	<u>11</u>	<u>295</u>
Pdo	Dry Mixedgrass	1	
Pend	Central Mixedwood	2	
Pf	Alpine	1	
Pf	Central Mixedwood	0	1
Pf	Foothills Fescue	0	9
Pf	Foothills Parkland	0	5
Pf	Montane	<u>20</u>	<u>336</u>
Pf	Subalpine	<u>4</u>	<u>117</u>
Pj	Athabasca Plain	0	<u>58</u>
Pj	Central Mixedwood	<u>9</u>	<u>40</u>
Pj	Dry Mixedwood	<u>6</u>	8
Pj	Kazan Uplands	0	15
Pj	Lower Boreal Highlands	0	8
Pl	Alpine	1	1
Pl	Boreal Subarctic	2	
Pl	Central Mixedwood	<u>10</u>	20
Pl	Dry Mixedwood	<u>7</u>	3
Pl	Foothills Parkland	1	

Species	Natural Subregion	Bulk*	Single*
Pl	Lower Boreal Highlands	<u>28</u>	<u>89</u>
Pl	Lower Foothills	<u>82</u>	<u>898</u>
Pl	Montane	<u>30</u>	<u>89</u>
Pl	Subalpine	<u>42</u>	<u>121</u>
Pl	Upper Boreal Highlands	<u>14</u>	6
Pl	Upper Foothills	<u>70</u>	<u>743</u>
PlxPj	Boreal Subarctic	1	
PlxPj	Central Mixedwood	<u>14</u>	1
PlxPj	Dry Mixedwood	<u>5</u>	
PlxPj	Lower Boreal Highlands	<u>7</u>	<u>63</u>
PlxPj	Lower Foothills	<u>3</u>	
PlxPj	Northern Mixedwood	1	
PlxPj	Peace River Parkland	1	
PlxPj	Upper Boreal Highlands	2	
Pv	Central Mixedwood	1	
Sb	Central Mixedwood	<u>9</u>	<u>53</u>
Sb	Dry Mixedwood	2	<u>31</u>
Sb	Lower Boreal Highlands	0	17
Sb	Lower Foothills	<u>3</u>	<u>38</u>
Sb	Montane	0	1
Sb	Subalpine	1	

*Collections with adequate samples are underlined

Species	Natural Subregion	Bulk*	Single*
Sb	Upper Foothills	<u>4</u>	7
Se	Montane	0	10
Se	Subalpine	2	
Se	Upper Foothills	1	
Sw	Athabasca Plain	0	1
Sw	Central Mixedwood	<u>5</u>	<u>465</u>
Sw	Central Parkland	0	1
Sw	Dry Mixedwood	<u>3</u>	<u>92</u>
Sw	Lower Boreal Highlands	2	<u>108</u>
Sw	Lower Foothills	<u>3</u>	<u>291</u>
Sw	Montane	<u>3</u>	<u>85</u>
Sw	Northern Mixedwood	<u>3</u>	5
Sw	Peace River Parkland	1	
Sw	Subalpine	0	9
Sw	Upper Boreal Highlands	1	2
Sw	Upper Foothills	<u>4</u>	<u>71</u>
SwxSe	Central Parkland	0	1
SwxSe	Montane	2	10
SwxSe	Upper Foothills	1	

Appendix 1B: Wild seed collections of indigenous species by seed zone

Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*
Aw	CM 2.4	2	0	Lt	CM 2.2	1	4	Pa	SA 4.3	<u>3</u>	<u>117</u>
Aw	CM 3.2	1	0	Lt	CM 2.3	0	10	Pdo	DMG 1.1	1	0
Bw	CM 3.2	1	0	Lt	CM 3.1	1	0	Pf	A 1.5	1	0
Bw	LBH 1.5	1	1	Lt	CM 3.2	1	1	Pf	CM 3.2	0	1
Fa	M 5.5	1	10	Lt	CM 3.3	1	19	Pf	FF 1.1	0	9
Fa	SA 1.2	0	6	Lt	CM 3.5	0	3	Pf	FP 1.1	0	5
Fa	SA 3.2	0	14	Lt	DM 1.2	1	21	Pf	M 4.1	<u>4</u>	<u>65</u>
Fb	LF 1.4	0	1	Lt	DM 1.3	<u>3</u>	9	Pf	M 4.4	1	24
Fd	CP 1.1	1	0	Lt	DM 2.1	1	0	Pf	M 4.5	<u>6</u>	<u>44</u>
Fd	M 2.2	1	0	Lt	DM 2.3	1	20	Pf	M 5.1	0	8
Fd	M 4.1	1	0	Lt	LF 1.3	1	0	Pf	M 5.4	2	<u>33</u>
Fd	M 4.4	1	0	Lt	LF 2.1	0	1	Pf	M 5.5	<u>3</u>	<u>37</u>
Fd	M 4.5	0	10	Lt	NM 1.1	1	0	Pf	M 5.6	<u>4</u>	<u>125</u>
Fd	M 5.5	0	19	Lt	UF 1.3	1	0	Pf	SA 1.2	1	0
Fd	M 5.6	1	0	Pa	A 1.2	2	<u>41</u>	Pf	SA 3.1	0	<u>48</u>
Fd	SA 3.1	1	0	Pa	A 1.5	0	5	Pf	SA 3.2	2	0
Jrm	M 5.6	1	1	Pa	M 5.6	1	2	Pf	SA 3.3	0	<u>55</u>
LI	A 1.4	0	2	Pa	SA 1.2	0	21	Pf	SA 4.2	1	0
LI	SA 1.1	1	0	Pa	SA 2.1	2	<u>102</u>	Pf	SA 4.3	0	14
LI	SA 4.2	<u>3</u>	2	Pa	SA 3.3	1	14	Pj	AP 1.1	0	<u>58</u>
Lt	CM 2.1	1	1	Pa	SA 4.2	<u>5</u>	<u>41</u>	Pj	CM 1.3	1	0

Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*
Pj	CM 2.1	0	8	PI	DM 2.2	1	0	PI	M 5.6	<u>3</u>	7
Pj	CM 2.2	1	0	PI	FP 1.1	1	0	PI	SA 1.1	<u>13</u>	<u>93</u>
Pj	CM 2.3	1	1	PI	LBH 1.1	<u>7</u>	23	PI	SA 1.2	<u>5</u>	3
Pj	CM 2.4	2	5	PI	LBH 1.4	2	0	PI	SA 2.1	0	11
Pj	CM 3.1	2	19	PI	LBH 1.6	<u>19</u>	<u>66</u>	PI	SA 2.2	1	0
Pj	CM 3.2	0	7	PI	LF 1.1	<u>4</u>	5	PI	SA 3.1	<u>8</u>	13
Pj	CM 3.3	1	0	PI	LF 1.2	<u>10</u>	16	PI	SA 3.2	<u>5</u>	1
Pj	CM 3.4	1	0	PI	LF 1.3	<u>7</u>	<u>119</u>	PI	SA 3.3	<u>5</u>	0
Pj	DM 1.1	<u>3</u>	<u>0</u>	PI	LF 1.4	<u>20</u>	<u>310</u>	PI	SA 4.1	2	0
Pj	DM 1.2	2	0	PI	LF 1.5	<u>10</u>	<u>115</u>	PI	SA 4.2	2	0
Pj	DM 2.1	0	8	PI	LF 2.1	<u>25</u>	<u>139</u>	PI	SA 4.3	1	0
Pj	DM 2.2	1	0	PI	LF 2.2	<u>4</u>	<u>173</u>	PI	UBH 1.1	1	0
Pj	KU 1.1	0	15	PI	LF 2.3	2	21	PI	UBH 1.2	<u>3</u>	0
Pj	LBH 1.5	0	8	PI	M 1.1	<u>8</u>	<u>43</u>	PI	UBH 1.3	<u>10</u>	6
PI	A 1.2	1	1	PI	M 2.1	<u>3</u>	7	PI	UF 1.1	2	<u>152</u>
PI	BSA 1.1	1	0	PI	M 3.2	0	1	PI	UF 1.2	<u>11</u>	1
PI	BSA 1.2	1	0	PI	M 4.1	1	5	PI	UF 1.3	<u>22</u>	<u>415</u>
PI	CM 1.3	1	0	PI	M 4.3	1	2	PI	UF 1.4	<u>16</u>	<u>121</u>
PI	CM 2.3	1	0	PI	M 4.4	2	4	PI	UF 1.5	<u>12</u>	<u>47</u>
PI	CM 3.3	0	4	PI	M 4.5	1	0	PI	UF 2.4	1	1
PI	CM 3.4	<u>8</u>	8	PI	M 5.1	1	0	PI	UF 2.5	<u>6</u>	6
PI	CM 3.5	0	8	PI	M 5.3	2	5	PlxPj	BSA 1.1	1	0
PI	DM 1.2	<u>5</u>	3	PI	M 5.4	<u>5</u>	10	PlxPj	CM 1.3	<u>4</u>	0
PI	DM 1.3	1	0	PI	M 5.5	<u>3</u>	5	PlxPj	CM 2.3	2	1

Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*
PixPj	CM 3.2	1	0	Sb	CM 3.3	<u>3</u>	20	Sw	CM 1.3	<u>3</u>	<u>33</u>
PixPj	CM 3.3	<u>5</u>	0	Sb	CM 3.4	1	3	Sw	CM 2.1	0	19
PixPj	CM 3.4	2	0	Sb	DM 1.2	2	20	Sw	CM 2.2	0	6
PixPj	DM 1.2	1	0	Sb	DM 1.3	0	10	Sw	CM 2.3	0	14
PixPj	DM 1.3	<u>4</u>	0	Sb	DM 2.1	0	1	Sw	CM 2.4	0	<u>62</u>
PixPj	LBH 1.1	1	0	Sb	LBH 1.3	0	2	Sw	CM 3.1	0	<u>65</u>
PixPj	LBH 1.2	1	<u>31</u>	Sb	LBH 1.4	0	11	Sw	CM 3.2	0	<u>174</u>
PixPj	LBH 1.3	2	<u>32</u>	Sb	LBH 1.5	0	4	Sw	CM 3.3	1	<u>34</u>
PixPj	LBH 1.4	2	0	Sb	LF 1.3	1	3	Sw	CM 3.4	0	<u>31</u>
PixPj	LBH 1.5	1	0	Sb	LF 1.4	1	21	Sw	CP 1.1	0	1
PixPj	LF 1.1	1	0	Sb	LF 1.5	0	7	Sw	DM 1.1	2	9
PixPj	LF 1.4	1	0	Sb	LF 2.1	0	7	Sw	DM 1.2	0	<u>49</u>
PixPj	LF 1.5	1	0	Sb	LF 2.3	1	0	Sw	DM 1.3	0	7
PixPj	NM 2.1	1	0	Sb	M 3.2	0	1	Sw	DM 2.1	1	7
PixPj	PRP 1.1	1	0	Sb	SA 1.1	1	0	Sw	DM 2.2	0	20
PixPj	UBH 1.1	2	0	Sb	UF 1.3	<u>3</u>	7	Sw	LBH 1.1	1	9
Pv	CM 2.4	1	0	Sb	UF 1.5	1	0	Sw	LBH 1.2	0	2
Sb	CM 1.3	1	0	Se	M 4.5	0	10	Sw	LBH 1.3	1	2
Sb	CM 2.1	1	6	Se	SA 1.1	1	0	Sw	LBH 1.4	0	2
Sb	CM 2.2	1	1	Se	SA 4.2	1	0	Sw	LBH 1.5	0	5
Sb	CM 2.3	0	3	Se	UF 1.3	1	0	Sw	LBH 1.6	0	<u>88</u>
Sb	CM 2.4	1	2	Sw	AP 1.1	0	1	Sw	LF 1.1	0	16
Sb	CM 3.1	0	7	Sw	CM 1.1	0	18	Sw	LF 1.2	0	<u>45</u>
Sb	CM 3.2	1	11	Sw	CM 1.2	1	9	Sw	LF 1.3	0	<u>79</u>

Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*	Species	Seed zone	Bulk*	Single*
Sw	LF 1.4	0	<u>86</u>	Sw	M 5.5	1	10	Sw	UF 1.3	2	13
Sw	LF 1.5	2	<u>31</u>	Sw	NM 1.1	<u>3</u>	5	Sw	UF 1.4	0	27
Sw	LF 2.1	0	<u>32</u>	Sw	PRP 1.1	1	0	Sw	UF 1.5	2	20
Sw	LF 2.2	1	2	Sw	SA 1.1	0	9	SwxSe	CP 1.1	0	1
Sw	M 1.1	2	<u>63</u>	Sw	UBH 1.2	1	0	SwxSe	M 5.5	1	10
Sw	M 4.5	0	2	Sw	UBH 1.3	0	2	SwxSe	M 5.6	1	0
Sw	M 5.3	0	10	Sw	UF 1.1	0	11	SwxSe	UF 2.4	1	0

*Collections with adequate samples are underlined.

Appendix 2: Ex situ gene conservation seed collection maps and species' ranges

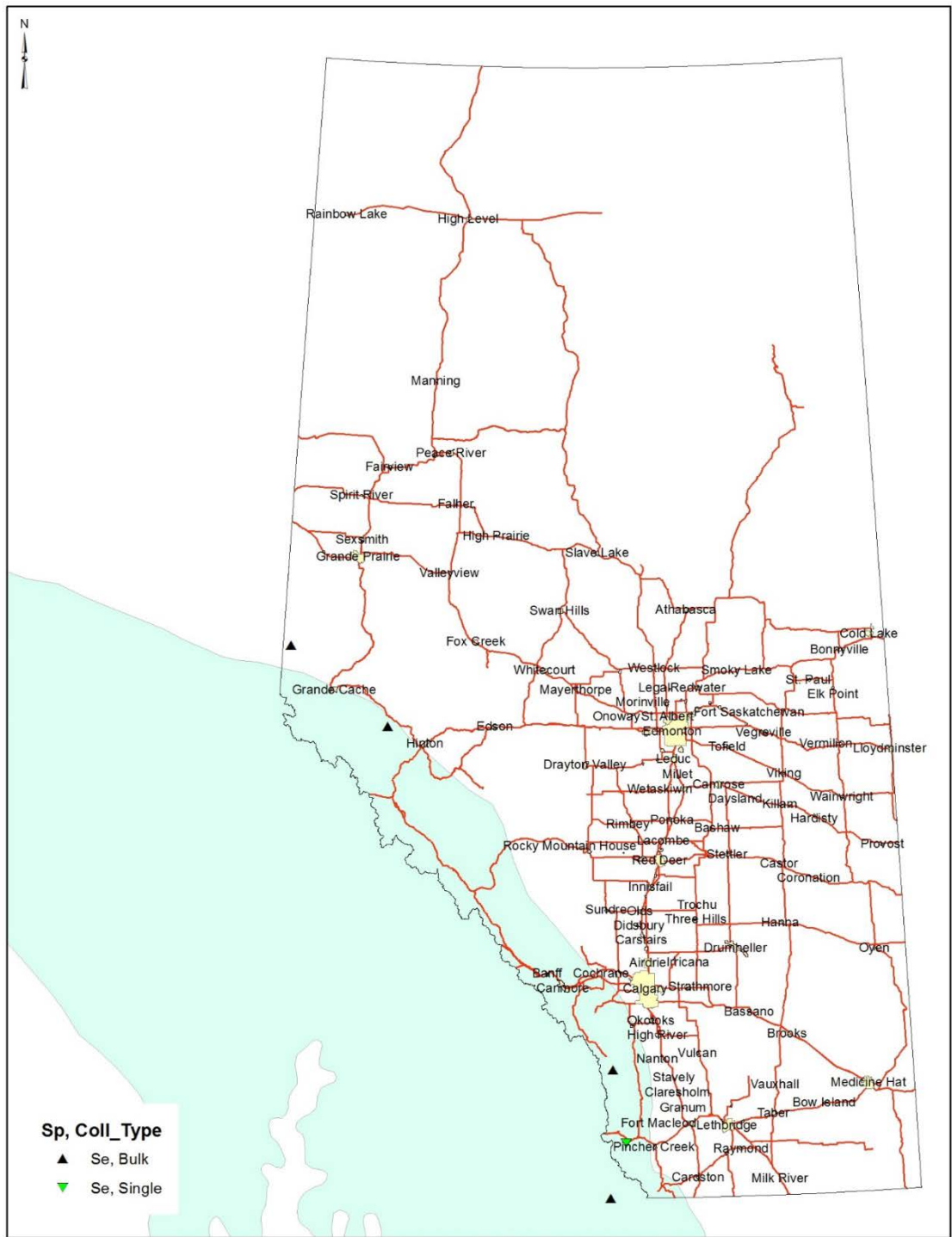


Figure A2.1. Engelmann spruce

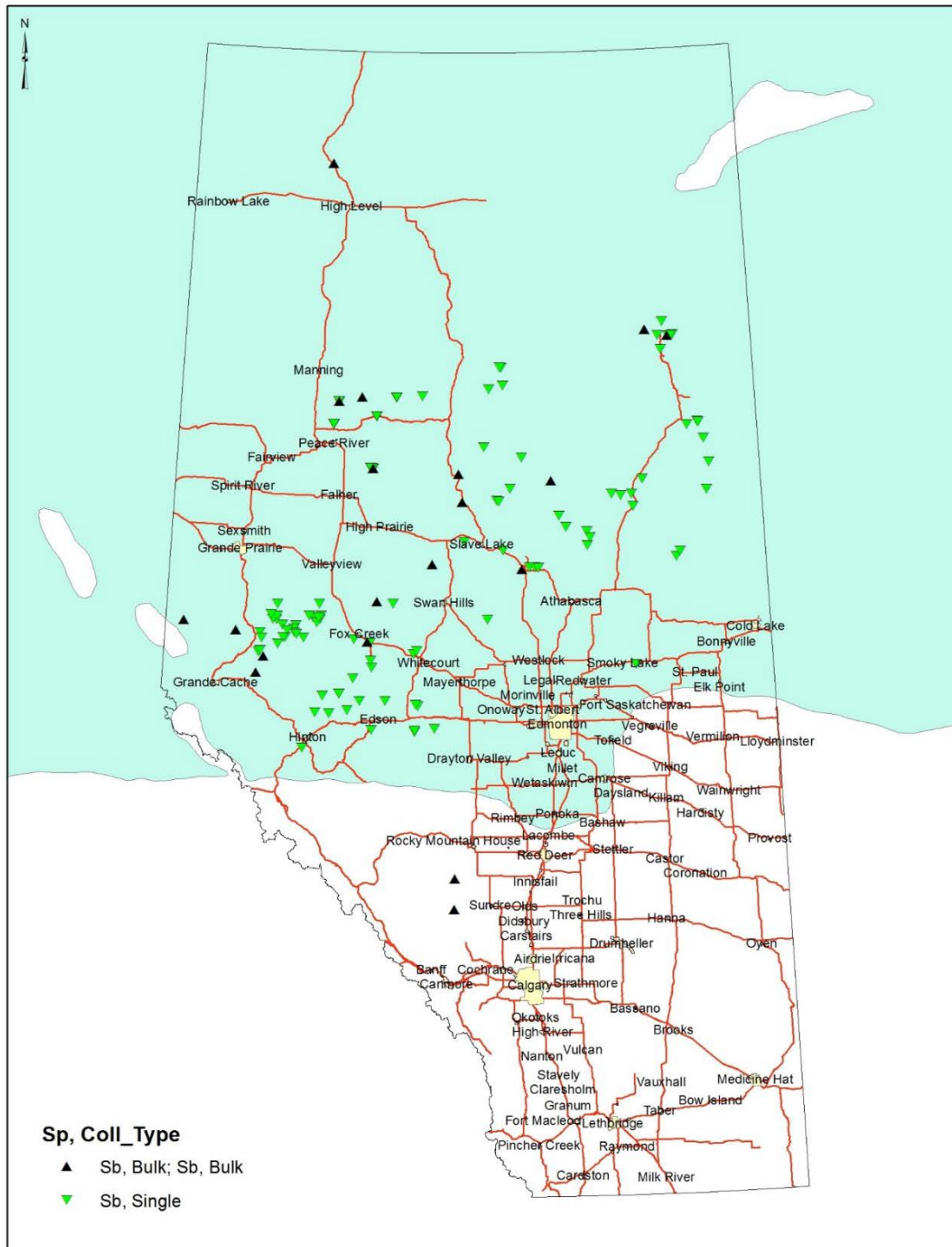


Figure A2. 2. Black spruce

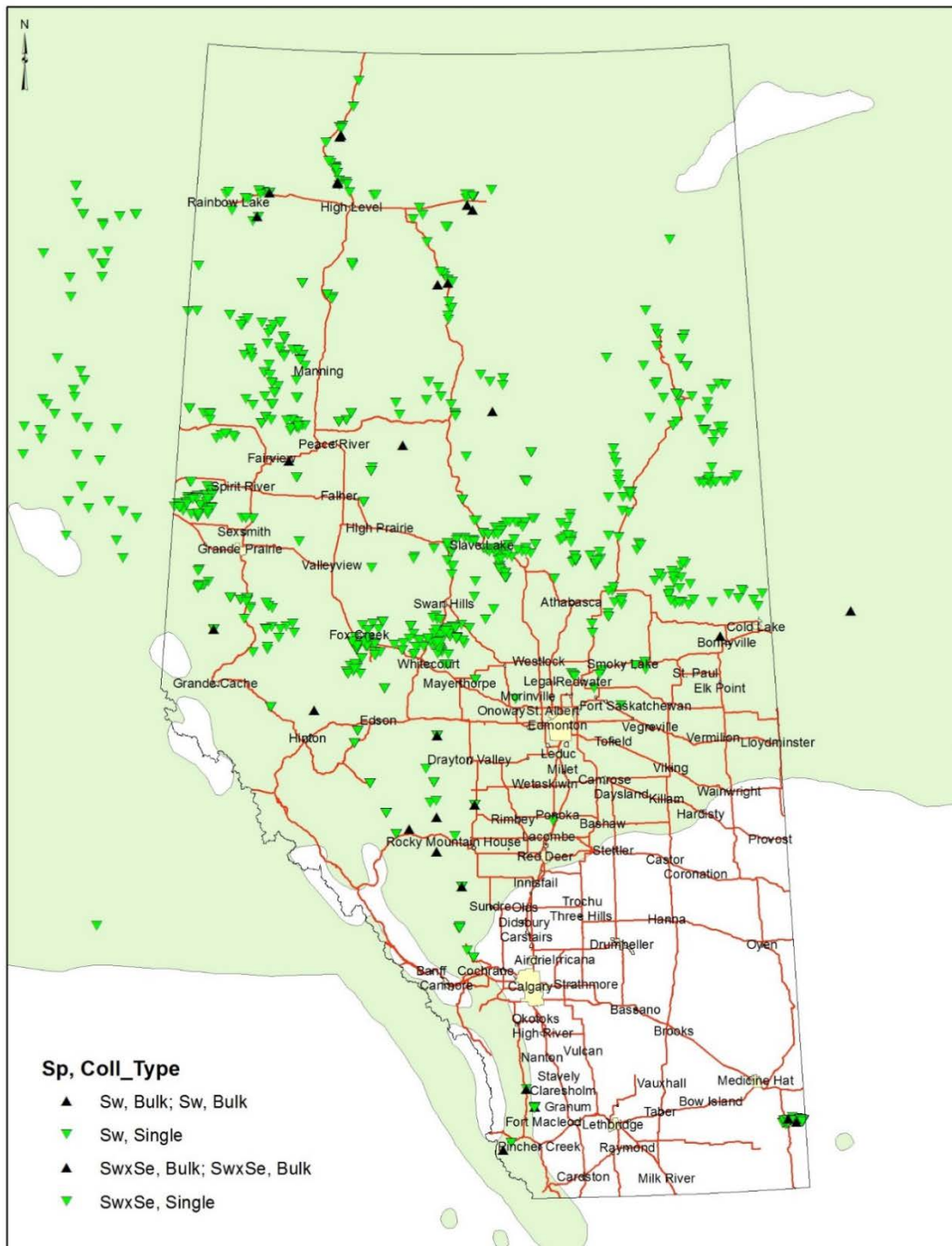


Figure A2.3. White spruce and white x Engelmann spruce hybrids

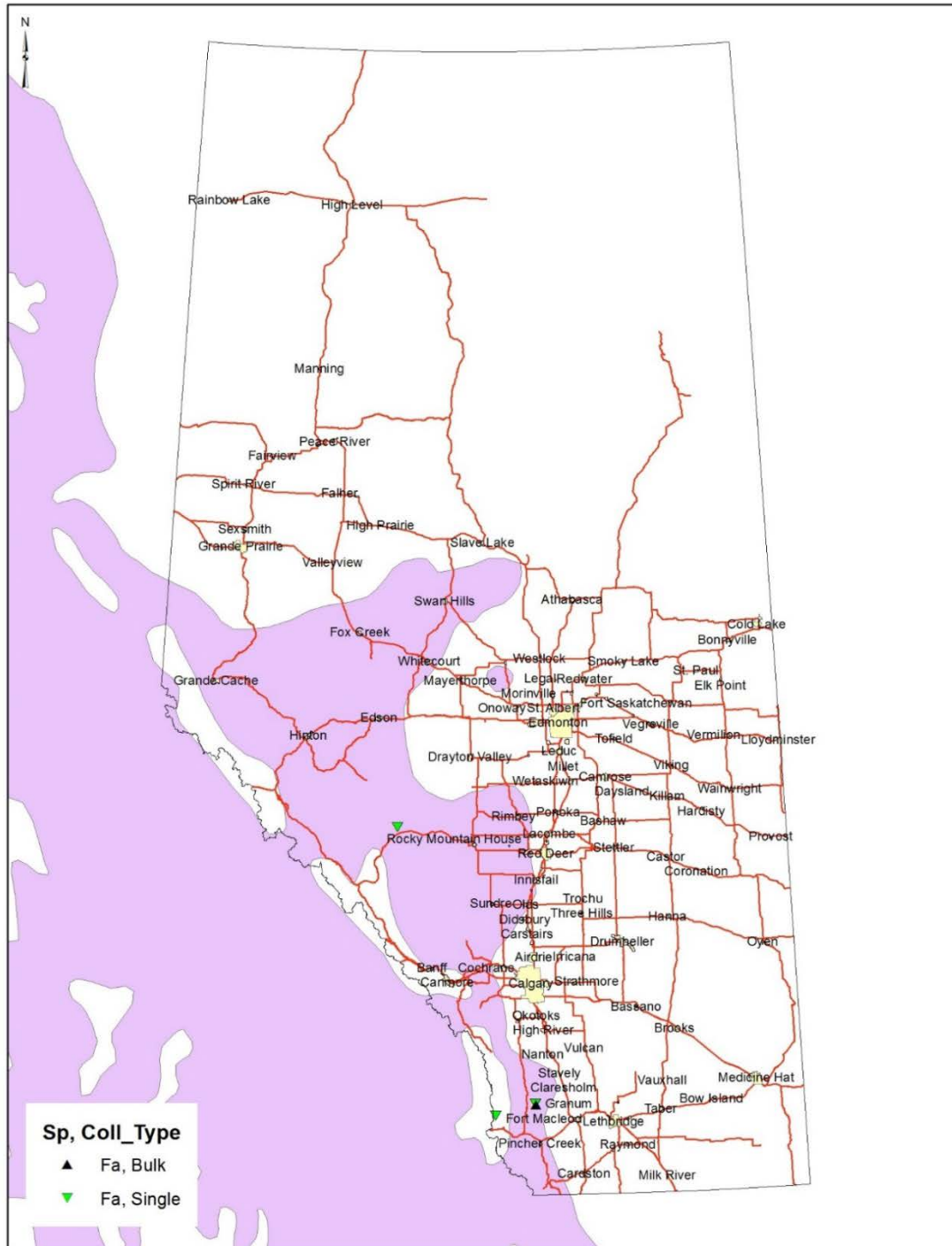


Figure A2.4. Subalpine fir

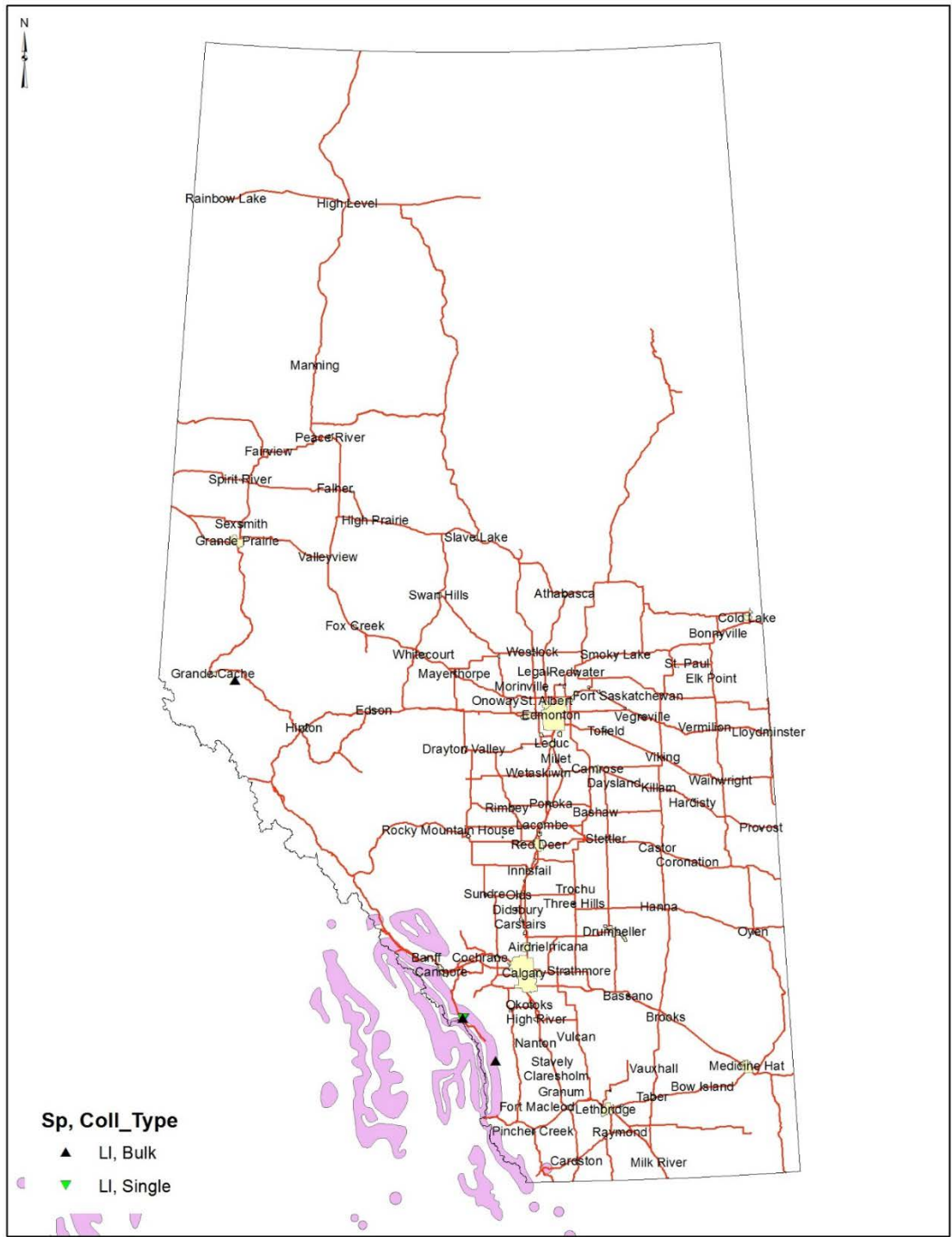


Figure A2.5. Subalpine larch

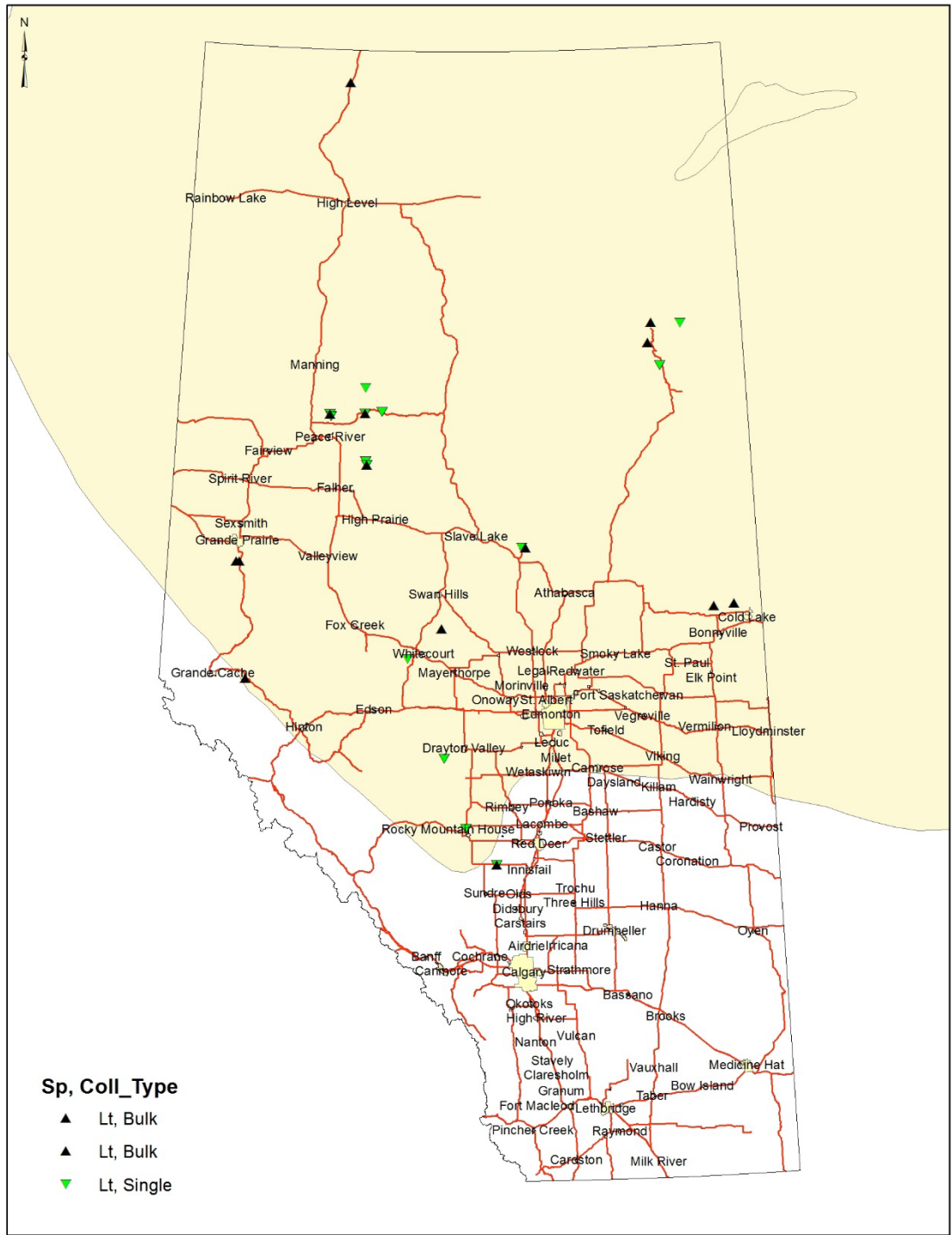


Figure A2.6. Tamarack



Figure A2.7. Paper birch



Figure A2.8. Rocky mountain juniper

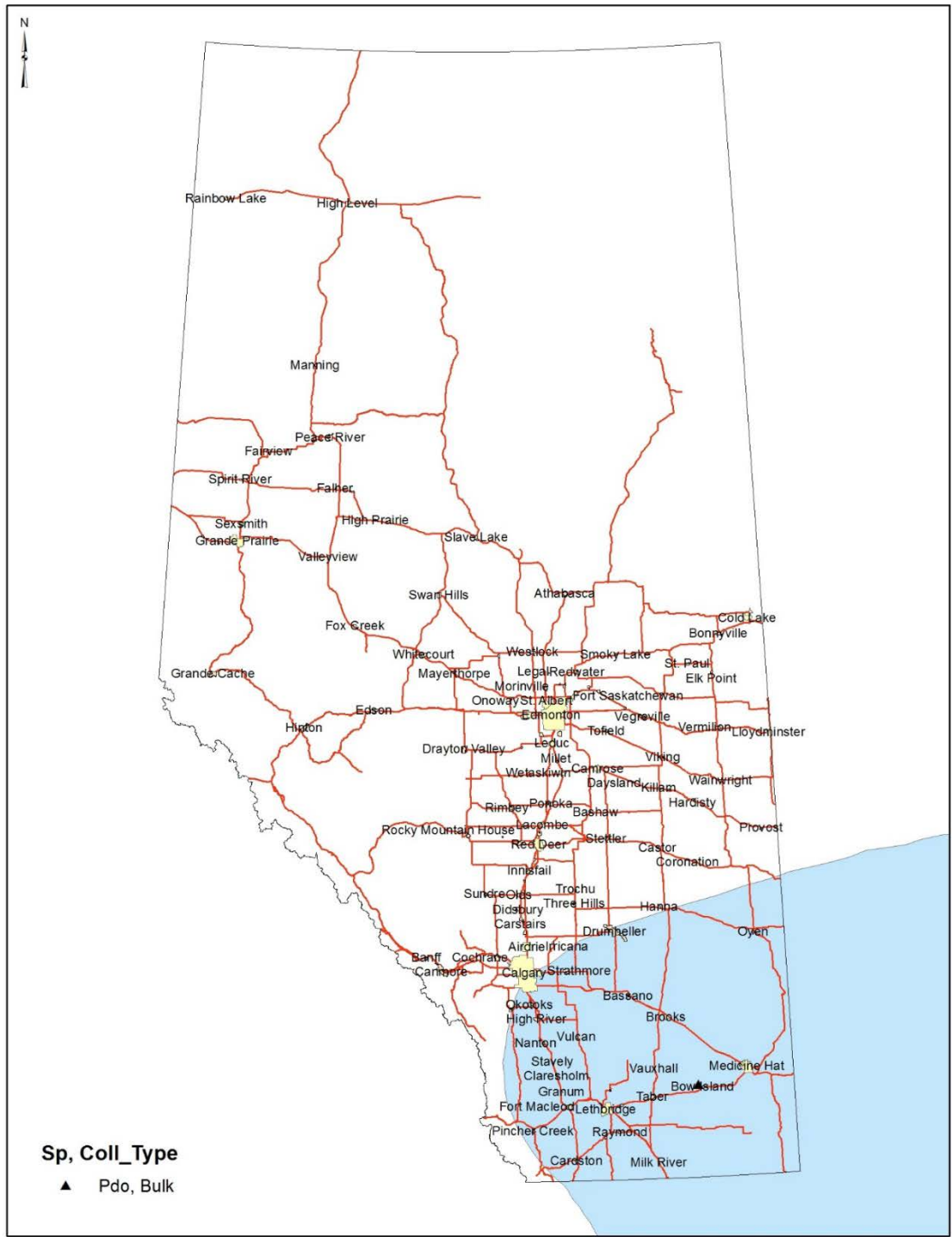


Figure A2.9. Eastern cottonwood



Figure A2.10. Douglas-fir

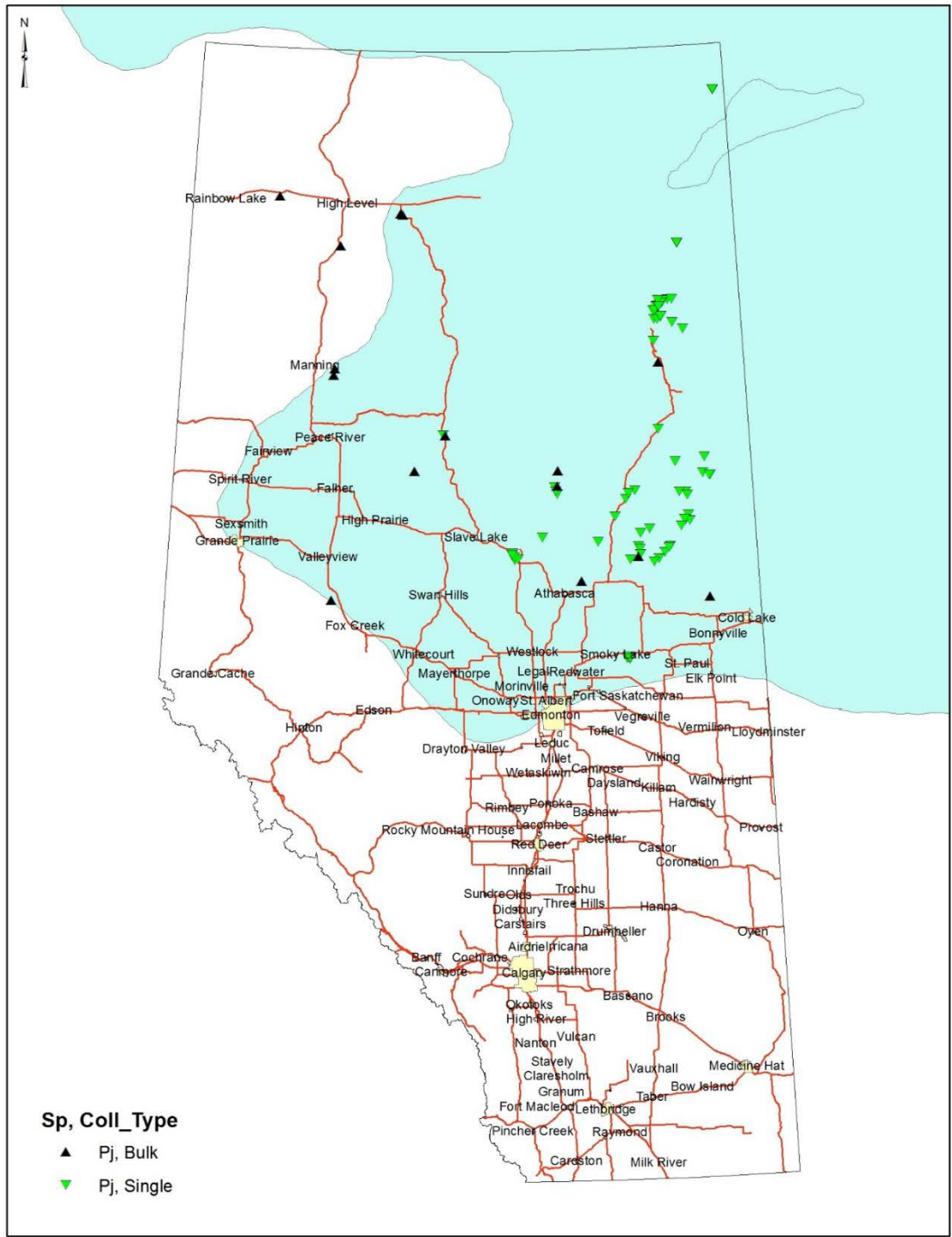


Figure A2.11. Jack pine

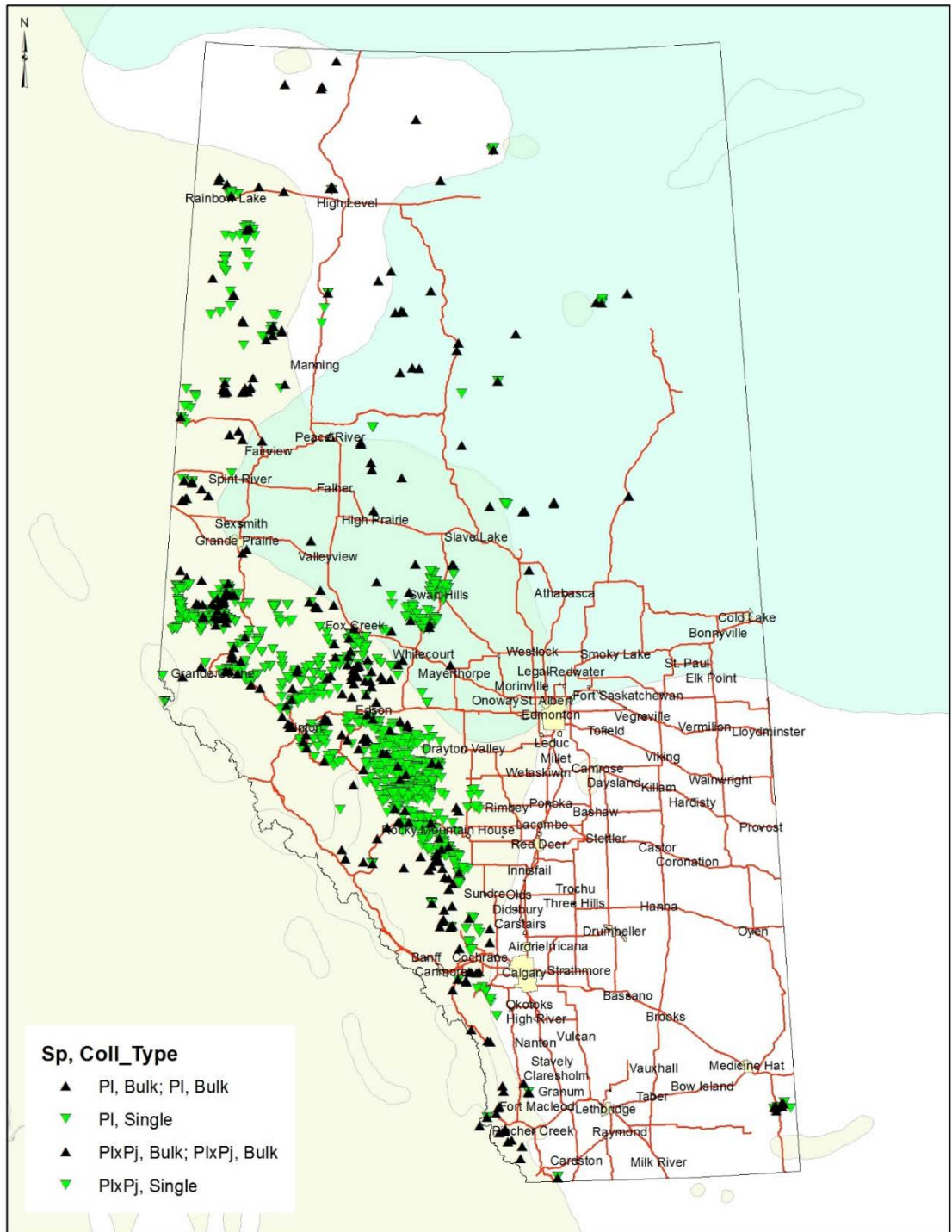


Figure A2.12. Lodgepole pine and jack pine x lodgepole pine hybrid

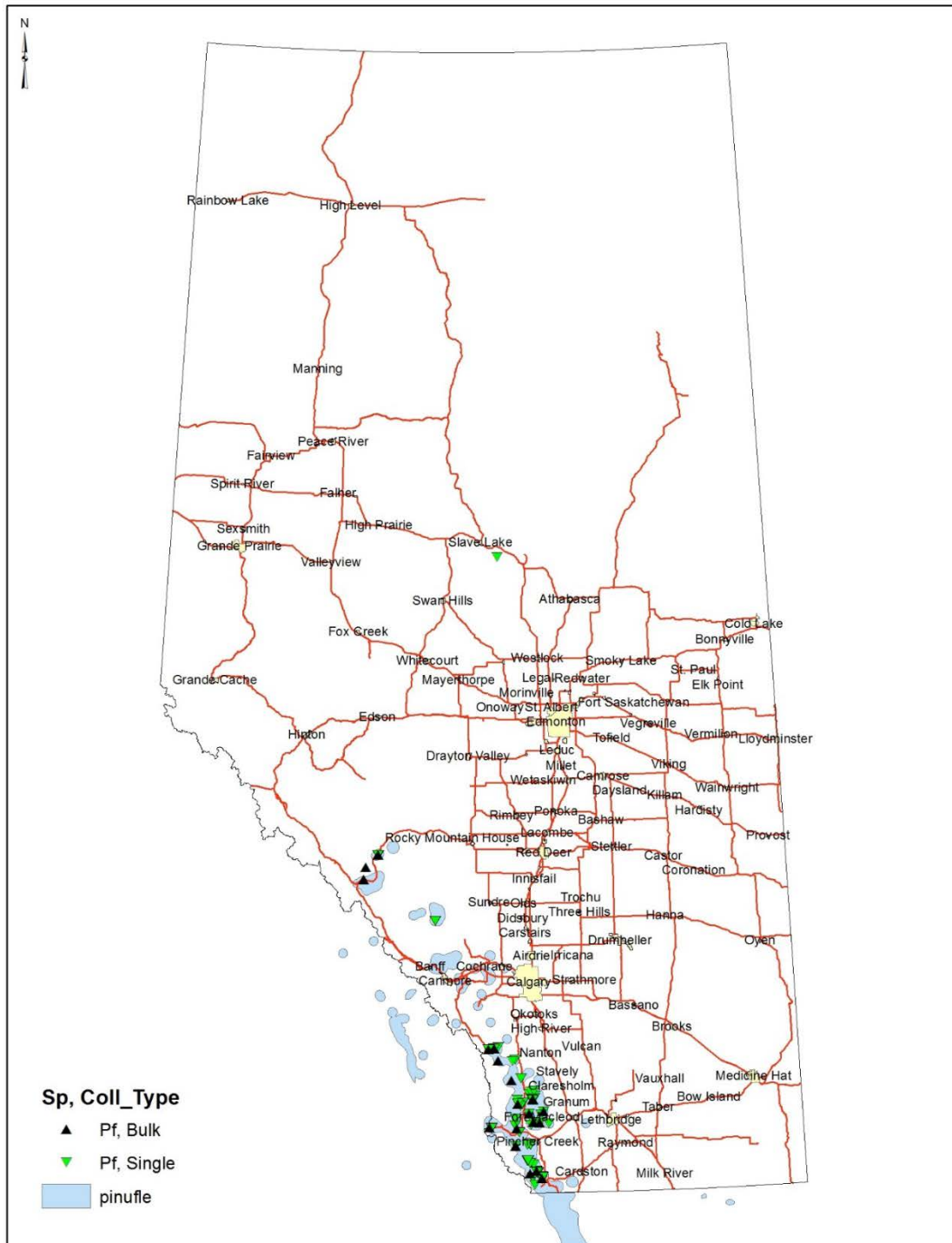


Figure A2.13. Limber pine

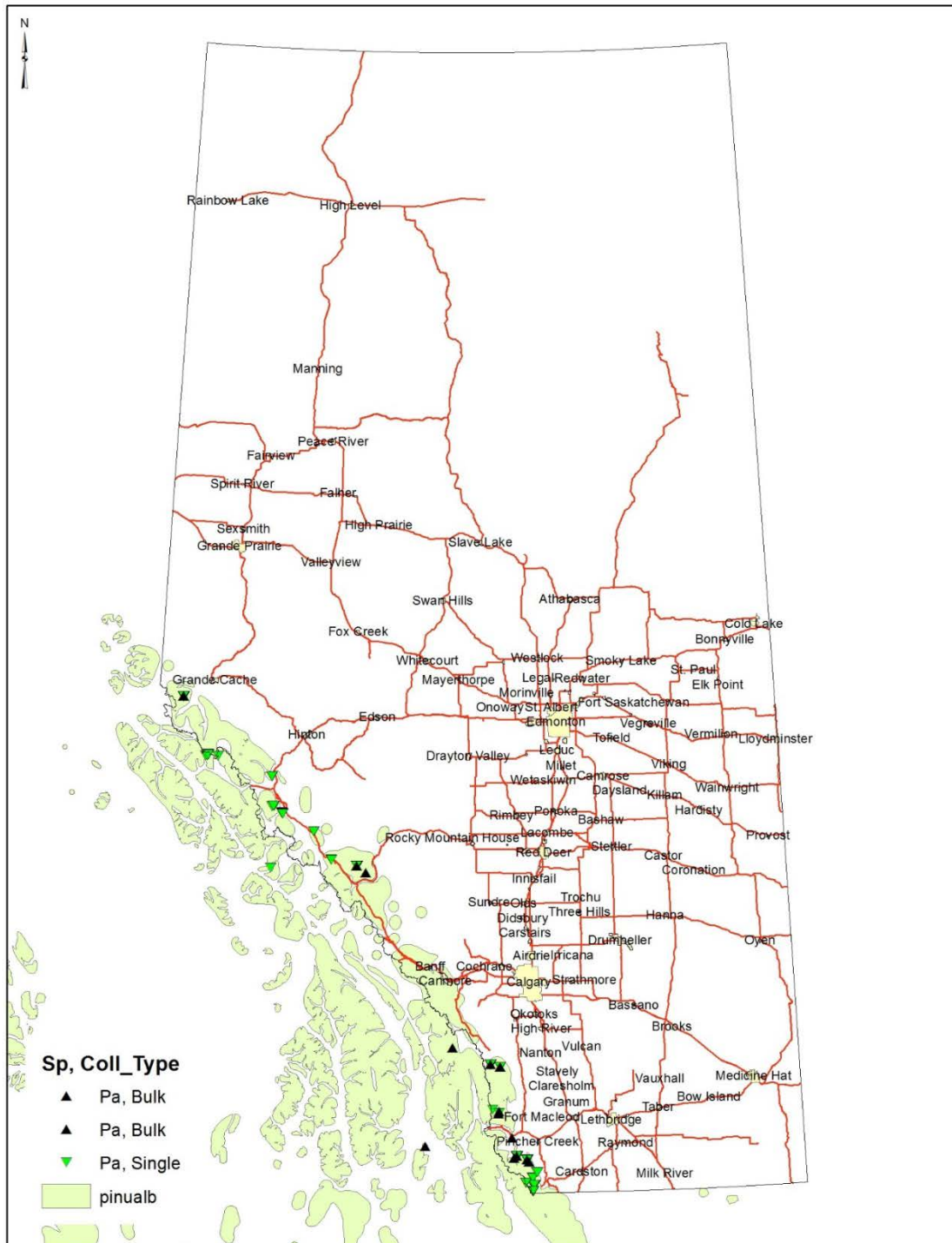


Figure A2.14. Whitebark pine

Appendix 3: Description and list of ex situ gene conservation facilities in Alberta

Alberta Tree Improvement and Seed Centre (ATISC)

ATISC was initially established in 1976, and was organized into its present form in 1978. The facility and staff are central to provincial seed registration, processing, storage, documentation, and conservation for the province of Alberta and supports the stewardship and scientific functions of the Forest Management Branch, Agriculture and Forestry. The program is carried out in cooperation with the forest and resource industry clients. The entire inventory of forest tree seed for reforestation in Alberta is held in storage in specially designed cold storage and seed handling facilities at ATISC. The ex situ collections are held in a separate facility on site. The entire facility is fenced off and secure. Keeping detailed documentation on the identities, status, history, objectives, and maintenance of all genetic trial installations also occurs at ATISC.

In addition to carefully controlled seed storage that reflects best practices of the International Seed Testing Association, staff conducts research to improve on the standards and understand seed morphology, biology, and handling to optimize efficiency, viability, and germination. ATISC has a range of cryogenic and environment-controlled facilities and a fully equipped laboratory.

ATISC has four small and two large greenhouses, all with current standard greenhouse equipment and controls, as well as one large cold frame. Field space, some with irrigation installed or available, is also on site for clone banks, arboreta, genetic archives and tests.

Crop Diversification Centre

The Crop Diversification Centre South, near Brooks, contains several genetic trial installations, seed orchards, and field space that may support additional clone banks or research trials.

Jumpingpound Demonstration Forest

The Jumpingpound Demonstration Forest near Calgary includes a site with several demonstration, provenance, and other research trials including exotic species. It is administered by the Forest Area office in Calgary and currently there is interest in expanding the interpretive capacity of the site.

Genetic Research Sites

There are 93 research sites around the province (see Figure 1). Most contain several projects including provenance and progeny trials, and several include non-native species (not described here). These sites are typically designated with a legal land disposition conferring varying degrees of protection from other land uses. These require notification to or consultation with Forest Management Branch when a proponent submits an application for adjacent or overlapping land use.