Alberta Forest Genetic Resource Management and Conservation Standards

Third Revision of STIA

Volume 1: *Stream 1* and *Stream 2*

Forestry Division
Alberta Agriculture and Forestry
December 21, 2016

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Corrigendum

Section	Standard	December 21, 2016	Change (Effective April 1, 2018)
19.0	19.1	*Wild* transplants and *propagules* from within 5 km and 100 m elevation of the target planting site or from within 20 km of the planting site and in the same *seed zone*, may be deployed without *registration*. These transplants and *propagules* may not be multiplied or serially propagated.	*Wild* transplants and ***vegetative*** *propagules* from within 5 km and 100 m elevation of the target planting site or from within 20 km of the planting site and in the same *seed zone*, may be deployed without *registration*. These transplants and ***vegetative*** *propagules* may not be multiplied or serially propagated.

Addendum

The following appendices were updated.

Appendices	Updated appendices can be found here: https://www.alberta.ca/forest-management-manuals-and-guidelines.aspx	Effective date
Appendix 2	Registration Request Form for Stream 1 Material (page 40)	May 1, 2020
Appendix 3	Registration Request Form for Stream 2 Material (page 41)	
Appendix 8	Request for Deployment Variance for Stream 1 Material (page 55)	
Appendix 10A	Authorization to Collect Plant Material Request Form for Stream 1 Material (page 59)	
Appendix 11 A	Parent Tree Selection Form – Wild Stand or Plantation Comparison Tree Method (page 61)	
Appendix 11 B	Parent Tree Selection Form – Wild Stand or Plantation Non-Comparison Tree Method (page 62)	
Appendix 11 C	Parent Tree Selection Form – Geographic Selection Method (page 63)	
Appendix 12	Parent Tree Selection Form – Genetic Test Materials (page 64)	
Appendix 15	Parent Tree Selection Form for Material Collected Outside Alberta (page 69)	
Appendix 16	Research, Conservation or Controlled Parentage Program Transportation and Interim Storage of Plant Material Form (page 70)	
Appendix 17	Seed and Vegetative Materials Withdrawal and Transportation Form (page 71)	
Appendix 22	Request for Deployment Variance for Stream 2 Material (page 89)	
Appendix 29	Genetic Test Site Information Form (page 103)	

This document is available on the government website by searching Alberta Forest Genetic Resource Management and Conservation Standards.

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This major revision of the Alberta Forest Genetic Resource Management and Conservation Standards (FGRMS), completed in 2016, was undertaken through the concerted efforts of a Steering Committee that included both Government of Alberta (*Alberta*) and industry representatives, and a Technical Committee made up of geneticists and other experts. Numerous other individuals provided comments and suggestions considered by the two committees.

Alberta wishes to thank the following individuals for their dedication and diligence in the revision of these standards.

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NOTE: Standards inside a double-lined box apply exclusively to CPPs (see Figure 5.1, Stream 2) (refer to page 5 second paragraph).

Table of Contents

List of Figures

List of Tables

List of Appendices

List of Appendix Tables

GENERAL

In this manual, all texts in italics are terminologies defined in the glossary at the end of the manual; species Latin names are underlined not italicized.

1.0 Authority, Principles and Rationale

Alberta Forest Genetic Resource Management and Conservation Standards (these Standards) are rules under the Timber Management Regulation 144.2 (1) ("The Minister may establish rules governing the source and type of tree seed and vegetative propagules used to reforest public land"). All rules in this manual facilitate the collection, development, processing, documentation, tracking, custody and eventual use of forest reproductive materials.

The forest genetic resources of Alberta are crucial to the long-term economic and ecological stability of the province.

The Government of Alberta (*Alberta)* and industry operating on Alberta *public lands*:

i) endeavour to ensure the adaptability, diversity and health of *wild* and managed plant populations, and to conserve the genetic integrity of *wild* forest plant populations on the landscape; and
ii) recognize the value of genetic improvement in enhancing the productivity of the forest landbase and generating economic benefit.

Resource managers operating on Alberta *public lands* have responsibilities for maintaining the value of the genetic resources of the province. This is an ethical commitment to future generations as well as support to *Alberta* in meeting its commitments under the 1992 Convention on Biological Diversity to conserve and sustainably use forest genetic resources.

In meeting these commitments, the role of *Alberta* is to:

i) protect the public interest and conserve the forest genetic resource by implementing conservation and sustainable use programs and enacting and enforcing policies, regulations and standards;
ii) promote development of that resource for the economic benefit of the people of Alberta; and
iii) participate in the development and implementation of genetic improvement and related technologies.

The role of industry and other resource users is to:

i) respect the public interest by complying with enacted policies, regulations and standards; and
ii) develop objectives and strategies that will increase the value derived from the forest genetic resource.

The need for standards related to sustainable use and conservation of forest genetic resources arises largely from human activity and development, which may interrupt natural genetic processes on the landscape. Without management, human activity can lead to genetic erosion, reduced fitness and loss of evolutionary resilience in *wild* populations, and can also reduce opportunities for development of new and useful plant varieties and gene products.

Although plant breeding can result in significant benefits, it also typically results in the displacement of *wild* plants by domesticated varieties, and is generally recognized to have the potential to reduce genetic variation and alter population gene frequencies (through *Stream 2* activities). Not as well understood is the potential of *artificial regeneration* using *wild* plant materials (through *Stream 1* activities) to pose similar risks, through human interference in natural selection (through collection and deployment of seed and other *propagule*s), and gene migration (through plant transport to new locations).

Maintaining adequate levels of *genetic diversity* is important for conserving the adaptive potential of species and populations in changing environments. It is also essential for minimizing inbreeding, which can reduce the fitness (survival, growth and reproductive capability) of a population.

Ideally, *genetic diversity* of a population would be measured through direct genomic assessment; however this is not yet practical. *Effective population size* (*Ne*) is a surrogate diversity measure used in many tree breeding programs. The concept of *Ne* is also used in risk assessment and management strategies for endangered animal species. *Ne* is the number of individuals in an idealized population that would undergo inbreeding or genetic drift at the same rate as the population of interest (e.g., a *seed orchard*) if left to reproduce naturally. *Ne* is a function of the number of *genotype*s (i.e., parents) in the population, the degree of variation in genotypic representation among *genotype*s, and the degree of relatedness among *genotype*s.

The minimum *Ne* of 18 required for *unrestricted registration* of *Stream 2* material in FGRMS (see Standard 34.2 for exception) was based on the following factors:

i) Natural stands of open-pollinated conifers exhibit inbreeding coefficients of about 0.05 - 0.125. Based on a precautionary approach, it was determined that planted stands of genetically improved trees should be able to reproduce naturally for at least three generations without exceeding an inbreeding coefficient of 0.1.
ii) Each step required in the calculation of *Ne* introduces error into the estimation and the result is therefore imprecise.

For *unrestricted registration* of *Stream 1* materials (see Appendix 4), collections are based on the same principle of meeting a minimum *Ne* ≥18.

2.0 Development and Review of the Standards

Management and conservation standards were developed through extensive consultation with geneticists and other scientific and management professionals. The Alberta Forest Legacy document guided the original development of the standards.

The standards were implemented in 2003, under the name Standards for Tree Improvement in Alberta (STIA), and were revised in 2005, 2009 and 2016; they were renamed Alberta Forest Genetic Resource Management and Conservation Standards (FGRMS) in 2009.

The original 2003 standards represented science-based policy that was developed to maintain the genetic integrity, health and productivity of Alberta's *wild* and managed forests. The standards guided the management of forest genetic resources in *reforestation* and tree improvement activities on public forest lands.

With ongoing industrial development, the use of appropriate plant genetic material in *reclamation* is essential for the maintenance of ecosystem function and biological diversity. One of the main outcomes of the 2016 review is that the revised standards now apply to the use of all woody plants in *reclamation* of land within the *Green Area*, as well as to *reforestation* and tree improvement.

In revising the standards, it was recognized that *reclamation* personnel will generally utilize *Stream 1* materials (seed or vegetative material collected from stands of *wild* or *artificially regenerated* native species), rather than *Stream 2* materials (seed or vegetative material produced in *production units*). Consequently, the standards are presented in two separate documents. The first, entitled "Alberta Forest Genetic Resource Management and Conservation Standards Volume 1*: Stream 1* and *Stream 2*" will contain all standards. The second, entitled "Alberta Forest Genetic Resource Management and Conservation Standards Volume 1A: *Stream 1*", will contain only those standards that apply to *Stream 1* material. This will facilitate use by *reclamation* personnel and those not involved in tree improvement activities.

The major changes in FGRMS 2016 are:

i) new clonal deployment standards;

ii) standards applicable to shrubs;
iii) enabling of deployment of *Stream 2* seed on more than 50% of *species-specific target strata* area;
iv) incorporation of a new method of estimating *genetic gain* at rotation age;
v) a revised process for establishment of *species-specific seed zones*;
vi) revised seed testing and storage standards;
vii) a revised and expanded section on Policy Issues and International Agreements; and
viii) *in situ gene conservation* standards.

The current version (FGRMS 2016) could not resolve all issues, largely due to insufficient knowledge. Issues to be addressed before completion of the next review include:

i) inclusion of other vascular plants (herbaceous native species) for *reclamation*;
ii) implications of seed sales on *cumulative Ne* reporting of deployed populations;
iii) implications of seed sales for *in situ conservation* areas required for *controlled parentage programs* (*CPP*s);
iv) consideration of mapping requirements in Standard 21.2.3 and 21.2.5 with respect to Alberta Regeneration Information System (ARIS) spatial capability;
v) consideration of an FGRMS stated criterion on when to permit use of seed with *restricted registration* and the amount to approve;
vi) duration of orchard phenology monitoring and implications of results; and
vii) age-age correlation.

Issues to be addressed to support future development of standards include:

i) development of a provincial shrub provenance testing research program to inform shrub seed transfer standards and *species-specific seed zone*s (SSSZs) for shrubs;
ii) development of seed transfer and deployment standards to address adaptation to climate change, through continued testing of populations and species over a wide environmental range, including extreme environments;
iii) development of standardized protocols for realized gain *trial*s, and for assessment of gain in plantations established with *Stream 2* materials; and
iv) consideration of the use of exotic species, hybrids and provenances in *reclamation* and *reforestation*.

3.0 Applicability

These standards apply to lands in the *Green Area*. In addition, the standards for Material Collection, Handling, Registration and Storage (MCHRS) apply to material collected from *public land* as well as all material intended for *deployment* in the *Green Area*, regardless of where the material was collected. Native trees and shrubs commonly encountered in Alberta are listed in Appendix 38; species codes are provided for *registration* purposes. For species not listed in Appendix 38 contact *Alberta*.

Users of these standards are:

i) all forest companies and public institutions that collect *Stream 1* and *Stream 2* material and vegetative materials or develop genetically improved seed and vegetative materials for reforestation and/or research on public land;
ii) all energy companies that use woody plants (trees and shrubs) for assisted revegetation on public land (ref. Alberta Energy Regulator Integrated Standards and Guidelines 200.2.7(c) and 200.2.9) & other Environmental Protection Enhancement Act approvals that mandate use of FGRMS when planting woody plants on public land);

iii) all private collectors and/or distributors of plant propagation materials from public land intended for commercial use and/or reforestation, revegetation and research on public land or research elsewhere, and gene conservation;
iv) all individuals and institutions intending to conduct planted genetic experiments (trials) on public land or other types of planted experiments which if installed on public land have potential to compromise the genetic integrity of wild stands of native species (e.g., through hybridization with native species) irrespective of the origin of propagation materials; and
v) All collectors of plant materials of trees and shrubs on public land for research including non-propagation uses where the government collection permit is required.

If unsure whether or not these standards are applicable to your case, consult *Alberta*.

Submission and Approval of Documents

Plans and forms that are required to be submitted to *Alberta* will receive one of four responses:

i) approved;
ii) approved with conditions;
iii) requires additional information; and
iv) rejected with reasons.

4.0 Document Structure

As noted in Section 2, these standards are published in two documents, i.e., a complete document including all standards, and a reduced document containing standards applicable to *Stream 1* materials only.

In the complete document, a double-lined box has been placed around standards that apply exclusively to *CPPs* (see Figure 5.1, *Stream 2*) or research programs (RPs). Standards appearing outside boxes apply to both *Stream 1* and *Stream 2* material.

Following this general information section are five sections containing goals and standards. Goal statements describe the intent and scope of each section. Standards define the specific results that must be attained or, in some cases, specific procedures that must be followed.

The five sections are:

i) Policy Issues and International Agreements;
ii) Material Collection, Handling, Registration and Storage (MCHRS);
iii) Green Area Deployment (GAD);
iv) Breeding, Testing and Verification (BTV); and
v) Production of Controlled Parentage Materials (PCPM).

This document also contains a glossary, a list of acronyms, and a number of appendices containing tables, forms and other supplements to the standards. The glossary provides definitions of terms specific to their usage in this policy.

5.0 Standards Framework

Figures 5.1 and 5.2 below illustrate the functional arrangement of components of FGRMS 2016, as applicable to *Stream 1* and *Stream 2* materials.

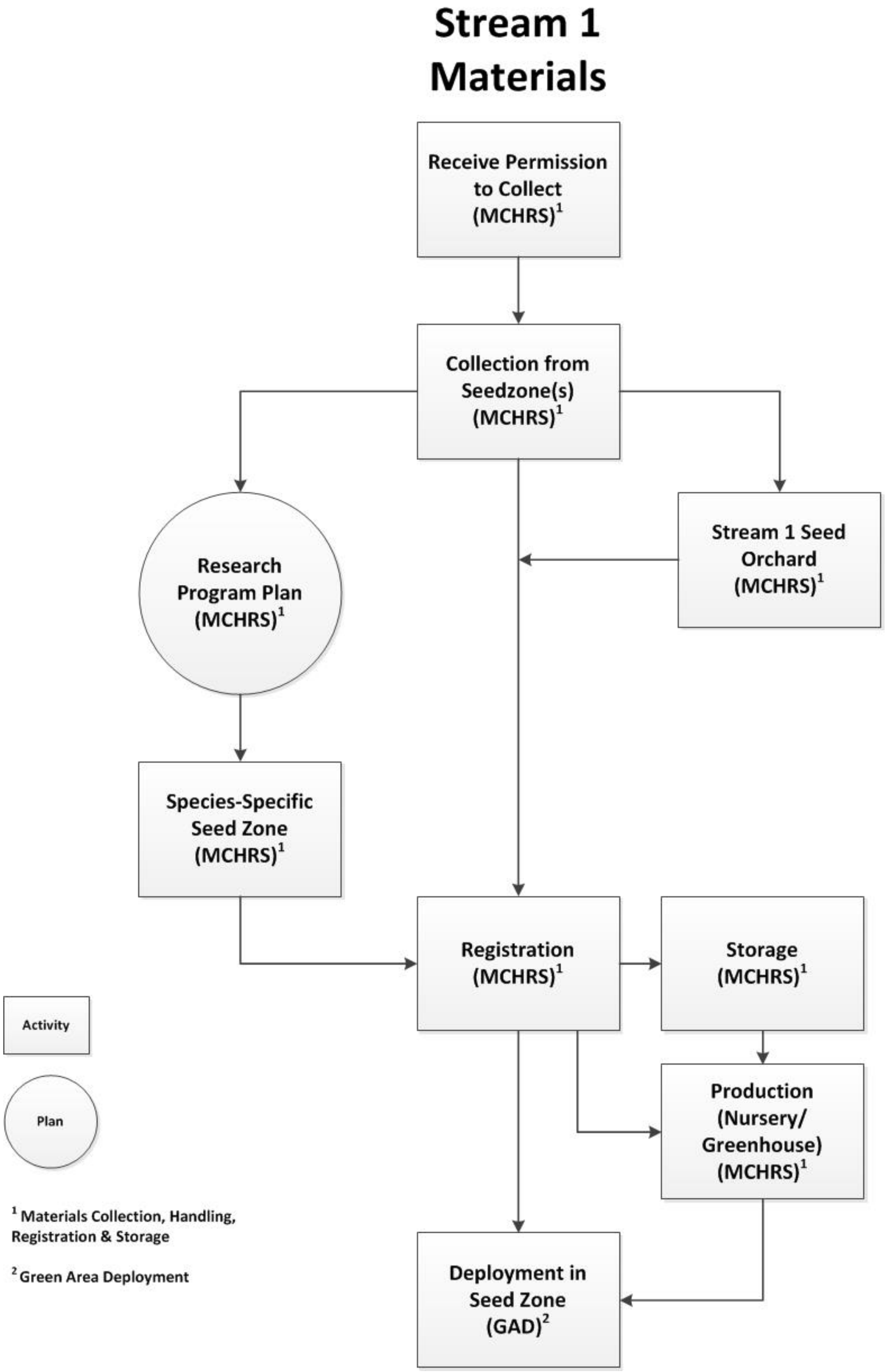
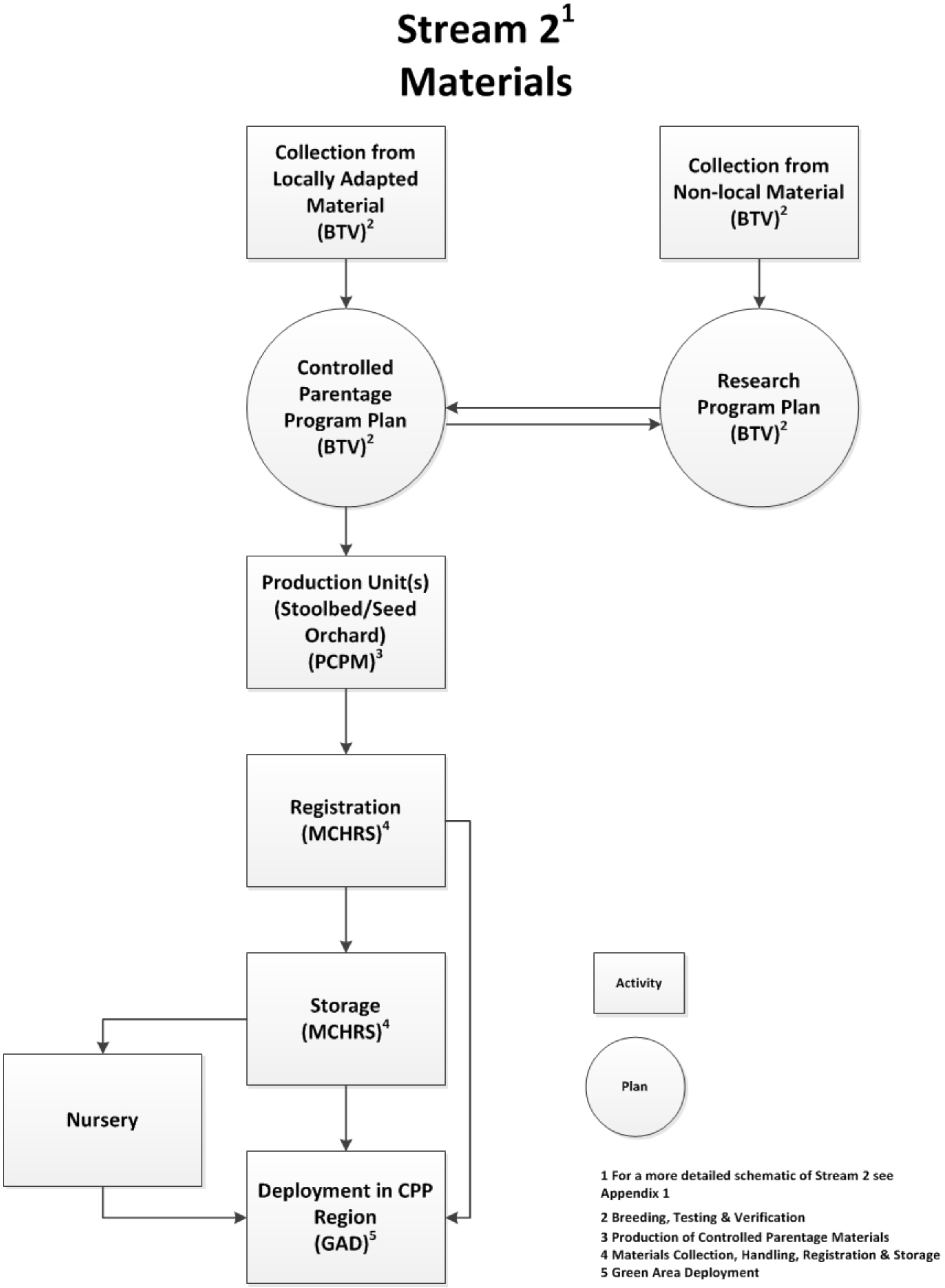


Figure 5.1. Functional arrangement for Stream 1 components of the Alberta Forest Genetic Resource Management and Conservation Standards (FGRMS) 2016.



1 For a more detailed schematic of Stream 2 see Appendix 1

2 Breeding, Testing & Verification

3 Production of Controlled Parentage Materials

4 Materials Collection, Handling, Registration & Storage

5 Green Area Deployment

Figure 5.2 Functional arrangement for Stream 2 components of Alberta Forest Genetic Resource Management and Conservation Standards (FGRMS) 2016.

6.0 Effective Date and Retroactivity

The standards were enabled through *Alberta's* Timber Management Regulation 144.2 and were effective as of May 01, 2003. FGRMS 2016 is effective as of its date of publication.

Controlled parentage programs and research programs that already existed or were under development prior to May 01, 2003 will be implemented or upgraded to the standards through discussion between *Alberta* and the proponent(s). The intent is to capitalize on work in progress while phasing in standards.

POLICY ISSUES AND INTERNATIONAL AGREEMENTS

Preamble

The Government of Alberta (*Alberta*) has stewardship responsibility for the management of forest genetic resources on *public land* in Alberta. *Alberta*, resource-based industries, research organizations, and tree improvement cooperatives undertake research, conservation, genetic improvement, and breeding programs jointly or individually, and are involved in the collection of forest genetic resources and *deployment* of trees and shrubs on *public land* in Alberta.

Goals

The goals of this section are to:

i) establish the requirements for access rights to *Alberta*'s forest genetic resources;
ii) clarify the requirements for benefit-sharing in relation to the commercialization of forest genetic resources obtained from *public land* in Alberta;
iii) enhance awareness of international agreements that address access and benefit-sharing of genetic resources; and
iv) provide *Alberta's* policy on *genetically modified organism*s.

7.0 Prior Informed Consent, Benefit-Sharing and Material Transfer Agreements

All genetic resources collected from *public land* in Alberta require prior and informed consent, obtained from *Alberta*. Forest genetic material collected from *public land* in Alberta, and utilized for commercial purposes other than fiber production in Alberta, could be subject to a benefit-sharing agreement, or *material transfer agreement (MTA)*, with *Alberta*. The province will endeavour to retain benefits in the form of revenue when such material from *public land* is utilized for commercial means. However, the province will not seek to obtain revenue when material is used for operational *deployment* of trees and shrubs in Alberta, or for strengthening genetic improvement programs in Alberta.

Exchanges of material between *Alberta* and other jurisdictions might require an *MTA*, or other type of agreement, indicating the terms of benefit-sharing and third-party use. *MTAs* may be required between *Alberta* and other entities (e.g., industrial, academic or research organizations) involved in forest genetic resource use activities in Alberta, nationally, or internationally. Requirements will be determined on a case-by-case basis. Situations where these agreements may apply include:

i) where a third party wishes to use material and associated *genotypes* from *Alberta public land* for propagation or further breeding for commercial or profit objectives; and
ii) where a member of a cooperative involving *Alberta* wishes to use material and associated *genotypes* for propagation or further breeding outside the cooperative(s) in which they are participants.

Once authorized by the province, through licenses, permits or otherwise, and subject to any terms of benefit-sharing, including in relation to *intellectual property rights* and any conditions on subsequent third party use, an organization or person(s) shall become the owner(s) or holder(s) of the trees or shrubs that have been harvested, or of other physical material that is collected from *public land* for the purpose of genetic improvement. Their right remains until the material is deployed back on to *public land*, at which time ownership transfers to the province (*Alberta*).

The province (*Alberta*) reserves the right to retain some collected material for conservation or research purposes (see Standards 17.0, 29.2, 29.3 and 29.4).

Forest Management Agreement (FMA) holders have ownership rights to timber on land subject to an FMA, and are entitled to compensation for any damages to timber or improvements they have created (such as to genetically improved material that has been deployed on *public land*).

8.0 Intellectual Property Rights

For existing and future genetic improvement cooperatives involving the province, *Alberta* will endeavour to establish agreements that define the respective *intellectual property rights* of all parties.

For collections of material by parties who do not hold timber dispositions with associated *reforestation* obligations in Alberta, a letter of authorization, map, and collection plan are required as per Standards 11.1.3 and 11.1.4. A condition may be placed on such authorizations stating that the province will retain all *intellectual property rights* to material collected, unless otherwise defined in an agreement.

The province will endeavour to define commercialization arrangements by way of an agreement at the earliest opportunity, wherever possible. The province may also directly charge a collection fee or royalty on material collected from *public land* when material is for commercial ventures (e.g., sale of genetically improved material and associated information) that are unrelated to genetic improvement or are outside Alberta.

If these standards conflict with copyright, patent and/or intellectual property laws, or other federal laws, such legislation would supersede these standards.

9.0 Access to Data and Information

Alberta will have access to data and information pertaining to improved stock or research and breeding programs. Access to, and retention and long-term storage or archiving of data is required because of *Alberta's* stewardship responsibility to monitor diversity and adaptation of materials to be deployed on forested *public land.* Specific data needs will be outlined in requirements for plan submission and reporting as detailed in other sections of this document.

All information provided to *Alberta*, or in the custody or control of *Alberta*, may be disclosed under Freedom of Information and Protection of Privacy (FOIP) legislation, if a request for disclosure is made. It is recognized that information submitted to *Alberta* regarding cooperative genetic improvement programs involving *Alberta* is subject to FOIP legislation, and that other parties may request access to such information through FOIP requests. *Alberta* will refuse to release information from cooperative programs that meet all conditions as per section 16 of the FOIP Act.

In summary, disclosure would be refused where information:

i) would reveal trade secrets or scientific/technical information of a third party; and
ii) would harm the competitive position of a third party or result in undue financial loss or gain to any person or organization; and
iii) is supplied in confidence to *Alberta*.

9.1 International Treaties and Agreements on Access to Genetic Resources and Benefit-Sharing, and Safe Transfer of *Living Modified Organisms*

Individuals, organizations, industry, and governments that import genetic resources from outside Canada or that export genetic resources including forest genetic resources for any purpose, including research, should be aware of international treaties and protocols with respect to genetic resources. Such treaties and protocols may contain legally binding commitments in regard to obtaining genetic resources from other countries, benefit-sharing arrangements, and the safe transfer of *living modified organisms*.

i) The Convention on Biological Diversity came into force in 1993. Canada is a party to this Convention, which contains general provisions for accessing genetic resources from other countries that are parties to the Convention. This requires prior informed consent from the party providing the genetic resources, based on mutually agreed terms.

ii) The Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity came into force in October of 2014. Canada has not yet become a party to this Protocol. The Nagoya Protocol is a complex legal document that aims to enhance legal certainty and transparency for both providers and users of genetic resources. Obligations to support compliance with domestic legislation or regulatory requirements of the party providing genetic resources, and contractual obligations reflected in mutually agreed terms, are considered innovations of the Protocol. The Protocol also supports benefit-sharing arising from the utilization of traditional knowledge associated with genetic resources. The Protocol sets out a number of administrative arrangements, including a certificate of compliance; it also establishes clear rules for prior informed consent and mutually agreed terms. It will be important for any person or organization that accesses forest genetic resources from other countries for any purpose, including research, to be aware of the obligations of the Nagoya Protocol and its administrative arrangements, including any measures that might be required in Canada, should Canada become a party to this Protocol.

iii) The Cartagena Protocol on Biosafety to the Convention on Biological Diversity came into force in 2003. The Nagoya – Kuala Lumpur Supplementary Protocol was open for signature in 2011, but has not yet come into force. Canada is not a party to the Cartagena Protocol. Both Protocols address the safe transfer of *living modified organisms* and are only relevant here to individuals or organizations that are engaged in the transfer and handling of any *living modified organisms* to other countries.

9.2 Genetically Modified Organisms

G*enetically modified organism* (*GMO*) refers to an organism that, through human intervention in a laboratory, has had its genome, or genetic code, deliberately altered through the mechanical insertion of a specific identified sequence of genetic coding material (generally DNA) that has been either manufactured or physically excised from the genome of another organism. This definition of *GMO* is substantially equivalent to that of *living modified organism*, as defined in the Cartagena Protocol on Biosafety to the Convention on Biological Diversity.

Although it is recognized that *GMO* material has possible utility for *reforestation* and *reclamation*, the potential performance and impacts on forest ecosystems are poorly understood. In view of the risks associated with *reforestation* and *reclamation* with *GMOs,* and in accordance with the current position of the Alberta Forest Genetic Resources Council, *GMOs* are not approved for use on *public land* in Alberta at this time.

The federal government has jurisdiction over testing and use of *GMOs* in Canada. Proponents should contact the appropriate federal department prior to undertaking a program for testing of *GMOs*. If federal approval for testing of *GMOs* is granted, FGRMS 2016 outlines provincial requirements for review, testing, and research (see Standards 23.5 and 25.3).

MATERIAL COLLECTION, HANDLING, REGISTRATION AND STORAGE (MCHRS)

Goals

Genetic materials of forest plants intended for *deployment* on *public land* will be collected, handled, registered and stored in a way that is designed to:

i) ensure adaptation and diversity;
ii) maintain documented *genetic identity* and ensure materials are appropriately tracked; and
iii) ensure that the genetic integrity and physical quality of materials are maintained.

MCHRS Standards

10.0 Registration

10.1 All material to be deployed on *public land*, with exceptions as noted in Standard 19, must be registered with *Alberta*. See Appendix 2 (re: *Stream 1*) and Appendix 3 (re: *Stream 2*).

10.2 Requests for *registration* are subject to review and acceptance by *Alberta*. If one or more of the relevant standards are not met, material may not be registered.

10.3 Required *registration* information must be complete and submitted to *Alberta*. All collection, handling, storage and processing information is to be made available for *Alberta's* review upon request.

10.4 Material that does not meet requirements for *unrestricted registration* may be eligible for *restricted registration* or for holding, pending *registration* eligibility, See Appendices 2, 3, 4, and 5 for *registration* requirements.

10.4.1 A *Stream 2* seed or vegetative lot with *effective population size* (*Ne*) insufficient for *unrestricted registration* may be blended with a *Stream 1* seed or vegetative lot of the same species to produce a new (blended) *Stream 2* lot with *unrestricted registration* under the following conditions:

i) the *Stream 1* lot has *unrestricted registration*;
ii) the *Stream 2* lot has an *Ne* of at least 5;
iii) the *seed zone* of the *Stream 1* lot and *CPP region* of the *Stream 2* lot overlap; and
iv) no gain is requested for *deployment* of the blended lot.

The blended lot shall be deployed within the area of overlap of the *seed zone* of the *Stream 1* lot and the *CPP region* of the *Stream 2* lot. The maximum proportion of the *Stream 2* lot allowed in the blended lot is defined in Table 10.1.

Table 10.1. Maximum proportion of Stream 2 material in a blended *Stream 1* and Stream 2 lot.

***Ne* of *Stream 2* lot**	**Maximum proportion of *Stream 2* lot in blended lot**
5 – 10	25% x (germination rate of *Stream 1* lot)
>10 – 18	50% x (germination rate of *Stream 1* lot)

10.5 Upon *registration*, *Alberta* will assign a *registered lot number*.

10.6 For *Stream 1* material, the material collection criteria defined in Appendix 4 must be met.

10.7 For *registration* of *Stream 1* material the information in Appendix 2 is required.

10.7.1 For *registration* of *Stream 1* seed, the following additional information is required: *temporary lot number*, volume of material collected (e.g., cones, berries, catkins), yield, and a *moisture measurement*. (See Standard 14.0, Seed Testing.)

10.7.2 For *registration* of *Stream 1* vegetative material, no additional information is required.

10.8 Material meeting *unrestricted registration* requirements of Table A4.1 (see Appendix 4; *point collections*) is eligible for *deployment* up to 1 km outside the *seed zone* of origin (see Appendix 7) provided the difference in elevation between point of collection and point of *deployment* does not exceed 100 m. Such material is also eligible for transfer across a *seed zone* boundary according to Standard 18.2.5 and Appendix 13.

10.9 For *registration* of *Stream 2* material (see Appendix 3), the *effective population size (Ne)* criteria contained in Appendix 5 must be met.

10.10 *Stream 2* material must originate from an *Alberta* approved *production site* and *production unit* (see Standards 32.2, 32.4 and 32.7).

10.11 For *registration* of *Stream 2* material, Appendix 3 must be completed.

10.11.1 For *registration* of *Stream 2* seed, the following additional information is required: volume of cones collected (conifer), yield, and a *moisture measurement*. Refer to Standard 14.0, Seed Testing.

10.11.2 For *registration* of *Stream 2* vegetative material**,** the contribution (%) of each *clone* to the vegetative lot is required.

10.12 *Restricted registration* (see Appendices 1, 2 3 and 4) may apply where:

i) documentation requirements in Standard 10.7 have not been met; or

ii) collections (*Stream 1*) do not meet *point* or *seed zone collection* requirements for *unrestricted registration* (see Appendix 4); or

iii) documentation standards of 10.11 have not been met; or

iv) *effective population size* (*Stream 2*) is less than that required for *unrestricted registration* (see Appendix 5); or

v) *Stream 2* material is not derived from *locally adapted material* (i.e., is derived from non-local provenances, non-local species, non-local hybrids, or *GMOs* as determined on a case-by-case basis); or

vi) genetic risks have been identified through the *Stream 2* risk assessment process (see Appendix 9). Such risks may lead to constraints on deployment. These will be dealt with through standards or through deployment conditions in the Forest Management Plan (FMP).

10.13 Conditions on *deployment* may be applied to *restricted registration* material. (See Standard 18.2.6 and Appendix 8 [for *Stream 1*], and Standards 18.4.3.2, 18.4.7 and Appendix 9 [for *Stream 2*]).

10.14 For locally infrequent species or *rare species*, special *registration* and deployment provisions may be enabled by *Alberta* for conservation, restoration or *reclamation* purposes.

11.0 Collection

11.1 Collections from *public land*

11.1.1 All collections of plant material from *public land* require authorization from *Alberta* (except as noted below).

11.1.2 *Forest tenure holders* responsible for *reforestation* will outline their intent to collect in their *Reforestation* Program Plan. *Alberta* is to be notified of the target species and general location of a collection not less than two working days prior to collection taking place.

11.1.3 Collections of forest tree or plant material by other than *forest tenure holders* require a letter of authorization from an *Alberta* Forest Area Office. The proponent(s) will submit a map and collection plan identifying the area of collection, type of material, method of harvest, timing, and target species (see Appendix 10A).

11.1.4 REPEALED.

11.1.5 For collections outside *Alberta*'*s* jurisdiction (e.g., on federal lands), collections must satisfy the requirements of the agency responsible for the land on which collection occurs.

11.1.6 Genetic material collected from *public land* for research or *CPPs* will be documented on the appropriate form (see Appendix 11A, 11B, 11C or 12) and submitted in report format (see Standard 26.1.1) to *Alberta* (in either hard copy or electronic format) within six months of collection completion.

11.2 Each *forest tenure holder* will maintain a minimum of one registered *Stream 1* lot, for each species and in each *seed zone,* where *artificial regeneration* is planned using *Stream 1* seed or seedlings of that species. Exceptions may be made when other appropriate seed sources are demonstrated to meet *reforestation* commitments.

11.3 The maximum size of a registered seedlot or vegetative lot depends on numerical restrictions on *deployment* from a single seedlot or vegetative lot. See Appendix 14 for maximum number of seedlings or vegetative propagules deployable by *seed zone* size.

11.4 *Stream 1* vegetative material may be multiplied in *stoolbed*s established from collections that contain the required minimum number of plants per collection for *Stream 1* material (see Appendix 4 – Material Category D).

11.4.1 *Alberta* reserves the right to inspect *Stream 1 stoolbed* sites and facilities.

11.4.2 Collections from approved *Stream 1 stoolbed*s do not require *Alberta* authorization.

11.5 Genetic material collected outside Alberta will be documented on the form provided in Appendix 15. This form will be submitted (in either hard copy or electronic format) to *Alberta* upon inclusion in an approved *CPP* or prior to *deployment* in research *tests* on *public land*.

11.6 Collections from approved *production units*, *production sites*, or *production populations* do not require *Alberta* authorization.

11.7 *Stream 1* seed may be produced in *Stream 1 seed orchards* (see Appendix 2, 4, 14, 25 and 32A for requirements).

11.7.1 Prior to initiating development of a *Stream 1 seed orchard*, the proponent(s) must submit a letter of intent to *Alberta*.

11.7.2 *Alberta* reserves the right to inspect proposed *Stream 1 seed orchard* sites and facilities.

11.7.3 Collections from approved *Stream 1 seed orchard*s do not require *Alberta* authorization.

12.0 Transportation of Material

12.1 An identification tag must accompany each container of material (e.g., cones) from the time of collection to the time of delivery to the processing or storage facility.

i) Identification for *Stream 1* material must include the *temporary lot number,* holder's name, collection location (Section, Township, Range, and Meridian, or latitude and longitude in decimal degrees), year of collection, and species.

ii) Identification for *Stream 2* material must include the *temporary lot number*, holder's name, *production unit* or *production population* identifier number, year of collection, and species.

12.2 When conservation, research or *CPP* genetic material is collected, shipped or stored, it must be accompanied by the Research, Conservation or Controlled Parentage Program Transportation and Interim Storage of Plant Material Form (see Appendix 16) which lists all material by either the *accession number*, *temporary lot number/registered lot number,* or *unique identifier (U.I.)*. In addition, each genetic entity will also be labelled unambiguously with the *U.I.*, *accession number*, or *temporary* *lot number* or *registered lot number*, both inside and outside its container. Where material is documented on a parent tree selection form (one of Appendices 11A, 11B, 11C, 12, or 15), these forms meet documentation requirements for transportation and storage.

12.3 Transportation of materials from *public land*

12.3.1 A completed *Registration* Request Form (Appendix 2 [*Stream 1*]) must accompany all shipments of *public land collections* of seed and vegetative material intended for *reforestation* or *reclamation*.

12.4 Transportation of materials from an approved *production site*

12.4.1 A completed *Registration* Request Form (Appendix 2 [*Stream 1*] or Appendix 3 [*Stream 2*]) must accompany all cones, fruits and material shipments.

12.5 Withdrawal and transportation

12.5.1 A Seed and Vegetative Materials Withdrawal and Transportation Form (see Appendix 17) must be received by *Alberta* before a seed or vegetative material withdrawal may be made.

12.5.2 Unless approved by *Alberta*, withdrawals of seed or vegetative material for *deployment* are not permitted until *registration* is complete.

12.5.3 A Seed and Vegetative Materials Withdrawal and Transportation Form (see Appendix 17) must be used for tracking materials from withdrawal from storage through to arrival at nurseries or related facilities. *Alberta* must be notified of any deviation from original documentation.

13.0 Processing

13.1 Processing of seed for operational *deployment* must be carried out at a seed processing facility approved by *Alberta*. In order to be approved, seed processing facilities must have the verifiable capability to maintain accurate identity and seedlot integrity. For a list of approved seed processing facilities, see *Alberta*'*s* website.

13.2 Seed and vegetative materials must have verifiable identity documentation, and the integrity of individual lots must have been maintained throughout. Any mixing of collections must be done and documented in such a way that the eventual distribution of individuals can reasonably be assumed to be random within the *deployment* lot.

13.3 Seed shall be processed and delivered for storage to *Alberta* or other approved storage facility within six months of collection (see Standard 15.7).

13.4 The completed *Registration* Request Form (see Appendix 2 [*Stream 1*] or Appendix 3 [*Stream 2*]) must accompany the seed to *Alberta* or other approved storage facility.

13.5 Where seed or vegetative material lots are divided for any reason, the *Registration* Request Form (see Appendix 2 or 3) must be included with each portion.

13.6 Seed processing facilities are not permitted to withhold any *reforestation* or *reclamation* seed, or ship that seed to any location except Alberta Tree Improvement and Seed Centre (ATISC) or another approved storage facility, without written permission from the seed owner and *Alberta*.

14.0 Seed Testing

14.1 Testing of seed for operational *deployment* must be conducted in accordance with *Alberta's* Seed Testing Standards, which are published on the *Alberta* website.

14.2 Seed testing must be conducted in an a*pproved facility*, and seed test result reports must be signed by an experienced seed testing technician or laboratory scientist responsible for the seed testing laboratory.

14.3 For all tree species except Pinus albicaulis, seed test results other than a *moisture measurement* must be provided to *Alberta* within four months of receipt of seed for storage. Test results for Pinus albicaulis and all non-tree species must be submitted within one year of receipt of seed for storage. For *moisture measurement* see Standard 15.1.1.

15.0 Storage

15.1 All registered seed must be stored at ATISC or another storage facility approved by *Alberta*.

15.1.1 All seed submitted for storage to *Alberta* or other approved storage facility must be accompanied by a *moisture measurement*.

15.2 *Production population* materials that need to be maintained in growing conditions for *propagule* production must be stored or maintained at an approved storage facility. An approved *production site* undertaking *propagule* production for *deployment* on *public land* is considered an approved storage facility.

15.3 *Alberta* will review requests for approval of storage facilities on the basis of physical infrastructure and management processes. Contact *Alberta* for approval process.

15.4 Seed and vegetative material received for storage must be securely packaged and clearly labelled with the *temporary lot number* or *registered lot number* as written on the accompanying *Registration* Request Form - *Stream 1* (see Appendix 2). Containers must have one tag inside and one tag securely affixed to the outside.

15.5 All seed and vegetative materials storage facilities must follow handling and storage procedures that maintain lot identity and integrity.

15.6 For storage of unregistered collections from other agencies, the minimum information required is: date of collection, owner, species, seed source, a *moisture measurement*, and total seed amount submitted for storage.

15.7 When submitted for cold storage, seedlots of lodgepole pine, jack pine, white spruce, Engelmann spruce, black spruce, Douglas-fir, tamarack and hybrids of any of these species must have 4-8% *moisture content* (MC) or 15-40% *equilibrium relative humidity* (eRH) at 20-30˚C; seed of all other *orthodox* species will only be accepted with 15-25% *e*RH at 20-30˚C. See Standard 14.0.

16.0 Excess Seed, Seedlings and Vegetative Material

16.1 Nurseries and/or propagation facilities are not permitted to sell or distribute excess seed, seedlings or vegetative material for *deployment* on *public land* without prior approval of the material owner and *Alberta*. An exchange of material between material owners does not require *Alberta* approval as long as all FGRMS 2016 standards are followed.

17.0 Retention of Material for ***Ex* *Situ*** Gene Conservation

17.1 *Alberta* has the right to retain samples of seed and vegetative material collected from *public land* for the purpose of conservation of *wild* seed or vegetative genetic material resources.

17.1.1 For *Stream 1* seedlots, *Alberta* may, at the time of *registration*, retain up to 30,000 viable seeds or 5% of the initial total seedlot, whichever is less. In the absence of seed viability test data, *Alberta* may retain up to 60,000 seeds or 10% of the initial total seedlot, whichever is less. *Alberta* will notify the owner of any withdrawals. Amounts greater than this will require written consent from the owner.

17.1.2 REPEALED.

17.1.3 For seed collections from *public land* intended for inclusion in research or *CPPs* in Alberta, *Alberta* may retain 5% of the seed.

17.1.4 For all other *public land* seed or vegetative material collections not intended for *reforestation, reclamation* or tree improvement in Alberta, the owner may be required to provide 10% of seed or vegetative material to *Alberta*.

GREEN AREA DEPLOYMENT (GAD)

Goals

Genetic resources of forest vegetation will be deployed within the *Green Area* in a manner that strives to:

- i) conserve the genetic integrity, adaptability, diversity and health of *wild* and managed populations while recognizing that genetic change will occur through evolutionary pressure, breeding and *deployment*,
- ii) maintain or enhance forest productivity, and plant and landscape diversity,
- iii) be consistent with sustainable forest management principles (economic, social and environmental sustainability), and
- iv) recognize that Forest Management Plans (FMPs) and *reclamation* plans, or plans of an equivalent level, guided by this and other policies, will determine how *deployment* will occur.

GAD Standards

18.0 Deployment of Registered Material

18.1 General

18.1.1 Except as noted in Standard 19.0, only registered materials – *unrestricted* or *restricted* – may be deployed within the *Green Area*.

18.2 Deployment of *Stream 1* materials

18.2.1 *Stream 1* materials will be deployed within the *seed zone* of origin. *Seed zones* are those delineated on the *Seed Zone* Maps provided in Appendix 7.

18.2.2 For seed and vegetative material collections made before May 1, 2003, the need for a variance approval to move seed outside the *seed zone* of origin will be determined using the decision tree in Appendix 13.

18.2.3 To maintain population diversity within a *seed zone*, total seedling and/or vegetative material *deployment* from *Stream 1* seed or vegetative lots with *unrestricted registration* will be limited on the basis of *seed zone* size as set out in Appendix 14.

18.2.4 Unrestricted *point collection*s that meet requirements in Appendix 4 are eligible for application for *deployment* outside the *seed zone* of origin (see Appendices 8 and 13). Without applying for a variance, *deployment* may occur within 1 km of the *seed zone* boundary, provided the difference in elevation from the point of collection (mid-point of range) to the point of *deployment* does not exceed 100 m. See Appendix 14 for additional *deployment* considerations.

18.2.5 Movement of seed or *vegetative propagules* outside the *seed zone* of origin requires variance approval by *Alberta*.

- i) Variances for *Stream 1* material may be requested by submitting a Request for Deployment Variance for *Stream 1* Material (see Appendices 8 and 13) to *Alberta*;
- ii) Where the same variance to deploy seed outside the *seed zone* of origin is requested several times, a standing approval may be issued for a five-year period;
- iii) Any three requests for the same variance, or a standing approval for variance, may initiate a request from either *Alberta* or the deploying party to review the *seed zone* boundaries or seed or vegetative material collection practices.

18.2.6 For *deployment* of *Stream 1* material with *restricted registration*, a determination is to be made by *Alberta* on the basis of a request for variance (see Appendix 8).

18.2.7 For deployment of *Stream 1* materials originating outside Alberta, a variance request for *registration* and deployment in Alberta may be applied for where all of the following are met:

i) Lots proposed for transfer will be deployed within a 50 km radius and 100 m elevation of origin;

ii) The lot meets *registration* requirements for a *point collection* and other requirements for *unrestricted registration*;

iii) The lot originates in a comparable ecological region with similar climate;

iv) A completed Request for Deployment Variance for *Stream 1* Material (see Appendix 8) is submitted;

v) A completed *Registration* Request Form – *Stream 1* (see Appendix 2) is submitted.

18.3 *Species-specific seed zone* development and amendment

18.3.1 A proponent is required to submit a letter of intent to *Alberta* prior to developing a *species-specific seed zone* (SSSZ) research program plan, outlining *propagule* collection and *trial* design. Alberta will respond within three months.

18.3.2 Development of *species-specific seed zone*s will require testing according to the following standards:

18.3.2.1 Establishment of *species-specific seed zones* will require a research program plan (see Appendix 24) and provenance testing for adaptation.

18.3.2.2 For establishment of *species-specific seed zones*, the number of *test* sites will be specified in the research program plan in consultation with *Alberta*. A minimum of five *test* sites is required. The number required may vary depending on characteristics of the proposed *species-specific seed zone* (e.g., *seed zone* size and heterogeneity). The number required may also depend on a review of ecological similarity (e.g., climate, taxonomy, crossability, ecological classification).

18.3.2.3 Sites will be well distributed geographically and elevationally across, and representative of, the existing climatic variability in the actual or proposed *species-specific seed zone*.

18.3.2.4 For revision of *species-specific seed zone* boundaries, the number of *test* sites will be specified in the research program plan.

18.3.2.5 Research program plans for *species-specific seed zones* must also comply with Standards 25, 27, and 30.

18.4 Deployment of *Stream 2* materials

Stream 2 materials originating from programs for *CPP regions* listed in Table A19.1, Appendix 19, and marked as approved for deployment may be registered and deployed prior to *CPP* plan approval provided the following conditions are met:

i) the *CPP production populations* contain only *locally adapted material*;

ii) previous project planning and implementation schedules are being followed;

iii) *production population* or *production unit(s)* meet FGRMS 2016 monitoring and reporting standards; and

iv) *deployment populations* meet FGRMS 2016 diversity and documentation standards.

18.4.1 Materials originating from programs for *CPP regions* not listed in Appendix 19 may be registered and deployed if the following conditions are met:

i) *CPP* plan approval has been obtained;

ii) proponent complies with *CPP* plan implementation schedule;

iii) *CPP production population* contains only *locally adapted material*;

iv) *production population* or *production unit(s)* meet FGRMS 2016 monitoring and reporting standards; and

v) *deployment populations* meet FGRMS 2016 diversity and documentation standards.

18.4.1.1 In addition to the topics to be addressed in *CPP* plan preparation (see Appendix 18), prior to *deployment*, the *CPP* plan must also contain:

i) a schedule for progeny/clonal *test* establishment;

ii) a reference to the approved Parent Tree Selection Report(s); and

iii) a reference, using *Alberta* assigned identifier(s), to an approved *production population* or *production unit(s)* containing only *locally adapted material*.

18.4.2 Total seedling and/or vegetative material *deployment* from *Stream 2* sources from a given *production population* and its associated *production unit(s)* will be limited by *CPP region* as defined in the *CPP* plan (see Appendix 18). For a list of existing *CPP regions*, see Appendix 19.

18.4.3 *Stream 2 deployment* limits

18.4.3.1 Seed: total *deployment* of *Stream 2* seed for a given *CPP region* will be limited by the *cumulative effective population size (Ne)* of the output from the associated orchard(s). The area of *deployment* from the associated orchard(s), where estimated *cumulative Ne* summed over the life of the orchard(s) is less than 30, may not exceed 25% of the total area of *species-specific target strata* over a rotation.

i) Where 30 ≤ *cumulative Ne* < 42, *Stream 2* seed may be deployed over a maximum of 50% of total *species-specific target strata* area over a rotation.

ii) Where 42 ≤ *cumulative Ne* < 54, *Stream 2* seed may be deployed over a maximum of 75% of total *species-specific target strata* area over a rotation.

iii) Where *cumulative Ne* ≥ 54, *Stream 2* seed may be deployed over the total *species-specific target strata* area over a rotation (see Appendix 21A).

iv) Appendix 20 provides methodology for calculating *cumulative Ne deployment* levels.

v) The foregoing is subject to constraints imposed by Standards 20.2 through 20.8, relating to *in situ conservation*.

18.4.3.2 Vegetative Materials: for native Alberta species existing naturally as *clone*s, clonal *deployment* may be used in reforesting voids, *reclamation*, and planting of extensively and intensively managed forest lands. Materials may be deployed as random mixtures or monoclonal blocks in accordance with the following.

18.4.3.2.1 Three *deployment options* are enabled: *rehabilitation*, *extensive* and *intensive* (see Appendix 9); specific standards apply to each.

18.4.3.2.2 Total *deployment* may not exceed one million *ramet*s per *clone* for all *deployment* scenarios (18.4.3.3, 18.4.3.4, 18.4.3.5).

18.4.3.2.3 The cumulative area for the *extensive* and *intensive* options may not exceed 50% of the *species-specific target strata* in a *CPP region* without prior approval by *Alberta*.

18.4.3.2.4 Areas planted with *Stream 2* clonal material using the *extensive* or *intensive deployment* options will be mapped and reported in the five year FMP Stewardship Report (standard 21.2.3).

18.4.3.3 ***Rehabilitation*** *deployment* option: *deployment* of vegetative materials as clonal mixtures or monoclonal blocks for planting roads, landings, decking areas, voids in *opening*s and for *reclamation* may occur subject to the following:

18.4.3.3.1 A minimum *Ne* of 18 must be met for each planted area.

18.4.3.3.2 Areas planted under this option do not contribute to the maximum area *deployment* cap (as listed in 18.4.3.4.2, 18.4.3.5.2).

18.4.3.3.3 Total *deployment* on voids, roads, landings and decking areas must not exceed 15% of the *opening*'s net harvest area (as submitted to ARIS).

18.4.3.3.4 Where *deployment* is in a contiguous area exceeding 10ha, at least 20% of deployed *clone*s must be known to be male and 20% known to be female.

18.4.3.4 ***Extensive*** management *deployment* option: *deployment* of vegetative materials as clonal mixtures or monoclonal blocks may occur subject to the following standards:

18.4.3.4.1 A minimum *Ne* of 18 must be met for each planted area.

18.4.3.4.2 The cumulative area where the *extensive* option may be used may not exceed 50% of *species-specific target strata* area in a *CPP region*.

18.4.3.4.3 The area planted with clonal material within an *opening* may not exceed 75% of any *opening*'s net area (as reported to ARIS); the remaining 25% must represent the original species mix and must be left for *natural regeneration*; however, remedial planting with *Stream 1* material is permitted.

18.4.3.4.4 Where vegetative materials are planted in monoclonal blocks, a block may not exceed 0.5 ha.

18.4.3.4.5 Proponents must report to *Alberta* at years 7 and 14 after initial planting (see Appendix 39), describing *deployment* outcomes, including all obvious signs of clonal success or failure from weather and climate-related damage, and insects and disease problems.

18.4.3.4.6 *Deployment* of up to 5,000 ha in a *CPP region* is enabled under this option with *CPP* plan approval. *Deployment* of an additional 10,000 ha must be authorized by *Alberta* and will be considered only after the year 7 report (18.4.3.4.5; Appendix 39) is approved by *Alberta*. Cumulative *deployment* exceeding 15,000 ha must be approved by *Alberta*, and will be considered only after the year 14 report (18.4.3.4.5; Appendix 39) is approved by *Alberta*.

18.4.3.5 ***Intensive*** *deployment* option: *deployment* of vegetative materials as clonal mixtures or monoclonal blocks may occur subject to the following standards:

18.4.3.5.1 A minimum *Ne* of 10 must be met for each area planted.

18.4.3.5.2 The total area of all plantings must not exceed 5% of the *species-specific target strata* area as listed in the *CPP* plan.

18.4.3.5.3 Where *deployment* is in a contiguous area exceeding 10 ha, at least 20% of deployed *clone*s must be known to be male and at least 20% known to be female.

18.4.3.5.4 Where vegetative materials are planted in monoclonal blocks, block size may not exceed 1.0 ha.

18.4.3.5.5 Proponents must report to *Alberta* at years 7 and 14 after initial planting (see Appendix 39), describing *deployment* outcomes, including all obvious signs of clonal success or failure from weather and climate-related damage, and insects and disease problems.

18.4.3.5.6 *Deployment* of up to 5,000 ha in a *CPP region* is enabled under this option with *CPP* plan approval. *Deployment* of an additional 10,000 ha must be authorized by Alberta and will be considered only after the year 7 report (18.4.3.5.5; Appendix 39) is approved by *Alberta*. Cumulative *deployment* exceeding 15,000 ha must be approved by *Alberta*, and will be considered only after the year 14 report (18.4.3.5.5; Appendix 39) is approved by *Alberta*.

18.4.4 *Deployment* numbers by proponent will be presented in the FMP or Annual Operating Plans (AOP) and in the current *CPP* plan. Appendix 20 provides details of methods for calculating *cumulative Ne*. Appendix 21A provides the method for calculating allowed *deployment* levels for seedlings based on *cumulative Ne*, and an example of the information and format for planning and reporting *production populations* under a *CPP* plan.

18.4.5 *CPP region* boundaries may be periodically reviewed and revised (Standard 28.0).

18.4.6 Minor changes to existing *CPP region* boundaries may be made with the mutual consent of proponent(s) and *Alberta*.

18.4.7 Prior to *deployment* of restricted *Stream 2* material, the FMP is to contain a summary of the research *test*s and analysis undertaken, monitoring required, and methods of ameliorating the risks identified in Appendix 9.

18.4. 8 A request for movement of seed or *vegetative propagules* outside the *CPP region* of origin will only be considered in emergencies, and is initiated by submitting a Request for *Deployment* Variance for *Stream 2* Material (see Appendix 22) to *Alberta*. Without applying for a variance, *deployment* may occur within 50 km outside a *CPP region* boundary provided the transfer of material does not exceed 100 m up in elevation and 50m down in elevation from the *CPP region* elevation limits (see Appendix 19).

18.4.9 REPEALED

19.0 Deployment of Unregistered Material (for limited use only)

19.1 *Wild* transplants and *vegetative propagule*s from within 5 km and 100 m elevation of the target planting site, or from within 20 km of the planting site and in the same *seed zone*, may be deployed without *registration*. These transplants and *vegetative propagule*s may not be multiplied or serially propagated.

19.2 Where *deployment* will be without nursery production, and will be completed within nine months of the collection date, a maximum of 5,000 *propagules*, cumulative over years, from a single *genotype* may be deployed without *registration*.

19.3 Records must be maintained for review by *Alberta* to ensure standards have been met.

20.0 *In Situ* Gene Conservation

20.1 *In situ gene conservation* for *Stream 1* material or for species not identified in a CPP for a specified seed zone will be implemented through the provincial gene conservation plan.

20.2 Proponents of a tree improvement program shall collectively implement *in situ gene conservation* for each CPP region by conserving wild stands in each of the seed zones found in the CPP region. A single conservation stand may serve as a conservation area for more than one species.

20.2.1 The number of wild stands to be conserved under each CPP plan is determined by the total size of the seed zone in Alberta and the size of the target stratum of the CPP region located in that seed zone. Table 20.1 is used to determine the required number of conservation areas per CPP region.

20.2.1.1 As a guide, conservation stands will be selected to capture topographic, climatic and stand productivity variability, and the geographic distribution of the species in the CPP region.

20.2.1.2 Where desired, proponent(s) may consult *Alberta* when selecting areas for *in situ gene conservation*.

Table 20.1. Number of *in situ gene conservation* stands for each seed zone in a CPP region[1, 2].

	E (%)				
D (%)	<15	>15-25	>25-50	>50-75	>75
<5	0	0	0	0	0
5-15	0	0	0	0	1
>15	0	2	3	4	4

[1] If the calculated number of conservation stands (Table 20.1) is greater than 1 but the area of the seed zone in the CPP region (B) is less than 0.5 million ha, one conservation stand is required.

[2] If the calculated number of conservation stands (Table 20.1) is greater than 2 but the area of the seed zone in the CPP region (B) is between 0.5 and 1.0 million ha, two conservation stands are required.

A = Area (ha) of the seed zone in Alberta (see Table A7.1) (Figure 20.1)
B = Area (ha) of the seed zone in the CPP region (Figure 20.1)
C = Area (ha) of the *species-specific target stratum* of the CPP region located in the seed zone (Figure 20.1)
D = Percentage of the seed zone located in the CPP region (B/A) × 100
E = Percentage of the *species-specific target stratum* within seed zone within CPP region (C/B) × 100

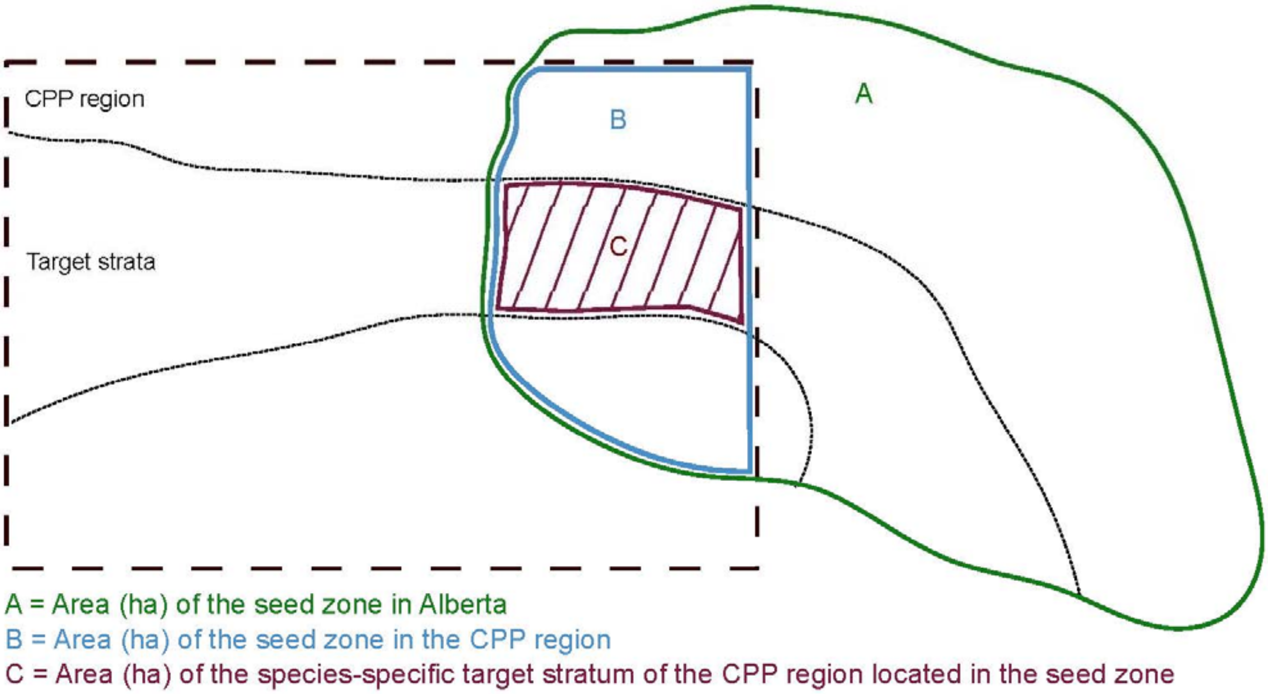


Figure 20.1. **Illustration of areas used to determine *in situ* conservation stands.**

Gene conservation areas may be chosen from:

20.3 existing reserves, or

20.4 subjective landbase deletions that meet *in situ conservation* objectives (e.g., streamside buffers, non-merchantable, inoperable), or

20.5 harvestable areas dedicated for *natural regeneration* (e.g., natural seeding or partial cutting), or for planting with seed specifically from the site or with *wild Stream 1* collections from adjoining areas, or

20.6 understory protection and variable retention areas (retain some naturals, supplement with planting with seed from the core conservation area (Appendix 4) or if not available, *wild Stream 1* collections from adjoining areas).

20.7 *In situ gene conservation* areas will be implemented as follows:

20.7.1 Areas designated for gene conservation will be dispersed across the *seed zone* to minimize risk of loss.

20.7.2 Areas designated for gene conservation will be chosen with consideration for long-term protection. A disposition is required for these areas.

20.7.3 Areas will be large enough to meet a reasonable expectation of 5,000 trees of the target species (at rotation) in a core area with an additional buffer of 200 m around it.

20.8 For a given species, in any *seed zone* where *Stream 2* material is being planted, the *CPP* plan(s) will indicate how *in situ conservation* standards are being addressed. Because *CPP regions* may include more than one *seed zone* and more than one cooperator, cooperative planning among parties in each *CPP region* may be required.

20.9 *CPP* proponents are required to make *Stream 1* collections from *wild* stands within *in situ conservation* areas or adjoining areas within the cooperator's area of influence to ensure that *wild* genetic resources are preserved and available for *reforestation* of conservation areas.

21.0 Deployment Planning and Reporting

21.1 Planning for *Stream 2 deployment*

21.1.1 Annual *deployment* schedules, as shown in the Annual Silviculture Schedule of an AOP, will be consistent with the approved FMP *deployment* strategies.

21.1.2 In the absence of approved FMP *deployment* strategies, annual *deployment* schedules will be approved when consistent with production objectives as defined in the approved *CPP* plan (see Standard 24.0).

21.1.3 Areas designated for *in situ gene conservation* will be described in the FMP, which will also include a statement of intended management with a time horizon of two rotations.

21.2 Reporting

21.2.1 Compliance monitoring for timber disposition holders' *deployment* activities (*Streams 1 and 2*) will be reported in the five year Stewardship Report of the FMP. Performance measures will be FMP-specific and designed to assure plan assumptions are adequately monitored. At a minimum, cumulative *deployment* of each source and type of material will be reported.

21.2.1.1 Reporting of *cumulative Ne* (see Appendix 20) for *Stream 2 deployment populations* produced by each *production unit* shall be included in the Annual Operations Report (see Appendix 35).

21.2.1.2 Reporting of *cumulative Ne* (see Appendix 20) for *Stream 2* populations deployed by each proponent in a *CPP region* shall be included in the FMP five year Stewardship Report.

21.2.2 *Deployment*

21.2.2.1 *Deployment* by timber disposition holders, of all registered material will be reported annually to *Alberta* in the Alberta Regeneration Information System (ARIS).

21.2.2.2 *Deployment* by non-timber disposition holders of all plant material used in *reforestation* or *reclamation* requires documentation of: the registered seed lot number; *deployment* location (centroid decimal degrees or geospatial representation); area of *reclamation* unit/polygon; number of individuals planted by species; *deployment* date; and type of *deployment* area, i.e., one of a) linear feature (road, seismic, pipeline), b) polygon (e.g., well pad, borrow pit, mine, compressor station). This information shall be maintained by the disposition holder and made available to the regulatory body upon request.

21.2.3 A map of appropriate scale showing *deployment* by cutblock or *opening* for the past five years' activities, will be submitted, when:

21.2.3.1 *Stream 2* material with *restricted registration* is planted, or

21.2.3.2 *deployment* of *Stream 2* seed material with *unrestricted registration* from a given *production population* exceeds 50% of the total area reforested by *target stratum* and species in a five year period, or

21.2.3.3 clonal *deployment* of vegetative materials occurs as per Standard 18.4.3.2.

21.2.4 Deployment mapping information will be reported in conjunction with the five year Stewardship Report of the FMP. Digital files will be accepted in lieu of hard copy.

21.2.5 Compliance with *in situ gene conservation* standards will be indicated by specifying, in the five year Stewardship Report, the status of designated areas.

22.0 Post-Deployment Monitoring

22.1 Growth and yield monitoring will be as per FMP and FMA requirements.

22.2 Monitoring requirements for *deployment of* material with *restricted registration* will be determined through a case-by-case assessment (see Appendix 9).

23.0 Genetic Research Plantings

23.1 Research *tests* may be established covering an area of up to 17 ha per site and a cumulative area of not greater than 85 ha. Contiguous research plantings larger than 17 ha or with a cumulative area of 85 ha must be identified in the RP plan (see Appendix 24) or *CPP* plan (see Appendix 18).

23.2 All materials included in research *tests* must have a *genetic identity* (*U.I.*, *accession number* or *registered lot number*).

23.3 Research *tests* must meet all applicable BTV standards.

23.4 Research *tests* that include material of uncertain or unknown adaptation (non-local) require approval through an RP plan or *CPP* plan (Appendices 1, 18 and 24).

23.5 Research *tests* including *GMOs* must comply with both federal regulations and provincial policy.

23.6 REPEALED.

23.7 Where a previously untested, non-local species or provenance (including hybrids) is to be planted in a research *test* that exceeds 17 ha per site or 85 ha cumulatively across sites, a benefit/risk assessment is required (see Appendices 18 and 24).

23.8 *Non-local material* may require enhanced monitoring.

BREEDING, TESTING AND VERIFICATION (BTV)

Goals

Programs that produce *Stream 2* material or information relating to *Stream 1* or *Stream 2* material for *deployment* on *public land* in the *Green Area* shall:

i) use testing, analysis and documentation protocols that are effective, efficient and scientifically sound, and

ii) be designed to ensure long-term flexibility in direction and development of RPs or *CPP* plans, and

iii) produce reliable estimates of *genetic gain* for *Stream 2* material when gain is included as an objective of the *CPP* plan.

BTV Standards

24.0 Controlled Parentage Programs

24.1 Proponent(s) of *controlled parentage programs* (*CPP*s) that existed prior to May 01, 2003 (see Appendix 19) and are intended to produce material for *deployment* on *public land* will submit a *CPP* plan in electronic or hard copy that capitalizes on existing work (see Standard 6.0 for clarification of intent) while addressing, as completely as possible, the *CPP* plan requirements (see Appendix 18). The date for submission will be determined by consultation between the proponent(s) and *Alberta*.

24.2 New *CPP*s require an approved *CPP* plan. Proponent(s) of new *CPPs* that are intended to produce material for *deployment* on *public land* will submit a *CPP* plan in electronic or hard copy (see Appendix 18). The *CPP* plan approval process is initiated when the proponent sends a letter of intent to *Alberta*. *Alberta* will respond within three months of receiving the letter of intent. Provided the proponent submits its *CPP* plan within 18 months of the letter of intent, *Alberta* will respond within six months of receipt (see Section 3.0 for submission and approval of documents).

24.2.1 For establishment of *CPPs* primarily based on *non-local material*, testing under an RP plan is required prior to approval of a *CPP* plan (see Appendix 1).

24.3 Where a new or revised *CPP* plan is not approved by *Alberta*, the proponent(s) may request that *Alberta* appoint a third party to review the technical merit of the plan. *Alberta* will consider the third party's advice and provide a decision.

24.4 *Controlled parentage program* plans will identify the following (see Appendices 21A and 21B):

i) the total area (ha) by participating tenure holder within the target *CPP region*,

ii) the total *operable area* (*contributing landbase*) (ha) by tenure holder within the *CPP region*,

iii) the *species-specific target strata* (species by *CPP region*, not necessarily yield stratum) for which the *Stream 2 production population(s)* is designed,

iv) the total area (ha) of *species-specific target strata* by tenure holder.

For *Stream 2* seed material, the following additional calculations and information are required (see Appendix 21A):

i) estimated plants required for 100% planting of *species-specific target strata* area per rotation for each participating tenure holder,

ii) estimated annual number of seedlings from a *production population* allocated to each participating tenure holder, and

iii) planned total production of seedlings over the life of the *production population.*

24.4.1 To determine *deployment* limits for a *production population* and for an example of information and presentation format for *CPP* planning for both seed and vegetative based programs, refer to Appendices 21A, 21B and Standard 18.4.

i) For *Stream 2* material with *restricted registration*, see also Standard 18.4.7 and Appendix 9.

24.5 **Revisions to *CPP* plans**

24.5.1 When significant changes (e.g., *CPP region* boundaries, program direction) occur, revised *CPP* plans or addenda will be submitted to *Alberta* for review. *Alberta* will respond within three months of submission (see Section 3.0 for submission and approval of documents).

25.0 Research Programs

25.1 All genetic testing (of *Stream 1* or *Stream 2* material) intended to provide information relating to *deployment* on *public land*, and not currently covered in a *CPP* plan, will require a RP plan to be submitted for approval by *Alberta* (see Appendices 1, 24 and 24A).

25.1.1 Proponents of RP plans will submit plans for *Alberta's* review at least six months prior to any planned *deployment* of *test* materials in the *Green Area*. *Alberta* will respond within three months of receiving the RP plan (see Section 3.0 for submission and approval of documents).

25.1.2 Where genetic *tests* in the *Green Area* are required by an RP plan, plans will be accompanied by minimum requirements for the *Genetic Test Site* Information Form (Appendix 29).

25.2 All genetic research field *tests* on *public land* will comply with GAD standards and field *test* standards where applicable.

25.3 Upon a request to deploy *non-local material* or *GMOs* (with prior federal approval) on *Green Area public land*, *Alberta*:

i) will review relevant scientific information on a case-by-case basis to evaluate the risks and benefits of *deployment;* and

ii) may request an RP plan and additional testing prior to considering inclusion of such material in a *CPP* (see Appendix 1).

25.4 Genetic research *tests* intended to produce information relating to *deployment* on *public land* in the *Green Area* will follow applicable sections of Standards 23 and 30.

25.5 All *genotype*s destined for testing and for inclusion in a *CPP* selected *population* will be labelled using *U.I.*s, assigned by proponents (see Appendix 25 for codes, and Appendices 11A, 11B, 11C, 12, or 15 for the appropriate submission form).

25.6 Consultation with *Alberta* is advised if a proponent is intending to establish a realized gain *trial*. *Alberta* can provide clarification regarding an acceptable design and methodology to provide information on stratum level *genetic gain*.

25.7 Where a new or revised RP plan is not approved by *Alberta*, the proponent(s) may request in writing that *Alberta* appoint a third party to review the technical merit of the plan. *Alberta* will consider the third party's advice and provide a decision.

26.0 Parent Tree Reporting, Genotype Information and Pedigree Records

26.1 Proponents involved in *CPPs* and RP plans with the intent of developing genetic material for *deployment* on *public land* will maintain and submit to *Alberta* the following:

26.1.1 Parent Tree Selection Report(s) establishing records of parentage and/or *pedigree* for all parent trees collected from *public land.* Report(s) will include:

26.1.1.1 completed parent tree forms (see Appendices 11A, 11B, 11C, 12 and 15) or an Excel file containing all required information, 26.1.1.2 an introduction summarizing the objectives, timing, participants, general location and other information of interest, and

26.1.1.3 for *wild* selections, a map to scale showing locations of parent trees and geographic reference information.

26.1.2 Parentage and/or *pedigree* for *genotypes* in *production populations* and *production units* (see Standards 33.5 and 34.4).

26.1.3 Associated *genotype* information related to species, origin, traits identified in the *CPP* plans and issues of adaptation or claims for gain (as per genetic *test* analysis reports or requirements arising out of *CPP* and RP plans).

27.0 Field Test Data Handling, Storage and Access

27.1 For genetic *tests* established as part of a *CPP* or RP, an electronic listing will be prepared that will allow the unambiguous identification of each *test* tree in the field when accompanied by the appropriate map(s). This listing will contain:

- i) *Alberta* assigned project number and site identifier (e.g., G625C);
- ii) *test* site name;
- iii) replication/block;
- iv) experimental tree position/location; and
- v) *genetic identity* (*accession number*, *registered lot number* or *U.I.*).

27.2 This file will be submitted to *Alberta* as part of the Genetic Test Establishment Report (see Standard 30.12.1 and Appendix 26).

27.3 Each successive measurement of a genetic *test* is to use the same listing to allow compiling of time series data sets.

27.4 Checked raw data will be submitted to *Alberta* as electronic files, using the listing defined in Standard 27.1 to identify individual trees.

27.5 Checked raw data will be accompanied by a data dictionary describing measurement methods and procedures, variables, format, measurement units and measurement codes, quality control procedures and results, assessors, assessment dates and any field assessment comments. Submission of data must follow the reporting standards outlined in Standard 30.12 and Appendix 27.

27.6 Any data or tree code discrepancies identified by *Alberta* in checked raw data sets will be reviewed and corrected by the measuring agency (i.e., company, contractor, scientific cooperator).

27.7 For each genetic research *test*, checked raw data files will be compiled by *Alberta* as new data is submitted and archived in a secure system with backup.

27.8 Data sets used to support claims of adaptation, diversity or performance of *tests* established under *CPP* or RP plans must be submitted to *Alberta.*

27.9 On request, *Alberta* will provide proponents with checked raw *test* data, along with required supporting documentation, contingent on the proponent's right to such material and knowledge.

28.0 Planning, Delineation and Revision of Controlled Parentage Program Regions

28.1 Processes used to delineate a new *CPP region* (e.g., provenance/progeny *tests*) will be included in the associated *CPP* plan or supporting RP plan.

28.2 Revision of an existing *CPP region* may be conducted under an RP plan or revision to an existing *CPP* plan.

28.3 A request submitted to *Alberta* for the establishment of a new *CPP region* or the revision of an existing *CPP region* must include all supporting documentation. *Alberta* will respond within three months of submission.

28.4 REPEALED (see Standard 18.3).

28.5 Material originating from outside a given *CPP region* shall, prior to inclusion in a *production population*, be tested for adaptation, or approved by *Alberta*. Such approval may be given for material deemed equivalent to local, based on evaluation of surrogates for genetic distance (e.g., climate, taxonomy, ecological classification).

29.0 *Ex Situ* Conservation of Native Species

29.1 General

Alberta will be notified of plans to terminate any genetic *test*, *clone* bank or orchard of native Alberta material on public or private land prior to termination. Documentation of genetic material identity will be made available to *Alberta*.

29.2 Samples of genetic *test*s – *public land*

29.2.1 When genetic *tests* on *public land* have fulfilled their purpose, *Alberta* may select and maintain a sample of *tests* for gene conservation purposes.

29.3 Samples of genetic *test*s – private land

29.3.1 When genetic *tests* that include material of native species collected from *public land* are conducted on private land, *Alberta* will have the opportunity to negotiate for maintenance of a sample of *tests* or to collect genetic material before *test*s are destroyed. An *MTA* may be required or a lease agreement considered.

29.4 *Clone* banks or orchards

29.4.1 *Alberta* retains the right to obtain and propagate vegetative material from each parent selected from *public land*. Access may be provided to third parties, and an *MTA* may be required.

29.4.2 Notification and access to the clonal material will be provided to *Alberta* or affected partners prior to destruction of any *clone* (e.g., through roguing).

29.5 Reporting and documentation

29.5.1 Documentation for gene conservation in *clone* banks and samples of genetic *tests* will include a map showing access to the site, a list of included genetic materials and their origins, a map showing tree location/position, and the name, e-mail address and phone number of the contact company(ies) and person(s), as well as (where it exists) a copy of the *MTA*.

30.0 Genetic Research Tests

30.1 Analyses of genetic *tests* conducted under a *CPP* or RP will be reported as outlined in Appendix 28.

30.1.1 Where a genetic analysis report is to be submitted in support of a claim for gain, the proponent will submit a letter of intent to *Alberta* specifying which of the following options will be followed:

i) Follow procedures outlined in the example report “Genetic Analysis Report for Region E White Spruce Tree Improvement” or

ii) Submit a proposal to *Alberta* for alternate procedures. *Alberta* must approve any alternative procedures prior to analysis.

30.2 Genetic field testing for adaptation or gain

30.2.1 *Genotypes* to be included in *production populations* under an approved *CPP* plan require field testing to confirm that the material is locally adapted and to provide data for analysis in support of claims for *genetic gain*.

30.2.2 REPEALED (see Standard 30.2.10).

30.2.3 Material originating from outside the *CPP region* shall be tested for adaptation prior to inclusion in a *production population* unless declared to be *locally adapted material* as per Standard 30.2.5.

30.2.4 Where material to be included in genetic field *tests* originates from inside an approved *CPP region*, testing for adaptation may occur concurrently with assembly of a *production population* and production of *deployment populations*, or as scheduled in the *CPP* plan.

30.2.5 Where material to be included in a *production population* originates outside the *CPP region*, proponents may request that *Alberta* consider it equivalent to material originating from within the *CPP region* for purposes of testing and *deployment*. Approval will be based on review by *Alberta* of ecological and geographic adjacency.

30.2.6 *Genotypes* to be included in *production populations* must be tested on no fewer than three *test* sites or the number specified in the *CPP* plan. Data from these *tests* will be used for analysis to confirm adaptation and support claims for gain.

30.2.7 A RP plan directed toward the establishment of a *CPP region* using *non-local material* must propose a minimum of five *test* sites. The number required may vary depending on characteristics of the proposed *CPP region* (e.g., size and heterogeneity). The number required may also depend on a review of ecological similarity and genetic distance of the *test* material, based on surrogates of genetic distance (e.g., climate, taxonomy, crossability, ecological classification).

30.2.8 For revision of *CPP region* boundaries, the number of *test* sites will be specified in the *CPP* plan or RP plan.

30.2.9 REPEALED (see Standard 18.3).

30.2.10 For incorporation of *non-local material* into a *CPP*, adaptation may be assessed on the basis of performance at a minimum age of 15 years or as determined in consultation with *Alberta*. Based on this assessment, material may then be considered to be locally adapted and included in a *production population*. The following factors will be considered in the assessment:

i) geographical and ecological proximity;

ii) rotation length;

iii) taxonomy and potential to hybridize with local material; and

iv) *test* results (see Standard 30.2.7).

30.3 Site selection and documentation

30.3.1 Sites will be well distributed geographically and elevationally across, and representative of the existing climatic variability in the actual or proposed *CPP region*.

30.3.2 For acceptance and approval of a *trial series* identified in an RP or *CPP* plan, a draft *Genetic Test Site* Information Form (Appendix 29) must be submitted for each *test* site at least six months prior to *test* establishment in the *Green Area*. Approved *trials* will be issued a *trial* number by *Alberta* and completed *Genetic Test Site* Information Forms are to be submitted with *test* Establishment Reports (see Appendices 26 and 29).

30.4 Site protection

30.4.1 A protective notation or reservation or appropriate *public land* disposition will be obtained prior to *test* establishment (e.g., industrial sample plot designation [ISP] or miscellaneous lease [MLL], consultative notation [CNT], protective notation [PNT], disposition reservations [DRS]).

30.5 Field marking

- 30.5.1 Field marking will be established and maintained that allows for identification of each *test* tree (see Appendix 26) complete with an establishment report map(s) and details of all coding systems used. An example of an appropriate format is provided in Appendix 30.
- 30.5.2 The starting point for assessments will be clearly and permanently marked in the field and on establishment report map(s).
- 30.5.3 At least 5% of *test* trees, or the number or proportion specified in the *CPP* or RP plan, will have a permanent marker stake.

30.6 Site maintenance – competition and ingress control

- 30.6.1 Competing vegetation and ingress of the target species will be managed in a manner specified in the *CPP* or RP plan to allow free growth and identification of *test* trees.
- 30.6.2 Ingress of target species, if present or anticipated, will be monitored annually for the first three years and as needed thereafter.

30.7 Site maintenance – maintenance of tree identification

- 30.7.1 Field labelling will be checked in the year following establishment and at the time of each scheduled measurement. Missing or illegible labels will be replaced within four months of each labelling check.

30.8 Measurements – data submission

- 30.8.1 Quality control procedures associated with *test* assessments will be detailed in the Genetic Test Measurement Report (see Appendix 27). Recommended best measurement practices should be used (see Alberta Tree Improvement Field Measurement Guidelines, available from *Alberta*).
- 30.8.2 Trees selected for quality control measurements shall exclude the shortest 20% of trees and all atypical trees (e.g., multi-top, broken top, leaning).

30.9 Measurements – timing

- 30.9.1 Growth traits on a given field *test* site will be measured within one dormant season.

30.10 Measurements – variables

- 30.10.1 Survival codes and other variables specified in the *CPP* or RP plan will be recorded at each measurement.
- 30.10.2 The height of trees shorter than 3 m will be measured to the nearest centimetre. Trees of height greater than 3 m will be measured to the nearest decimetre (i.e., 0.1 m). Units of measurement must be consistent for traits in the measurement period (e.g., all heights in centimetres).
- 30.10.3 Height will be measured to within 10% of the check value 90% of the time across the *test series*.
- 30.10.4 Diameter at breast height (DBH) will be measured to the nearest millimetre and recorded in centimetres.
- 30.10.5 The DBH of trees will be measured to within 10% of the check value 90% of the time across the *test series*.

30.11 Measurements – duration of measurements and long-term monitoring

- 30.11.1 Duration of measurements will be specified in the *CPP* or RP plan.
- 30.11.2 Long-term monitoring will be specified in the *CPP* or RP plan.

30.12 Measurements – reporting

- 30.12.1 A Genetic Test Establishment Report (see Appendix 26) will be submitted to *Alberta* by November 30 of the year following establishment.

30.12.2 A Genetic Test Measurement Report (see Appendix 27) will be completed and submitted to *Alberta* together with checked raw data sets and quality control summary statistics in electronic format within eight months of completion of the current year's measurements. Data sets will be cleaned and formatted.

30.13 Termination of genetic *test*, *clone* bank or orchard

30.13.1 See *Ex situ conservation*, Standard 29.0.

31.0 Genetic Gain Approval

31.1 The process for approval of *genetic gain* begins with a request by a proponent to *Alberta*, stating average values expected for specific trait(s). *Alberta* will provide a response to a request within three months of receipt.

31.2 Approval of a *genetic gain* value will be based on review of the *CPP* plan and one or more of:

i) 2% gain in height at rotation for clonal *seed orchard*s when parents have been selected using the comparison parent tree selection method (see Appendix 11A);

ii) 1% gain in height at rotation for seedling *seed orchard*s when parents have been selected using the comparison parent tree selection method (see Appendix 11A);

iii) results of genetic *tests* (e.g., *genetic worth* calculation – see Appendix 31);

iv) associated RP plans; and

v) other relevant information.

31.3 Any increase to the Annual Allowable Cut (AAC) attributable to *genetic gain* must be approved through the FMP process as per Alberta Forest Management Planning Standard.

31.4 Currently, claims for *genetic gain* are based on height.

31.5 The minimum age of *test* evaluation in support of a claim for *genetic gain* based on progeny testing will be calculated as:

Minimum age in years = 4 + 0.1 * (midpoint of rotation age class), as shown in Table 31.1 below.

Table 30.1. Minimum test evaluation age to support claims for genetic gain.

Rotation age	Midpoint of rotation age class	Minimum evaluation age
6-15	10	5
16-25	20	6
26-35	30	7
36-45	40	8
46-55	50	9
56-65	60	10
66-75	70	11
76-85	80	12
86-95	90	13
96-105	100	14
106-115	110	15
116-125	120	16

31.6 For *non-local material*, adaptation may be assessed on the basis of performance at the minimum age of 15 years, or as determined in consultation with *Alberta*. The following factors will be considered:

i) performance for adaptive traits from field *tests*;
ii) geographic proximity;
iii) ecological compatibility;
iv) genetic distance; and
v) sampling intensity.

PRODUCTION OF CONTROLLED PARENTAGE MATERIALS (PCPM)

Goals

Stream 2 seed and vegetative materials of controlled parentage for *deployment* on *public land* will be produced:

i) in *production sites*, *production units* and/or *production populations* approved by *Alberta*, using established procedures;

ii) in a manner that maintains the potential to produce a crop (*deployment population*) that can be registered with a calculated *effective population size* (diversity) and *genetic worth*; and

iii) in a manner that ensures adequate documentation and reporting for *registration* of materials produced.

PCPM Standards

32.0 General

32.1 *Production sites*, *production units* and *production populations* must have the potential to produce registered *deployment populations* of seed or vegetative materials for *deployment* on *public land* (see Appendix 35 for a production systems schematic).

32.2 *Alberta* will approve *production sites* for production of materials on the basis of a review of an application submitted to *Alberta*. An application will include a risk assessment that will address the following where appropriate:

i) pollen contamination for proposed orchard(s);

ii) infrastructure (e.g., roads, water source, labour supply, expansion capability, *production site* modification);

iii) environment;

iv) potential pest risks;

v) security in space and time; and

vi) pre-conditioning/adaptation (e.g., for production environments differing significantly from *deployment* environments).

32.3 A *production site* on *public land* must be protected by a *public land* disposition or other protective notation.

32.4 Each *production unit* requires *Alberta* approval and is designated for a single specified *CPP region* to ensure adaptation (contact *Alberta*).

32.5 Production of controlled parentage materials must be integrated with an approved *CPP* plan or with a *CPP* included in the list in Table A19.1. For details on plan development, approval and materials *deployment* see Standards 24.1, 24.2, 18.4 and 18.4.1.

32.6 The maximum amount of registered *Stream 2* material, over the life of a *production population* and its associated *production unit(s)* for a given *CPP region*, will depend on numerical restrictions on total *deployment* from the *production population* (see Appendices 20 and 21A for seed deployment limits and Standard 18.4.3.2 for vegetative material use limits). The maximum number deployable will vary by *CPP region*, and will be included in the *CPP* plan as per Standard 24.0.

32.7 A *production site* and *production unit* review will include inspection to assess the ability of the owner to fulfill *Alberta's* requirements:

32.7.1 Owners of existing *production sites* and *production units* will provide *Alberta* with information supporting approval.

32.8 Continued compliance with approval conditions is required to maintain approval to produce material for *public land deployment*. Technical audits may be used to verify compliance.

- 32.8.1 Completed *production unit* establishment reports must be submitted by June 30 of the year following establishment (see Appendix 32).
- 32.8.2 All orchards must follow the Permanent Sample Tree (PST) protocols contained in Appendix 33.
- 32.8.3 All orchards must follow the Pollen Contamination Monitoring protocols (see Appendix 34A) and Phenology Monitoring protocols (see Appendix 34B); see Appendix 35A for reporting requirements.
- 32.8.4 An annual operations report shall be submitted to *Alberta* by June 30 for *seed orchard* production (see Appendix 35A) and June 30 for *vegetative propagule* production (see Appendix 35B).

32.9 A *production site* and *production unit* review will be conducted every five years, or sooner where significant changes to the *production site* or *production unit* have occurred.

32.10 An approval may be cancelled for failure to comply with the standards or for submitting information that is known to be incorrect or purposely misleading.

33.0 Seed Material Production

33.1 An orchard must be designed to produce a *deployment population* (seed crop) of a minimum *effective population size* (*Ne*) of 18.

33.2 Orchards must be designed using specialized design software (e.g., SOL32 or SOMAD).

33.3 When required, *deployment population genetic worth* is to be calculated according to the procedures outlined in Appendix 31 and reported as per Appendix 35A.

33.4 *Effective population size* is to be calculated according to procedures outlined in Appendices 36 and 37 and reported as per Appendix 35A:

- 33.4.1 The basis for collecting required data to calculate the *effective population size* is through the sampling of contributing parents as outlined in Appendix 37.
- 33.4.2 Calculations will be documented and records/data retained for auditing purposes; they will be provided upon request by *Alberta*.
- 33.4.3 With *Ne* of at least 18, proponents may deploy up to 25% of species-specific target strata. The *cumulative Ne* of deployed populations produced from all *production unit*s (*seed orchard*s) for a given *CPP* must be at least:
  - i) 30 when 50% of the *species-specific target strata* area has been regenerated with material from those *production unit*s;
  - ii) 42 when 75% of the *species-specific target strata* area has been regenerated with that material; and
  - iii) 54 when 100% of the *species-specific target strata* area has been regenerated with that material.

See Standard 18.4.3 and Appendix 21A. Methods for calculating *cumulative Ne* are detailed in Appendix 20.

- 33.4.4 REPEALED

33.5 The *genetic identity*, and where available the *pedigree*, of *seed orchard* parents must be maintained.

33.6 Documentation for each *deployment population* (seed crop) must be submitted for *registration* (see Appendix 3).

33.7 *Alberta* will assign a *production unit* identifier for approved seed *production populations* and associated *production units* (see Appendix 35A for reporting).

34.0 Vegetative Material Production

34.1 When required, *deployment population genetic worth* is to be calculated according to procedures in Appendix 31 and reported as per Appendix 35B.

34.2 A vegetative lot must be assembled from a *production population* or *production unit(s)* capable of producing a *deployment population* with a minimum *effective population size* of 18 for *unrestricted registration* except in the case of *intensive deployment* of clonal material (see Appendices 5 and 9).

34.3 *Effective population size* is calculated according to procedures in Appendix 36.

34.3.1 The individual clonal contribution to a *deployment population* must be known in order to meet data requirements for calculating *effective population size* for *Stream 2* vegetative materials in Appendix 36.

34.3.2 Calculations will be documented and records/data retained for auditing purposes; they will be provided upon request by *Alberta* (see Appendices 3, 36 and 37).

34.4 The *genetic identity*, and where available the *pedigree*, of *clone*s in the *production population* and *production unit(s),* must be maintained.

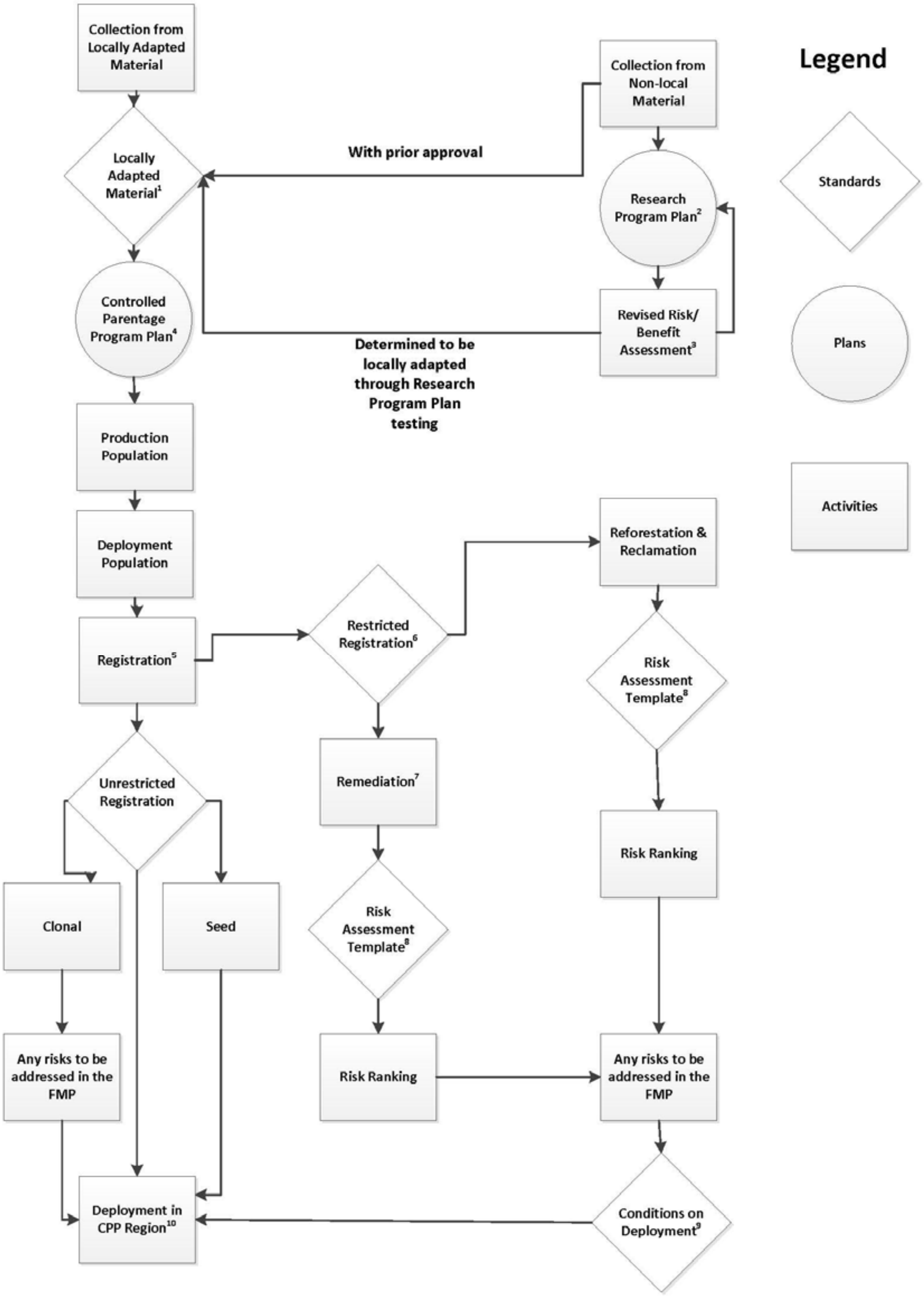
34.5 Documentation for each *deployment population* (vegetative crop) must be submitted for *registration* (see Appendix 3).

34.6 *Alberta* will assign a *production population* identifier for approved vegetative *production populations* (see Appendix 35B for reporting).

APPENDICES

Appendix 1. Flow Diagram for Registration and Deployment of *Stream 2* Material

See Standards 5.0, 10.12, 23.4, 24.2.1, 25.1 and 25.3.



Appendix 1. Flow Diagram for Registration and Deployment of *Stream 2* Material (continued)

[1] See Glossary for definitions. Note that material originally classified as having unproven adaptation may be determined to be locally adapted either by *Alberta* or based on genetic testing.

[2] See Appendix 24. Research Program Plan – Contents.

[3] The risk/benefit assessment conducted as a part of the research plan will be revised on the basis of information resulting from implementation of the research plan.

[4] See Appendix 18. *Controlled Parentage Program* Plan – Contents.

[5] See Appendix 5. Collection Effective Population Size (*Ne*) Requirements for *Registration* of *Stream 2* Material; also see Material Collection, Handling, *Registration* and Storage (MCHRS) Standards for additional *Stream 2 registration* requirements.

[6] See Appendix 9. Assessment of Risk for *Stream 2* and *Restricted Registration* Material: also Standard 10.0 for *Stream 2 registration* requirements.

[7] *Remediation* may be governed by different sustainability objectives, legislation and jurisdiction than *reforestation* and *reclamation*.

[8] See the Risk Assessment Template, Appendix 9.

[9] Refer to Appendix 9 for assessment of risk procedures for *Stream 2* and *restricted registration* materials.

[10] *Deployment* standards within the Alberta Forest Genetic Resource Management and Conservation Standards (FGRMS 2016) apply, but no additional conditions are necessary as per restricted *registration* stream.

Appendix 2. Registration Request Form for *Stream 1* Material (Updated May 1, 2020)

See Standards 10.1, 10.4, 10.7, 10.12, 12.3.1, 13.4, 13.5, 15.4 and 18.2.7.

All plant seed and vegetative materials to be used on *public land* must be registered with *Alberta*. Completion of this form initiates the *registration* process for materials collected on *public land*. The agency or company doing the collection assigns a *temporary lot number*, writes it on the tag with the material, and completes the *Registration* Request Form. *Alberta* assigns a *registered lot number* once *registration* is complete.

Alberta Government

STREAM 1 REGISTRATION REQUEST (APPENDIX 2 FGRMS)

1. ADMINISTRATIVE INFORMATION

OWNER/ADDRESS	(For Department Use Only) SIMS INVENTORY NO.
	REGISTRATION CATEGORY ☐ UNRESTRICTED ☐ RESTRICTED ☐ PENDING REGISTRATION[1]
REGISTERED LOT NUMBER (For Department Use Only)	

2. STAND AND SITE INFORMATION

SPECIES		ARIS CODE[2]	
TEMPORARY LOT NUMBER THE TEMPORARY LOT NUMBER IS ASSIGNED BY THE AGENCY AND MUST CORRESPOND WITH LABELLING ON SACKS, CONTAINERS, ETC.			
ELEVATION RANGE (m)	min	max	SEED ZONE[3]
LEGAL LOCATION			

PROVIDE LATITUDE & LONGITUDE INFORMATION BELOW: Record the four most outside collection points using degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456). If the collection was made within ONE legal subdivision, report the legal subdivision in the space above and provide only one latitude and longitude below.

LATITUDE		LONGITUDE	
LATITUDE		LONGITUDE	
LATITUDE		LONGITUDE	
LATITUDE		LONGITUDE	

3. COLLECTION INFORMATION

COLLECTION SUPERVISOR	CONTRACTOR

COLLECTION METHOD						PICKING METHOD		TYPE OF MATERIAL COLLECTED & TOTAL VOLUME AND/OR AMOUNTS COLLECTED
Aerial ☐	Felled trees ☐	Slash ☐	Cuttings ☐	Climbing /ladder/lift ☐	Squirrel cache ☐	Hand picked ☐	Mechanically picked ☐	

COLLECTION DATES	NUMBER OF PLANTS FROM WHICH THE COLLECTION WAS MADE[4]	COLLECTION PERMIT (APPENDIX 10A) YES ☐ NO ☐ OTHER[5] ☐

4. INTERIM STORAGE AND SHIPPING INFORMATION

INTERIM STORAGE DATES (INCLUDES COLD STORAGE)	DATE SHIPPED TO PROCESSING FACILITY
PROCESSING FACILITY	

5. DECLARATION I HEREBY DECLARE THAT THE INFORMATION GIVEN ABOVE (SECTIONS 1, 2, 3 & 4) IS VALID AND CORRECT FOR THIS LOT.

NAME		POSITION
SIGNATURE OF REGULATED PROFESSIONAL	DESIGNATION	COMPANY
REMARKS		

6. EXTRACTION AND CLEANING INFORMATION (TO BE COMPLETED BY PROCESSING FACILITY FOR SEED ONLY).

DATE RECEIVED	DATES EXTRACTED	AMOUNT CLEANED (KG)	SEED MOISTURE MEASUREMENT eRH MC

Approval Decision (Department use only)	
Reviewed by	Date

A COPY OF THIS FORM MUST ACCOMPANY MATERIAL TO PROCESSING AND/OR STORGE FACILITIES IN COMPLIANCE WITH T/M REGULATION 144.3

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[1] Pending fulfillment of all requirements for registration such as adequate number of trees sampled.

[2] See Alberta Regeneration Information System code listing in Appendix 6 FGRMS.

[3] If material from outside Alberta indicate province or state.

[4] Provide exact number of plants if minimum trees per collection for unrestricted registration (see relevant table in Appendix 4) has not been exceeded; provide estimates if minimum number of trees has been exceeded.

[5] Annual Operating Plan, or other plans.

Appendix 3. Registration Request Form for *Stream 2* Material (Updated May 1, 2020)

See Standards 10.1, 10.4, 10.9, 10.11, 10.12, 12.4.1, 13.4, 13.5, 33.6 and 34.5.

Alberta
Government

STREAM 2 REGISTRATION REQUEST (APPENDIX 3 FGRMS)

1. ADMINISTRATIVE INFORMATION

TEMPORARY LOT NO.	(FOR DEPARTMENT USE ONLY)
REGISTERED LOT NO. (FOR DEPARTMENT USE	SIMS INVENTORY No.
APPROVED PRODUCTION UNIT or PRODUCTION POPULATION NO.	REGISTRATION CATEGORY
PRODUCTION SITE LOCATION(S)	☐ UNRESTRICTED ☐ RESTRICTED ☐ PENDING REGISTRATION

2. OWNERSHIP

COMPANY	% OF LOT ALLOCATED

3. GENETIC INFORMATION

SPECIES	CPP Region	
EFFECTIVE POPULATION SIZE	GENETIC WORTH	ARIS CODE[1]

4. COLLECTION INFORMATION

COLLECTION SUPERVISOR	CONTRACTOR
COLLECTION DATES	TYPE OF MATERIAL COLLECTED AND TOTAL VOLUME AND/OR AMOUNTS COLLECTED

5. INTERIM STORAGE AND SHIPPING INFORMATION

INTERIM STORAGE DATES (INCLUDES COLD STORAGE)	DATE SHIPPED TO PROCESSING FACILITY
PROCESSING FACILITY	

6. EXTRACTION AND CLEANING INFORMATION (TO BE COMPLETED BY PROCESSING FACILITY FOR SEED ONLY)

DATE RECEIVED	DATES EXTRACTED	AMOUNT CLEANED (KG)	SEED MOISTURE MEASUREMENT eRH MC

7. DECLARATION

THE ABOVE INFORMATION (SECTIONS 1, 2, 3, 4, & 5) WAS COMPLETED BY:

NAME	POSITION
SIGNATURE (of regulated professional)	COMPANY
REMARKS	

A COPY OF THIS FORM MUST ACCOMPANY MATERIAL TO PROCESSING AND/OR STORAGE FACILITIES IN COMPLIANCE WITH T/M REGULATION 144.3

Approval Decision (Department use only)	
Reviewed by	Date

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[1] See Alberta Regeneration Information System code listing in Appendix 6 FGRMS.

Appendix 4. Requirements for Registration of *Stream 1* Material

See Standards 10.4, 10.6, 10.8, 10.12, 11.4, 18.2.4 and 20.

POINT COLLECTIONS

Where a collection meets the number, area and elevation requirements as shown in Table A4.1 and is otherwise eligible for *unrestricted registration*, material may be deployed up to 1 km outside the *seed zone* of origin, provided the difference in elevation from point of collection to point of *deployment* does not exceed 100 m. Such collections are also eligible for wider movement outside the *seed zone* of origin through application for a *Stream 1* variance (see Appendices 8 and 13). See Appendix 14 for *deployment* limits.

Table A4.1. Requirements for point collections of *Stream 1* Material.

Material category	***Stream 1* material**	**Minimum plants per collection for *unrestricted registration* or establishment of *serial propagation***	**Range of plants per collection eligible for *restricted registration*[1]**	**Maximum elevation range from which plants collected**	**Maximum area from which collection is made**
A	All seedlot collections **except** aspen and balsam poplar, and clonal shrubs[4]	30	20-29	100 m	2 km radius
B	Aspen and balsam poplar and clonal shrubs[4] seedlot collections	10 (well-spaced *clones*/patches)[2]	7-9 (well-spaced *clones*/patches)[2]	100 m	5 km radius
C	Vegetative lots (deployed without *serial propagation*)	75[3]	N/A	100 m	5 km radius
D	Vegetative lots (*serial propagation* before *deployment*)	120[3]	75-119	100 m	5 km radius

[1] Collections from plants fewer than listed in this column may be stored "pending *registration*" (see Appendix 2) and will only be registerable when combined to meet *unrestricted* or *restricted registration* requirements.

[2] Must be collected from aspen and balsam poplar *clones* separated by a minimum of 500 m, or by 50 m for clonal shrubs (separation between nearest edges of patches or *clones*).

[3] Must be collected from plants separated by at least 10 m.

[4] See Table A38.4 (Appendix 38).

SEED ZONE COLLECTIONS

Where a collection does not meet the area and elevation requirements in Table A4.1 but is collected within a *seed zone* and meets the minimum number requirements in Table A4.2, and *Stream 1 unrestricted registration* requirements, this collection is eligible for *registration*. However, variance requests for *deployment* outside the *seed zone* of origin will not be considered. See Appendix 14 for *deployment* limits.

Table A4.2. Requirements for seed zone collections of *Stream 1* Material.

Material category	***Stream 1* material**	**Minimum plants per collection for *unrestricted registration* or establishment of *serial propagation***	**Range of plants per collection eligible for *restricted registration*[1]**	**Collection area**
A	All seedlot collections **except** aspen and balsam poplar, and clonal shrubs[4]	30	20-29	Within *seed zone*
B	Aspen and balsam poplar and clonal shrubs[4] seedlot collections	10 (well-spaced *clones*/patches)[2]	7-9 (well-spaced *clones*/patches)[2]	Within *seed zone*
C	Vegetative lots (deployed without *serial propagation*)	75[3]	N/A	Within *seed zone*
D	Vegetative lots (*serial propagation* before *deployment*)	120[3]	75-119	Within *seed zone*

[1] Collections from plants fewer than listed in this column may be stored "pending *registration*" (see Appendix 2) and will only be registerable when combined to meet *unrestricted* or *restricted registration* requirements.

[2] Must be collected from aspen and balsam poplar *clone*s separated by a minimum of 500 m, or by 50 m for clonal shrubs (separation between nearest edges of patches or *clones*).

[3] Must be collected from plants separated by at least 10 m.

[4] See Table A38.4 (Appendix 38).

STREAM 1 SEED ORCHARD COLLECTIONS

Where a collection meets the requirements in Table A4.3 and *Stream 1 unrestricted registration* requirements, it is eligible for *registration*. Variance requests for *deployment* outside the *seed zone* of origin will not be considered. See Appendix 14 for *deployment* limits.

Table A4.3. Requirements for *Stream 1* seed orchard collections.

Material Category[1]	***Seed orchard* type**[2]	**Minimum number of *clones* or families for establishment of a *Stream 1 seed orchard***	**Requirements for representation of *genotypes* in *Stream 1 seed orchard***	**Collection area for *seed orchard* establishment**
A1	Clonal *seed orchard*	100 - 300 *clones*/patches[3]	Plants per *clone* must be between 0.5% and 10% of orchard total, or minimum *Ne* = 18	Within *seed zone*
A2	Clonal *seed orchard*	>300 *clones*/patches [3]	Documentation at establishment	Within *seed zone*
B1	Seedling *seed orchard*	50 - 150 parents/patches[3]	Minimum 4 plants /parent and maximum plants/parent must not exceed 10% of orchard total	Within *seed zone*
B2	Seedling *seed orchard*	>150 parents/patches[3]	Documentation at establishment	Within *seed zone*

[1] These orchards can also be used for vegetative lot collections provided requirements in Table A4.2 are met.

[2] Spatial design requirements for *seed orchard*s must be followed (see Appendix 32a).

[3] Plants collected for *seed orchard* establishment must be separated by at least 50 m (between *clone* or patch edges) and they cannot be sourced from *artificially regenerated* areas.

RESTRICTED REGISTRATION COLLECTIONS

Collections not fully meeting *point collection* or *seed zone collection* requirements may be eligible for *restricted registration* (see Appendix 2).

COLLECTIONS PENDING REGISTRATION

Lots that do not meet requirements for *unrestricted or restricted registration* (e.g., lots collected from fewer than the minimum number of plants specified above) may be collected and stored, pending fulfillment of *registration* requirements (which can include combining lots from the same *seed zone* to meet *registration* requirements).

Geographic collection limits and *deployment* number caps (see Appendix 14) are in place to safeguard *genetic diversity* by considering biological differences among species, patterns of natural variation, and quantitative implications of vegetative and sexual reproduction.

Appendix 5. Effective Population Size (Ne) Requirements for Registration of *Stream 2* Material

See Standards 10.4, 10.9 and 10.12.

Table A5.1 shows effective population size requirements for *Stream 2 reforestation* seed or vegetative material destined for *deployment* in the *Green Area*.

Table A5.1. Effective population size (Ne) requirements for registration of *Stream 2* Material.

***Stream 2* material**	***Ne*[1] required**	***Registration* category**	**Maximum deployable numbers from a *production population***
Seedlots	≥18	*Unrestricted*	see Appendix 21A
Vegetative lots	≥18	*Unrestricted*	see Standard 18.4.3.2
Seedlots	6 – < 18[2]	*Restricted*	see Appendices 1, 9
Vegetative lots	6 – < 18[2,4]	*Restricted*	see Appendices 1, 9
Seedlots	< 6[2,3]	pending *registration*	None
Vegetative lots	< 6[2,3]	pending *registration*	None

[1] See Appendix 36 for *Ne* calculation methods.

[2] Lots with *Ne* < 18 may be combined to achieve threshold *Ne* levels of 6 and 18 for *restricted* and *unrestricted registration* respectively. Lots to be combined must be from *production units* or *production populations* targeting the same *controlled parentage program (CPP) region*. See Appendix 20 for calculation methods.

[3] Lots with *Ne* < 6 may be held in interim storage, pending combination with other lot(s) to achieve registerable *Ne* levels.

[4] *Ne* = 10 does not imply *restricted registration* in *intensive deployment* (see Appendix 9).

Appendix 6. Stream Categories and Genetic Class Codes for Alberta Regeneration Information System (ARIS) Reporting

See Standard 10.7.

A. SEED

List of potential materials for *deployment* on provincial *public land*

	Material Type	Stream	Genetic Class Code[1]
a.	**Native seed collections in *wild* stands**		
1.	Unselected parents in unselected stands	1	AIa1
2.	Unselected parents in selected stands[2]	1	AIa2
3.	Selected parents[2] in unselected stands	1	AIa3
4.	Selected parents[2] in selected stands[2]	1	AIa4
b.	**Native seed collections in *artificially regenerated* stands**		
5.	Unselected parents in unselected stands	1	AIb5
5.i	Unselected parents in *Stream 1 seed orchard*s		AIb5so
6.	Unselected parents in selected stands[2]	1	AIb6
7.	Selected parents[2] in unselected stands	1	AIb7
8.	Selected parents[2] in selected stands[2]	1	AIb8
c.	**Seed collections in *production units*[3]**		
9.	Improved orchard	2	AIc9
10.	Unimproved orchard	2	AIc10
11.	Seedlot with *Ne* < 18 (*registration restricted*)[4]	2	AIc11
12.	*Hybrid orchard* [5]	2	AIc12
13.	*Non-local material*	2	AIc13
14.	*Genetically Modified Organisms (GMOs)*	2	AIc14

List of potential precursor materials for *deployment* on provincial *public land*

a.	**Local seed**	
15.	Individual family	R
16.	Pollen	R
17.	*GMOs*	R
b.	**Non-local seed**	
18.	Provenances	R
19.	Species	R
20.	Hybrids	R
21.	Individual family	R
22	*GMOs*	R
23.	Pollen	R

Stream 1 = traditional *reforestation* stream (see glossary)
Stream 2 = controlled parentage stream (see glossary)
R = *research material* (see glossary)

[1] *Genetic class code*s assigned only to *Stream 1* and *2* materials; research materials cannot be deployed operationally.

[2] A selected parent tree or stand refers to a tree or stand of trees that has been systematically selected from a population of trees or stands based on a documented process of selection for one or more desirable phenotypic traits (e.g., height, form, canopy position).

[3] Orchards may include some trees from adjacent areas with *Alberta* approval or based on testing.

[4] If material fits this category in addition to any other category, this category over-rides.

[5] Orchard designed to produce hybrid seed.

B. VEGETATIVE PROPAGULES

List of potential materials for *deployment* on provincial *public land*

	Material Type	Stream	Genetic Class Code[1]
a.	**Native *propagule* collections in *wild* stands[2]**		
1.	Unselected parents in unselected stands	1	BIa1
2.	Unselected parents in selected stands	1	BIa2
3.	Selected parents[3] in unselected stands	1	BIa3
4.	Selected parents[3] in selected stands	1	BIa4
b.	**Native *propagule* collections in *artificially regenerated* stands**		
5.	Unselected parents in unselected stands	1	BIb5
5.i	Unselected parents in *Stream 1 stoolbed*s		BIb5sb
6.	Unselected parents in selected stands	1	BIb6
7.	Selected parents[3] in unselected stands	1	BIb7
8.	Selected parents[3] in selected stands	1	BIb8
c.	***Propagule*s generated in *production units* or *production populations*[4]**		
9.	*Selected population*	2	BIc9
10.	Tested population	2	BIc10
10.i	Tested population used in *intensive deployment*[5]	2	BIc10i
10.ii	Tested population used in *extensive deployment*[5]	2	BIc10e
11.	Lot with *Ne*<18 (*registration restricted*)[6]	2	BIc11
12.	*Amplified family*	2	BIc12
13.	Hybrids	2	BIc13
14.	*Non-local material*	2	BIc14
15.	*GMOs*	2	BIc15

List of potential precursor materials for *deployment* on provincial *public land*

	Material Type	Stream
a.	**Local material**	
16.	Individual family	R
17.	Individual *clone*s	R
18.	Pollen	R
19.	*GMOs*	R
b.	***Non-local materia*l**	
20.	Provenance material	R
21.	Species material	R
22.	Hybrid material[7]	R
23.	Individual *clone*s	R
24.	Pollen	R
25.	*GMOs*	R

Stream 1 = traditional *reforestation* stream (see glossary)
Stream 2 = controlled parentage stream (see glossary)
R = *research material* (see glossary)

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[1] *Genetic Class Code*s assigned only to *Stream 1* and *2* materials; research materials cannot be deployed operationally.

[2] Materials may be multiplied in *stoolbeds* that meet the minimum number of trees required per collection for *Stream 1* material (see Standard 11.4 and Appendix 4.

[3] A selected parent tree or stand refers to a tree or stand of trees that has been systematically selected from a population of trees or stands based on a documented process of selection for one or more desirable phenotypic traits (e.g, height, form, canopy position).

[4] *Production unit*s and populations may include some trees from adjacent areas with *Alberta* approval or based on testing.

[5] See standards 18.4.3.4 and 18.4.3.5.

[6] If material fits this category in addition to any other category, this category over-rides. *Propagule*s in *intensive deployment* are allowed to have *Ne* below 18 and thus should not be reported in this category (Standard 18.4.3.5.1).

[7] Hybrid with at least one non-local parent.

Appendix 7. Seed Zone Descriptions, Areas and Maps

See Standards 10.8, 18.2.1, 18.3 and 20.2.

Plant populations' exhibit genetic variation associated with differences in geography and climate of origin. Such variation is the result of long-term evolutionary processes and is key to biological adaptation to regional habitats, and to maintenance of future evolutionary potential. For these reasons, movement of all plant material for *reforestation* and *reclamation* on *public land* is regulated.

SEED ZONES

A seed zonation system for Alberta has been developed for natural seed movement, and replaces the old Seed Provenance Rule (*deployment* within a 50 mile [80 km] radius and plus/minus 500 feet (150 m) elevation movement from location of collection). *Seed zones* are geographic subdivisions of Natural Regions and Subregions, and are based on general genetic and ecological criteria. They limit seed movement to a conservative area where native plants of all species can be moved without risk of maladaptation or erosion of genetic integrity. Seed collections from natural stands of all species that meet *unrestricted registration* requirements can be moved freely within a *seed zone* of origin. There are a total of 90 described *seed zones* for Alberta, which cover all species and areas of the province. Seventy-four *seed zones* are applicable to the *Green Area*.

Forestry *Seed Zone*s of Alberta are delineated for all areas of the province, and are applicable to all native forest plant species. The intent of *seed zones* is to provide delineated ecological land units within which planning, collection, inventory maintenance, conservation and *deployment* can occur for reproductive materials of natural forest plant species.

Seed zone delineation is hierarchical and based on Alberta's six Natural Regions, their Natural Subregions and Ecodistricts. Where there was a concern that the Natural Regions, Subregions or Ecodistricts did not adequately capture natural adaptive genetic variation, elevation contours were used for further subdivision. While current seed zones were developed for trees, the current scientific opinion is that they work sufficiently well for shrubs to guard against maladaptation; however, when new information is available, shrub-specific seed zones may be created.

Seed zone labelling is structured so that:

a. the designated alphabetic descriptor denotes the Natural Subregion in which the *seed zone* falls;
b. the number preceding the decimal designates groupings of *seed zones* within a subregion that are similar in climate; and
c. the decimal portion designates the individual *seed zone* within a climate grouping. Numbering generally follows a pattern of cooler growing seasons, milder winters and increased precipitation.

*Seed zone*s are listed in Table A7.1 and mapped in Figures A7.1, A7.2, and A7.3. *Species-specific seed zone*s may be developed (see Standards 18.3 and Appendix 24A).

For s*eed zone* shape files, maps, and an electronic listing of *seed zone*s, contact *Alberta*.

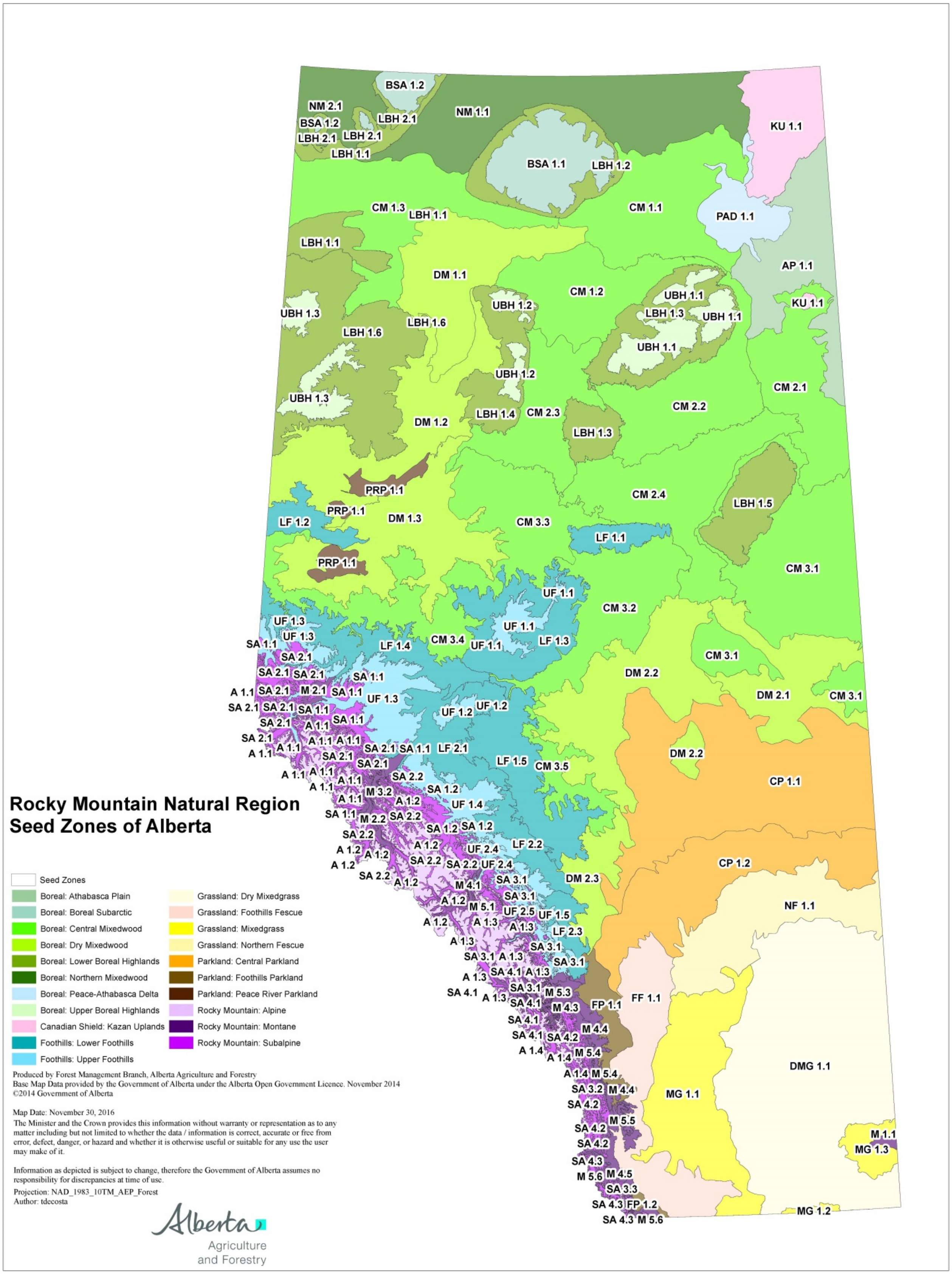
Table A7.1. Seed zones of Alberta.

SEED ZONE LABEL	2014 REVISED AREA IN HECTARES	NATURAL REGION	NATURAL SUBREGION	SEED ZONE NAME	MIN. ELEV*	MAX. ELEV*	MEAN. ELEV*	SD. ELEV*
A 1.1	341,795	Rocky Mountain	Alpine	Kakwa-Athabasca Alpine	1306	3280	2211	182
A 1.2	572,916	Rocky Mountain	Alpine	Athabasca-Kootenay Alpine	1325	3637	2419	249
A 1.3	491,424	Rocky Mountain	Alpine	Kootenay-Bow Alpine	1739	3498	2405	220
A 1.4	86,951	Rocky Mountain	Alpine	Bow-Crowsnest Alpine	1867	3275	2390	187
A 1.5	15,371	Rocky Mountain	Alpine	Crownsest-Waterton Alpine	1876	2901	2281	137
AP 1.1	1,352,525	Boreal	Athabasca Plain	Athabasca Plain	199	646	311	101
BSA 1.1	952,530	Boreal	Boreal Subarctic	Caribou Mountains Boreal Subarctic Uplands	655	1000	847	62
BSA 1.2	229,742	Boreal	Boreal Subarctic	Cameron Hills Boreal Subarctic Uplands	581	825	697	47
CM 1.1	1,675,648	Boreal	Central Mixedwood	Great Slave Central Mixedwood Plains	196	522	253	37
CM 1.2	1,209,780	Boreal	Central Mixedwood	Vermillion Central Mixedwood Lowlands	241	696	367	82
CM 1.3	1,739,345	Boreal	Central Mixedwood	Hay River Central Mixedwood Lowlands	279	630	391	55
CM 2.1	1,243,579	Boreal	Central Mixedwood	Saskatchewan Central Mixedwood Plains	210	670	438	85
CM 2.2	1,384,867	Boreal	Central Mixedwood	Mackay Central Mixedwood Lowlands	228	682	482	83
CM 2.3	1,103,602	Boreal	Central Mixedwood	Loon Lake Central Mixedwood Lowlands	358	690	556	55
CM 2.4	1,786,122	Boreal	Central Mixedwood	Wabasca Central Mixedwood Lowlands	222	759	558	65
CM 3.1	2,524,589	Boreal	Central Mixedwood	Mostoos Hills Central Mixedwood Uplands	443	867	628	58
CM 3.2	1,301,511	Boreal	Central Mixedwood	Swan Hills-Pelican Central Mixedwood Uplands	510	897	657	50
CM 3.3	1,402,207	Boreal	Central Mixedwood	Swan Hills-Utikuma Central Mixedwood Uplands	551	877	671	52
CM 3.4	992,783	Boreal	Central Mixedwood	Wapiti-Smoky Central Mixedwood Uplands	576	928	763	50
CM 3.5	421,425	Boreal	Central Mixedwood	Drayton Central Mixedwood Plains	733	1039	863	52
CP 1.1	3,487,579	Parkland	Central Parkland	Northern Central Parkland Plains	497	1028	705	77
CP 1.2	1,883,038	Parkland	Central Parkland	Southern Central Parkland Plains	601	1254	825	130
DM 1.1	1,476,415	Boreal	Dry Mixedwood	Vermillion Dry Mixedwood Lowlands	194	613	340	57
DM 1.2	1,735,991	Boreal	Dry Mixedwood	Peace River Dry Mixedwood Lowlands	259	829	588	86
DM 1.3	1,704,194	Boreal	Dry Mixedwood	Smoky River Dry Mixedwood Lowlands	286	969	625	72
DM 2.1	1,138,702	Boreal	Dry Mixedwood	Lac La Biche Dry Mixedwood Plains	488	739	604	46
DM 2.2	1,951,240	Boreal	Dry Mixedwood	Edmonton Dry Mixedwood Plains	487	934	689	67
DM 2.3	525,537	Boreal	Dry Mixedwood	Red Deer Dry Mixedwood Plains	828	1235	994	71
DMG 1.1	4,693,714	Grassland	Dry Mixedgrass	Southeastern Dry Mixedgrass Plains	567	1102	798	81
FF 1.1	1,362,345	Grassland	Foothills Fescue	Southwestern Foothills Fescue	799	1524	1106	128
FP 1.1	355,167	Parkland	Foothills Parkland	Southwestern Foothills Parkland	1022	1533	1235	78
FP 1.2	37,001	Parkland	Foothills Parkland	Waterton Foothills Parkland	1245	1587	1380	55
KU 1.1	971,882	Canadian Shield	Kazan Uplands	Kazan Upland	165	409	273	41
LBH 1.1	624,356	Boreal	Lower Boreal Highlands	Bistcho Lower Boreal Highlands	389	792	523	62
LBH 1.2	469,632	Boreal	Lower Boreal Highlands	Caribou Mountains Lower Boreal Highlands	410	896	607	86
LBH 1.3	1,042,176	Boreal	Lower Boreal Highlands	Birch Mountains Lower Boreal Highlands	437	838	666	54

SEED ZONE LABEL	2014 REVISED AREA IN HECTARES	NATURAL REGION	NATURAL SUBREGION	SEED ZONE NAME	MIN. ELEV*	MAX. ELEV*	MEAN. ELEV*	SD. ELEV*
LBH 1.4	595,419	Boreal	Lower Boreal Highlands	Buffalo Head Hills Lower Boreal Highlands	468	834	687	49
LBH 1.5	665,699	Boreal	Lower Boreal Highlands	Stony Mountain Lower Boreal Highlands	558	871	689	36
LBH 1.6	1,985,568	Boreal	Lower Boreal Highlands	Clear Hills Lower Boreal Highlands	510	1064	738	74
LBH 2.1	178,450	Boreal	Lower Boreal Highlands	Cameron Hills Lower Boreal Highlands	563	777	655	42
LF 1.1	253,333	Foothills	Lower Foothills	Pelican Mountains Lower Foothills	663	1021	800	76
LF 1.2	295,179	Foothills	Lower Foothills	Saddle Hills Lower Foothills	641	1019	816	57
LF 1.3	952,135	Foothills	Lower Foothills	Swan Hills Lower Foothills	678	1141	882	84
LF 1.4	779,453	Foothills	Lower Foothills	Wapiti-Athabasca Lower Foothills	675	1210	916	75
LF 1.5	999,615	Foothills	Lower Foothills	McLeod-North Saskatchewan Lower Foothills	704	1168	932	63
LF 2.1	663,891	Foothills	Lower Foothills	Athabasca-McLeod Lower Foothills	817	1575	1042	72
LF 2.2	335,231	Foothills	Lower Foothills	Brazeau-Clearwater Lower Foothills	965	1700	1100	66
LF 2.3	211,005	Foothills	Lower Foothills	Clearwater-Bow Lower Foothills	1067	1648	1268	92
M 1.1	30,948	Rocky Mountain	Montane	Cypress Hills Montane	1119	1474	1340	80
M 2.1	48,420	Rocky Mountain	Montane	Grande Cache Montane	825	1555	1141	135
M 2.2	33,608	Rocky Mountain	Montane	Jasper Lower Montane	926	1314	1053	68
M 3.2	94,211	Rocky Mountain	Montane	Jasper Upper Montane	941	1864	1212	120
M 4.1	17,078	Rocky Mountain	Montane	Kootenay Lower Montane	1198	1640	1326	61
M 4.2	2,170	Rocky Mountain	Montane	Ya Ha Tinda Montane	1533	1749	1609	42
M 4.3	71,657	Rocky Mountain	Montane	Bow Lower Montane	1176	1921	1358	76
M 4.4	139,316	Rocky Mountain	Montane	Bow-Porcupine Lower Montane	1198	1687	1385	75
M 4.5	137,019	Rocky Mountain	Montane	Crowsnest Lower Montane	1151	1793	1417	91
M 5.1	25,298	Rocky Mountain	Montane	Kootenay Upper Montane	1195	2015	1418	77
M 5.3	77,029	Rocky Mountain	Montane	Bow Upper Montane	1241	2100	1545	108
M 5.4	102,078	Rocky Mountain	Montane	Bow-Old Man Upper Montane	1362	1908	1557	75
M 5.5	20,759	Rocky Mountain	Montane	Porcupine Hills Upper Montane	1407	1814	1590	71
M 5.6	77,150	Rocky Mountain	Montane	Crowsnest Waterton Upper Montane	1242	1917	1506	89
MG 1.1	1,719,776	Grassland	Mixedgrass	Western Mixedgrass Plains	648	1341	953	88
MG 1.2	38,334	Grassland	Mixedgrass	Sweetgrass Mixedgrass Uplands	942	1262	1066	36
MG 1.3	249,066	Grassland	Mixedgrass	Cypress Hills Mixedgrass Uplands	825	1446	1099	95
NF 1.1	1,493,335	Grassland	Northern Fescue	Northern Fescue Plains	643	1096	809	68
NM 1.1	2,380,309	Boreal	Northern Mixedwood	Great Slave Northern Mixedwood Plains	159	521	316	60
NM 2.1	570,971	Boreal	Northern Mixedwood	Bistcho Lake Northern Mixedwood Uplands	445	660	568	30
PAD 1.1	553,542	Boreal	Peace-Athabasca Delta	Peace-Athabasca Delta Plains	188	261	216	11
PRP 1.1	312,042	Parkland	Peace River Parkland	Peace River Parkland Lowlands	302	797	620	86
SA 1.1	574,886	Rocky Mountain	Subalpine	Wapiti-Athabasca Lower Subalpine	1030	2126	1496	107
SA 1.2	307,191	Rocky Mountain	Subalpine	Athabasca-Kootenay Lower Subalpine	1036	2319	1629	119
SA 2.1	384,771	Rocky Mountain	Subalpine	Wapiti-Athabasca Upper Subalpine	1275	2697	1837	126

SEED ZONE LABEL	2014 REVISED AREA IN HECTARES	NATURAL REGION	NATURAL SUBREGION	SEED ZONE NAME	MIN. ELEV*	MAX. ELEV*	MEAN. ELEV*	SD. ELEV*
SA 2.2	333,920	Rocky Mountain	Subalpine	Athabasca-Kootenay Upper Subalpine	1247	2754	1950	137
SA 3.1	270,422	Rocky Mountain	Subalpine	Kootenay-Bow Lower Subalpine	1401	2329	1766	101
SA 3.2	172,157	Rocky Mountain	Subalpine	Bow-Crowsnest Lower Subalpine	1371	2319	1772	97
SA 3.3	65,679	Rocky Mountain	Subalpine	Crowsnest-Waterton Lower Subalpine	1383	2419	1727	118
SA 4.1	232,365	Rocky Mountain	Subalpine	Kootenay-Bow Upper Subalpine	1558	2730	2020	113
SA 4.2	139,361	Rocky Mountain	Subalpine	Bow-Crowsnest Upper Subalpine	1707	2694	2045	109
SA 4.3	41,073	Rocky Mountain	Subalpine	Crowsnest Waterton Upper Subalpine	1429	2648	2027	129
UBH 1.1	601,181	Boreal	Upper Boreal Highlands	Birch Mountains Upper Boreal Highlands	647	870	759	39
UBH 1.2	168,900	Boreal	Upper Boreal Highlands	Buffalo Head Upper Boreal Highlands	668	911	789	31
UBH 1.3	415,729	Boreal	Upper Boreal Highlands	Clear Hills Upper Boreal Highlands	772	1112	961	63
UF 1.1	215,721	Foothills	Upper Foothills	Swan Hills Upper Foothills	908	1388	1133	72
UF 1.2	85,116	Foothills	Upper Foothills	Mayberne Upper Foothills	1015	1457	1204	67
UF 1.3	912,772	Foothills	Upper Foothills	Wapiti-Athabasca Upper Foothills	807	1737	1214	99
UF 1.4	471,904	Foothills	Upper Foothills	Athabasca-North Saskatchewan Upper Foothills	1033	1703	1305	113
UF 1.5	196,392	Foothills	Upper Foothills	North Saskatchewan-Bow Upper Foothills	1131	1860	1391	100
UF 2.4	75,247	Foothills	Upper Foothills	Brazeau Upper Foothills	1288	1972	1537	68
UF 2.5	196,549	Foothills	Upper Foothills	Red Deer Upper Foothills	1286	2145	1588	83

* The elevation data was calculated from gridded raster cells.



Rocky Mountain Natural Region
Seed Zones of Alberta

Produced by Forest Management Branch, Alberta Agriculture and Forestry
Base Map Data provided by the Government of Alberta under the Alberta Open Government Licence. November 2014

Map Date: November 30, 2016

Projection: NAD_1983_10TM_AEP_Forest
Author: tdecosta

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Figure A7.1. Seed zones of Alberta.

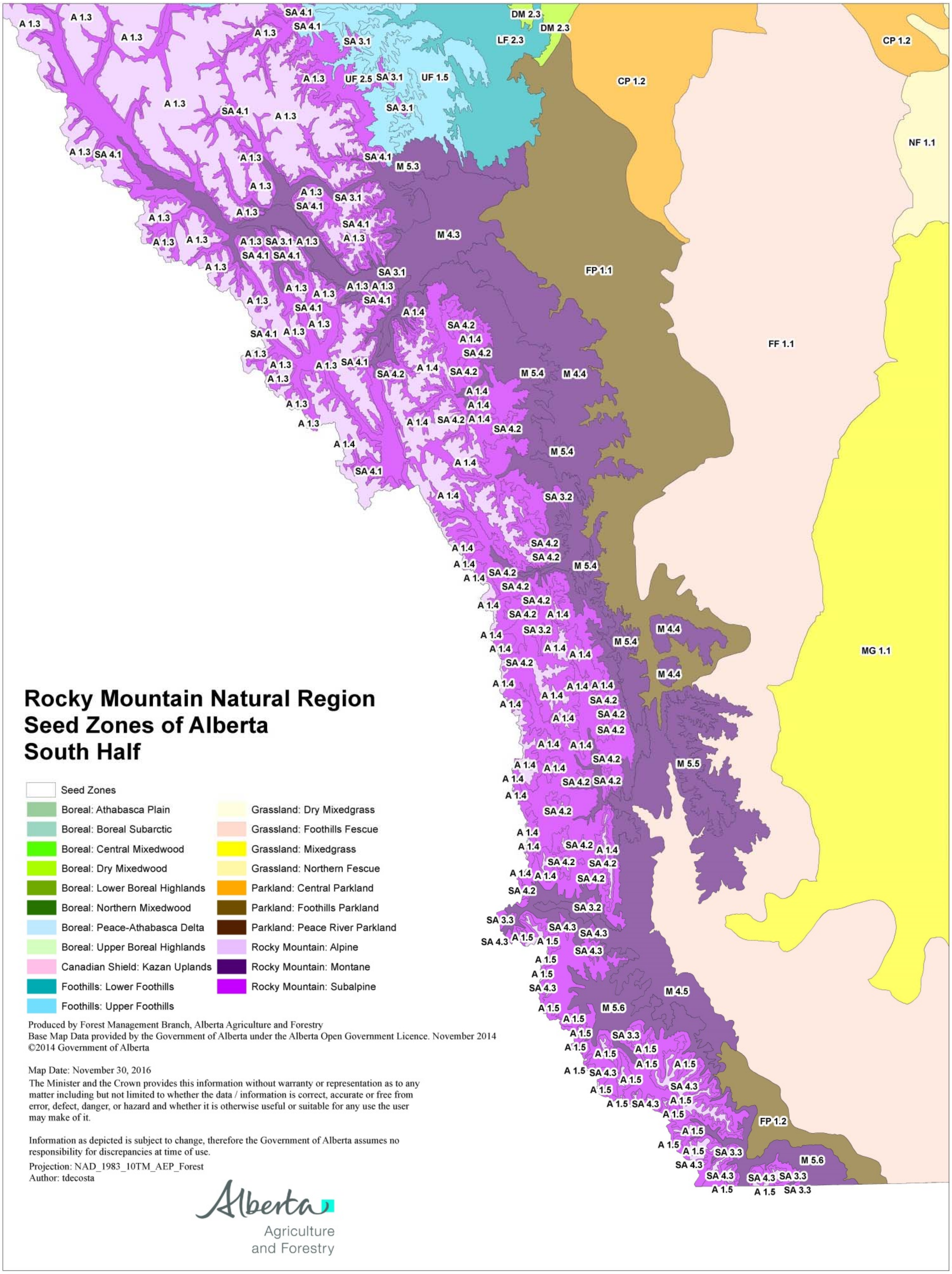
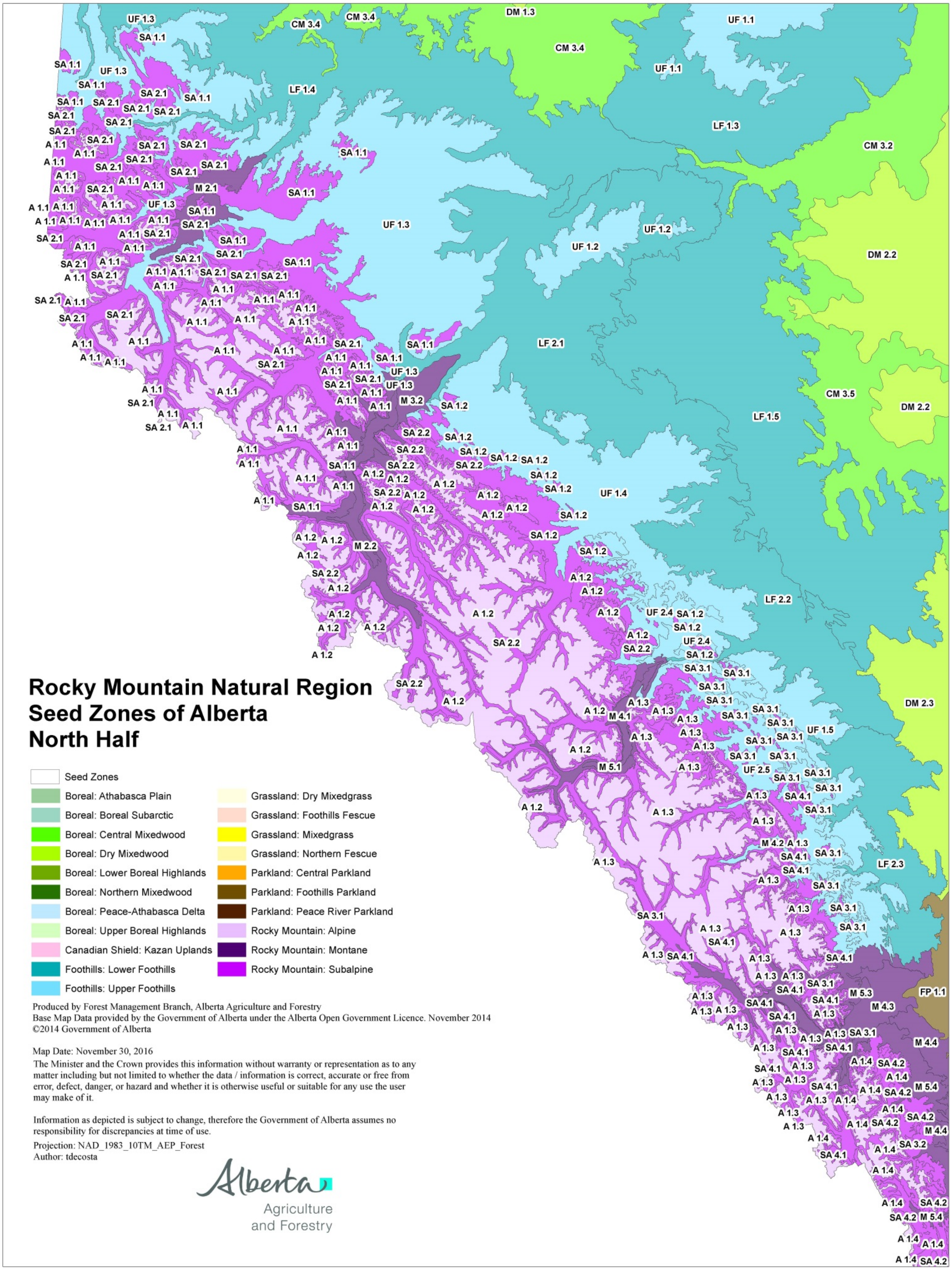


Figure A7.2. Seed zones of Alberta. Southern Rocky Mountains.



Rocky Mountain Natural Region Seed Zones of Alberta North Half

- Seed Zones
- Boreal: Athabasca Plain
- Boreal: Boreal Subarctic
- Boreal: Central Mixedwood
- Boreal: Dry Mixedwood
- Boreal: Lower Boreal Highlands
- Boreal: Northern Mixedwood
- Boreal: Peace-Athabasca Delta
- Boreal: Upper Boreal Highlands
- Canadian Shield: Kazan Uplands
- Foothills: Lower Foothills
- Foothills: Upper Foothills
- Grassland: Dry Mixedgrass
- Grassland: Foothills Fescue
- Grassland: Mixedgrass
- Grassland: Northern Fescue
- Parkland: Central Parkland
- Parkland: Foothills Parkland
- Parkland: Peace River Parkland
- Rocky Mountain: Alpine
- Rocky Mountain: Montane
- Rocky Mountain: Subalpine

Produced by Forest Management Branch, Alberta Agriculture and Forestry
Base Map Data provided by the Government of Alberta under the Alberta Open Government Licence. November 2014

Map Date: November 30, 2016

Projection: NAD_1983_10TM_AEP_Forest
Author: tdecosta

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Figure A7.3 Seed zones of Alberta. Northern Rocky Mountains.

Appendix 8. Request for Deployment Variance for *Stream 1* Material (Updated May 1, 2020)

See Standards 10.13, 18.2.4, 18.2.5 , 18.2.6 and 18.2.7.

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STREAM 1 REQUEST FOR DEPLOYMENT VARIANCE (APPENDIX 8 FGRMS)

REQUESTING AGENCY DATE

Agency Name

Mailing Address

Contact

Phone Fax

E-mail

REQUEST CATEGORY

Lot has restricted registration Transfer outside of seed zone origin Transfer from outside Alberta

TYPE OF VARIANCE REQUESTED

☐ Annual ☐ Standing

REASONS FOR REQUEST

CROP DESCRIPTION

Registered lot number Species

Seed Zone[1] Legal Location (to Section)[2] sec twp rge W

Mean Lat., Long.[3] and Elev.(m) Lat. Long[3]. andElev. Range (m) min max

☐ Seed ☐ Seedling ☐ Vegetative Crop size

PROPOSED DEPLOYMENT

ARIS Opening No(s) or Disposition No(s).
Attach sheet for additional openings

Seed Zone Legal Location (to Section) sec twp rge W

Mean Lat., Long[3]. and Elev.(m) Lat., Long[3]., and Elev. Range (m) min max

Years of Deployment (Standing Variance only)

# of seedlings/propagules to be deployed in proposed deployment

PROPONENT/AGENCY

Name	Position
Signature	Date

VARIANCE APPROVAL (DEPARTMENT USE ONLY) Date

Reviewed By:

Date

☐ Approved ☐ Denied Approved by

Approved with conditions ☐

Conditions

Variance No.

---

[1] If material from outside Alberta indicate province or state.

[2] Optional.

[3] Degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456).

Appendix 9. Assessment of Risk for *Stream 2* Material with Restricted and Unrestricted Registration*

See Standard 18.4.

This risk assessment template is a generic form to be applied to *Stream 2* materials with restricted and unrestricted registration. It is to be applied at both stand and landscape levels, and to plantings where seedlings or vegetative material are deployed as mixes or where materials are proposed for *deployment* as single *clone*s or single-family blocks. Where a row in Table A9.1 is completed with "A"s, *deployment* risks and conditions for *registration* have been reviewed and enabled within the FGRMS 2016 review process. Where rows in the matrix are blank for a planned *controlled parentage program* (*CPP*) production and *deployment* strategy/scenario, the proponent is to notify *Alberta*, complete the appropriate matrix line for the proposed *deployment* strategy/scenario and submit an explanation of how the risk categories (columns in the matrix) are proposed to be managed under the planned production and *deployment* strategy/scenario.

Table A9.1. Risk assessment template.

LANDSCAPE LEVEL risk[5]					STAND LEVEL risk[5]					
Group[1]	**Seed or veg.**	**Ne[2]**	**Planting strategy[3]**	**Mgmt. intensity[4]**	**Sustainability[6]**	**Genetic diversity[7]**	**Eco-system Impact[8]**	**Sustainability[6]**	**Genetic diversity[7]**	**Eco-system Impact[8]**
Conifer/ Birch	Seed	≥18	mixed	*rehabilitation*	A	A	A	A	A	A
Conifer/ Birch	Seed	≥18	mixed	*intensive*	A	A	A	A	A	A
Conifer/ Birch	Seed	≥18	mixed	*extensive*	A	A	A	A	A	A
Conifer	Seed	≥18	family blks	*rehabilitation*						
Conifer	Seed	≥18	family blks	*intensive*						
Conifer	Seed	≥18	family blks	*extensive*						
Conifer	Veg	≥18	mixed	*rehabilitation*	A	A	A	A	A	A
Conifer	Veg	≥18	mixed	*intensive*						
Conifer	Veg	≥18	mixed	*extensive*						
Conifer	Veg	≥18	clonal blks	*rehabilitation*						
Conifer	Veg	≥18	clonal blks	*intensive*						
Conifer	Veg	≥18	clonal blks	*extensive*						
Conifer	Veg	≥18	family blks	*rehabilitation*						
Conifer	Veg	≥18	family blks	*intensive*						
Conifer	Veg	≥18	family blks	*extensive*						
Populus	Seed	≥18	mixed	*rehabilitation*	A	A	A	A	A	A
Populus	Seed	≥18	mixed	*intensive*	A	A	A	A	A	A
Populus	Seed	≥18	mixed	*extensive*	A	A	A	A	A	A
Populus	Seed	≥18	family blks	*rehabilitation*						
Populus	Seed	≥18	family blks	*intensive*						
Populus	Seed	≥18	family blks	*extensive*						
Populus	Veg	≥18	mixed	*rehabilitation*	A	A	A	A	A	A
Populus	Veg	≥10	mixed	*intensive*	A	A	A	A	A	A
Populus	Veg	≥18	mixed	*extensive*	A	A	A	A	A	A
Populus	Veg	≥18	clonal blks	*rehabilitation*	A	A	A	A	A	A
Populus	Veg	≥10	clonal blks	*intensive*	A	A	A	A	A	A
Populus	Veg	≥18	clonal blks	*extensive*	A	A	A	A	A	A
Populus	Veg	≥18	family blks	*rehabilitation*						
Populus	Veg	≥10	family blks	*intensive*						
Populus	Veg	≥18	family blks	*extensive*						
Other[9]										

*For risk assessment of *restricted registration* material, contact *Alberta*.

Explanatory Notes for Risk Assessment Template

[1]Group	"<u>Populus</u>" refers specifically to trembling aspen and balsam poplar.
[2]*Effective Population Size (Ne)*	a) ≥18 or ≥10: Current strategy/scenario matrix is for material with *unrestricted registration* to have an *Ne* ≥18 or, in the case of <u>Populus</u> in *intensive* management, *Ne* ≥10. Otherwise material with *Ne* of <18 has *restricted registration* with specified limits on *deployment*.
[3]Planting Strategy	a) Mixed: planting to occur as a random mixture of *genotypes*; b) Family Blocks: planting to occur in blocks composed of genetic members belonging to a family; c) Clonal Blocks: planting to occur in blocks composed of a single genetic individual.
[4]Management Intensity	Refers to the following management (silviculture) intensity categories in the Risk Assessment Template table: a) ***Rehabilitation:*** Stand "non-conversion" plantings, including fill planting of small areas in cutblocks to remedy localized poor *reforestation* success due to natural site conditions, and planting of block roads, landings and decking areas. Also includes all *reclamation* sites. b) ***Intensive*****:** Planting of an entire cutblock, or cutblocks across a large area, with recurrent near-complete control of native vegetation prior to canopy closure. Site is dominated by *artificial regeneration* material through use of vegetation management techniques. c) ***Extensive*****:** artificial *reforestation* of a cutblock or cutblocks across large areas where there is minimal follow-up treatment that would impact re-establishment of native vegetation.
[5]Stand and Landscape Risks	a) Landscape: deals with risks associated with *deployment* aggregate effects at the 10,000 ha scale; b) Stand: deals with risks at the cutblock level, 30-100 ha scale.
[6]Sustainability	Ability to persist through *natural regeneration* without management intervention, and with low risk to sustained productivity. May refer to inbreeding potential from reduced number of parents or poor reproductive performance of specific *clone*s.
[7]*Genetic Diversity*	Risks due to reduced *genetic diversity*: increased vulnerability to pests, diseases and weather, and reduced evolutionary potential. Also risks due to genetic recombination in hybrids.
[8]Ecosystem Impacts	Potential for deployed material to serve as centres for pest dispersal and weediness. Potential for gene flow and impacts on non-target species.
[9]Other	Contact *Alberta*

Options for accommodating risks include limits on area of *deployment*, establishment of buffers around plantations of restricted material, limits on the distance from where the wood will be used, requirements for an intermediate level ("pilot-scale") of *deployment* before *deployment* to specified area limits, agreements to prevent *natural regeneration* on areas occupied by material of *restricted registration*, etc. These conditions may be addressed through standards or the Forest Management Plan (see Standards 10.12 and 18.4.7).

Appendix 10. Temporary Field Authorization Form

REPEALED

Appendix 10A. Authorization to Collect Plant Material Request Form for *Stream 1* Material (Updated May 1, 2020)

See Standards 7.0, 11.1 and 17.

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Authorization to Collect Plant Material Request Form for *Stream 1*material: Collections of plant material by other than *forest tenure holders* require authorization by *Alberta.* A request for authorization is made by completing this form and submitting it to *Alberta*. **(Appendix 10A FGRMS)**

AAF Region:

Date of application:

Applicant name/organization:

Address:

City:

Province:

Postal code:

Telephone:

Fax:

Email:

Requested start date:

Estimated completion date:

1. Purpose of collection:

2. Collection location: Provide *seed zone* and attach maps of the collection area(s) (add lat. and long. in decimal degree format where applicable; e.g.,: Lat. 56.123456, Long. 118.123456).

3. Target species (attach list)*:

4. Material type and amounts expected (attach list)*:

5. Harvest method: (attach list)*

6. Will collected materials be used for *reforestation* or *reclamation* on Alberta *public lands*?

☐ Yes ☐ No ☐ Other and specify:

7. **Retention of seed**

For *Stream 1* seedlots, *Alberta* may, at the time of *registration*, retain up to 30,000 viable seeds or 5% of the initial total seedlot, whichever is less. In the absence of seed viability test data *Alberta* may retain up to 60,000 seeds or 10% of the initial total seed lot, whichever is less. *Alberta* will notify the owner of any withdrawals. Amounts greater than this will require written consent of the owner. **(Standard 17.1.1).** For all other *public land* seed or vegetative material collections not intended for *reforestation, reclamation* or tree improvement in Alberta, the owner may be required to provide 10% of harvested seed or vegetative material to *Alberta*. **(Standard 17.1.4).**

Signature of Applicant:

8. Other permission(s) and/or notifications required (Area office department use only)

Road access: ☐ Yes ☐ No ☐ Not required

Land use TFA: ☐ Yes ☐ No ☐ Not required

Disposition permission: ☐ Yes ☐ No ☐ Not required

Other (specify)

If TFA is required, attach application and submit to Area Office for approval.

9. Approval Decision: (Department Use Only) **Date:**

☐ **Approved** ☐ **Approved with conditions** ☐ **Denied**

Approved by:

*If there are two or more species attach an Excel file to the application, with the following four columns for items 3, 4 and 5: Target species, Material type, Amounts expected, and Harvest method.

Information for completing an authorization to collect plant material request form.

1. Purpose of collection: State the purpose of the collection (e.g., research, education, *reclamation*, conservation, or saleable product).
2. Collection location: Provide the *seed zone* name and attach maps of the collection area(s).
3. Target species: Provide the scientific or accepted common name of the species to be collected.
4. Material type and amounts: Provide the material to be collected (e.g., cones, cuttings, seed, catkins, or berries) and provide an estimate of the amounts to be collected (volumes or weights).
5. Harvest method: Include the harvesting method to be used (e.g., felling trees, climbing trees, aerial rakes, slash collections, ladders, pruning poles, secateurs, hand collections).
6. The issuance of an authorization to collect plant material does not necessarily eliminate the need for other approvals for the use of *public land*. For example, a Temporary Field Authorization (TFA) is required for staging areas and camps, and private roads or rights of way may require access permission. The applicant is required to ensure all additional approvals required are obtained prior to entry or commencement of the activity.
7. Materials collected for *reforestation* or *reclamation* purposes on Alberta *public land* must be collected, transported, processed, tested, registered and stored in accordance with FGRMS, 2016, which can be found on the *Alberta* website. For collections intended for *public land* use, a completed *Registration* Request form – *Stream 1* (see Appendix 2) must accompany all material shipments.
8. *Alberta* requires a minimum of five full working business days from receipt of application for review. An *Alberta* representative will contact the applicant within that time to discuss the application and status of approval.
9. Conditions may include requirements for stakeholder notification, TFAs, existing land reserves, road restrictions, and debris disposal methods. The amount of material to be retained by *Alberta* for conservation purposes may be established at the time of collection authorization, or at the time of *Stream 1* material *registration*.

Appendix 11A. Parent Tree Selection Form – Wild Stand or Plantation Comparison Tree Method (Updated May 1, 2020)

See Standards 11.1.6, 12.2, 25.5 and 26.1.1.1.

The comparison-tree selection method was developed for selecting individual *genotypes*. This method is not appropriate for selecting and comparing putative *clone*s which may be difficult to identify in the field and are often too dispersed to allow meaningful information to be gathered on individual *phenotype* performance.

Alternatively, required information may be submitted electronically in an Excel file.

PARENT TREE SELECTION FORM – WILD STAND or PLANTATION
Comparison Tree Method (APPENDIX 11A FGRMS)

SPECIES		*FIELD NUMBER*		*UNIQUE IDENTIFIER*
SELECTION AGENCY		*SELECTION DATE*		

PARENT TREE LOCATION AND STAND INFORMATION			
COLLECTION SITE NAME		NATURAL SUBREGION	
LATITUDE (decimal degrees)[2]		SEED ZONE	
LONGITUDE (decimal degrees)[2]		*LEGAL LOCATION	twp range meridian
ELEVATION (m)		STAND OR SITE TYPE	

*Stand Comments

PARENT TREE AND MATERIALS COLLECTION INFORMATION									
SEX	MALE	☐	FEMALE	☐	UNKNOWN	☐	MONOECIOUS	☐	
WOOD SAMPLE	YES	☐	NO	☐	COLLECTION DATE				
VEGETATIVE SAMPLE	YES	☐	NO	☐	COLLECTION DATE		SCIONS	☐	OTHER ☐
OPEN POLLINATED SEED	YES	☐	NO	☐	COLLECTION DATE				

Trait[1]		Select Tree	Dom.1	Dom.2	Dom.3	Superiority (%)	*Comments
Height (m)							
DBH (cm)							
Age (DBH) (yrs)							
Natural Pruning (%)							
Height/Age (cm/yr)							
Radial Increment	Last 10 yrs (mm)						
	Last 11-20 yrs (mm)						
Stem Form							
Branch Angle							
Branch Thickness							
Crown Width							
***Other Trait**							
***Damage** (e.g pest/diease/climate)							

Parent Tree Location and Access Information			
Parent Tree Location Map			Access Information
Photo Attached	Yes ☐ No ☐	Map Attached Yes ☐ No ☐	*Tree Marking

Agency Representative	Signature	Date

Approved for entry into Alberta Tree Improvement & Seed Centre Parent Tree Registry Yes ☐ No ☐ **(Department use only)**	
Reviewed by	Date

* Optional fields

[1] Trait coding as per the Superior Tree Selection Collection Project – Comparison Tree Method manuals

[2] Degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456)

Appendix 11B. Parent Tree Selection Form – Wild Stand or Plantation Non-Comparison Tree Method (Updated May 1, 2020)

See Standards 11.1.6, 12.2, 25.5 and 26.1.1.1.

Alternatively, required information may be submitted electronically in an Excel file.

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PARENT TREE SELECTION FORM – WILD STAND or PLANTATION
non-Comparison Tree Method (APPENDIX 11B FGRMS)

SPECIES		*FIELD NUMBER*		*UNIQUE IDENTIFIER*
SELECTION AGENCY		*SELECTION DATE*		

PARENT TREE LOCATION AND STAND INFORMATION			
COLLECTION SITE NAME		NATURAL SUBREGION	
LATITUDE (decimal degrees)[2]		SEED ZONE	
LONGITUDE (decimal degrees)[2]		*LEGAL LOCATION	twp range meridian
ELEVATION (m)		STAND OR SITE TYPE	

*Stand Comments

PARENT TREE AND MATERIALS COLLECTION INFORMATION					
SEX	MALE ☐	FEMALE ☐	UNKNOWN ☐	MONOECIOUS ☐	
WOOD SAMPLE	YES ☐	NO ☐	COLLECTION DATE		
VEGETATIVE SAMPLE	YES ☐	NO ☐	COLLECTION DATE	SCIONS ☐	OTHER ☐
OPEN POLLINATED SEED	YES ☐	NO ☐	COLLECTION DATE		

Trait[1]	Data/Score	Comments	Trait[1]	Data/Score	Comments
***Height (m)**			***Stem Form**		
***DBH (cm)**			***Branch Angle**		
***Age (DBH) (yrs)**			***Branch Thickness**		
***Natural Pruning (%)**			***Crown Width**		
***Height/Age (cm/yr)**			***Parent Tree Comments (pest damage, etc)**		
***Radial Increment Last 10 yrs (mm)**					
***Last 11-20 yrs (mm)**					
***Other Trait**					

Parent Tree Location and Access Information			
Parent Tree Location Map		Access Information	
*Tree Marking			
Photo Attached	Yes ☐ No ☐	Map Attached Yes ☐ No☐	

Agency Representative	Signature	Date

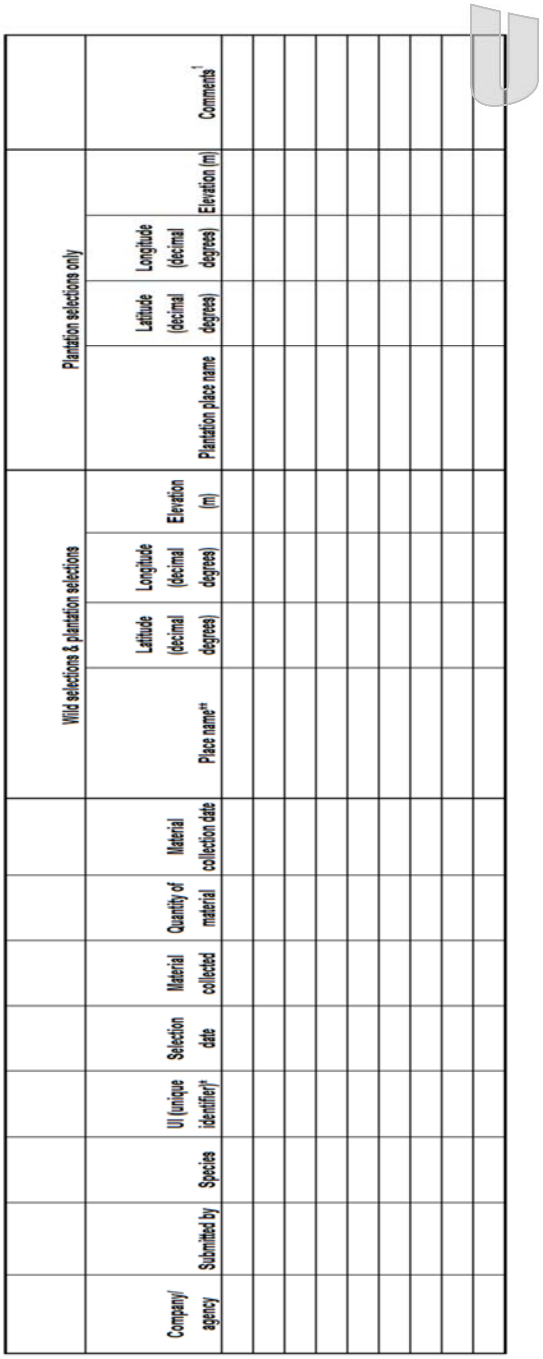
Approved for entry into Alberta Tree Improvement & Seed Centre Parent Tree Registry Yes ☐ No ☐ **(Department use only)**			
Reviewed by		Date	

*Optional fields
[1] Trait coding as per the Superior Tree Selection Project Standards and Code Sheet for Field Use
[2] Degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456)

Appendix 11C. Parent Tree Selection form– Geographic Selection Method

See Standards 11.1.6, 12.2, 25.5 and 26.1.1.1. (Updated May 1, 2020)

Submission in Excel format is preferred.



								Wild selections & plantation selections				Plantation selections only				
Company/ agency	Submitted by	Species	UI (unique identifier)*	Selection date	Material collected	Quantity of material	Material collection date	Place name**	Latitude (decimal degrees)	Longitude (decimal degrees)	Elevation (m)	Plantation place name	Latitude (decimal degrees)	Longitude (decimal degrees)	Elevation (m)	Comments[1]

Reviewed by: Date

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* to be assigned by the selecting agency (Reference Appendix 25)

** location of wild selection, or location of original seed source for plantation selections

[1] If selection is to be included in deployment population before testing, include age estimate in the Comments. The age of selection must be at least half of the estimated rotation age in the CPP.

Appendix 12. Parent Tree Selection Form – Genetic Test Materials (Updated May 1, 2020)

See Standards 11.1.6, 12.2, 25.5 and 26.1.1.1.

Alternatively, required information may be submitted electronically in an Excel file.

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PARENT TREE SELECTION FORM –
Genetic Test Materials (APPENDIX 12 FGRMS)

SPECIES		*FIELD NUMBER*		*UNIQUE IDENTIFIER*
SELECTION AGENCY		*SELECTION DATE*		

PARENT TREE LOCATION COLLECTION SITE AND TRIAL/PLANTATION INFORMATION	
COLLECTION SITE NAME	LATITUDE (decimal degrees)[1]
TRIAL CODE	LONGITUDE (decimal degrees)[1]
*LEGAL LOCATION sec twp range meridian	ELEVATION (m)
Age at Selection	Seedlot # (as applicable)
Rep. # (as applicable)	Set or Block # (as applicable)
Row # (as applicable)	Position # (as applicable)
Selection Criteria or Analysis Report Reference	
Purpose of Selection	

*TRIAL COMMENTS

PARENT TREE AND MATERIALS COLLECTION INFORMATION								
SEX	MALE	☐	FEMALE	☐	UNKNOWN ☐	MONOECIOUS ☐		
WOOD SAMPLE	YES	☐	NO	☐	COLLECTION DATE			
VEGETATIVE SAMPLE	YES	☐	NO	☐	COLLECTION DATE		SCIONS ☐	OTHER ☐
OPEN POLLINATED SEED	YES	☐	NO	☐	COLLECTION DATE			

TRAITS	***DATA**	***COMMENTS**
Height (m)		
DBH (cm)		
(other measured traits, list all)		
*Damage (e.g. Pest/Disease/Climate)		

INFORMATION ON PARENTS OF THIS SELECTION	
*Breeding Date/Year	
MOTHER	**FATHER** (if known)
Unique Identifier/Genetic Identity	Unique Identifier/Genetic Identity
Latitude (decimal degrees)[1]	Latitude (decimal degrees)[1]
Longitude (decimal degrees)[1]	Longitude (decimal degrees)[1]
Elevation (m)	Elevation (m)

GENERAL REMARKS

Agency Representative	Signature	Date

Photo of selected tree attached	☐ Yes	☐ No

Approved for entry into Alberta Tree Improvement & Seed Centre Parent Tree Registry Yes ☐ No ☐ **(Department use only)**	
Reviewed by	Date

*Optional fields

[1] Degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456)

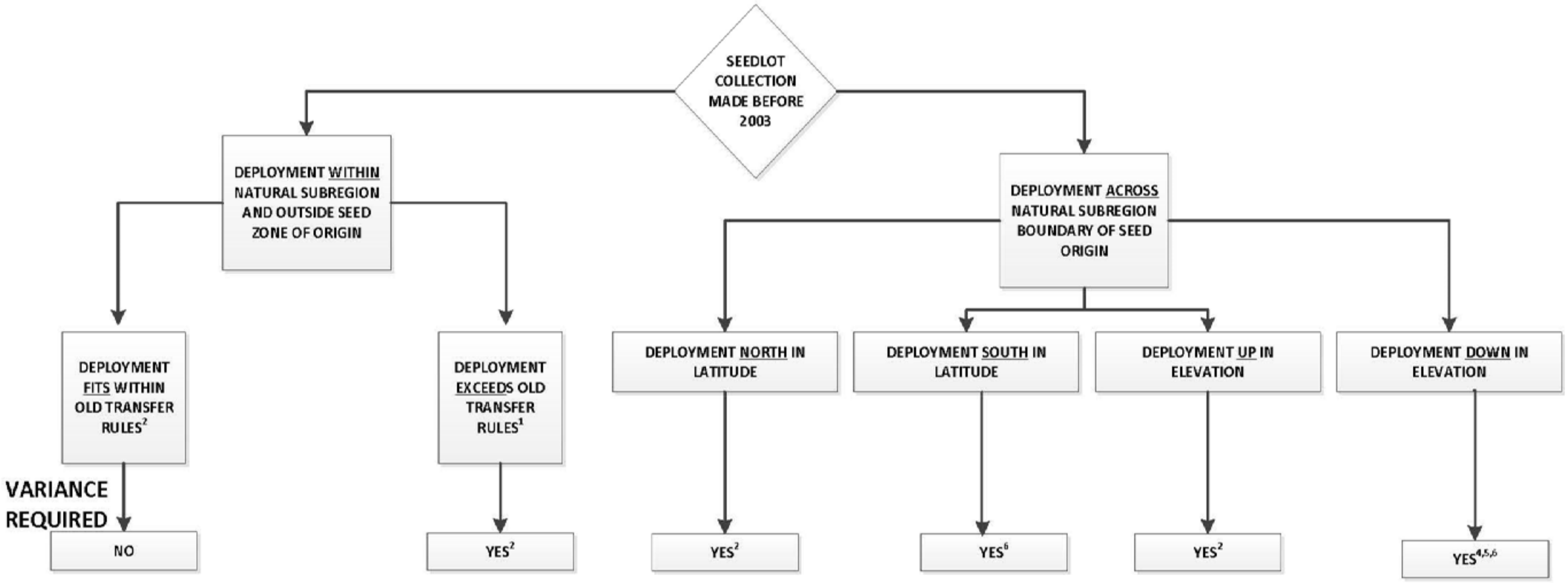
Appendix 13. Decision Tree for Deployment of *Stream 1* Material Outside the Seed Zone of Origin

See Standards 10.8, 18.2.2 and 18.2.4.

These *deployment* decision trees (Figures A13.1 and A13.2) are based on seedlot type, seed collection and use history, ecological classification, the known relationship between climate and plant population genetics, and results from Alberta conifer provenance *trial*s in Alberta. These conifer provenance *trial*s show that:

i) moderate movement up in elevation is neutral or can increase growth without reducing survival, whereas downward movement in mountains and hill systems can seriously reduce growth;
ii) populations from mid latitudes and mid elevations have high genetic growth potential over much of Alberta, whereas populations from high latitudes and high elevations have high genetic growth potential only when planted in their native areas.

It is recognized that locally adapted populations have other attributes, such as tolerance to local strains of insects and diseases, tolerance of extreme weather conditions, and optimal reproduction, which have yet to be systematically tested in Alberta. The risk for these traits is mitigated through progressive moderate seed transfers as research data become available.



[1] "Old transfer rules" refers to ***deployment*** within 50 miles (80 km) and within 500 feet (150 metres) elevation from the collection location.

[2] Quality of seed origin information, potential for undesirable hybridization numbers being transferred and adaptation to current and future predicted climate will be considered in reviews.

[3] For a description of point collection see Appendix 4.

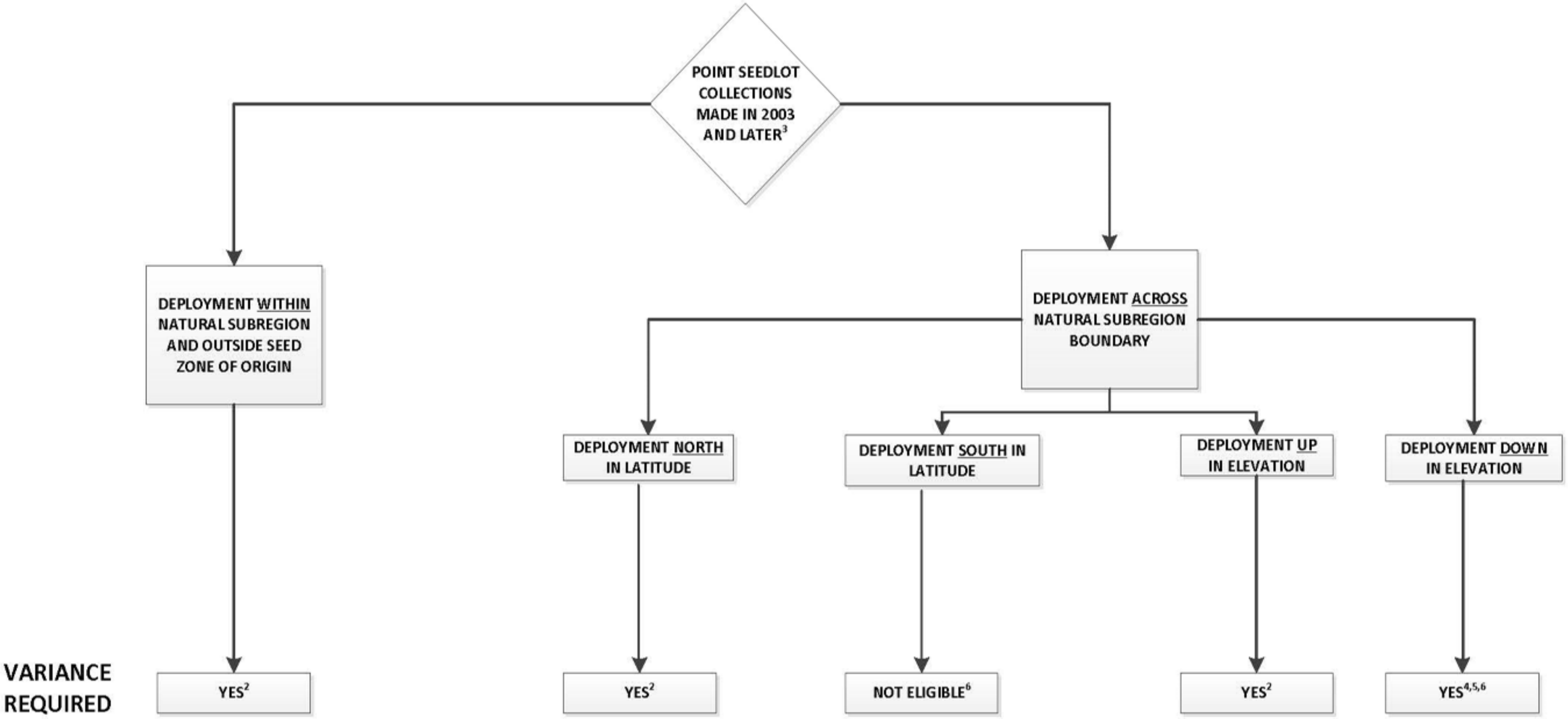
[4] Eligible in the boreal forest region where transfer North in latitude coincide with transfer down in elevation.

[5] Not eligible in mountainous regions (Foothills, Boreal highlands, Montane, Alpine).

[6] Eligible only where the opening bisects seed zone boundaries.

Fuzzy Boundary Note:
Point collections are eligible for deployment up to 1 km outside the seed zone of origin boundary without variance provided the difference in elevation from the point of collection to point of deployment does not exceed 100 m.

Figure A13.1. Pre-2003 seedlot collections: variance requirements.



[1] "Old transfer rules" refers to ***deployment*** within 50 miles (80 km) and within 500 feet (150 metres) elevation from the collection location.

[2] Quality of seed origin information, potential for undesirable hybridization numbers being transferred and adaptation to current and future predicted climate will be considered in reviews.

[3] For a description of point collection see Appendix 4.

[4] Eligible in the boreal forest region where transfer North in latitude coincide with transfer down in elevation.

[5] Not eligible in mountainous regions (Foothills, Boreal highlands, Montane, Alpine).

[6] Eligible only where the opening bisects seed zone boundaries.

Fuzzy Boundary Note:
Point collections are eligible for deployment up to 1 km outside the seed zone of origin boundary without variance provided the difference in elevation from the point of collection to point of deployment does not exceed 100 m.

Figure A13.2. Point collections (2003 and later): variance requirements.

Appendix 14. *Stream 1* Seedling and Vegetative Propagule Lot Deployment Limit by Seed Zone

See Standards 11.3, 18.2.3 and 18.2.4.

*Seed zone collection*s are permitted; however *point collection*s are recommended, and are eligible for variance requests for transfer outside *seed zone* boundaries.

Table A14.1 provides limits on *deployment* for *seed zone* and *point collections*; Table A14.2 provides limits on *deployment* for *Stream 1 seed orchard* (*seed zone* specific) collections.

Table A14.3 provides examples showing the amount of seed required to produce 1,000,000 seedlings, and the area of land that could be planted, for a number of different species.

Table A14.1. Deployment limits for seed zone and point collections.

Size category	***Seed zone* area (ha)[1]**	**Maximum number deployable per lot[2]**	
		Seedlings	***Vegetative propagules***
1	> 1 million	25 million	20 million
2	500,000 to 1 million	20 million	16 million
3	100,000 to 500,000	15 million	12 million
4	< 100,000	10 million	8 million

[1] See Appendix 7 for *seed zone* sizes.

[2] *Deployment* limit includes seed and *vegetative propagules* from a single lot.

Table A14.2. Deployment limits for Stream 1 seed orchard/vegetative collections.

Size category	***Seed zone* area (ha)[1]**	**Maximum number deployable [2]**	
		Seedling	***Vegetative propagules*[3]**
1	> 1 million	82.5 million	66 million
2	500,000 to 1 million	66 million	53 million
3	100,000 to <500,000	50 million	40 million
4	< 100,000	33 million	26 million

[1] See Appendix 7 for *seed zone* sizes.

[2] Contact *Alberta* if greater *deployment* is wanted.

[3] Refers to material from Appendix 4 Table A4.3 Orchard types A2 and B2 only.

Table A14.3. Examples: seed required to produce one million seedlings, and area to be covered.

Species[1]	**Average seeds/kg**	**Seeds required per delivered seedling**	**Seed required (kg)**	**Planting density (/ha)**	**Coverage (ha)**
Pl	250,000	2.5	10.0	1800	555
Sw	425,000	2.5	5.9	1800	555
Aw	8,100,000	5.0	0.617	1800	555
Pb	4,600,000	5.0	1.09	1800	555
Alnuvir	4,500,000	5.0	1.11	200[2]	5000
Cornser	35,000	4.0	114.3	200[2]	5000
Shepcan	135,000	4.0	29.6	200[2]	5000
Amelaln	330,000	4.0	12.12	200[2]	5000

[1] See Appendix 38 for common and Latin names associated with species codes.

[2] Average from oil sands mine closure plans.

Appendix 15. Parent Tree Selection Form for Material Collected Outside Alberta (Updated May 1, 2020)

See Standards 11.5, 12.2, 25.5 and 26.1.1.1.

To be used for documenting genetic materials intended for use in *controlled parentage programs* where materials did not originate in Alberta.

Alternatively, required information may be submitted electronically in an Excel file.

Alberta Government

PARENT TREE SELECTION FORM – MATERIAL COLLECTED OUTSIDE ALBERTA[1] (APPENDIX 15 FGRMS)

Company/Agency in Possession

Submitted by

Unique Identifier

COLLECTION INFORMATION

Origin Place Name

	Original Source[2]	Plantation Collection Site[3]
Latitude (decimal degrees)[4]		
Longitude (decimal degrees)[4]		
*Legal Location	twp range meridian	
Elevation (m)	m	m

*Comments

GENETIC INFORMATION

Species

*Male Parent Information

*Female Parent Information

*Comments

PHYSICAL INFORMATION

Type of Material

*Quantity of Material

*Comments

Approval Decision (Department use only)

Approved for entry into the Alberta Tree Improvement & Seed Centre Parent Tree Registry **Yes** ☐ **No** ☐

Reviewed by	Date

---

[1] To be used for documenting genetic materials intended for use in controlled parentage programs where materials did not originate from Alberta.

[2] Original location of initial wild collection to be documented where known.

[3] Plantation location where material is collected from a non-wild source.

[4] Degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456).

*Optional fields.

Appendix 16. Research, Conservation or Controlled Parentage Program Transportation and Interim Storage of Plant Material Form (Updated May 1, 2020)

See Standard 12.1 and 12.2.

Research, Conservation or Controlled Parentage Program Transportation and Interim Storage of Plant Material Form) (APPENDIX 16 FGRMS) [1]

UNIQUE IDENTIFIER ____________________

(or other genetic identifier including accession, temporary or registered lot number)

OWNER(S)

DESTINATION FACILITY

Mailing Address ____________________

Contact ____________________ Phone ____________________ Fax ____________________

E-mail ____________________

COLLECTING AGENCY

Representative ____________________

Phone ____________________

E-mail ____________________

DATE OF COLLECTION

DATE OF SHIPPING

MATERIAL DESCRIPTION

Species	Collection Location
Latitude[2]	Longitude[2]

Type of Material (e.g. cones, fruit, seed, pollen, cuttings, roots)

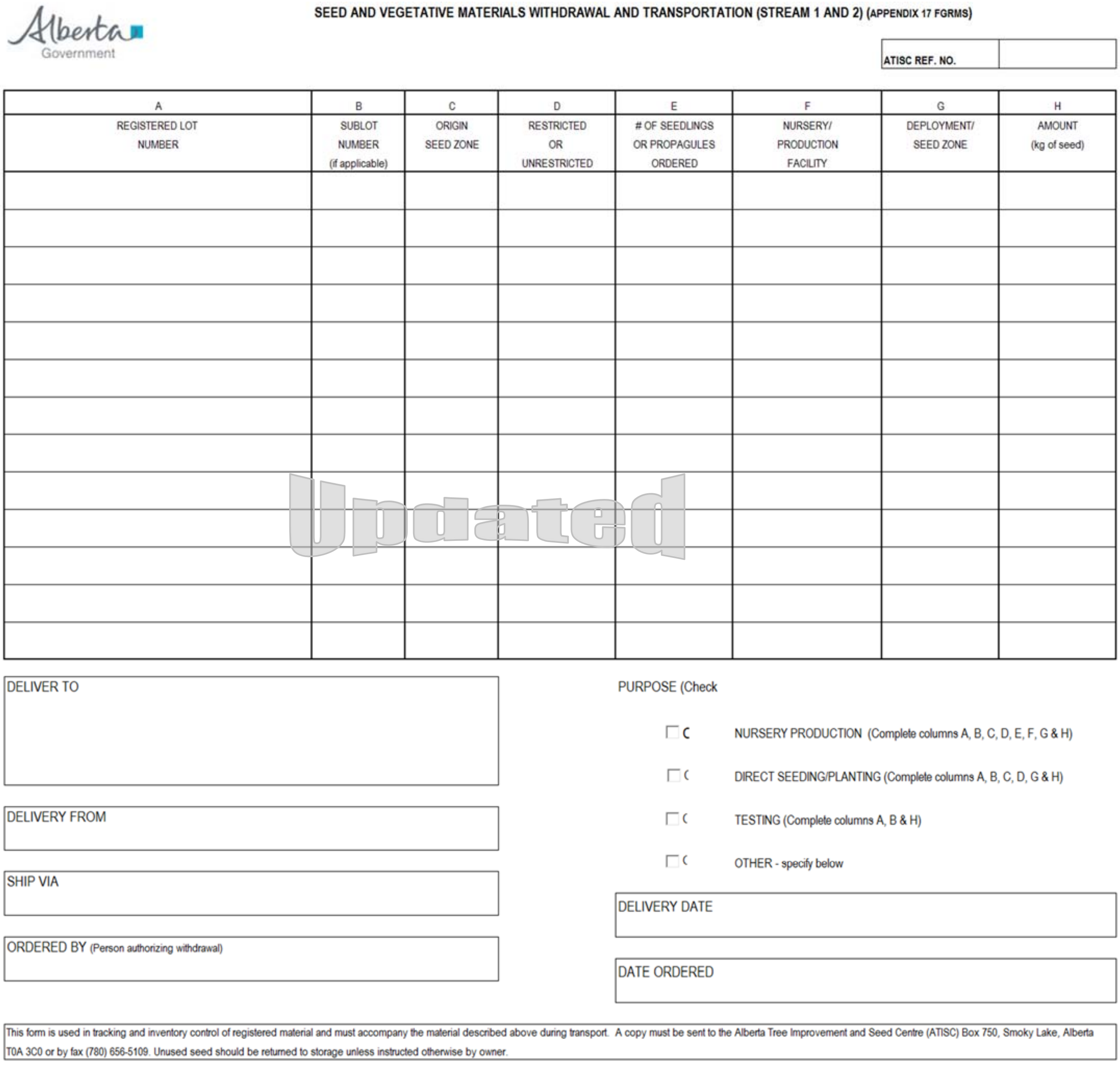
Quantity of Material (specify measurements units: e.g. grams of seed, metres of roots, number or volume of cones)

[1] This form is to accompany all genetic material (seed, pollen, cuttings, tissue etc.). Where there are multiple genetic identities, an attached sheet listing the individual genetic identities in the shipment may be used. Material representing each genetic identity in the shipment must be unequivocally labelled with a label both inside and outside the container clearly identifying its genetic identity number.

[2] Degrees in decimal format, to six decimal places (Example 56.123456).

Appendix 17. Seed and Vegetative Materials Withdrawal and Transportation Form (Updated May 1, 2020)

See Standards 12.5.1, 12.5.3 and 16.1.



Alberta Government

SEED AND VEGETATIVE MATERIALS WITHDRAWAL AND TRANSPORTATION (STREAM 1 AND 2) (APPENDIX 17 FORMS)

ATISC REF. NO.	

A	B	C	D	E	F	G	H
REGISTERED LOT NUMBER	SUBLOT NUMBER (if applicable)	ORIGIN SEED ZONE	RESTRICTED OR UNRESTRICTED	# OF SEEDLINGS OR PROPAGULES ORDERED	NURSERY/ PRODUCTION FACILITY	DEPLOYMENT/ SEED ZONE	AMOUNT (kg of seed)

DELIVER TO

DELIVERY FROM

SHIP VIA

ORDERED BY (Person authorizing withdrawal)

PURPOSE (Check

☐ C NURSERY PRODUCTION (Complete columns A, B, C, D, E, F, G & H)

☐ (DIRECT SEEDING/PLANTING (Complete columns A, B, C, D, G & H)

☐ (TESTING (Complete columns A, B & H)

☐ (OTHER - specify below

DELIVERY DATE

DATE ORDERED

This form is used in tracking and inventory control of registered material and must accompany the material described above during transport. A copy must be sent to the Alberta Tree Improvement and Seed Centre (ATISC) Box 750, Smoky Lake, Alberta T0A 3C0 or by fax (780) 656-5109. Unused seed should be returned to storage unless instructed otherwise by owner.

Appendix 18. Controlled Parentage Program Plan – Contents for *Stream 2* Material

See Standards 18.4.1.1, 18.4.2, 23.1, 23.4, 23.7, 24.1, 24.2, 30.2 and 30.6.1.

The following topics are to be addressed in a *controlled parentage program* (*CPP*) plan.
An example of an approved *CPP* plan is posted on the *Alberta* website.

Introduction

Submission Objective: *Controlled Parentage Program* plan approval, revision, or addendum.

History

i) Early project development (e.g., motivating factors, general development history, changes in cooperative structure, partners, *CPP region* boundaries, administration);
ii) Cooperative structure (current partners, partnership arrangements, agreements, and percent ownership);
iii) Present status (e.g., general status of development of the program, including objectives, orchards, roguing, gain, *trials,* and challenges).

CPP description and objectives

i) Target species (a brief description of the species, its taxonomy and geographic range);
ii) Ecology (the species' successional role, site, climate and soil preferences, common plant community associates, geographic range, etc.);
iii) Genetics (e.g., mating system, range-wide adaptive variation, distribution of variation among regional populations, variation within populations, and observed heritabilities for traits of interest);
iv) Objectives (genetic improvement, seed production, seed supply, *propagule* production targets, etc.);
v) Improvement traits (traits to be considered for improvement, improvement targets, and any available information on selected traits, such as heritabilities and variation);
vi) Similar programs in other regions where available (review of other programs working with genetic improvement of the same species).

CPP region description and delineation

i) Topography (general description of terrain and surface expression);
ii) Climate (e.g., precipitation, frost-free-period, growing degree days, average July and average January mean daily temperatures, wind patterns, chinooks);
iii) Information on adaptive genetic variation that is pertinent to the description and delineation of the *CPP region*;
iv) Administration and land use information (land management jurisdiction, main land use activities and planning objectives for the area);
v) Process used to delineate the *CPP region* (see Standard 28.1);
vi) An *Alberta*-approved scalable digital map of *CPP region* boundaries and exclusion areas suitable for project planning, conceptual depiction in the *CPP* plan and approved *deployment* (see Standard 28.3);
vii) Location description (latitude, longitude, elevation, range).

Parent selection plan

i) Selection traits (traits to be selected on and description of traits);
ii) Selection method (e.g., comparison, non-comparison, geographic, selection from genetic *trials*);
iii) Selection strategy, including consideration of correlated traits (e.g., wood density and growth);
iv) Collection of materials (shoots, scions, root sections, seed, wood samples etc.).

Breeding/clonal plan

a) Seed-based programs

- i) First generation plan
  - a. Traits to be selected for;
  - b. *Base population* description;
  - c. *Breeding population* description;
  - d. Description of planned *production population*s;
  - e. Schedule and predicted timelines for establishment of *production site*s, *production unit*(s), establishment and measurement of progeny, provenance, or other *test*s, orchard roguings etc.;
  - f. Gain estimates where applicable;
- ii) Advanced generation/*pedigree* information (where available).

b) Clonal programs

- i) Traits to be selected for;
- ii) *Base population* description;
- iii) *Breeding population* description where employed;
- iv) Description of planned p*roduction populations* (e.g., clonal turnover, stand level and landscape level *effective population size* (*[Ne])* management, pest and disease screening program);
- v) Schedule and predicted timelines for establishment of *production sites* and *production unit(s)* where applicable; establishment of genetic field *trials* (provenance, progeny, clonal) and their measurements;
- vi) Gain estimates where applicable;
- vii) Selection intensity and target *Ne* (stand and landscape).

Genetic field testing plan

- i) *Test* objective (e.g., *CPP region* delineation, progeny testing, provenance testing, clonal testing for adaptation/gain);
- ii) *Test* material (description);
- iii) *Test* sites
  - a. Selection criteria in terms of relevance to *test* objectives;
  - b. Number of *test* sites and geographic, elevation and climatic coverage;
  - c. *Test* site(s) description (see Appendix 29).
- iv) *Test* site protection (land reservation or disposition type, and other e.g., fire protection, fencing) (Standard 30.4);
- v) *Test* design
  - a. Content and structure (controls, plot structure, blocking, replication);
  - b. Trees per treatment per site.
- vi) *Trial* establishment
  - a. Field marking (method of field marking that allows verification of field layout design and experimental tree location and genetic identification) (see Standard 30.5).
- vii) Site maintenance
  - a. Competition and ingress control (see Standard 30.6);
  - b. Maintenance of tree identification and *trial* staking or monumentation;
  - c. Fencing and boundary maintenance.
- viii) *Trial* measurement
  - a. Variables/traits to be measured;
  - b. Measurement schedule;
  - c. Description of data management and analysis methods.

Field *test* area justification and risk/benefit assessment

- i) Where a *CPP* Genetic Field Testing Plan, in order to meet *test* objectives, requires *trials* that are more than 17 ha per site or more than 85 ha cumulatively across *test* sites, a justification must be made;
- ii) In addition, where a research *test* exceeds 17 ha per site, occupies more than 85 ha across *test* sites and includes previously untested non-local species or provenances, a benefit/risk assessment is required that addresses the pertinent issues from the following list:
  - a. Volume/growth expectations, benefit(s);

b. Genetic make-up (i.e., based on flowering, leaf morphology analysis, DNA analysis);
c. Gender;
d. Fertility (hybridization potential [phenology, viability, control]);
e. Gene flow;
f. Suckering potential (possible control [if a *genetically modified organism* (*GMO*), may be specific to type]);
g. Planting location, design, timeline, size;
h. Buffer requirements, maintenance standards;
i. Harvesting method, clean-up, *reclamation*;
j. Potential for release of toxins;
k. Potential to be a centre for insect and disease outbreaks;
l. Potential to ameliorate risk (e.g., through silviculture practices);
m. Invasiveness;
n. Ecosystem impact;
o. Monitoring.

Production plan

a) Seed-based programs

- i) *Production unit* (orchard) design
  - a. Production planning (e.g., number of trees in orchard, production assumptions and seed needs) and *deployment* limits (see Appendix 21A) (Forest Genetic Resource Management and Conservation Standards 24.4);
  - b. *Production unit* design and layout (e.g., seedling, clonal or *rolling front orchard*; number of trees, inbreeding control). Include a general description, to be followed up in more detail in the orchard establishment report (see Appendix 32).
- ii) *Production unit* establishment
  - a. *Production site*;
  - b. Establishment dates (planned or known initiation and completion dates);
  - c. P*roduction unit* number when known (issued by *Alberta*).
- iii) *Production unit* management
  - a. Pollen contamination;
  - b. Pollen management;
  - c. Weed, insect, and disease monitoring and control;
  - d. Tree management;
  - e. *Crop* management;
  - f. Permanent sample tree (PST) monitoring.

b) Clonal programs

- i) Where *production units* are employed such as *stoolbeds*, s*toolbed* design and production planning (program production needs, *production sites*, *stoolbed* design, size and number, production expectations and projections).
- ii) *In vitro* micro-propagation
  - a. Production design including production needs, methods and systems, planned *production sites*, approach to *production population* assembly, and *deployment population* production; expectations and projections;
  - b. *Alberta* -issued *production population* numbers when issued and available.
- iii) *Production unit* establishment
  - a. *Production unit*(s) description (due to the nature of potential production systems for clonal material, description may vary, particularly if *production units* are dispersed or ephemeral);
  - b. Proposed or existing *production site(s).*
- iv) *Production unit* or *production population* management
  - a. Weed, insect, and disease monitoring and control for *production units* (e.g., in *stoolbeds*);
  - b. General description of production controls and tracking procedure for assembly of *deployment populations* from *production populations* and *production units.*

Deployment plan

a) Seed-based programs

- i) All requirements met as per Standards 18.4.31, 18.4.4, 24.4 and Appendix 21A including:
  - a. Identification of *species*-*specific target strata* and landscape level *deployment Ne* limits;
  - b. Stand level *Ne* planning and *deployment* strategies (e.g., proposed use of unrestricted or *restricted registration* materials, targeted ecosites, productivity classes);
  - c. *Deployment* strategies specific to sites and strata.

b) Clonal programs

- ii) All requirements met as per Standards 18.4.3.2,18.4.4, 24.4 and Appendix 21B including:
  - a. Identification of *species*-*specific target strata* and landscape level *clone deployment* limits;
  - b. Stand level *Ne* planning and *deployment* strategies (e.g., number of *clone*s per *deployment population*, number of planned populations, stand level *Ne* objectives and spatial arrangement on the landscape, proposed use of unrestricted or restricted materials);
  - c. *Deployment* strategies specific to sites and strata.

Genetic conservation plan

- i) In situ (status of reserves for the *CPP* plan species and *CPP region*) (see Standard 20.2 and 20.8).
- ii) Ex situ
  - a. Clone banking plan;
  - b. Seed collections;
  - c. Other.
- iii) Considerations upon termination of *tests*.

Link to supporting research plan(s)

- i) Listing of research plans (e.g., pest and disease research, preliminary adaptation testing to address *CPP* risks).

Reference to additional relevant reports

- i) Genetic *test* establishment report;
- ii) Genetic *test* measurement report;
- iii) Genetic *test* analysis report;
- iv) Parent tree selection report.

Appendix 19. Current Controlled Parentage Program Regions and Associated Programs for *Stream 2* Material

See Standards 18.4, 18.4.1, 18.4.2 and 24.1.

Controlled parentage program (CPP) seed movement guidelines and *deployment* rules differ from natural stand seed movement guidelines because seed or *vegetative propagule* production is carried out under several production scenarios involving various *production sites*, *production populations* and *production units* (see Appendix 35).

Deployment of improved varieties is controlled by a *CPP region* system. Each *CPP region* is based on a target *deployment* area for a single species. *Seed orchards* are mostly developed on agricultural land outside the forest zone to reduce outcrossing with contaminating pollen. Repeated collections are made from the same trees, and control is exercised on genetic composition, genetic quality and *genetic diversity* of seedlots. *CPP regions* are not necessarily coincident with *seed zones*, as they are based on a target *deployment* area for a single species, and are generally accompanied by provenance, progeny and/or clonal testing.

Controlled parentage program regions are initially delineated and mapped on the basis of general genetic and ecological information, as well as administrative boundaries, and are reviewed and modified on the basis of further progeny and provenance testing. *Controlled parentage program regions* are also delineated on the basis of testing for adaptiveness of genetic material.

Seed and *vegetative propagule* movement, and *deployment* from *production populations* and associated *production units,* are generally unrestricted within their *CPP region*. However, *Alberta* may place conditions on the use of these materials within the *CPP region* if warranted by scientific considerations. Areas within a *CPP region* boundary that are suspected to be environmentally atypical are dealt with as exclusion areas.

The *CPP region* zoning system will be periodically updated to accommodate new projects, new scientific information, changes in genetic improvement objectives, or other biological considerations.

The 24 currently approved *CPP regions* in Alberta include nine white spruce, three black spruce, six lodgepole pine, one jack pine, one Douglas-fir, one western larch, one balsam poplar and two trembling aspen (see Table A19.1).

Figures A19.1 through A19.4 are for conceptual use only. For *CPP region* digital boundary line work, contact *Alberta*.

Table A19.1. Approved Controlled Parentage Program regions[1].

Species	*CPP region*	Area (ha)	Latitudinal range (° N)	Elevation operational range[2] (m)	Description
Lodgepole pine (Figure A19.3)	A	1,965,478[3]	52.09 - 54.15	950 - 1350[4]	West-central lower foothills *CPP region* represented by mixedwood forest types at lower elevations and conifer-dominated forest types at upper elevations.
Lodgepole pine (Figure A19.3)	B1	1,660,031	53.27 - 54.94	800 - 1200	Northern lower foothills *CPP region* dominated by mixedwood forest types.
Lodgepole pine (Figure A19.3)	B2	1,106,686	52.65 - 54.67	1200 - 1600	Northern upper foothills *CPP region* dominated by conifer forest types.
Lodgepole pine (Figure A19.3)	C	1,193,752	53.98 - 55.29	800 - 1200	Swan Hills area outlier foothills *CPP region* dominated by pure and mixed conifer forest types. Area of lodgepole and jack pine hybridization.
Lodgepole pine (Figure A19.3)	K1	822,072	51.29 - 53.25	1100 - 1500	Southern upper foothills *CPP region* dominated by conifer forest types.
Lodgepole pine (Figure A19.3)	J	2,649,575	56.24 - 58.65	600 - 1000 (see description for exceptions)	Clear Hills area outlier foothills *CPP region* dominated by mixedwood and conifer forest types, including areas of lodgepole and jack pine hybridization. Approved operational elevations are 600 m to 1000 m, except for an area on the north slope of Zama Ridge which follows the NM to LBH Natural Subregion boundary.
Jack pine (Figure A19.3)	P1	3,927,769	55.36 - 58.08	250 - 600	Northeastern lowlands boreal *CPP region* dominated by mixedwood forest types.
Western larch (Figure A19.2)	M	78,723	49.17 - 49.72	1450 - 1700	Southern lower subalpine *CPP region* dominated by conifer forest types. This species is rare in Alberta. The main project objectives are conservation and restricted use for *CPP region deployment*.
White spruce (Figure A19.1)	D	1,655,448	53.66 - 55.36	650 - 1050	Swan Hills area outlier lower foothills *CPP region* dominated by mixedwood forest types.
White spruce (Figure A19.1)	D1	5,201,616	54.41 - 56.77	500 - 800	Slave Lake area boreal *CPP region* dominated by boreal lowland and upland mixedwood forest types.
White spruce (Figure A19.1)	E	3,286,019	54.76 - 57.03	300 - 650	Northeastern boreal lowland *CPP region* dominated by mixedwood forest types.
White spruce (Figure A19.1)	E1	3,943,262	55.64 - 58.08	250 - 600	Northeastern boreal lowland *CPP region* dominated by mixedwood forest types. Northern extension of *CPP* Region E.
White spruce (Figure A19.1)	E2	4,526,268	52.93 - 55.05	550 - 750	East central sub-boreal and parkland *CPP region* dominated by mixedwood and parkland forest types. Project objectives include conservation and restricted *deployment*.
White spruce (Figure A19.1)	G1	2,646,147	54.24 - 56.29	650 - 1050 (see description for exceptions)	Northern lower foothills *CPP region* dominated by mixedwood forest types. Approved operational elevations are 650 m to 1050 m except along the Smoky River where the lower elevation limit is 600 m.
White spruce (Figure A19.1)	G2	3,071,738	55.91 - 58.25	500 - 900	Northwestern outlier foothills *CPP region* dominated by mixedwood forest types.

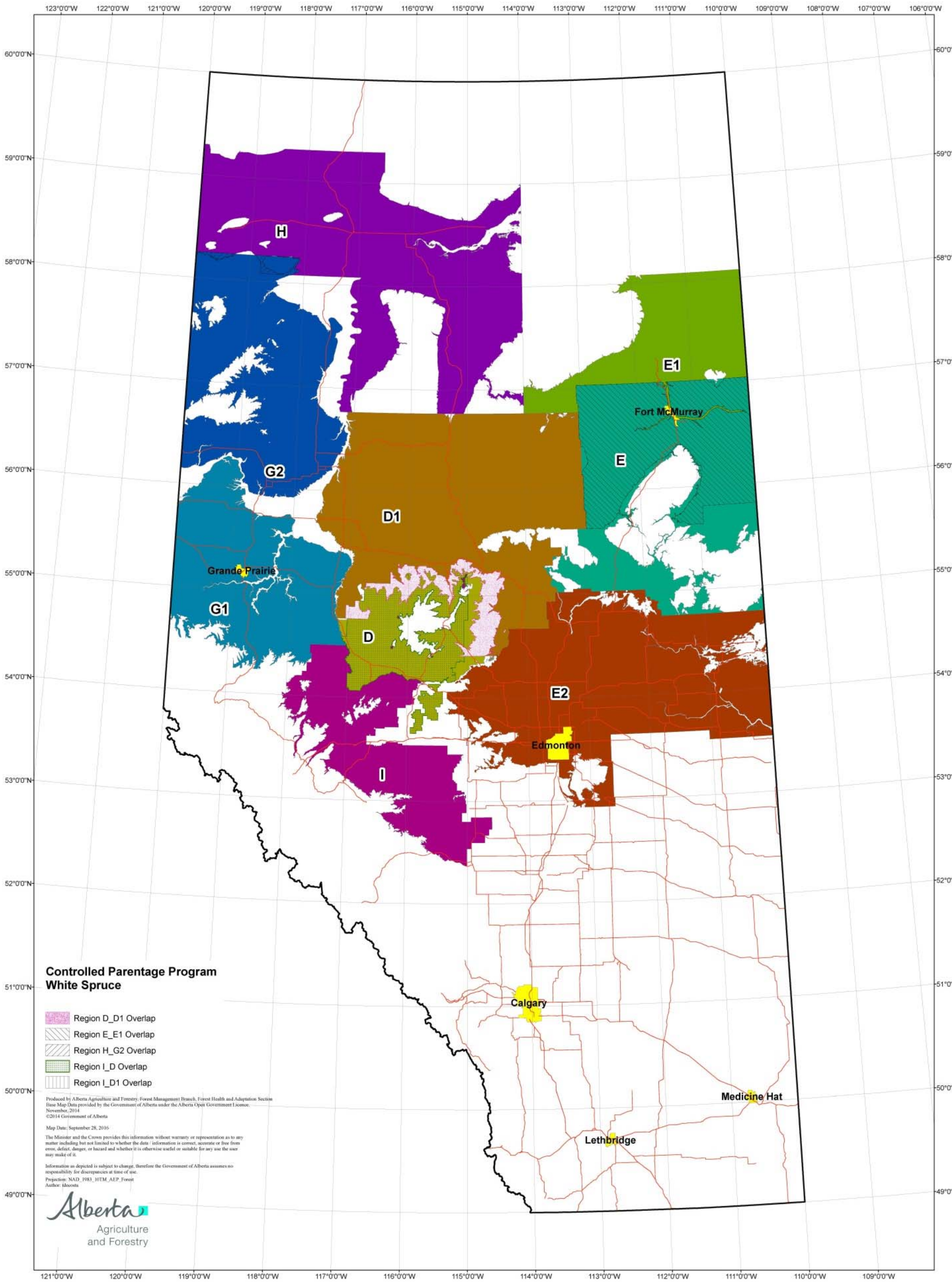
Species	*CPP region*	Area (ha)	Latitudinal range (° N)	Elevation operational range[2] (m)	Description
White spruce (Figure A19.1)	H	5,005,519	56.77 - 59.30	250 - 550	Northwestern boreal lowlands *CPP region* dominated by mixedwood forest types.
White spruce (Figure A19.1)	I	3,310,385	52.36 - 55.36	800 - 1200 in south and 700 - 1050 in north	North-central lower foothills *CPP region* dominated by mixedwood forest types.
Interior Douglas-fir (Figure A19.4)	F1	528,830	49.18 - 51.36	1300 - 1550 (to 1700 in the Porcupine Hills)	Southern montane *CPP region* dominated by montane mixedwood forest types.
Black spruce (Figure A19.2)	L1	2,776,820	53.02 - 55.30	800 - 1200	North-central lower foothills *CPP region* dominated by mixedwood forest types.
Black spruce (Figure A19.2)	L2	1,074,023	54.15 - 55.99	800 - 1200	Northern lower foothills *CPP region* dominated by mixedwood forest types.
Black spruce (Figure A19.2)	L3	4,806,252	54.67 - 57.38	300 - 650	Northeastern boreal lowlands *CPP region* dominated by mixedwood forest types.
Balsam poplar (Figure A19.4)	Pb1	4,818,407	54.76 - 57.65	250 - 650	Northeastern boreal lowlands *CPP region* dominated by mixedwood forest types.
Trembling aspen (Figure A19.4)	AW1	6,594,381[3]	56.00 – 58.00	350 – 750 north of 57°N and 450 – 850 south of 57°N	Lower boreal highlands Central mixedwood Dry mixedwood Peace River parkland
Trembling aspen (Figure A19.4)	AW2	5,416,633[3]	52.50 - 55.50	650 - 1050	Lower foothills Central mixedwood Dry mixedwood Upper foothills

[1] Approved *CPP region* does not mean approved *CPP* plan.

[2] These are approved operational elevation ranges (there are often “islands” in the CPP regions that are outside the approved altitudinal limits).

[3] Areas outside the elevation range (“islands”) are included in this total area, pending completion of mapping; these “islands” are not approved for operational *deployment*.

[4] Elevation operational range is under review.



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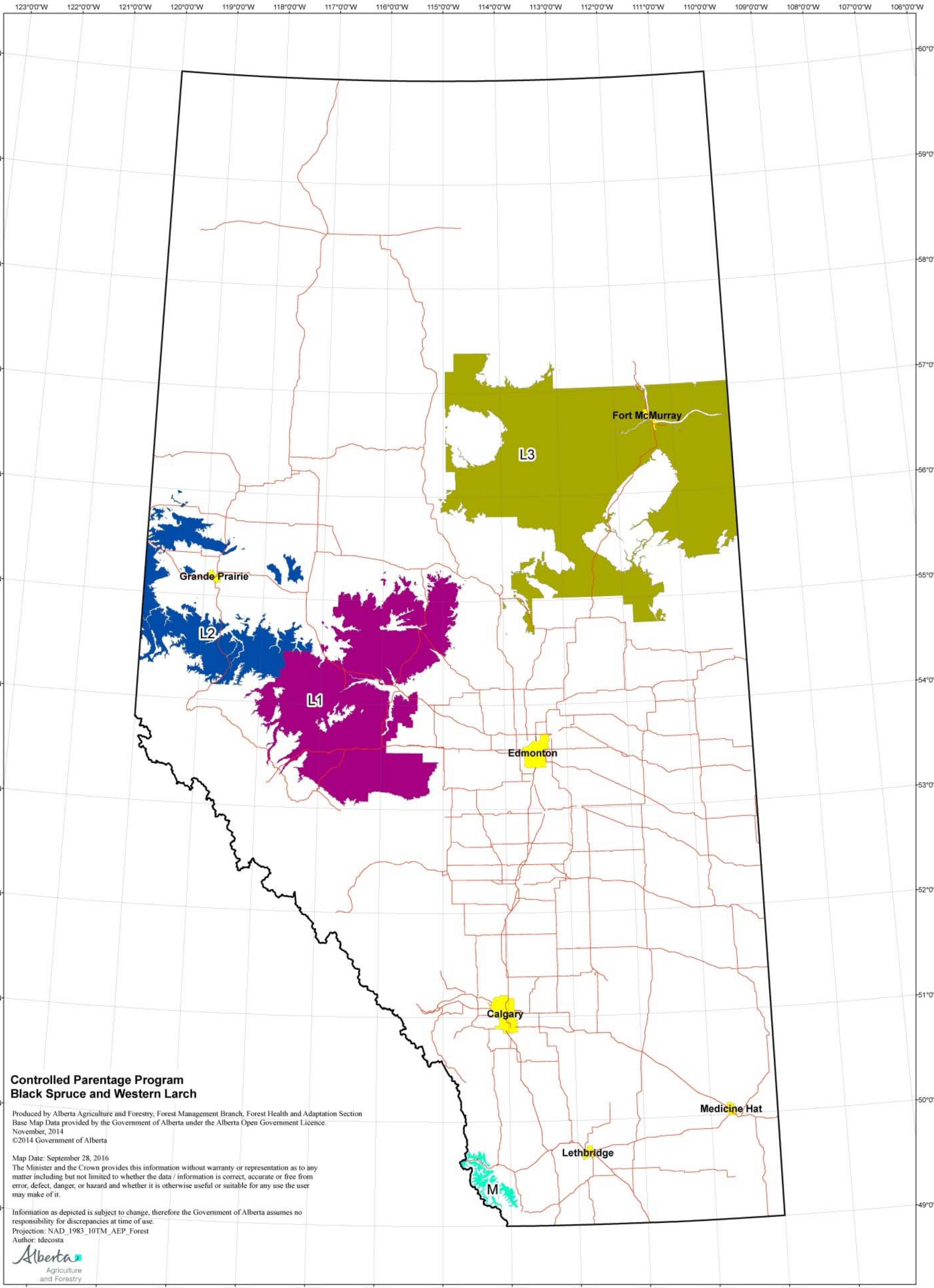
Information as depicted is subject to change, therefore the Government of Alberta assumes no responsibility for discrepancies at time of use.

Projection: NAD_1983_10TM_AEP_Forest
Author: tdecosta

Figure A19.1. Controlled parentage program regions for white spruce.



Controlled Parentage Program
Black Spruce and Western Larch

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Author: tdecosta

Figure A19.2. Controlled parentage program regions for black spruce and western larch.

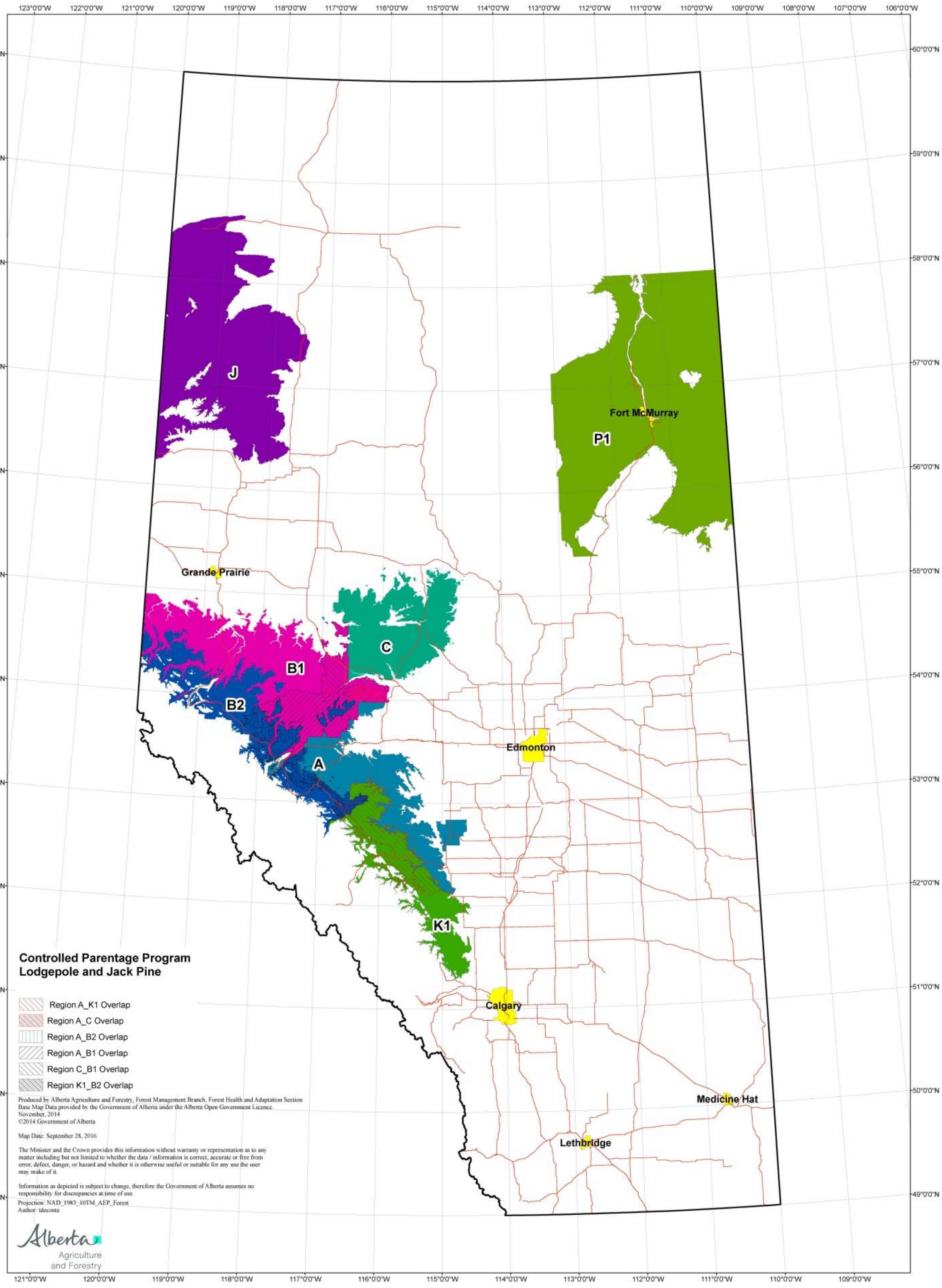
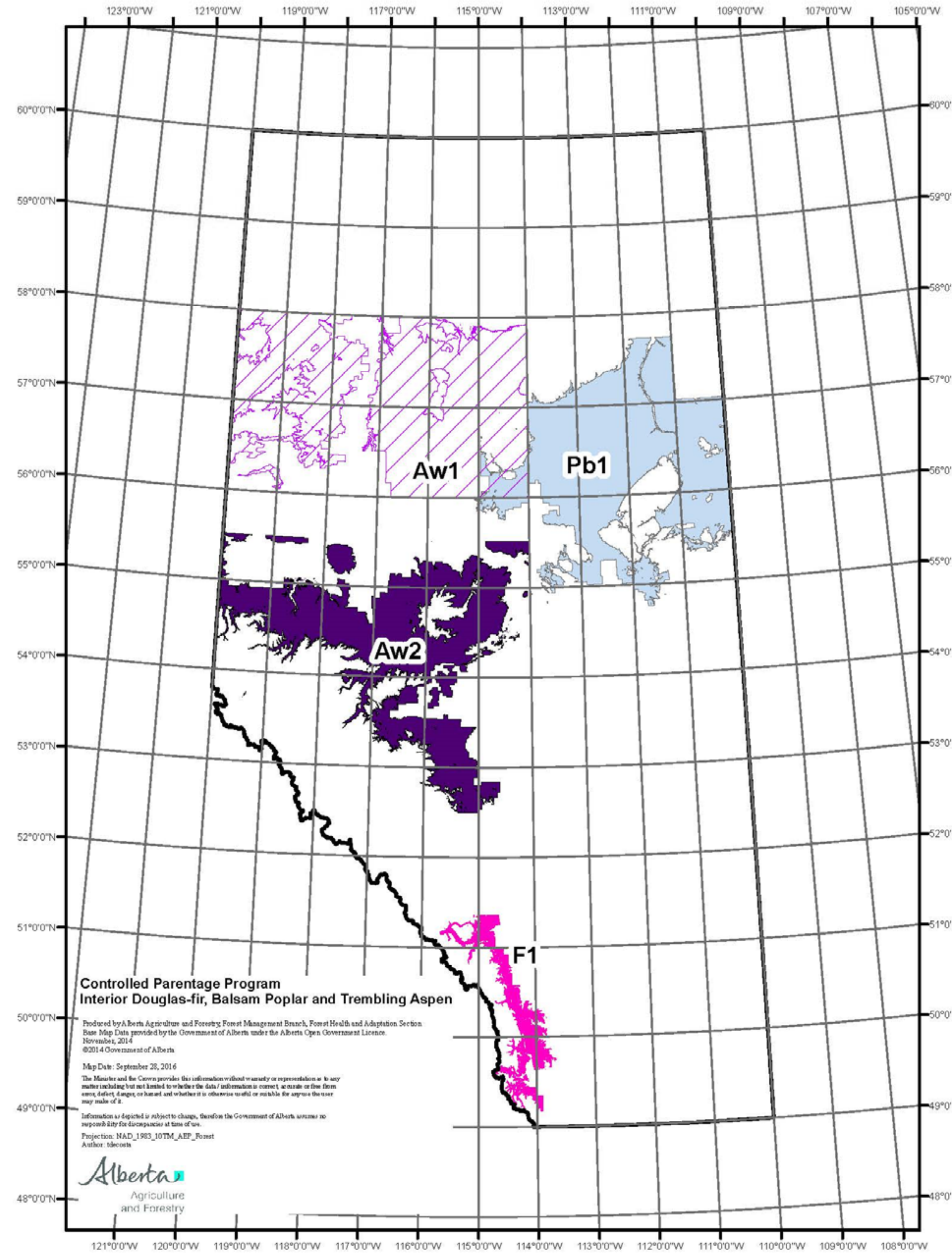


Figure A19.3. Controlled parentage program regions for lodgepole pine and jack pine.



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Information as depicted is subject to change, therefore the Government of Alberta assumes no responsibility for discrepancies at time of use.

Projection: NAD_1983_10TM_AEP_Forest
Author: tdecosta

Figure A19.4. Controlled parentage program regions for interior Douglas-fir, balsam poplar, and trembling aspen.

Appendix 20. Calculation of Cumulative Effective Population Size (Ne) for *Stream 2* Material

See Standards 18.4.4, 21.2.1.1, 32.6 and 33.4.3.

It may apply to two distinct types of populations:

1. the cumulative output (*deployment populations*), summed over years, of one or more *production units* for a *CPP*; or
2. the actual cumulative *deployment*, summed over years, of these *deployment populations* on a given area (e.g., a Forest management Agreement area (FMA) or *CPP region*).

Although these two populations are conceptually distinct, *cumulative Ne* calculation methods are the same for both.

Cumulative effective population size, or *cumulative Ne*, is the total *effective population size* (*Ne*) of multiple populations, calculated over years and/or across *production units* or *production populations*, for a given *CPP region*.

There are three distinct classes of *deployment population*s:

1. Those derived from unrelated, clonally-propagated *genotypes* (e.g., from a first generation clonal orchard);
2. Those derived from related, clonally-propagated *genotypes* (e.g., an advanced orchard, based on forward selections, some of which might be from the same family);
3. Those made up of families of sexually-propagated *genotypes* (e.g., a seedling orchard), or a combination of sexually-propagated and clonally-propagated *genotype*s (e.g., combined seedling & clonal orchards).

Steps in calculating *cumulative Ne*

Class 1. See below for an example including three populations with subsets of 60 unrelated and non-inbred *genotypes*. Columns in Table A20.2 are referenced in steps.

1. For each population to be included in the cumulative assessment, calculate $\mathbf{p_{ij}}$, the proportional contribution to population **i** by *genotype* **j** (example: $\mathbf{p_{1j}}$, $\mathbf{p_{2j}}$ and $\mathbf{p_{3j}}$ are listed in columns 2, 4 and 6 for populations 1, 2 and 3 respectively). See Appendix 36 for $\mathbf{p_i}$ estimation procedures.
2. Multiply the proportional contribution by the total number of plants deployed from that population (example: Table A20.1) to obtain $\mathbf{n_{ij}}$ (example: $\mathbf{n_{1j}}$, $\mathbf{n_{2j}}$ and $\mathbf{n_{3j}}$ are shown in columns 8, 9 and 10 for populations 1, 2 and 3 respectively).
3. Sum each *genotype's* contribution $\mathbf{ntot_j}$ across populations (column 11).
4. Express that number as a proportion of the total number of plants deployed (divide $\mathbf{ntot_i}$ by the sum of column 11 entries to give $\mathbf{pc_j}$ values in column 12).
5. For an orchard containing unrelated and non-inbred *genotypes*, square $\mathbf{pc_j}$ values and sum over *genotypes* ($\Sigma\, pc_j^2$; table row 61, column 13).

   And finally:

6. C*umulative Ne* = $1/\Sigma\, pc_j^2$ (table row 62, column 13).

Class 2. Note: For a *production population* containing related and/or inbred clonally-propagated *genotypes*, *cumulative Ne w*ould be calculated as outlined in Appendix 36, using $\mathbf{pc_j}$ values as calculated for Class 1, above (e.g., column 12, rows 1-60) as the **p** vector, and generating the covariance matrix **C** (defined in Appendix 36); then *cumulative Ne* = $0.5/\mathbf{p'Cp}$.

Note that *Ne* values for each individual population are shown in columns 3, 5 and 7, row 62. The *cumulative Ne* in this example is less than the largest and greater than the smallest individual population *Ne*. *Cumulative Ne* will always be greater than the smallest *Ne* of individual populations, and may be larger or smaller than the largest.

Class 3. For seedling or combined seedling and clonal orchards, *cumulative Ne* may, if desired, be calculated as the weighted average *Ne* of the component *deployment population*s. It has been demonstrated that *cumulative Ne* calculated in this manner will never exceed c*umulative Ne* calculated according to Appendix 36, so provides a conservative estimate. However, it is computationally simpler than the method in Appendix 36.

Example Class 1

Three years' production from a *seed orchard* is considered here. One bulk seedlot is collected in each of the three years. Sixty *clone*s are included in the orchard initially; the orchard is successively rogued to 40 and then to 20 *genotypes* before seedlots are produced in years 2 and 3 respectively. *Genotypes* are non-inbred and unrelated.

Table A20.1. Numbers deployed from each of the three seedlots.

Seedlot	Seedlot 1	Seedlot 2	Seedlot 3	Total
# deployed	600,000	850,000	200,000	1,650,000

Table A20.2. Genotypic contributions and calculated Ne values.

	Column 1	2	3	4	5	6	7	8	9	10	11	12	13
Table row	Geno-type	p_{1j}	p_{1j}^2	p_{2j}	p_{2j}^2	p_{3j}	p_{3j}^2	n_{1j}	n_{2j}	n_{3j}	$ntot_j$	pc_j	pc_j^2
1	1	0.032	0.00102	0.098	0.00960	0.057	0.00325	19200	83300	11400	113900	0.069	0.00477
2	2	0.031	0.00096	0.035	0.00123	0.054	0.00292	18600	29750	10800	59150	0.036	0.00129
3	3	0.029	0.00084	0.015	0.00023	0.043	0.00185	17400	12750	8600	38750	0.023	0.00055
4	4	0.016	0.00026	0.042	0.00176	0.041	0.00168	9600	35700	8200	53500	0.032	0.00105
5	5	0.012	0.00014	0.023	0.00053	0.060	0.00360	7200	19550	12000	38750	0.023	0.00055
6	6	0.020	0.00040	0.022	0.00048	0.058	0.00336	12000	18700	11600	42300	0.026	0.00066
7	7	0.022	0.00048	0.006	0.00004	0.056	0.00314	13200	5100	11200	29500	0.018	0.00032
8	8	0.027	0.00073	0.047	0.00221	0.053	0.00281	16200	39950	10600	66750	0.040	0.00164
9	9	0.006	0.00004	0.031	0.00096	0.037	0.00137	3600	26350	7400	37350	0.023	0.00051
10	10	0.005	0.00003	0.004	0.00002	0.049	0.00240	3000	3400	9800	16200	0.010	0.00010
11	11	0.025	0.00063	0.016	0.00026	0.065	0.00423	15000	13600	13000	41600	0.025	0.00064
12	12	0.001	0.00000	0.030	0.00090	0.044	0.00194	600	25500	8800	34900	0.021	0.00045
13	13	0.008	0.00006	0.001	0.00000	0.042	0.00176	4800	850	8400	14050	0.009	0.00007
14	14	0.007	0.00005	0.048	0.00230	0.049	0.00240	4200	40800	9800	54800	0.033	0.00110
15	15	0.008	0.00006	0.026	0.00068	0.065	0.00423	4800	22100	13000	39900	0.024	0.00058
16	16	0.014	0.00020	0.002	0.00000	0.036	0.00130	8400	1700	7200	17300	0.010	0.00011
17	17	0.028	0.00078	0.016	0.00026	0.055	0.00303	16800	13600	11000	41400	0.025	0.00063
18	18	0.023	0.00053	0.003	0.00001	0.044	0.00194	13800	2550	8800	25150	0.015	0.00023
19	19	0.002	0.00000	0.037	0.00137	0.042	0.00176	1200	31450	8400	41050	0.025	0.00062
20	20	0.008	0.00006	0.002	0.00000	0.05	0.00250	4800	1700	10000	16500	0.010	0.00010
21	21	0.028	0.00078	0.025	0.00063	0	0.00000	16800	21250	0	38050	0.023	0.00053
22	22	0.022	0.00048	0.039	0.00152	0	0.00000	13200	33150	0	46350	0.028	0.00079
23	23	0.004	0.00002	0.035	0.00123	0	0.00000	2400	29750	0	32150	0.019	0.00038
24	24	0.027	0.00073	0.047	0.00221	0	0.00000	16200	39950	0	56150	0.034	0.00116
25	25	0.017	0.00029	0.023	0.00053	0	0.00000	10200	19550	0	29750	0.018	0.00033
26	26	0.008	0.00006	0.035	0.00123	0	0.00000	4800	29750	0	34550	0.021	0.00044
27	27	0.026	0.00068	0.006	0.00004	0	0.00000	15600	5100	0	20700	0.013	0.00016
28	28	0.004	0.00002	0.041	0.00168	0	0.00000	2400	34850	0	37250	0.023	0.00051
29	29	0.010	0.00010	0.034	0.00116	0	0.00000	6000	28900	0	34900	0.021	0.00045
30	30	0.022	0.00048	0.021	0.00044	0	0.00000	13200	17850	0	31050	0.019	0.00035
31	31	0.005	0.00003	0.002	0.00000	0	0.00000	3000	1700	0	4700	0.003	0.00001
32	32	0.032	0.00102	0.005	0.00003	0	0.00000	19200	4250	0	23450	0.014	0.00020
33	33	0.017	0.00029	0.011	0.00012	0	0.00000	10200	9350	0	19550	0.012	0.00014
34	34	0.024	0.00058	0.020	0.00040	0	0.00000	14400	17000	0	31400	0.019	0.00036
35	35	0.001	0.00000	0.005	0.00003	0	0.00000	600	4250	0	4850	0.003	0.00001
36	36	0.013	0.00017	0.021	0.00044	0	0.00000	7800	17850	0	25650	0.016	0.00024
37	37	0.006	0.00004	0.028	0.00078	0	0.00000	3600	23800	0	27400	0.017	0.00028
38	38	0.012	0.00014	0.039	0.00152	0	0.00000	7200	33150	0	40350	0.024	0.00060
39	39	0.008	0.00006	0.041	0.00168	0	0.00000	4800	34850	0	39650	0.024	0.00058
40	40	0.020	0.00040	0.018	0.00032	0	0.00000	12000	15300	0	27300	0.017	0.00027
41	41	0.006	0.00004	0	0.00000	0	0.00000	3600	0	0	3600	0.002	0.00000
42	42	0.004	0.00002	0	0.00000	0	0.00000	2400	0	0	2400	0.001	0.00000
43	43	0.009	0.00008	0	0.00000	0	0.00000	5400	0	0	5400	0.003	0.00001
44	44	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012
45	45	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012
46	46	0.008	0.00006	0	0.00000	0	0.00000	4800	0	0	4800	0.003	0.00001
47	47	0.018	0.00032	0	0.00000	0	0.00000	10800	0	0	10800	0.007	0.00004
48	48	0.020	0.00040	0	0.00000	0	0.00000	12000	0	0	12000	0.007	0.00005
49	49	0.010	0.00010	0	0.00000	0	0.00000	6000	0	0	6000	0.004	0.00001
50	50	0.021	0.00044	0	0.00000	0	0.00000	12600	0	0	12600	0.008	0.00006
51	51	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012
52	52	0.019	0.00036	0	0.00000	0	0.00000	11400	0	0	11400	0.007	0.00005
53	53	0.010	0.00010	0	0.00000	0	0.00000	6000	0	0	6000	0.004	0.00001
54	54	0.049	0.00240	0	0.00000	0	0.00000	29400	0	0	29400	0.018	0.00032
55	55	0.030	0.00090	0	0.00000	0	0.00000	18000	0	0	18000	0.011	0.00012

	Column 1	2	3	4	5	6	7	8	9	10	11	12	13
Table row	Geno-type	p_{1j}	p_{1j}^2	p_{2j}	p_{2j}^2	p_{3j}	p_{3j}^2	n_{1j}	n_{2j}	n_{3j}	$ntot_j$	pc_j	pc_j^2
56	56	0.009	0.00008	0	0.00000	0	0.00000	5400	0	0	5400	0.003	0.00001
57	57	0.015	0.00023	0	0.00000	0	0.00000	9000	0	0	9000	0.005	0.00003
58	58	0.011	0.00012	0	0.00000	0	0.00000	6600	0	0	6600	0.004	0.00002
59	59	0.020	0.00040	0	0.00000	0	0.00000	12000	0	0	12000	0.007	0.00005
60	60	0.021	0.00044	0	0.00000	0	0.00000	12600	0	0	12600	0.008	0.00006
61	**Sum**	1.00000	0.02284	1.00000	0.03881	1.00000	0.05145	**600000**	**850000**	**200000**	**1650000**	1.000	0.02496
62	**Ne**		**43.78**		**25.77**		**19.44**						**40.07**

where:

p_{1j} = proportional contribution of the jth *genotype* in the first population (seed or vegetative lot, or deployed population) to be included in the cumulative assessment

p_{2j} = proportional contribution of the jth *genotype* in the second population

p_{3j} = proportional contribution of the jth *genotype* in the third population

n_{1j} = total contribution of the jth *genotype* in the first population

n_{2j} = total contribution of the jth *genotype* in the second population

n_{3j} = total contribution of the jth *genotype* in the third population

$ntot_j$ = total contribution of the jth *genotype*, summed over populations

pc_j = proportional contribution of the jth *genotype*, over populations

Appendix 21A. Limits for Numbers of *Stream 2* Seedlings Deployed from a Production Population

See Standards 18.4.3.1, 18.4.4, 24.4, 24.4.1, 32.6 and 33.4.3.

To maintain forest *genetic diversity* and associated sustainability, a limit is placed on the total number of *Stream 2* seedlings to be deployed from a *production population.* (The *production population* is the aggregate of all *genotype*s included in *production units* for the *CPP region*.) This limit depends on the *cumulative Ne* of the output of *production units* for that *CPP region*, and is applied to an entire *CPP region*, recognizing that there is often more than one tenure holder and/or *production unit* per *CPP region*.

The limit is calculated on the basis of:

i) total area of *species-specific target strata* in the region/zone,
ii) the number of seedlings planted per hectare (trees per ha), and
iii) the planned *cumulative Ne* of the deployed output of all *production units.*

Seedling *production population* limits are calculated as follows.

i) Where the *cumulative Ne* is <30 (cumulative over the life of the *production population;* see Appendix 20):
   Total *deployment* limit (column 6, in example below) = area of *species-specific target strata* (e.g., column 4) x trees per ha x 0.25;

ii) Where 30 ≤ *cumulative Ne* < 42, these limits are:
   Total *deployment* limit (column 7) = area of *species-specific target strata* (column 4) x trees per ha x 0.50.

iii) Where 42 ≤ *cumulative Ne* < 54, these limits are:
   Total *deployment* limit (column 8) = area of *species-specific target strata* (column 4) x trees per ha x 0.75.

iv) Where the *cumulative Ne* is ≥ 54, these limits are:
   Total *deployment* limit (column 9) = area of *species-specific target strata* (column 4) x trees per ha x 1.00.

The example in Table 21A.1 illustrates how the size of *production populations* may be planned to meet the landscape level *cumulative Ne* limits as calculated above.

Table A21A.1. Stream 2 *CPP production population* planning - seedling example.

1	2	3	4	4a	5	6	7	8	9
Tenure holder(s) (also unallocated areas in *CPP region*)	**Total *CPP region area* by tenure holder[3] (ha)**	***Operable area* within *CPP region*[3] (ha)**	**Area of *species-specific target strata* [1,3] (ha)**	**Planting density (plants/ha)**	**Estimated plants required for 100% planting of *target strata* (million seedlings)**	***Deployment* limit, all *production units;* (*cumulative Ne* <30) (million seedlings)**	***Deployment* limit, all *production units;* (30 ≤ *cumulative Ne* < 42) (million seedlings)**	***Deployment* limit, all *production units;* (42 ≤ *cumulative Ne* < 54) (million seedlings)**	***Deployment* limit, all *production units;* (*cumulative Ne* ≥ 54) (million seedlings)**
TI Co-op member X	1,595,000	1,096,250	150,000	1,800	270.00	67.50	135.00	202.50	270.00
TI Co-op member Y	957,000	817,750	87,000	1,500	130.50	32.63	65.25	97.88	130.50
Non-Co-op member Z[2]	638,000	478,500	50,000	1,200	60.00	15.00	30.00	45.00	60.00
Unallocated[2]	445,000	310,000	35,000	1,800	63.00	15.75	31.50	47.25	63.00
Totals	3,635,000	2,702,500	322,000	N/A	523.50	130.88	261.75	392.63	523.50

[1] *Species-specific target strata* refers to the area to be regenerated to the species produced by the *production unit(s).* This may or may not be the same as the area of regenerated yield strata.

[2] Data are to be provided by *Alberta*. Where data are not available, a weighted average of cooperators' holdings will be used for estimating values in columns 3, 4 and 4a for these rows.

[3] Proponent must provide details on how these areas were determined (e.g., water bodies excluded, stand conversion).

Appendix 21B. Production and Deployment Population Planning for *Stream 2* Vegetative Propagules

See Standards 18.4.3.2, 24.4 and 24.4.1.

Unlike the tables in Appendix 21A, Table A21B.1 is not to be used to determine limits for plant production from a *production population*, but rather to provide planning information for *CPP* plan development and Forest Management Plan (FMP) reporting. Issues of landscape level diversity for vegetative production and *deployment* systems are addressed through Standard 18.4.3.2.

Table A21B.1. Stream 2 *CPP production population* planning – vegetative propagule example.

1	2	3	4
Tenure holder(s) (also unallocated areas in *CPP region*)	**Total *CPP region* area by tenure holder[3] (ha)**	***Operable area* within *CPP region*[3] (ha)**	**Area of *species-specific target strata*[1,3] by tenure holder (ha)**
TI Co-op member X	1,595,000	1,096,250	150,000
TI Co-op member Y	957,000	817,750	87,000
Non Co-op member Z[2]	638,000	478,500	50,000
Unallocated[2]	445,000	310,000	35,000
Totals	3,635,000	2,702,500	322,000

[1] *Species-specific target strata* refers to the area to be regenerated to the species produced by the *production population* which may, or may not, be the regenerated yield strata.

[2] Data in this row are to be provided by *Alberta*. Where data are not available, a weighted average of cooperators' holdings will be used for estimating values in columns 3 and 4.

[3] Proponent must provide details on how the area was determined (e.g., water bodies excluded, stand conversion).

Appendix 22. Request for Deployment Variance for *Stream 2* Material (Updated May 1, 2020)

See Standard 18.4.8.

Variance request to be submitted in emergencies only. Without applying for a variance, *deployment* may occur within 50 km outside a *CPP region* boundary, provided *deployment* is within 100 m up in elevation and 50 m down in elevation from the *CPP* elevation limits (see Appendix 19).

STREAM 2 REQUEST FOR DEPLOYMENT VARIANCE (Appendix 22 FGRMS)

REQUESTING AGENCY DATE

Agency Name Contact

Mailing Address

Phone Fax

E-mail

REQUEST CATEGORY ☐ Lot has restricted registry ☐ and/or transfer outside of CPP Region

REASON(S) FOR EMERGENCY REQUEST

DEPLOYMENT POPULATION (CROP) DESCRIPTION

Registered Lot Number ☐ Seed ☐ Seedling ☐ Vegetative

CPP Region

Production Unit Number (seed) Species

Production Population Number (vegetative)

Production Population Origins if not a fixed Production Unit (Additional pages added ☐ [attach as necessary])

Latitude (decimal degrees)[1]

Longitude (decimal degrees)[1]

*Legal Location twp range meridian

Deployment Population Effective Population Size

PROPOSED DEPLOYMENT

CPP Region

ARIS Opening No(s).
Attach sheet for additional openings

*Latitude (decimal degrees)[1,2] Elevation: Mean (m)

*Longitude (decimal degrees)[1,2] Elevation: Range (m) min max

Legal Location sec twp range meridian

# of seedlings/propagules to be deployed in proposed deployment area

PROPONENT/AGENCY

NAME	POSITION
SIGNATURE	DATE

VARIANCE APPROVAL (DEPARTMENT USE ONLY) Date

Reviewed by

Date

☐ Approved ☐ Denied Approved by

Approved with conditions ☐

Conditions

Variance No.

* Optional fields.

[1] Degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456).

[2] Location may be provided for vegetative lots.

Appendix 23. Request for Planting Variance for Research Material

REPEALED

Appendix 24. Research Program Plan – Contents

See Standards 23.1, 23.4, 23.7, 25.1, 28.1, 30.3.2, 30.11.1 and 30.11.2.

A proponent is advised to submit a letter of intent to *Alberta* prior to developing a research program (RP) plan.

The following topics are to be addressed in an RP plan.

Where the RP plan requires field testing, *Genetic Test Site* Information Form(s) (Appendix 29) shall be submitted as per Standard 30.3.2.

Introduction

i) Project title;
ii) Research proponents;
iii) Research problem;
iv) Traits of interest;
v) Research objective(s);
vi) Hypothesis test(s);
vii) *Deployment* objectives where applicable;
viii) Link to *controlled parentage program*, if relevant.

Field *test* area justification and risk/benefit assessment

i) Where a research *test* requires more than 17 ha per site, or more than 85 ha cumulatively across *test* sites, to meet *test* objectives, a justification must be made.
ii) In addition, where a research *test* exceeds 17 ha per site or occupies more than 85 ha across *test* sites, and includes previously untested non-local species or provenances, a risk/benefit assessment is required that addresses the pertinent issues from the following list:
    a. Volume/growth expectations, benefit(s);
    b. Genetic composition (i.e., based on flowering, leaf morphology analysis, DNA analysis);
    c. Gender;
    d. Fertility (hybridization potential [phenology, viability, control]);
    e. Gene flow;
    f. Suckering potential (possible control [if a *genetically modified organism* (*GMO*) may be specific to type]);
    g. Planting location, design, timeline, size;
    h. Buffer requirements, maintenance standards;
    i. Harvesting method and clean-up;
    j. Potential for release of toxins;
    k. Potential to be a centre for insect and disease outbreaks;
    l. Potential to ameliorate risk (e.g., through silviculture practices);
    m. Invasiveness;
    n. Ecosystem impact;
    o. Monitoring.

Materials

i) Target species;
ii) Genetic *test* material (provenances, populations, families, etc.);
iii) Genetic *test* material origin;
iv) Physical *test* material (seedling, seed, rooted cuttings, stock type, etc.);
v) Controls;
vi) Physical *test* environment (e.g., lab, green house, field *test*);
vii) *Test* environment (climate, soils, etc. at field *test* site locations; lab or greenhouse *test* environmental conditions).

Methods

i) Research hypothesis *test(s)*;
ii) Experimental design;
iii) Data collection;
iv) Criteria for selection and protection of *test* site(s) if applicable;
v) Description of assessed traits and assessment procedures;
vi) Analysis procedures.

Anticipated deliverables

i) Listing and/or discussion of deliverables in terms of research objectives.

References

i) Citation of pertinent literature.

Appendix 24A. Species-Specific Seed Zone Research Program Plan – Contents for *Stream 1* Material

See Standards 18.3, 25, 27 and 30.

Proponents are encouraged to discuss their proposal with *Alberta* prior to preparation of research program (RP) plan.

This appendix is to be used when a proponent wishes to establish a new *seed zone* for a species or group of species.

The following topics are to be addressed in a *species-specific seed zone (SSSZ)* RP plan.

Where the *SSSZ* RP plan requires field testing, *Genetic Test Site* Information Form(s) (Appendix 29) shall be submitted as per Standard 30.3.2.

Introduction

i) Project title;
ii) Research proponents;
iii) Research objective(s);
iv) Traits of interest (must include survival and growth; for shrub testing, reproduction must be considered).

Proposed *seed zone* description and delineation must include:

i) Current *seed zone*s existing within proposed boundary;
ii) Digital shape file of proposed boundary;
iii) Proposed SSSZ description (latitude, longitude, elevation, range);
iv) Ecological information (ecological classification at various scales and general biome description);
v) Forest types and plant communities (e.g., general description of ecosite types and plant communities) (see Natural Regions Committee, 2006);
vi) Topography (general description of terrain and surface expression);
vii) Climate (e.g., precipitation, frost-free period, growing degree days, average July and average January mean daily temperatures, wind patterns, chinooks);
viii) Information on adaptive genetic variation that is pertinent to the description and delineation of the SSSZ;
ix) Administration and land use information (land management jurisdiction, main land use activities, and planning objectives for the area);
x) Process used to delineate the SSSZ.

Materials

i) Target species or group of species;
ii) Genetic *test* material (e.g., provenances, populations, families);
iii) Genetic *test* material origin (must include material from all *seed zone*s within the proposed SSSZ);
iv) Physical *test* material (e.g., seedling, seed, rooted cuttings; also stock type).

Methods

i) *Propagule* collection (number of plants per site, number and location of sites);
ii) Experimental *trial* design;
iii) Criteria for selection and protection of *test* site(s) if applicable;
iv) Site description (completed *Genetic Test Site* Information Forms; Appendix 29);
v) Description of assessed traits and assessment methods;
vi) Data collection schedule;
vii) Analysis procedures.

Anticipated deliverables

i) List and discussion of deliverables in terms of research objectives.

Field *test* area justification and risk/benefit assessment for *test* sites greater than 17 ha

i) Where a research *test* requires more than 17 ha per site or more than 85 ha cumulatively across *test* sites to meet *test* objectives, a justification must be made.
ii) In addition, where a research *test* exceeds 17 ha per site or occupies more than 85 ha across *test* sites, and includes previously untested non-local species or provenances, a risk/benefit assessment is required that addresses the pertinent issues from the following list:
  a. Volume/growth expectations, benefit(s);
  b. Genetic composition (i.e., based on flowering, leaf morphology analysis, DNA analysis);
  c. Gender;
  d. Fertility (hybridization potential [phenology, viability, control]);
  e. Gene flow;
  f. Suckering potential (possible control [if a *genetically modified organism* (*GMO*) may be specific to type]);
  g. Planting location, design, timeline, size;
  h. Buffer requirements, maintenance standards;
  i. Harvesting method and clean-up;
  j. Potential for release of toxins;
  k. Potential to be a centre for insect and disease outbreaks;
  l. Potential to ameliorate risk (e.g., through silviculture practices);
  m. Invasiveness;
  n. Ecosystem impact;
  o. Monitoring.

References

i) Citation of pertinent literature.
ii) Provincial strategy (in preparation).

Literature cited

Natural Regions Committee. 2006. Natural Regions and Subregions of Alberta. Compiled by Downing, D.J. and W.W. Pettapiece. Government of Alberta. Pub. No. I/005.

Appendix 25. Unique Identifier (U.I.) Codes for *Stream 2* Material

See Standard 25.5, Appendix 32A and Appendix 38.

Agencies without a two-letter code in Table A25.5 should contact *Alberta* to have a code issued.

Introduction

U.I.s is one form of *genetic identity*. They differ from some others (e.g., *accession number*, *registered lot number*) in that they denote a single *genotype*, and can apply to different forms of that *genotype* (e.g., *ramets,* parents).

All *genotype*s included in *CPP*s or in *Stream 1 seed orchards* must be assigned *unique identifiers* (*U.I.s.*)

Selected *genotype*s should be identified with *U.I.s* at the time of selection. Identification of each *genotype* with a single coded label throughout the processes of (e.g.) selection, collection, storage, bulking up, and orchard establishment reduces the chance of confusion.

U.I.s is assigned by proponents. They do not require, or imply, parent registration by *Alberta*.

Each agency's identification number for a parent/selection/*clone* (fields 3 – 7) is a unique number for that agency, and is to be used only once by that agency, regardless of species.

Table A25.1 describes the structure of *U.I.s* for use only in *reforestation*, and Table A25.2 provides an example. Table A25.3 describes the structure of *U.I.s* for use in either *reclamation* or *reforestation*, and Table A25.4 provides an example.

A. UNIQUE IDENTIFIERS FOR USE IN REFORESTATION ONLY (TWO-DIGIT SPECIES CODES).

Table A25.1. U.I. field description for use in reforestation only (two-digit species codes), with example.

Field numbers*	**Character type**	**Mandatory/optional**	**Description**	**Example DM00045AW001S**	**Example description**
1 – 2	Alpha	Mandatory	Agency Code	DM	Daishowa-Marubeni
3 – 7	Numeric	Mandatory	Agency's unique *clone* identification number for the parent tree/selection/ *clone*	00045	*Clone* number 45
8 – 9	Alpha	Optional	Species Code	AW	Trembling aspen
10 – 12	Numeric	Optional	Agency's identification number for the individual or collection	001	First collection
13	Alpha	Optional	Type of material	S	Seedlot

*Fields 1 – 7 provide the unique *genotype* and are **compulsory** fields.

Fields 1 and 2 must be the agency code;
Fields 3 and 4 should be the last two digits of the selection year;
Fields 5, 6 and 7 are a unique (within the selection year) number assigned to the selection.

*Fields 8 – 13 provide the material description and are **optional** fields;

Fields 8 -9 are two digit species codes as listed in Tables A38.1 and A38.2, Appendix 38;
Fields 10-13 provide material description identifiers. See below for field 13 codes.

Type of Material (field 13):	*grafted ramet*	(G)
	rooted ramet	(C)

seedlot	(S)
scion	(N)
root	(R)
flower buds	(B)
pollen	(P)
whole tree/seedling/plant	(T)
other	(X)

Table A25.2. An example of an alternate unique identifier (only for tree species used in reforestation, with two-digit species codes).

Field number	1	2	3	4	5	6	7	8	9	10	11	12	13
Example	**H**	U	**0**	**0**	**0**	**4**	**5**	P	L	0	0	1	S

Each agency's identification number for a parent/selection/*clone* (fields 3 – 7) is a unique number for that agency, and is to be used only once by that agency, regardless of species.

B. UNIQUE IDENTIFIERS FOR USE IN RECLAMATION OR REFORESTATION (SEVEN-LETTER SPECIES CODES).

Table A25.3. U.I. field description for use in reclamation or reforestation (seven-letter species codes), with example.

Field numbers*	**Character type**	**Mandatory/ optional**	**Description**	**Example DM00045AW001S**	**Example description**
1 – 2	Alpha	Mandatory	Agency Code	AT	ATISC
3 – 7	Numeric	Mandatory	Agency's unique *clone* identification number for the selected individual	00045	*Clone* number 45 selected in year 2000
8 – 14	Alpha	Optional	Species Code	ARCTUVA	kinnikinnick
15 – 17	Numeric	Optional	Agency's identification number for the individual or collection	001	First collection
18	Alpha	Optional	Type of material	S	Seedlot

*Fields 1 – 7 provide the unique *genotype* and are **compulsory** fields.

Fields 1 and 2 must be the agency code;
Fields 3 and 4 should be the last two digits of the selection year;
Fields 5, 6 and 7 are a unique (within the selection year) number assigned to the selection;

*Fields 8 – 18 provide the material description and are **optional** fields.

Fields 8 -14 are seven digit species codes as listed in **Tables A38.1A, A38.1B and A38.2,** Appendix 38;
Fields 15-18 provide material description identifiers. See below for field 18 codes.

Type of Material (field 13):	*grafted ramet*	(G)
	rooted ramet	(C)
	seedlot	(S)
	scion	(N)
	root	(R)
	flower buds	(B)
	pollen	(P)
	whole tree/seedling/plant	(T)
	other	(X)

Table A25.4. An example of a unique identifier for use in reclamation.

Field number	**1**	**2**	**3**	**4**	**5**	**6**	**7**	8	9	10	11	12	13	14	15	16	17	18
Example	**A**	**T**	**1**	**5**	**0**	**4**	**5**	A	R	C	T	U	V	A	0	0	1	S

Each agency's identification number for a parent/selection/*clone* (fields 3 – 7) is a unique number for that agency, and is to be used only once by that agency, regardless of species.

Table A25.5. Agency names and codes.

Agency name	**Code**
770538 ALBERTA LTD	AA
AINSWORTH LUMBER COMPANY	AI
ALBIAN SANDS ENERGY INC	AS
ALBERTA-PACIFIC FOREST INDUSTRIES INC	AF
ALBERTA PLYWOOD LTD	AP
ALBERTA TREE IMPROVEMENT AND SEED CENTER	AT
ANC TIMBER LTD	AN
BLUE RIDGE LUMBER	BR
BOSS TIMBER LTD	BT
BOUCHER BROTHERS LUMBER	BB
BUCHANAN LUMBER	BL
CANADIAN FOREST PRODUCTS LTD, GRANDE PRAIRIE	CG
CANADIAN FOREST PRODUCTS LTD, HINES CREEK	CH
CARDINAL RIVER COALS	CR
CYPRESS HILLS INTERPROVINCIAL PARK	CY
DAISHOWA-MARUBENI INTERNATIONAL LTD	DM
FOOTNER FOREST PRODUCTS	FF
FOREST RESOURCE IMPROVEMENT ASSOCIATION	FR
HANSEN FOREST PRODUCTS	HF
HUALLEN SEED ORCHARD COMPANY	HU
INDIAN AND NORTHERN AFFAIRS, CANADA	IN
FORESTRY DIVISION, ROCKY MOUNTAIN HOUSE AREA	LC
FORESTRY DIVISION, EDSON FOREST AREA	LF
FORESTRY DIVISION, LAC LA BICHE FOREST AREA	LL
FORESTRY DIVISION, SLAVE LAKE FORESTAREA	LS
FORESTRY DIVISION, PEACE RIVER FORESTAREA	LP
FORESTRY DIVISION, GRANDE PRAIRIE FOREST AREA	LG
FORESTRY DIVISION, CALGARY FOREST AREA	LR
FORESTRY DIVISION, HIGH LEVEL FOREST AREA	LU
FORESTRY DIVISION, FORT MCMURRAY FORESTAREA	LW
FORESTRY DIVISION, WHITECOURT FOREST AREA	LO
FORESTRY DIVISION, PRFN	LN
L H REHN LUMBER LTD	RE
LITTLE RED RIVER FORESTRY LTD	RR
LUSCAR LTD –COAL VALLEY MINE	CV
LUSCAR LTD –GREGG RIVER MINE	GR
LUSCAR LTD –LINE CREEK MINES	CM
LUSCAR LTD –OBED MOUNTAIN MINE	OM

Agency name	Code
MANNING DIVERSIFIED FOREST PRODUCTS	MD
MEDICINE LODGE TIMBER PRODUCTS	ML
METIS SETTLEMENTS TRANSITION COMMISSION	MS
MILLAR WESTERN FOREST PRODUCTS – BOYLE	MB
MILLAR WESTERN FOREST PRODUCTS – WHITECOURT	MW
NATURAL RESOURCES CANADA	NR
NORTHLAND FOREST PRODUCTS LTD	NF
ROCKY WOOD PRESERVERS LTD	RW
SEEHTA FOREST PRODUCTS	SF
SLAVE LAKE PULP LTD	SA
SMOKY RIVER COALS LIMITED	SR
SOSNOWSKI, MIKE	SM
SPRAY LAKES SAWMILLS LTD	SL
ST JEAN LUMBER LTD	SJ
SUNCOR ENERGY INC	SE
SUNDANCE FOREST INDUSTRIES LTD	SU
SUNDRE FOREST PRODUCTS LTD	SP
SYNCRUDE CANADA LTD	SC
TALL PINE TIMBER COMPANY LTD	TP
TIMEU FOREST PRODUCTS	TF
TOLKO INDUSTRIES LTD – HIGH PRAIRIE	TH
TOLKO INDUSTRIES LTD – HIGH LEVEL	TL
VANDERWELL CONTRACTORS LTD	VC
WABASCA LAKES SAWMILL COMPANY LTD	WL
WALLACH, PAUL	WP
HINTON WOOD PRODUCTS	WW
WESTERN BOREAL ASPEN CORP	WB
WEYERHAEUSER COMPANY LTD, DRAYTON VALLEY	WD
WEYERHAEUSER COMPANY LTD, EDSON	WE
WEYERHAEUSER COMPANY LTD, GRANDE PRAIRIE	WG
ZAMA MILLS	ZM
PARENT MATERIAL COLLECTIONS MADE PRIOR TO May 1, 2003	XX[1]

[1] For all parent materials collected prior to May 1, 2003 and documented by *Alberta*, a *U.I.* is assigned for each unique *genotype* as outlined in the standards and Appendix 25. The agency code “XX” is used for such parent material collections.

Appendix 26. Genetic Test Establishment Report – Contents for *Stream 2* Material

See Standards 27.2, 30.3.2 and 30.12.1.

At a minimum, the genetic *test* establishment report will contain a clear description and/or listing of the following:

Header

i) Program and species;
ii) Agency/cooperators;
iii) *Trial* code;
iv) Site name;
v) Reference to associated *controlled parentage program* (*CPP*) or research plan (RP);
vi) List of associated *trials* (i.e., *tests* containing the same genetic material).

***Test* material**

i) Listing of seed or vegetative lots including *genetic identity* and origin.

Controls

i) Listing of seed or vegetative lots including *genetic identity* and origin.

Planting stock

i) Description and location of sowing/striking and growing, including nursery name and location, sowing/striking date, lift date and stock type; also any relevant descriptive details relating to growing, lifting, packing, and delivery.

Experimental and field design

i) Type (e.g., alpha, randomized complete block);
ii) Number of replicates;
iii) Number of blocks/rep;
iv) Plot size and shape;
v) Include outputs from design generation program showing treatment randomizations and replicate/block assignments;
vi) Border row(s) description;
vii) Spacing.

***Test* site**

i) Include the completed *Genetic Test Site* Information Form (Appendix 29) and access map.

Field marking

i) Description;
ii) Percent of trees/plants marked.

Planting

i) Names of contractors and supervisors;
ii) Dates;
iii) Planter allocation description (e.g., one planter/rep).

Map(s)

i) Must unambiguously define genetic and experimental design identity of each tree/plant.

***Test* content file**

i) Attach electronic listing as per Standard 27.1.

References

i) List of citations.

Appendix 27. Genetic Test Measurement Report – Contents for *Stream 2* Material

See Standards 27.5, 30.8.1, 30.10 and 30.12.2.

Contact *Alberta* for recommended field *trial* measurement equipment, measurement procedures and quality control procedures; also refer to Alberta Tree Improvement Field Measurement Guidelines (2016).

At a minimum, the genetic *test* measurement report will contain a clear description and/or listing of the following.

Introduction

i) *Trial* description and objective(s);
ii) Applicable *controlled parentage program* or Research Program Plan;
iii) Measurement objectives;
iv) Measurement schedule;
v) Measuring agency and personnel.

Methods

i) Variables assessed and measured;
ii) Assessment and measurement methods, procedures and equipment;
iii) Quality control procedures (e.g., measurement procedures, data handling and verification procedures, field measurement spot checking and sampling intensity, measurement instrument calibration).

Results

i) Data dictionary containing variable listing, description of values of variables, position in file, and file format;
ii) Data format;
iii) Measurement start and completion dates;
iv) Data summaries;
v) Tree counts by site, replicate, and treatment;
vi) Appropriate site means and ranges for quantitative traits;
vii) Trait means by replicate;
viii) Trait means by treatment;
ix) Survival by site;
x) Verified raw data set to be submitted electronically with report and in accordance with data handling standards outlined in Standard 27.0;
xi) Quality control summary results (see attached example [Table A27.1]).

Notes

i) Significant items of interest or concern relating to assessment or data.

TABLE A27.1 Genetic Test Measurement Report - Quality Control Summary Results (APPENDIX 27 FGRMS)

- **Replace *Site 1 ID*, 2 ID*, 3 ID*, 4 ID** with actual test site names in the trial series**

DATE: ____________________

- **Fill in ht & dbh columns for ea. *Site ID 1*, 2 ID*, ID 3*, ID 4** ; (the "all" ht & dbh columns will auto-complete in the Excel version)**
- **If more than 4 sites attach additional sheet(s)**

	item		*Site 1 ID**		*Site 2 ID**		*Site 3 ID**		*Site 4 ID**		**all**[1]	
			ht	**dbh**	**ht**	**dbh**	**ht**	**dbh**	**ht**	**dbh**	**ht**	**dbh**
a	number of test trees planted	*count*									**0**	**0**
b	number of test trees living and measured	*count*									**0**	**0**
c	number of living trees checked	*count*									**0**	**0**
d	number of checked trees included	*count*									**0**	**0**
e	number exceeding tolerance	*count*									**0**	**0**
f	% sample [= d/b]	*ratio*	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!	#DIV/0!
g	% exceeding tolerance [= e/d]	*ratio*	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**	**#DIV/0!**
h	reason for exclusion (include all applicable; see codes below)[2]	*list*										

[1] Values calculated across sites

[2] Reasons for exclusion from check . . .

1 tree now missing

2 tree now dead

3 tree broken between times of original measurement and check

4 other [describe]

* actual site name to be inserted in cell(s)

Appendix 28. Genetic Test Analysis Report – Contents for *Stream 2* Material

See Standard 30.1.

At a minimum, the genetic *test* analysis report will contain a clear description and/or listing of the following:

Name of *controlled parentage program* or research program plan

i) *Trial* identity;
ii) Filename of *checked dataset* (submitted with Genetic Test Measurement Report; see Appendix 27 for contents);
iii) Objective(s) of analyses;
iv) Editing procedure used to convert *checked dataset* to analyzed dataset (e.g., treatment of outliers, values deleted, reasoning);
v) Analytical procedure:
  a. Method (e.g., Analysis of Variance [ANOVA], Best Linear Predictor [BLP], Best Linear Unbiased Prediction [BLUP]);
  b. Model;
  c. Expected mean squares where appropriate.

Summary statistics for traits of interest (e.g., height and survival)

Estimates of genetic parameters (e.g., *breeding values* [*BV*s], heritability and genetic correlations)

i) Showing method and formulae used.

Standard errors

i) Calculated for parameter estimates used to calculate heritability and genetic correlations;
ii) Calculation methods to be shown.

Dataset analyzed

i) Submitted in electronic format with this analysis report.

Reference to additional relevant reports

i) Other Research program plan or *controlled parentage program* plan;
ii) Establishment report;
iii) Measurement report.

Appendix 29. Genetic Test Site Information Form for *Stream 1* and *2* Material (Updated May 1, 2020)

See Standards 25.1.2 and 30.3.2. See also Appendix 26.

Minimum required information for initial submission is identified by asterisks for *Alberta* assignment of a *trial* code. A completed form is to be included in the *trial* establishment report.

Alberta Government

GENETIC TEST SITE INFORMATION FORM (APPENDIX 29 FGRMS)

Relevant CPP or RP Plan*		
Proponent responsible for test site*		
Date form completed/updated*		
Trial code (provided by the Department)		
Site name (local feature or landmark)*		
Company ARIS Opening No.		
Land reservation (type: e.g. ISP or MLL, date, identification number, disposition number)		
Site location	Latitude*(decimal degrees)[2]	
	Longitude*(decimal degrees)[2]	
	Legal	twp range meridian
	UTM Northing (optional)	
	UTM Easting (optional)	
Site information	Elevation (m)*	
	Slope (%)	min max mean
	Slope Position (e.g. toe)	
	Aspect (e.g. NE)	
	Test site size (ha)	
	Parent material	
	Soil classification	
	Natural region*	
	Natural subregion*	
	Ecosite/Site classification*	
	Depth to any restricting layer (within 50 cm)	
	Drainage class (e.g. "well" or "hydric")	
	Nutrient class (e.g "rich" or "mesotrophic")	
	Other soil information (optional)[1]	
Site history	Harvest date	
	Post-harvest (site prep) treatment(s), date(s)	
	Other development info (fence, culvert, etc.)	
Maps (attach)	Site access (sketch ok)	
	Site (cutblock) map to scale	

Reviewed by: **Date:**

*** Minimum required information for initial submission for Department assignment of trial codes.**

A completed Genetic Test Site Information form is to be included in the trial establishment report submission.

[1] Indicate if the test is planted on a reconstructed site and add any additional information specific to this site.

[2] Degrees in decimal format, to six decimal places (Example: Lat 56.123456 Long 118.123456).

Appendix 30. Example of Data Collection Form and Corresponding Map for *Stream 2* Material

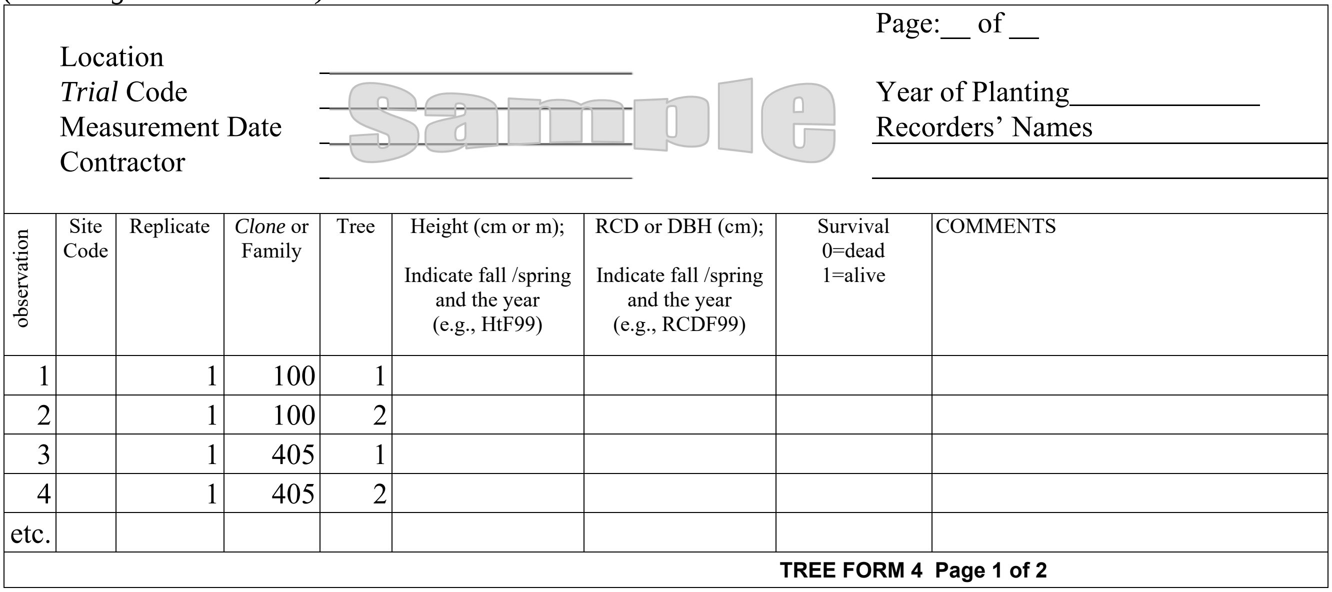
See Standards 27.1, 27.3 and 30.5.1.

EXAMPLE OF DATA COLLECTION FORM (Excel file)

This form may be used as a template for any *trial*; not all columns will be relevant to all *trials*. For silviculture *trials* there will be a treatment column; for genetics *trials* there may be provenance, family and/or *clone* columns. Although the site code must exist in the file, the column can be hidden when printing out the sheets for data entry purposes. Each year that the file is added to will require the insertion of new columns for the traits being measured (e.g., FHt99|FHt00|FHt01|FCp99|FCp00|FCp01|).

It is useful to print out at least the last year's measurements when preparing data sheets, while hiding all other information. This can also be done if data is being collected electronically.

(Fall Height 1999 : FHt99)



Page:__ of __

Location ____________________

Trial Code ____________________

Measurement Date ____________________

Contractor ____________________

Year of Planting_____________

Recorders' Names ____________________

observation	Site Code	Replicate	*Clone* or Family	Tree	Height (cm or m); Indicate fall /spring and the year (e.g., HtF99)	RCD or DBH (cm); Indicate fall /spring and the year (e.g., RCDF99)	Survival 0=dead 1=alive	COMMENTS
1		1	100	1				
2		1	100	2				
3		1	405	1				
4		1	405	2				
etc.								

TREE FORM 4 Page 1 of 2

EXAMPLE OF MAP GUIDE FOR *TRIAL* INSTALLATION MAP

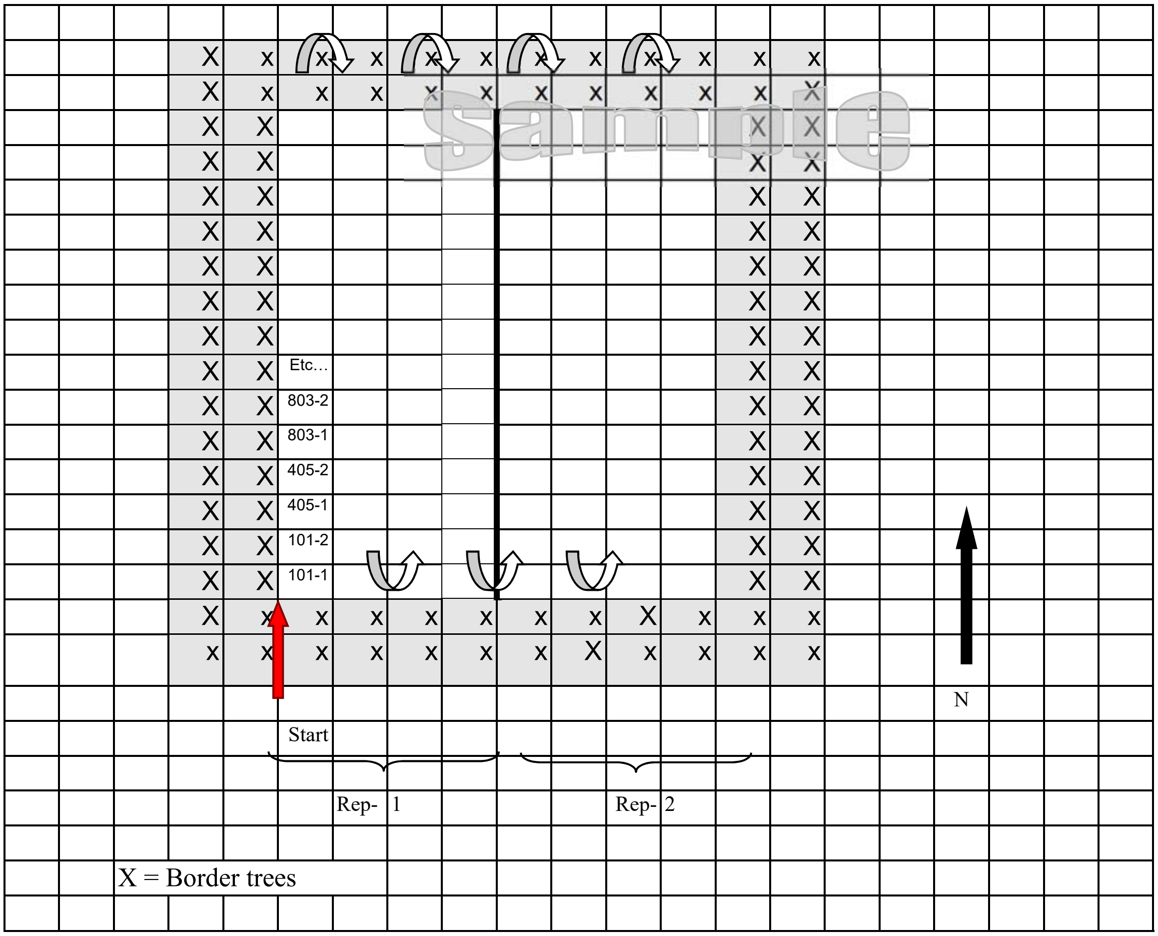
MAP GUIDE

Page__ of __

Location____________________________
Plantation name or *trial* code_________________
Measurement date____________________ Year of planting______________
Contractor___________________________ Initials of recorders____________________

On the grid indicate the tie point, direction of travel throughout plantation/*trial*.
Show North arrow.
Include replicate, *clone* or treatment and tree number per grid square.

Clearly indicate Start point of map to link with data file sequence.



Include as many grids as needed to cover plantation/*trial* and include tie points between maps.
Indicate border trees with shading or X's.
Comments:

MAP GRID

Appendix 31. Calculation of Genetic Worth for Vegetative Lots and Orchard Seedlots of *Stream 2* Material

See Standards 31.2, 33.3 and 34.1. See also Appendix 28.

INTRODUCTION

Genetic worth (*GW*) is an estimate of the expected performance of a vegetative lot or seedlot, and refers to individual traits such as height, volume or wood density. It is calculated as the average *breeding value* (*BV*) of *genotypes* represented in the lot, weighted by genotypic contribution (for vegetative lots), or by an estimate of the proportion of gametes contributed by each *genotype* (for seedlots). The *genetic worth* of orchard seedlots will be adjusted for genetic (pollen) contamination and supplemental mass pollination (SMP).

APPLICABILITY

Claim for *genetic gain* is contingent on the *GW* of a seedlot or seedlots used for *reforestation*. *GW* shall be calculated according to the protocols outlined below. Where no claim for *genetic gain* applies, GW, for the purpose of lot *registration*, can be considered to be 0.

Inclusion of *genetic gain* in a timber supply analysis requires prior approval by *Alberta*.

CALCULATIONS

1. 2% gain in height at rotation, based on Standard 31.2, may be used as a *BV* for *clone*s of parent trees selected intensively (using the *comparison tree method*) until *test* results are available (see Standard 31.5). Individuals in seedling *seed orchards* will be assigned a *BV* of 1% until *test* results are available.
2. *Breeding value*s for height, estimated from genetic *test* data, are calculated relative to unselected or operational control lots appropriate to the *controlled parentage program* (*CPP*), or to the mean performance of progeny of parents in the *breeding population* of the *CPP*. Where *BVs* are calculated relative to the mean of tested parents (rather than relative to control lots), and selections were made using the *comparison tree method* as described in Item 1 above, 2% will be added to the calculated *BV* for clonal orchards and 1% for open-pollinated seedling orchards.
3. For forward selections from progeny *test*s: Where the mean of all offspring of all intensively selected parents is used as the comparison then 1% can be added to the calculated *BV* (height at rotation). Where the mean of local check lots is used as a comparison then calculated *BV* can be assumed to reflect selection differential.
4. A correlation between heights at measurement and at rotation ages will be used to convert height *BV* at measurement age to height *BV* at rotation age. An appropriate correlation may be selected from Appendix 40 for conifer species, a *CPP*-specific correlation, or any other correlation approved by *Alberta*. For deciduous species contact *Alberta*.
5. It will be assumed that the *genetic worth* of contaminating pollen is 0, unless evidence to the contrary exists.

Other options will be considered by *Alberta* on a case-by-case basis.

A. Seedlots from clonal and/or uneven-aged *seed orchard*s (including clonal, seedling, and mixed clonal and seedling *seed orchard*s)

The method of estimation of genotypic frequencies will depend on the number of *genotypes* contributing to the *deployment population* (see Table A31.1). Where genotypic frequencies are based on both male and female contributions, male and female genotypic contributions may be calculated separately. Otherwise, male and female contributions for *genotype* **i** are both assumed to equal $\mathbf{p_i}$.

$\mathbf{p_i}$, the proportion of gametes produced by *genotype* i, will be estimated as follows.

Table A31.1. Method of genotypic contribution estimation for clonal and/or uneven-aged orchards.

Number of *genotype*s contributing	**Method of estimation of genotypic contribution**
Fewer than 50	As per Table A37.1, Appendix 37. Alternatively, if collections are made on a clonal basis, cone volume per *clone* may be used to estimate $\mathbf{p_i}$.
50 – 74	Sampling level: 50% sample of contributing trees. Material assessed: count of female flowers or cones. Alternatively, if collections are made on a clonal basis, cone volume per *clone* may be used to estimate $\mathbf{p_i}$.
75 or more	Genotypic frequency in the cone-bearing population may be used to estimate $\mathbf{p_i}$. Example: c*lone* x has 15 *ramets* that bear cones out of an orchard total of 250 cone-bearing *ramets*. $\mathbf{p_i} = 15/250 = 0.06$. Alternatively, if collections are made on a clonal basis, cone volume per *clone* may be used to estimate $\mathbf{p_i}$.

B. Seedlots from even-aged half-sibling seedling *seed orchard*s

Method of estimation will depend on the number of families contributing to the *deployment population* (see Table A31.2). Where genotypic frequencies are calculated based on both male and female contributions, male and female genotypic contributions may be calculated separately. Otherwise, male and female contributions for family **i** are both assumed to equal $\mathbf{p_i}$.

Table A31.2. Method of genotypic contribution estimation for even-aged half-sibling family orchards.

Number of families contributing	**Method of estimation of genotypic contribution**
Fewer than 25	As per Table A37.1, Appendix 37. Alternatively, if collections are made on a family basis, cone volume per family may be used to estimate $\mathbf{p_i}$.
25 – 37	Sampling level: 50% sample of contributing trees. Material assessed: count of female flowers or cones. Alternatively, if collections are made on a family basis, cone volume per family may be used to estimate $\mathbf{p_i}$.
38 or more	$\mathbf{p_i}$ = proportion of orchard trees of family **i**.

C. Vegetative lots

$\mathbf{p_i}$ = proportion of total *vegetative propagules* produced by *genotype* i

SEVERAL CASES ARE CONSIDERED.

CASE 1. Seed or vegetative lot produced with no pollen contamination or supplemental mass pollination (SMP)

$$\mathbf{GW} = \sum(p_i \, BV_i)$$

where

GW = *genetic worth* of the seed or vegetative lot;

BV_i = *breeding value* of *genotype* (*clone* or family) i

Example 1: *Breeding value*s and genotypic contributions are shown in Table A31.3.

Table A31.3. Breeding values and genotypic contributions.

Genotype	p_i	BV_i	$p_i x BV_i$
1	0.10	0.27	0.027
2	0.07	0.20	0.014
3	0.05	0.15	0.0075
4	0.09	0.22	0.0198
5	0.14	0.06	0.0084
6	0.07	0.10	0.007
7	0.05	0.08	0.004
8	0.04	0.12	0.0048
9	0.03	0.02	0.0006
10	0.11	0.02	0.0022
11	0.07	0.02	0.0014
12	0.06	0.02	0.0012
13	0.05	0.02	0.001
14	0.07	0.02	0.0014
Sum	**1.00**		**0.10**

Thus for this lot

GW = 0.10, or 10%

CASE 2. Seedlot produced where pollen contamination exists

GW = $0.5\sum[(1-PC) \times BVM + PC \times BVC + BV_i] \times p_i$

where

PC = proportion of contaminating pollen (see Appendix 34 for calculation methods)

BVM = average male *BV*, weighted by genotypic contributions

BVC = *BV* of contaminant pollen

[other variables as above]

If the contaminant pollen has a *BV* of 0, this simplifies to

$$GW = 0.5\sum\{(1-PC) \times BVM + BV_i\} \times p_i$$

$$= 0.5[(1-PC) \times BVM + \sum(BV_i) \times p_i]$$

Example 2: *Breeding value*s and genotypic contributions as in Table A31.3.

PC = 0.23

BVC is assumed to be 0.

Thus

$$GW = 0.5 \times [(1-0.23) \times 0.1003 + 0.1003]$$

$$= 0.5 \times [.0772 + .1003]$$

$$= 0.09\text{, or } 9\%$$

CASE 3. Seedlot produced with supplemental mass pollination (SMP), where pollen contamination exists

GW = $0.5\sum[PSMP_i \times BVSMP_i + (1-PSMP_i)[(1-PC) \times BVM + PC \times BVC] + BV_i] \times p_i$

where

$PSMP_i$ = proportion of successful SMP applied to *clone* i

$BVSMP_i$ = average *BV* of successful SMP applied to *clone* i

[other variables as above]

REFERENCES

Woods, J.H., M.U. Stoehr and J.W. Webber. 1996. Protocols for rating seed orchard seedlots in British Columbia. BC Ministry of Forests, 26 p.

Xie, C.-Y. and A.D. Yanchuk. 2003. Breeding values of parental trees, genetic worth of seed orchard seedlots and yields of improved stocks in British Columbia. West. J. Appl. For. 18(2):88-100.

Appendix 32. Production Unit Establishment Report for *Stream 2* Material

See Standard 32.8.1.

Establishment reports are due June30 in the year following the establishment of the *production unit*. Establishment reports for seed *production units* must contain the following information (Contact *Alberta* for a sample establishment report).

For vegetative *production units*, complete as appropriate. Contact *Alberta* for information.

Project Title

Project proponent(s)

Species

Anticipated life of orchard

Location

i) Site name;
ii) Legal land description;
iii) Latitude (decimal format, e.g., Lat 56.123456, Long 118.123456);
iv) Longitude (decimal format, e.g., Lat 56.123456, Long 118.123456);
v) Elevation.

Site information

i) Physical description;
ii) History of site use.

Description of orchard parental material

i) List of *genotypes*, identified by *unique identifier* (*U.I.*), in the orchard population.

Orchard stock

i) Description of rearing regime;
ii) Rootstock provenance.

Orchard design

i) Design software used;
ii) Constraints on spacing of related *clone*s.

Planting report

i) Planting dates;
ii) Temperature, precipitation and soil moisture status during plant (e.g., wet, moist, dry).

Table of origin of clones

i) *Unique identifier (U.I).* (and *clone* or family number, if different);
ii) Collection site;
iii) Latitude, longitude, and elevation.

Distribution of clones

i) *Ramets* per *clone* in the *clone* bank;
ii) Inventory of potted grafts per *clone*;
iii) List of grafts planted in the current year including *clone* and *ramet* number and planting position in the orchard.

Orchard layout map

i) Showing orchard design and positions with planted positions keyed to *genetic identity*.

Site layout map

i) Showing position of orchard in relation to other plantations on site.

Access map

i) Providing directions to the orchard.

As changes occur (e.g., mortality, replacement, roguing), the above items should be updated and submitted to *Alberta* annually in the *Production Unit* Annual Operations Report (see Appendix 35).

Appendix 32A. Stream 1 Seed Orchard Establishment Report

See Standards 11.7, 11.7.1 and 11.7.2; also Appendix 2, 4, 14 and 25.

Prior to initiating development of a *Stream 1 seed orchard*, proponent must submit a letter of intent to *Alberta*.

Establishment reports are due June 30 in the year following the establishment of the *Stream 1 seed orchard*. Establishment reports must contain the following information:

Project Title

Project proponent(s)
Seed zone
Species (include information about mating system)
Orchard type (see Table A4.3, Appendix 4)
Anticipated life of orchard

Location of *seed orchard*

i) Site name;
ii) Legal land description;
iii) Latitude, longitude (use decimal format), and elevation.

Site Information

i) Physical description;
ii) History of site use;
iii) Planting dates.

Description of orchard parental material

i) *Unique identifier* (*U.I.*) (assigned by proponent) for each *clone* or parent (parent registration not required);
ii) Collection site latitude, longitude, and elevation for each *clone* or parent;
iii) Number of plants per *clone* or per parent planted in the orchard.

Orchard design

i) Design software used.

Orchard layout map

i) Showing orchard design and positions with planted positions keyed to *genetic identity*.

Site layout map

i) Showing position of orchard in relation to other plantations on site.

Access map

i) Providing directions to the orchard.

Appendix 33. Permanent Sample Tree (PST) Protocols for *Stream 2* Material

See Standard 32.8.2.

PST system for flowering and seed production monitoring in *seed orchard*s

PURPOSE

i) To provide orchard-specific local data for monitoring *seed orchard* development, flowering, cone and seed production, and seed quality;
ii) To provide an estimate of reproductive contribution and a tool for cone crop forecasting.

SAMPLE SIZE AND DISTRIBUTION

i) For orchards with fewer than 600 trees planned, a minimum of 60 PSTs will be designated;
ii) For orchards with 600-2000 trees planned, a minimum of 10% of trees will be designated as PSTs;
iii) For orchards with more than 2000 trees planned, a minimum of 200 PSTs will be designated;
iv) PSTs will proportionately represent each planting year (with a tolerance of five trees or 20%, whichever is greater, to calculate yearly PST additions and tolerances) (see Excel spreadsheet [App33_PST _ assignment.xlsx], available from *Alberta*);
v) All *clone*s or families with five or more trees will be represented in PSTs;
vi) Mortality in the PST population will be replaced to ensure continued compliance with these rules;
vii) PSTs will be well distributed across the orchard.

After 50% of planned positions in an orchard have been filled, the number of designated PSTs divided by the planned final PST number will be equal to or greater than the number of filled orchard positions divided by the total number of orchard positions.

INDIVIDUAL PST TREE DATA REQUIREMENTS (SEE TABLE A33.1)

i) Height to the nearest centimetre to tip of terminal bud;
ii) Crown width at widest part of crown to nearest centimetre;
iii) Diameter at breast height (DBH) to nearest centimetre, once grafts reach breast height;
iv) Number of male and female flowers (actual count, or estimate if flowering is prolific);
v) Number of immature cones (pine species only) (actual count, or estimate if numbers are large);
vi) Number of mature cones (estimate if numbers are large). If a crop is collected in the given year, this information need not be collected; an average will be calculated from operational collection data;
vii) Where data or material collection is incompatible with orchard operations (e.g., sanitation picking), such data and/or material need not be collected.

Crown measurements (height, crown width and DBH) need not be reported for:

i) white spruce, black spruce, lodgepole pine, or jack pine orchards, or for
ii) orchards of other species, once crown management has been initiated.

For all other orchards, crown measurements must be reported every two years. All other data must be reported annually.

ADDITIONAL REQUIREMENTS, *SEROTINOUS* SPECIES

Where cones will be left on the tree for collection in a subsequent year, flowering and immature cone assessments will be done in each crop year.

MATERIAL COLLECTION, SEED YIELD CALCULATIONS AND GERMINATION TESTING

Applies only to species other than white spruce, black spruce, lodgepole pine, and jack pine.

In the years before operational crops are produced and collected, ripe cones will be collected from PSTs (five cones per tree, where available) and bulked into a single PST collection for extraction and testing. After an orchard comes into production, PST cones need not be collected separately. The following information shall be reported:

i) Mean number of cones per litre;
ii) Seed production (g);
iii) Number of seeds per cone;
iv) 1000 seed weight;
v) Seed germination %.

ASSESSMENT SCHEDULE

Assessments are completed annually, except for growth trait measurements, i.e., height, crown width, and DBH. These are done (where required) every second year.

DATA SUMMARIES

Data is added annually to an electronic database maintained for each orchard. Data is to be summarized and reported in the *Production Unit* Annual Operations Report (see Appendices 35 & 35A) as shown in Tables A33.1 and A33.2.

In Table A33.1:

i) lines 1 – 5 refer to the whole orchard, not just PSTs.
ii) where an orchard has a collectable crop in the given year:
  - lines 28 and 31-34 may be completed from operational crop data;
  - lines 27, 29 and 30 may be left blank.

Table A33.1. Template: annual summary of seed production and monitoring information for Region ___ seed orchard, year ____.

Line	**Orchard characteristics**	result
1	Planned orchard size	
2	Total no. of seed trees established	
3	Total no. of *clones*/families established	
4	Average age	
5	Age range	
6*	Average height (cm) PSTs only	
7*	Height range PSTs only	
8*	Average crown width (cm) PSTs only	
9*	Crown width range PSTs only	
10*	Average DBH (cm) PSTs only	
11*	DBH range PSTs only	
12	Total no. of PSTs	
	Reproductive balance	
13	Total # of PSTs flowering (male and female)	
	Male flowering	
14	No. of PSTs with male flowers	
15	Mean no. of male flowers or clusters/PST	
16	Range of male flowers or clusters/PST	
	Female flowering	
17	No. of PSTs with female flowers	
18	Mean no. of female flowers/PST	
19	Range female flowers/PST	
20	Mean male-female flower production ratio	

Line	**Immature cone production** **(pine spp. only)**	result
21	**Date assessed**	
22	No. of PSTs producing cones	
23	Mean no. of cones/PST	
24	Range of cones/PST	
25	Cone crop estimate (# of cones)[1]	
26	Cone crop estimate (hectolitres)[2]	
	Cone production	
27	No. of PSTs producing cones	
28	Mean no. of cones/PST	
29	Range of cones/PST	
30	Total no. of cones collected from all PSTs; max. 5/tree; (developing orchards only)	
31	Mean no. of cones/litre	
	Seed production	
32	Seed production (g)	
33	1000 seed weight	
34	Germination %	

Table A33.2. Template: summary over years of mean PST data for Region ______ seed orchard.

Year	**Height* (cm)**	**Crown* width (cm)**	**DBH* (cm)**	**Male flowers**	**Female flowers**	**Immature cones**	**Mature cones**	**Seed per cone**

* optional for white spruce, black spruce, lodgepole pine and jack pine.

[1] For all species except pine, cone crop estimate equals (line 2) x (line 18); for pine species it equals (line 2) x (line 23)

[2] To estimate hectolitres, divide (line 25) by the appropriate factor:
For white spruce – 15,000 cones/hl
For black spruce – 24,000 cones/hl
For lodgepole pine – 3,800 cones/hl

Appendix 34A. Pollen Contamination Monitoring

See Standard 32.8.3.

Pollen contamination can reduce the *genetic worth (GW)* of a seedlot or, in extreme cases, render a seedlot maladapted. Pollen flight monitoring or, for conifer orchards, chloroplast DNA (cpDNA) analysis will be used where required to estimate pollen contamination levels. It is left to the orchard manager to decide which of these two monitoring methods to use.

Pollen differentiation by visual means is virtually impossible within genera. Thus white spruce pollen cannot be distinguished from black spruce pollen, nor lodgepole pine from jack pine, nor aspen from balsam poplar.

Pollen monitoring is required (subject to Figure 34A.1) in the season of pollination for any crop that will be collected. This applies to *serotinous* species where crops may remain on the tree for one or more years. If a given crop will not be collected, pollen monitoring will not be required.

In years when no collectible crop is anticipated in the given orchard, pollen monitoring is not required in that orchard. The flowchart (Figure 34A.1) below will be used to determine pollen monitoring requirements in each orchard.

If gain is requested, proponent must demonstrate how pollen contamination will be factored into gain estimates.

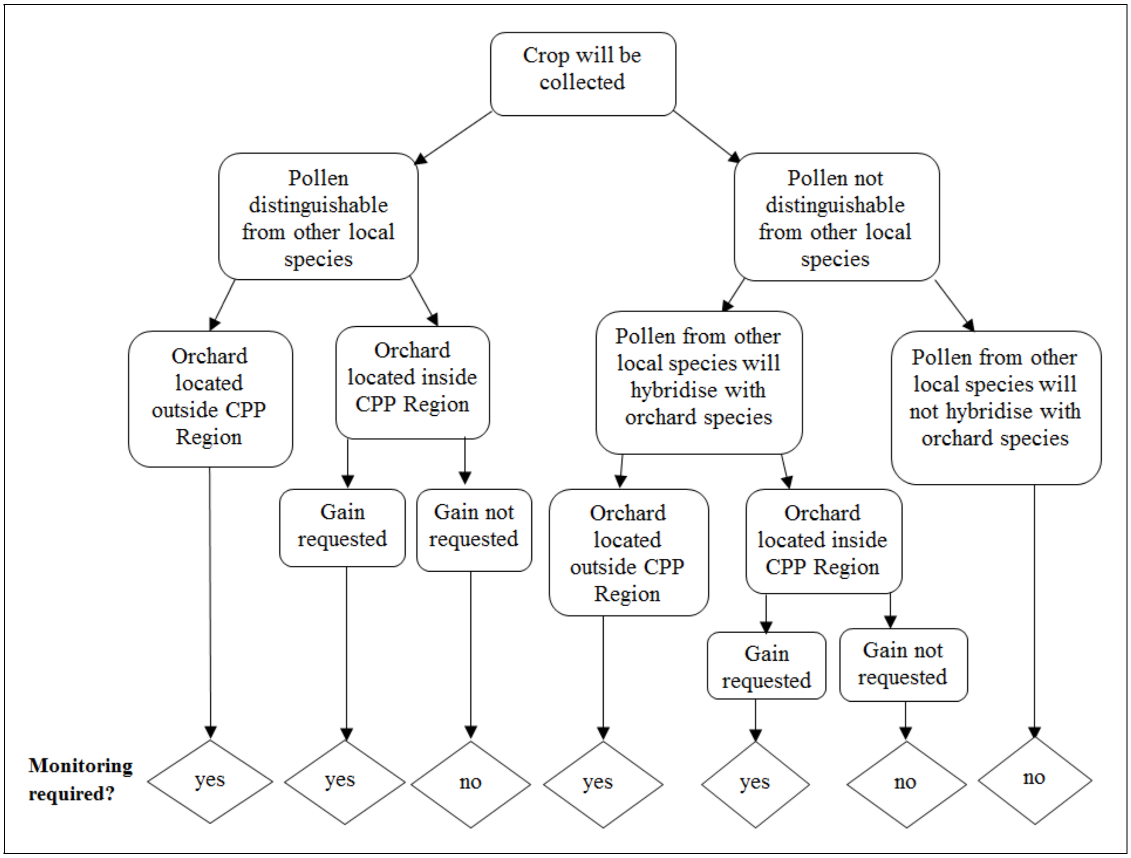


Figure A34A.1. Flowchart to determine pollen monitoring requirements.

Part 1. Pollen Contamination Estimation Using Pollen Flight Monitoring

PROCEDURES FOR POLLEN FLIGHT MONITORING

- i) The orchard manager will monitor pollen flight within each orchard at a minimum of two locations.
- ii) The orchard manager will monitor pollen flight outside the orchard with a minimum of two regional monitors for each orchard complex. Regional monitors may be established within orchards that have not yet begun to produce pollen.
- iii) Regional monitors are to be located in an open area a minimum of 300 m from the orchard boundary. The orchard manager is expected to be knowledgeable about the location of contaminant pollen sources and to situate regional monitors where there is a high expectation that they will trap pollen from these contaminant sources and not pollen from the orchard.
- iv) The type of pollen monitoring device used is the responsibility of the orchard manager but the manager must ensure that daily pollen cloud density values can be reliably generated.
- v) Traps are to be changed at least every two days.
- vi) A dissecting microscope is required to count pollen grains. To estimate pollen density in grains per square mm over the change interval (i.e., 24-48 hours), pollen grains will be counted in at least 10 1 mm^2 samples from each monitor and then averaged. These counts will be summed over the monitoring period. Total counts will then be averaged over all monitors of each category (regional or within-orchard).
- vii) All traps will be installed several days before pollen flight (either locally or in the orchard) is expected to begin. Pollen trapping within each orchard will continue until the orchard manager has determined that the orchard has completed receptivity. Regional monitors will be maintained until all orchards on site have completed receptivity.
- viii) For pine orchards, within-orchard monitors should be located at a height of one-half of the average crown height of the orchard.
- ix) For spruce orchards, within-orchard monitors should be located at a height of three-quarters of the average crown height of the orchard.

ESTIMATION OF CONTAMINATION LEVELS

Since it is impossible to differentiate visually between pollen produced within an orchard and pollen of the same species originating outside the orchard, the amount of foreign pollen cannot be estimated directly. Instead, a surrogate species or genus with recognizably distinct pollen can be used to provide an estimate of the proportion of outside pollen that penetrates into an orchard (e.g., for a pine orchard, tamarack or spruce can be used as a surrogate).

The external (outside-orchard) pollen levels of the surrogate species and target species (**xs** and **xt**, respectively) are estimated by the orchard manager using regional monitors. The within-orchard pollen levels of the surrogate and target species (**ws** and **wt**, respectively) are measured using orchard monitors.

The ratio of pollen density within the orchard to pollen density outside the orchard, in the open, can then be calculated for the surrogate species. This ratio is assumed to be independent of time, so that the surrogate need not be flowering simultaneously with the target species. It is assumed that the proportion of target species pollen penetrating the orchard from outside will be the same as the proportion of surrogate species pollen penetrating from outside. Thus this ratio also reflects the ratio of within-orchard to outside-orchard levels of non-orchard, or contaminating, target species pollen. This ratio is expected to be considerably less than 1.0 for a mature orchard, due to altered wind speed and patterns, and the screening effect of the orchard trees.

Thus the contaminant pollen level for the target species, **ct**, within the orchard can be estimated as

$$\mathbf{ct} = R \times xt$$

where

$$\mathbf{R} = \min(ws/xs, 1)$$

and the proportion of contaminant pollen, pc, within the orchard can be estimated as

$$\mathbf{pc} = ct/wt$$

$$= \mathbf{R \times xt/wt}$$

where

ct = **contaminant pollen level of target species**

R = ratio of within orchard surrogate species pollen to external surrogate species pollen, with a maximum value of 1

ws = within-orchard pollen level of surrogate species

xs = outside orchard pollen level of surrogate species

xt = outside orchard pollen level of target species

wt = within-orchard pollen level of target species

pc = proportion of contaminant pollen (within-orchard target species pollen that originated outside the orchard)

This number, **pc**, is used in the calculation of *genetic worth* of orchard seedlots (see Appendix 31).

EXAMPLE
A pine orchard has been established in an area where spruce pollen is present in significant amounts; thus spruce can be used as the surrogate species. There are two regional monitors, R1 and R2, and three within-orchard monitors, O1-O3. Counts for both species are shown in Table A34A.1. Outside and within-orchard levels of target species pollen, pine in this example, are estimated with data from the receptive period of the orchard only as determined by phenology monitoring (see Part 2); target species pollen occurring in the orchard before and after this period will not affect pollen contamination. For surrogate species pollen, spruce in this example, outside and within-orchard pollen levels are estimated with data from the complete pollen flight period of the surrogate species in order to provide the most robust estimate of the contaminant pollen level of the target species (**ct**).

The format used in this example will be used for reporting pollen contamination results in the annual operations report (see Appendix 35A).

Table A34A.1. Pollen counts (grains/mm2) from orchard and regional pollen monitors.

Date	Spruce R1	Spruce R2	Spruce O1	Spruce O2	Spruce O3	Pine R1	Pine R2	Pine O1	Pine O2	Pine O3
02.05.15	0	0	0	0	0	0	0	0	0	0
02.05.17	0	0	0	0	0	0	0	0	0	0
02.05.19	0	0	0	0	0	0	0	0	0	0
02.05.21	0	0	0	0	0	0	0	0	0	0
02.05.23	0	0	0	0	0	0	0	0	0	0
02.05.24	0.7	0.8	0.3	0.4	0.3	0	0	0	0	0
02.05.25	1.4	1.6	0.7	0.8	0.6	0	5.9	0	0.4	13.7
02.05.26	0.8	0.8	0.3	0.4	0.3	4.5	5	12.6	12	11.4
02.05.27	0.2	0.2	0	0.2	0	9.2	10.2	25.9	24.7	23.4
02.05.28	0	0	0.2	0	0.1	4.8	5.3	13.5	12.9	12.3
02.05.29	1.6	1.7	0.7	0.9	0.7	0.8	0.9	2.2	2.1	2
02.05.30	1.5	1.6	0.7	0.8	0.6	0	0	0	0	0
02.05.31	2.3	2.6	1.1	1.3	1	10.1	11.1	28.3	20	25.6
02.06.01	0.4	0.5	0.2	0.2	0.2	9.4	10.3	26.2	24.9	23.7
02.06.02	0.8	0.9	0.4	0.5	0.3	15.1	16.6	42.1	40.1	38.1
02.06.03	2.9	3.2	1.3	1.6	1.2	2.7	3	7.5	7.2	7.2
02.06.04	7.3	8	3.4	4	3	5.4	5.9	15.1	14.3	13.6
02.06.05	5.4	6	2.5	3	2.3	18.8	20.7	52.7	50.2	47.7
02.06.06	3	3.3	1.4	1.7	1.2	67.1	51.8	101	95.8	119.3
02.06.07	1.1	1.2	0.5	0.6	0.4	34.9	38.4	97.8	93.2	88.5
02.06.08	0	0	0	0	0	19.2	21.2	53.9	51.3	48.7
02.06.10	1	1.1	0.4	0.5	0.4	6.8	7.4	19	18.1	17.2
02.06.12	0.1	0.1	0.1	0.1	0.1	0	0	0	0	0
02.06.14	0	0	0	0	0	6.2	6.9	17.5	16.6	15.8
02.06.16	0	0	0	0	0	0.9	0.9	1.9	2.3	2.2
02.06.18	0	0	0	0	0	0	0	0	0	0
02.06.20	0	0	0	0	0	0	0	0	0	0
02.06.22	0	0	0	0	0	0	0	0	0	0
02.06.24	0	0	0	0	0	0	0	0	0	0
Sum	**30.5**	**33.5**	**14.1**	**16.9**	**12.6**	**179.4**	**175.3**	**415.3**	**395.1**	**404.0**

🟨 receptive period of orchard
xs= spruce pollen density on regional monitors
ws= spruce pollen density on orchard monitors
xt= pine pollen density on regional monitors
wt= pine pollen density on orchard monitors
ct= (ws/xs)xt if ws/xs is < 1 or xt if ws/xs is > 1
pc= ct/wt

xs= (30.5+33.5)/2 = 32.0
ws= (14.1+16.9+12.6)/3 = 14.5
xt= (179.4+175.3)/2 = 177.4
wt= (415.3+395.1+404.0)/3 = 404.8
ct= 14.5/32.0 = 80.5
pc= 80.5/404.8 = 0.20

NOTE: xt and wt are averaged over the receptive period of the orchard, i.e., June 1-10, while xs and ws are averaged over the total period of surrogate species pollen flight.

Part 2. Estimation of Contamination Using Chloroplast DNA (CpDNA) Markers

There are many sources of error associated with contamination estimates based on pollen monitoring, some of which are listed below.

1) Orchard pollen may be captured on external traps, inflating estimates of **xt**.
2) Pollen of the same genus but of a different species than the orchard may be captured on both internal and external traps. Being indistinguishable from orchard pollen, it would affect estimates of both **xt** and **wt**.
3) Estimates of **xs** and **xt** are highly dependent on where the outside orchard monitors are located, and estimates of **ws** are highly dependent on the density of the surrogate species in the vicinity of the orchard.
4) Although orchard traps are placed to sample the pollen cloud density throughout the orchard, data can be biased if trees nearest to the traps are significantly above or below the average in male flower production. Nearby trees can also have a screening effect on pollen coming from more distant orchard trees.

CpDNA markers eliminate these sources of error, and provide an alternative method of estimating pollen contamination levels. However, this approach is also subject to errors. These errors involve possible violations of the following assumptions:

i) the background pollen haplotype frequencies estimated from bud samples taken from surrounding stands reflect the effective pollen contaminant cloud within the orchard, and

ii) outside and inside orchard pollen have an equal chance of fertilization success (Smith and Adams 1983) (Stoehr *et al*. 1998).

In addition, statistical issues associated with sampling will reduce precision of the estimate.

Of the species included in Alberta tree improvement projects, markers are currently available for white spruce, lodgepole pine, western larch, and Douglas-fir (Newton 2004).

Conifer chloroplasts contain their own DNA which is inherited from the pollen parent independently of nuclear genes; no recombination between parental genomes occurs, so that all the cpDNA found in the embryo after fertilization is from the pollen parent. Distinguishing orchard parental *clone*s by their cpDNA and counting the corresponding parental cpDNA in seed embryos provides a measure of paternal contribution to the seedlot and, therefore, an estimate of pollen contamination.

Chloroplast DNA is isolated from dormant vegetative buds or seed embryos, and *genotypes* (or, more correctly, haplotypes) are determined using a minimum of five cpDNA markers that are unique to the species. Each marker is a segment of chloroplast DNA from a specific locus. The markers are highly variable in size (i.e., in the number of nucleotides in the sequence at that locus) due to mutations and mistakes in replication. The size differences are assayed using electrophoresis and a cpDNA haplotype is comprised of the sizes, in base pairs, of all the loci assayed.

All orchard parents must be haplotyped. Background stands or plantations that are likely sources of contaminant pollen must also be sampled, to estimate the frequency of haplotypes common to both the background stands and the orchard. Approximately 50-100 trees should be sampled.

A sample of seeds from a given orchard seedlot is then haplotyped. The sample size depends up the number of unique haplotypes detected in the orchard and the level of precision required. Seed embryos can be categorized as detectable contamination if an embryo haplotype is not present in the orchard or as within-orchard pollination events adjusted for the presence of orchard-sized haplotypes in the background pollen.

Haplotyping of orchard and background pollen sources is a one-time undertaking. Once this is completed, estimates of pollen contamination for a seed crop require haplotyping of embryos only.

In addition to pollen contamination estimates, cpDNA markers can provide information on orchard pollen dynamics and their impact on seedlot makeup. Pollen contribution to a seedlot can be expressed as the proportion of seed embryos carrying an identical parental haplotype; pollen parent contributions that seriously violate panmixis indicate reductions in *effective population size (Ne)*.

If seed is sampled and haplotyped by *clone*, interactions between specific male and female parents can be assessed; some paternal haplotypes may show enhanced fertility with individual maternal *clone*s. Selfing rates can also be estimated if a given *clone* has a unique haplotype; because it is unique to one *clone*, seed with that haplotype could only be the result of selfing.

DNA extraction, amplification, electrophoresis and haplotyping are being done for *Alberta* by ATG Genetics Inc. (Craig Newton, PhD.), Nanaimo, British Columbia (www.atggenetics.com). In 2008, the cost of haplotyping using bud samples was $75-$100 per tree, depending upon the number of trees being haplotyped, and the cost per seed was $20.

EXAMPLE
This example follows the method described by Smith and Adams (1983). A white spruce orchard has 30 *clone*s represented by 14 cpDNA 5-locus haplotypes (Table A34A.2). In a sample of 50 trees from nearby white spruce stands and plantations, 22 trees had haplotypes that were not found in the orchard (Table A34A.3). Fifty seeds from the 2008 seed crop were haplotyped and 41 of these seeds matched haplotypes found in the orchard (Table A34A.2). Nine seeds did not match any of the 14 orchard haplotypes (Table A34A.3).

The expected proportion of orchard ovules fertilized by background pollen with a haplotype unique to the background stands is

$$\mathbf{b = m \times d}$$

where

m = the probability that an orchard ovule is fertilized by a pollen grain from the background stand, and
d = the probability that a background stand pollen grain has a haplotype unique to the background stand.

The rate of pollen contamination is then estimated as

$$\mathbf{m = b/d}$$

The fraction of seeds not matching any orchard haplotypes, 9/50 = 0.18, is **b** and represents the minimum level of unambiguous pollen contamination. The fraction of trees sampled from the background stands carrying haplotypes unique to the background, 22/50 = 0.44, is **d**. Therefore, pollen contamination in the 2008 seedlot is estimated as 0.18/0.44 = 41%.

The variance of **m** is calculated as follows:

$$\mathbf{Var(m) = (b(1-b))/nd^2}$$

where

n = the number of embryos sampled to estimate **b**.

This must be considered a minimum variance because it does not take into account the fact that both **b** and **d** are estimated, or the possibility of failure of assumptions.

For this example, the variance of **m** is 0.015 giving a standard error of 0.12. Pollen contamination is therefore estimated as 41% ± 12%.

Table A34A.2. Orchard haplotypes.

Haplotype number	Haplotype (cpDNA size in basepairs)[1]					*Clone*s per haplotype	Number of seed embryos
	Locus 1	Locus 2	Locus 3	Locus 4	Locus 5		
4	***188***	***166***	***151***	***137***	***123***	***6***	***8***
5	***188***	***167***	***146***	***136***	***131***	***4***	***12***
8	***188***	***167***	***149***	***137***	***128***	***3***	***4***
11	***189***	***162***	***146***	***136***	***122***	***3***	***3***
12	***189***	***162***	***146***	***136***	***123***	***3***	***5***
17	***190***	***162***	***146***	***136***	***122***	***2***	***3***
18	***190***	***162***	***146***	***136***	***123***	***2***	***2***
20	190	162	146	137	122	1	1
21	190	162	146	137	123	1	
22	190	163	145	136	124	1	2
23	190	163	146	136	122	1	
25	191	162	146	136	121	1	
26	191	162	146	136	122	1	1
27	191	162	146	136	123	1	
					Total	**30**	**41**

Table A34A.3. Background stand haplotypes.

Haplotype number	Haplotype (cpDNA size in basepairs)[2]					Trees per haplotype	Number of seed embryos[3]
	Locus 1	Locus 2	Locus 3	Locus 4	Locus 5		
1	186	165	146	136	127	1	1
2	187	161	146	138	126	1	
3	187	162	145	137	129	1	1
4	***188***	***166***	***151***	***137***	***123***	***5***	***(8)***
5	***188***	***167***	***146***	***136***	***131***	***9***	***(12)***
6	188	167	146	137	129	3	1
7	188	167	148	136	128	3	2
8	***188***	***167***	***149***	***137***	***128***	***3***	***(4)***
9	189	162	146	135	122	2	
10	189	162	146	135	123	2	1
11	***189***	***162***	***146***	***136***	***122***	***4***	***(3)***
12	***189***	***162***	***146***	***136***	***123***	***4***	***(5)***
13	190	161	146	136	123	1	
14	190	161	146	137	122	1	1
15	190	162	145	136	123	1	
16	190	162	146	135	123	1	1
17	***190***	***162***	***146***	***136***	***122***	***2***	***(3)***
18	***190***	***162***	***146***	***136***	***123***	***1***	***(2)***
19	190	162	146	136	124	1	
24	191	162	146	135	123	1	
28	191	162	146	137	122	1	1
29	191	162	146	137	125	1	
30	191	163	146	136	122	1	
					Total	**50**	**9**

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[1] bold and italicized haplotypes are also found in the background stands and plantations

[2] bold and italicized haplotypes are also found in the orchard parental *clone*s

[3] numbers in brackets are included in the Table A34A.2 total

References

Newton, C. 2004. Applications of DNA markers in BC tree improvement programs. Forest Genetics Council Extension Note 06. 5 pp.

Smith, D.B. and Adams, W.T. 1983. Measuring pollen contamination in clonal seed orchards with the aid of genetic markers. Proc. South. For. Tree Improv. Conf. 17:69-77.

Stoehr, M.U., Orvar, B.L., Vo, T.M., Gawley, J.R., Webber, J.E., and Newton, C.H. 1998. Application of a chloroplast DNA marker in seed orchard management evaluations of Douglas-fir. Can. J. For. Res. 28:187-195.

Appendix 34B. Phenology Monitoring

See Standard 32.8.3.

Phenology monitoring allows the orchard manager to identify *clone*s that are receptive either later or earlier than the bulk of the orchard population. Together with pollen monitoring, it also allows the manager to relate patterns of within-orchard pollen flight to periods of orchard receptivity, and to identify *clone*s that may not be successfully pollinated.

It is believed that periods of pollen flight of local and contaminating pollen are coincident in Alberta *seed orchards*. Monitoring the phenology of orchard trees and relating it to pollen flow within and outside the orchard will provide an empirical test of this assumption.

Phenology monitoring is required as follows:

i) each *clone* or family will be assessed for a minimum of five years after operational production begins;
ii) measurement years for individual *clone*s must overlap sufficiently that an accurate assessment of relative phenology can be made;
iii) each *clone* must have overlapping data from at least 10 other *clone*s.

Phenology monitoring is not required in orchards where:

i) pollen contamination estimation is not required (see Appendix 34A), or
ii) no crop collection is planned in the given year.

SAMPLING LEVEL

Permanent sample trees (PSTs) may be used for phenology monitoring. At least one *ramet* of each *clone* represented in the PST population will be monitored from approximately stage 3 (see Tables A34B.1 and 34.B2) until stage 7, at intervals of two days or less.

Table A34B.1. White spruce female reproductive phenology.

Stage	Female bud description
1	dormant bud – bud scales dry; no swelling
2	early bud swell – pointed tip; scales shiny, resinous, dark brown
3	late bud swell – bud elongates, becomes oblong; identifiable
4	early flushing – ovuliferous scales (o.s.) visible through bud scales; bud scales partially rip off
5	advanced flushing – cone becoming erect, some o.s. at central portion separate
6	fully receptive – cone erect, o.s. separate and bend perpendicular to cone axis
7	post-receptive – cone scales closing

Table A34B.2. Lodgepole pine female reproductive phenology.

Stage	Female bud description
1	seed cone still fully contained within shoot bud scales
2	seed cone bud still contained within flower bud scales
3	seed cone starting to emerge; rosette of cone scales just visible; not receptive
4	seed cone emerging; some pollen may reach ovules
5	advanced flushing seed cone emerged but not fully open; cone axis not elongated; pollen may reach ovules
6	fully receptive – seed cone emerged and spaces between scales allow pollen to sift down to the ovules
7	post-receptive- cone scales thickened, preventing pollen entry

i) A *clone* is considered receptive when 20% of the cones are fully receptive (stage 5 or 6).
ii) A *clone* is considered to have completed receptivity when 80% of the cones are post-receptive (stage 7).
iii) The orchard is considered receptive when 20% of *clone*s are receptive, and to have completed receptivity when 80% of *clone*s are post-receptive.

EXAMPLE

A 30-*clone* white spruce orchard is receptive from May 16 to 27. A summary and graph of the phenology and pollen monitoring data are shown in Table A34B.3 and Figure A34B.1.

Table A34B.3. Orchard receptivity and pollen flow.

Date May	*clone* receptivity			Pollen flow (grains/mm^2) (orchard)	Pollen flow (grains/mm^2) (regional)
	# receptive	# post-receptive	% receptive		
15	0	0	0	0.0	0.0
16	28	0	93	0.1	0.1
17	28	0	93	0.9	0.5
18	30	0	100	0.5	0.6
19	30	0	100	0.2	0.2
20	30	0	100	4.2	1.9
21	30	0	100	14.7	5.8
22	28	2	93	29.5	21.5
23	28	2	93	7.8	9.0
24	28	2	93	3.6	1.0
25	16	14	53	5.1	7.8
26	16	14	53	2.7	4.7
27	16	14	53	2.7	4.7
28	0	30	0	2.4	9.0
29	0	30	0	2.4	9.0
30				0.5	0.3
31				0.5	0.3

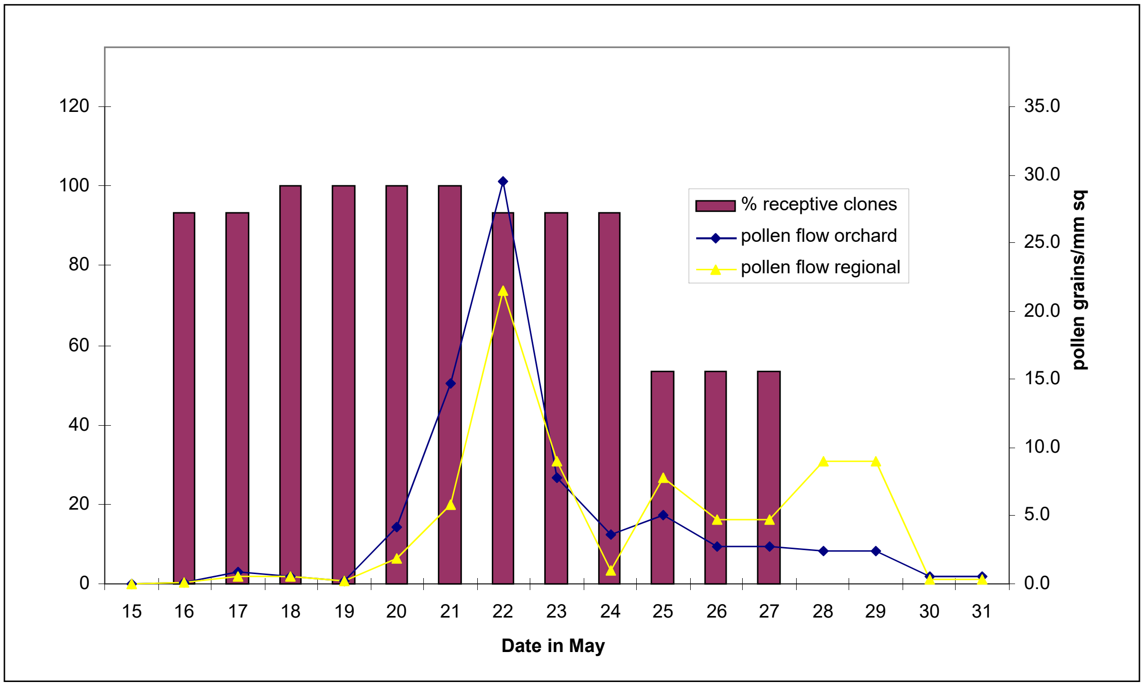


Figure A34B.1. Orchard receptivity and pollen flow.

REFERENCES

Owens, J.N. 1984. The reproductive cycle of lodgepole pine. BC Ministry of Forests. 29 p.

Owens, J.N. and Molder, M. 1984. The reproductive cycle of interior spruce. BC Ministry of Forests. 31p.

Appendix 35. Annual Operations Report for *Stream 2* Material

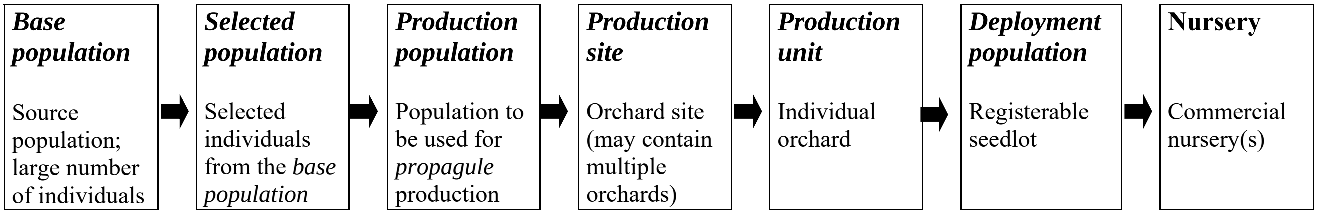
See Standard 32.1.

Annual operations reporting is required to establish that *Stream 2* programs have the ability to produce *deployment populations* (crops) which are eligible for *registration*, meet *genetic gain*, diversity and adaptation requirements and are capable of producing *reforestation* stock in sufficient quantities to meet Forest Management Plan *deployment* targets and yield expectations. The schematic provided below outlines various *Stream 2* production systems which correspond to reporting requirements in Appendices 35A and 35B. Materials used to assemble the *selected population* and *production population(s)* is taken from a *base population* which can include materials collected from *wild* stands, plantations, genetic *tests*, *clone* banks, or germplasm archives etc.

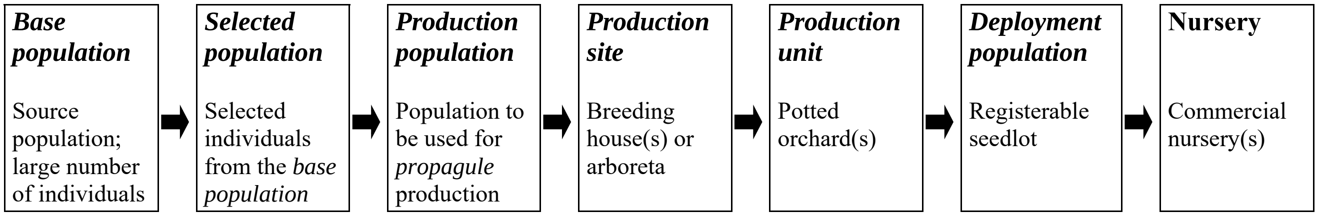
A. Sexual Production

Alberta will assign *production unit* identifiers.

1. Fixed *seed orchards*



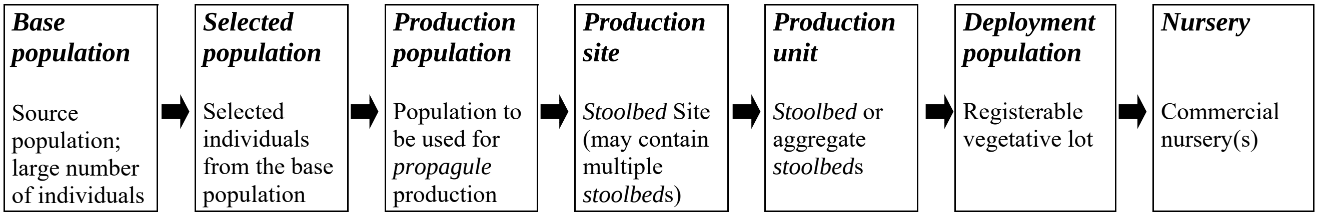
2. Potted *seed orchards*



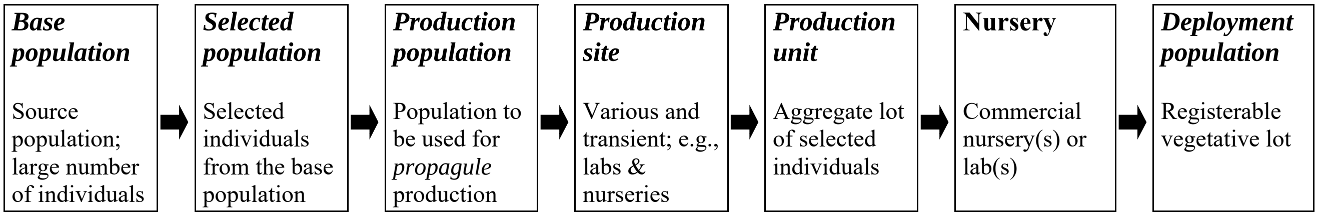
B. Vegetative Production

Alberta will assign *production population* identifiers.

1. Vegetative *stoolbeds*



2. Vegetative collections



Appendix 35A. Production Unit Annual Operations Report for Sexual Production Systems of *Stream 2* Material

See Standards 32.8.3, 32.8.4 and 33.7.

Annual operations reports are due June 30 in the year following the year in which the operations took place. Annual operations reports for seed facilities must contain the following:

Name of relevant *controlled parentage program* (*CPP*) plan

Base population

i) Population type (e.g., *wild* stands, plantations, genetic *tests*);
ii) *Trial series* name(s), numbers(s) related to this *seed orchard*.

***Production site* description**

i) Site name and location (decimal format, e.g., Lat 56.123456; Long 118.123456);
ii) Manager(s);
iii) Area occupied (ha).

Production unit

i) *Production unit* identifier (assigned by *Alberta*);
ii) Design capacity (planned final number of *clone*s, families, trees);
iii) Current number of trees in *production unit.*

Cultural activities

i) Cultural activities including irrigation, fertilization, mowing, herbicide applications, crown management, flower induction, root pruning, girdling, supplemental pollination.

Insect and disease incidence

i) Monitoring methods;
ii) Control measures.

Other activities

i) Activities that may not occur annually but have an impact on orchard composition, e.g., roguing, thinning, tree moving.

Orchard monitoring

i) PST report (see Appendix 33);
ii) Pollen density and phenology of orchard receptivity (in format shown in Table A34B.3 and Figure A34B.1, Appendix 34B) and a map showing monitor location (see Appendix 34);
iii) Pollen contamination.

***Deployment population* (cone and seed production)**

i) Timing and method of cone collection;
ii) Total cone production (hectolitres);
iii) Total seed production (grams);
iv) 1000 seed weight;
v) Germination percent;
vi) *Effective population size* (see Appendix 36) and a description of the data set upon which the calculation is based;
vii) *Cumulative effective population size* of crops produced (see Appendix 20);
viii) *Genetic worth* (see Appendix 31).

Subsequent year's planning

i) Report on items planned for the subsequent production season that may affect *registration* of crops, or licensing of *production site*s or *production unit*s.

Annual establishment summary

i) Report on planting including:
  - List trees planted in the current year including family (*accession*), *clone*, or *Unique Identifier (U.I.)*, and planting position in the orchard;
  - Planters;
  - Planting date;
  - Planting conditions (temperature and soil moisture).

ii) Report on mortality including:
  - Listing of trees identified by orchard position, and by family, *clone* or *U.I.* designation, which died in the previous winter and over the past growing season;
  - Known or suspected causes of mortality.

iii) Report on distribution of families/*clone*s including:
  - Listing of all trees by *U.I.*, *clone* or family planted in the orchard, keyed to planting position and year;
  - Percent of total orchard capacity planted;
  - *Ramets* per *clone* in the *clone* bank;
  - Inventory of potted grafts per *clone*;
  - A current orchard layout map showing all living trees identified by *U.I.*, *clone* or family number.

Appendix 35B. Production Unit Annual Operations Report for Vegetative Production Systems of *Stream 2* Material

See Standards 32.8.4 and 34.6.

Annual operations reports are due June 30 in the year following the year in which the operations took place. Annual operations reports for vegetative propagation facilities must contain the following information.

Name of relevant *controlled parentage program* plan

Base population

- i) Population type (e.g., *wild* stands, provenance *trial*, clonal *trial*);
- ii) *Trial series* name(s), number(s), location (decimal format, e.g., Lat 56.123456 Long 118.123456).

***Production population* and unit**

- i) *Production unit* identifier (assigned by *Alberta*);
- ii) *Genotypes* selected from *base population*;
- iii) Gender of *production population clones*[1].

***Production site*(s) description**

- i) Name(s), location(s) (decimal format, e.g., Lat 56.123456 Long 118.123456);
- ii) Manager(s).

***Production unit* (each *production site*)**

- i) Type (e.g., field, lab based production or greenhouse pots);
- ii) Physical capacity (e.g., square meters of *stoolbed*, number of beds, number of mother pots per *clone*);
- iii) Design capacity (number of *clone*s, number of *ramets* of each *clone*[2] or number of cultures of each *clone*).

Cultural activities (each *production site*)

- i) Silviculture management (e.g., mowing, cultivation, irrigation, fertilization, CO_2 enhancement, herbicide applications, root pruning).

Insect and disease incidence (each *production site*)

- i) Monitoring methods;
- ii) Control methods.

Other activities (each *production site*)

- i) Activities that may not occur annually but may have an impact on the production/composition of the *production unit* (e.g., roguing, *stoolbed* replacement, culture replacement, potting up additional mother plants of a specific *clone* [for aspen production]).

***Propagule* production (across all *production sites*)**

- i) Timing of harvest (e.g., s*toolbed* or potted mother plant);
- ii) Number of cuttings/*propagules*/root sections collected by *clone*/bed, culture, pot;
- iii) Total number of *clone*s in *deployment population* and total number of cuttings/plantlets;
- iv) Storage location and method;
- v) *Effective population size (Ne)* (see Appendix 36); and
- vi) *Genetic worth* (see Appendix 31).

Subsequent year's planning

- i) Report on items that may affect *registration* of *deployment population* or approval.

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[1] See standards18.4.3.3.4 and 18.4.3.5.3.

[2] If number of *ramet*s is being determined from root cuttings (e.g., aspen), the actual number produced will not be known until after the nursery production stage. The lot or d*eployment population* cannot be registered until after propagation is completed in the nursery and the contribution from each *clone* is known. For *stoolbeds*, for example, the d*eployment population* can be registered after the design capacity of the *production unit* has been determined, prior to nursery propagation.

Appendix 36. Calculation of Effective Population Size (Ne) for Deployment Populations of *Stream 2* Material

See Standards 33.4 and 34.3.

INTRODUCTION

Calculation methods presented here for *effective population size (Ne)* of seed or vegetative lots produced by unrelated, non-inbred *genotypes* are based on the work of Robertson (1961) and developed in Kang and Namkoong (1988); formulae developed elsewhere may give very different results.

Calculation methods for *Ne* of seed or vegetative lots produced by orchards or *stoolbeds* containing inbred or related *genotypes*, such as half-sib seedling orchards, involve coancestry values, and are based on the work of Lindgren and Mullin (1998), who generalized earlier work.

FORMULAE

Effective population size of a seed or vegetative lot can be calculated as

Ne = $0.5/(\Sigma\Sigma\, p_i\, p_j\, c_{ij}) \quad (i, j = 1, 2, \ldots, n)$ equation 1

or, in matrix notation

Ne = $0.5/\mathbf{p'Cp}$ equation 2

where

Ne = *effective population size*

$\mathbf{p_i}$ = the proportional genetic contribution of *clone* or *genotype* i

$\mathbf{p_j}$ = the proportional genetic contribution of *genotype* j

$\mathbf{c_{ij}}$ = coancestry between *genotypes* i and j

n = number of *genotypes*

p = the n x 1 vector of gametic proportions for *genotypes* i = 1, 2, . . . , n

C = the n x n coancestry matrix for *genotypes* i = 1, 2, . . . , n

The proportional genetic contribution, p_i, of *genotype* i is calculated as follows:

$\mathbf{p_i}$ = $f_i/\Sigma f_i$ for proportions based only on samples of female “flower” or cone counts

$\mathbf{p_i}$ = $(f_i/\Sigma f_i + m_i/\Sigma m_i)/2$ for proportions based on samples of both female and male “flower” counts

$\mathbf{p_i}$ = $n_i/\Sigma n_i$ for proportions based on total counts of cuttings per *clone*

where

$\mathbf{f_i}$ = the number of female “flowers” occurring on *genotype* i (alternatively, cone counts can be used)

$\mathbf{m_i}$ = the number of male “flowers” occurring on *genotype* i

$\mathbf{n_i}$ = the number of cuttings taken from *genotype* i

Where *genotypes* are unrelated and not inbred, formula (1) simplifies to

Ne = $1/\Sigma p_i^2$ equation 3

COANCESTRIES

Coancestry values for some common relationships between non-inbred individuals are shown in Table A36.1.

Table A36.1. Common co-ancestry values.

Relationship between *genotypes*	**Coancestry**
Identical (tree with itself or with *ramet* of the same *clone*)	0.500
Full-sib (two individuals with same mother and father)	0.250
Parent-offspring (individual with mother or with father)	0.250
Half-sib (two individuals with same mother or father but not both; e.g., members of open-pollinated family)	0.125
Unrelated individuals	0.000

CATEGORIES AND CALCULATIONS

Four classes of *deployment population* are addressed, with a worked example for each.

A. Vegetatively produced *deployment populations* from:

1. *production populations* producing vegetative lots of unrelated *clone*s;
2. *production populations* producing vegetative lots of related *clone*s (*amplified families;* full-sib or half-sib).

B. Sexually produced *deployment populations* from:

3. orchards of unrelated and non-inbred *genotypes* (e.g., most first generation clonal orchards, including potted orchards);
4. orchards of related, non-inbred *genotypes* (e.g., open-pollinated seedling *seed orchards* and advanced generation clonal orchards with related *clone*s).

No example is given of a *deployment population* produced from inbred *genotypes*, since no such populations are expected in Alberta in the near future. However, calculations would use equations (1) or (2) with no additional modification.

All calculations for categories 1 and 3 can be done easily in Excel, using equation (3). Calculations for most lots in categories 2 and 4 can be done by means of matrix manipulation using equation (2), in Excel; the coancestry matrix need only be constructed once for each *production unit* or *production population*, and the frequency vector **p** reconstructed for each annual *deployment population.*

An ACCESS program developed for calculation of *Ne* for orchards including related *genotypes* using equation (1) was developed by Weyerhaeuser Company, in collaboration with the British Columbia (BC) Ministry of Forests; this program is available from *Alberta.*

Excel-based *Ne* calculation methods have been developed for orchards including:

1. Half-sib seedling families;
2. Unrelated *clone*s and half-sib seedling families, where no *clone* is related to any seedling family;
3. Related clones; some *clone*s related as half-sibs (e.g., orchard established on the basis of forward selections from half-sib progeny *test*s);
4. Unrelated *clone*s and seedling families; one or more *clone*s are related to seedling families (e.g., orchard containing both clonally-propagated *ramet*s and seedling offspring of that *genotype*);
5. Related *clone*s, where some *clone*s are related as half-sibs and some *clone*s are related as parent-offspring (e.g., *rolling front orchard* including some original parents [backward selections] and clonally-propagated forward selections from half-sib progeny *test*s).

Annotated examples of *Ne* calculations for these five orchard types are detailed in the Excel workbook: Ne_calculation_procedures.xlsx, available from *Alberta.* These methods were developed by Isabella Point Forestry Ltd., with the support of the Huallen Seed Orchard Company (HASOC).

WORKED EXAMPLES

A. VEGETATIVE MATERIAL (*Stream 2*)

Note: *Effective population size* (*Ne)* calculations for vegetatively reproduced material are based on actual total numbers in a vegetative lot, not on a sample, as for *seed orchards*.

A.1 Vegetative lots of unrelated *clone*s

EXAMPLE 1: A vegetative lot containing 2360 individuals of 10 unrelated *clone*s
Note: see introduction for formula definitions.

Clone	**Number of cuttings or plants**	p_i	p_i^2
1	300	0.127	0.01616
2	10	0.004	0.00002
3	150	0.064	0.00404
4	240	0.102	0.01034
5	460	0.195	0.03799
6	300	0.127	0.01616
7	190	0.081	0.00648
8	200	0.085	0.00718
9	240	0.102	0.01034
10	270	0.114	0.01309
Total	**2360**		**0.12180**

Using equation (3)

$$Ne = 1/\Sigma p_i^2$$

$$= 1/0.1218 = 8.21$$

A.2. Vegetative lots of related *clone*s (*amplified families;* full-sib or half-sib)

This example is worked manually to show the application of equation (1), as well as in matrix notation using equation (2). Calculations for actual vegetative lots would normally be done using matrices in Excel or SAS, or by using the ACCESS program available from *Alberta*.

EXAMPLE 2: A vegetative lot containing five *clone*s, with two *clone*s belonging to one full-sib family, and three belonging to a second half-sib family, unrelated to the first family.

Coancestry table (showing c_{ij} for each pair of *clone*s i and j)

		Family 1		**Family 2**		
		***Clone* 1**	**2**	**3**	**4**	**5**
Family 1	***Clone* 1**	0.5	0.25	0	0	0
	2	0.25	0.5	0	0	0
Family 2	**3**	0	0	0.5	0.125	0.125
	4	0	0	0.125	0.5	0.125
	5	0	0	0.125	0.125	0.5

Clonal frequencies

Family	***Clone***	**Number of cuttings or plants**	**p_i**
1	1	910	0.13
1	2	1960	0.28
2	3	2870	0.41
2	4	1050	0.15
2	5	210	0.03
Total		**7000**	

Construct a weighted table where $x_{ij} = p_i \, p_j \, c_{ij}$

		Family 1		**Family 2**		
		***Clone* 1**	**2**	**3**	**4**	**5**
Family 1	***Clone* 1**	0.00845	0.0091	0	0	0
	2	0.0091	0.0392	0	0	0
Family 2	**3**	0	0	0.08405	0.007688	0.001538
	4	0	0	0.007688	0.01125	0.000562
	5	0	0	0.001538	0.000562	0.00045

summing over terms:

$$\Sigma\Sigma p_i \, p_j \, c_{ij} = 0.181175$$

and using equation (1)

$$Ne = 0.5/(\Sigma\Sigma p_i \, p_j \, c_{ij}) = 2.76$$

EXAMPLE 2 reworked using matrices

$$\mathbf{p} = \begin{bmatrix} 0.13 \\ 0.28 \\ 0.41 \\ 0.15 \\ 0.03 \end{bmatrix} \qquad \mathbf{C} = \begin{bmatrix} 0.5 & 0.25 & 0 & 0 & 0 \\ 0.25 & 0.5 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0.125 & 0.125 \\ 0 & 0 & 0.125 & 0.5 & 0.125 \\ 0 & 0 & 0.125 & 0.125 & 0.5 \end{bmatrix}$$

$$\mathbf{p'Cp} = 0.181175$$

and using equation (2)

$$Ne = 0.5/\mathbf{p'Cp} = 2.76\text{, as above.}$$

B. SEED ORCHARD DEPLOYMENT POPULATIONS OF *STREAM 2* MATERIAL

SAMPLING REQUIREMENTS

Sampling requirements for orchard *Ne* calculations are detailed in Appendix 37.

COMBINED SEEDLOTS

When seedlots from a single orchard, produced over two or more years, are held in storage pending testing and *registration* until sufficient amounts have been accumulated, the *Ne* of the combined seedlot may, if desired, be calculated as the weighted average *Ne* of the component seedlots. It has been demonstrated that *Ne* calculated in this manner will never exceed *Ne* calculated on the basis of individual genotypic contributions summed over component seedlots.

B.1. Seedlots from orchards of unrelated and non-inbred *genotype*s (e.g., most first generation clonal orchards)

The value of $\mathbf{p_i}$ may be calculated using only the female component, i.e., estimates of flower or cone numbers, or using both male and female components, with estimates of pollen cone numbers in addition to estimates of seed cone numbers. In this example we demonstrate both methods.

EXAMPLE 3: A clonal orchard with a total of 50 *ramet*s of 10 *clone*s

Count of female and male "flowers" for each *ramet*

Clone	*Ramet*	Females	Males	*Clone*	*Ramet*	Females	Males
x123	1	50	500	x699	1	475	3200
x123	2	50	600	x699	2	575	6000
x123	3	0	100	x699	3	275	1300
x123	4	75	660	x699	4	375	2900
x123	5	85	1000	x699	5	0	50
x123	6	80	450	x732	1	0	170
x123	7	0	120	x732	2	0	50
x123	8	230	1860	x732	3	0	60
x354	1	0	20	x732	4	60	590
x354	2	0	0	x732	5	0	0
x354	3	25	300	x732	6	80	680
x354	4	0	50	x744	1	50	370
x354	5	0	0	x744	2	0	210
x465	1	50	430	x744	3	35	250
x465	2	350	1980	x744	4	175	1500
x466	1	225	2100	x798	1	225	1900
x466	2	125	1490	x798	2	30	290
x466	3	425	3580	x798	3	450	5400
x466	4	0	0	x798	4	0	60
x466	5	900	7500	x798	5	75	650
x466	6	100	900	x900	1	80	870
x466	7	1450	9800	x900	2	0	50
x466	8	85	400	x900	3	0	110
x487	1	0	50				
x487	2	20	200				
x487	3	125	980				
x487	4	75	640				

Summarize by *clone* and calculate proportions:

i) for proportions based only on female counts: $p_i = f_i/\Sigma f_i$
ii) for proportions based on both female and male counts: $p_i = (f_i/\Sigma f_i + m_i/\Sigma m_i)/2$

Clone	***Ramets***	**Females (f_i)**	**Males (m_i)**	**p_i (f only)**	**p_i^2 (f only)**	**p_i (m only)**	**p_i (m & f)**	**p_i^2 (m & f)**
x123	8	570	5290	0.076	0.006	0.085	0.080	0.006
x354	5	25	370	0.003	0.000	0.006	0.005	0.000
x465	2	400	2410	0.053	0.003	0.039	0.046	0.002
x466	8	3310	25770	0.442	0.196	0.413	0.428	0.183
x487	4	220	1870	0.029	0.001	0.030	0.030	0.001
x699	5	1700	13450	0.227	0.052	0.216	0.221	0.049
x732	6	140	1550	0.019	0.000	0.025	0.022	0.000
x744	4	260	2330	0.035	0.001	0.037	0.036	0.001
x798	5	780	8300	0.104	0.011	0.133	0.119	0.014
x900	3	80	1030	0.011	0.000	0.017	0.014	0.000
Total	50	7485	62370	1.00	0.270	1.00	1.00	0.256
$Ne = 1/\Sigma(p_i^2)$					**3.70400**			**3.906**

In this example, *Ne* based only on female counts = 3.7, while including male counts increases the estimate of *Ne* to 3.91. Including male counts will increase the accuracy of *Ne* estimates, but may result in either increased or decreased *Ne* estimates. Note that *Ne* is considerably less than the number of *clone*s (10). This is due to imbalance in both numbers of *ramets*/*clone* and in reproductive activity.

B.2. Seedlots from orchards of related, non-inbred *genotypes* (e.g., open-pollinated seedling *seed orchard*s and advanced generation clonal orchards with related *clone*s)

EXAMPLE 4: a half-sib seedling orchard containing two families with three and two individuals respectively

$$\mathbf{p} = \begin{bmatrix} 0.24 \\ 0.32 \\ 0.09 \\ 0.20 \\ 0.15 \end{bmatrix} \qquad \mathbf{C} = \begin{bmatrix} 0.5 & 0.125 & 0.125 & 0 & 0 \\ 0.125 & 0.5 & 0.125 & 0 & 0 \\ 0.125 & 0.125 & 0.5 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & 0.125 \\ 0 & 0 & 0 & 0.125 & 0.5 \end{bmatrix}$$

$\mathbf{p'Cp} = 0.1546$

and using equation (2)

$Ne = 0.5/\mathbf{p'Cp} = 3.23.$

References

Kang, H. and G. Namkoong. 1988. Inbreeding effective population size under some artificial selection schemes. 1. Linear distribution of breeding values. Theor. Appl. Genet. 75:333-339.

Lindgren, D. and T. Mullin. 1998. Relatedness and status number in seed orchard crops. Can. J. For. Res. 28: 276-283.

Robertson, A. 1961. Inbreeding in artificial selection programmes. Genet. Res. 2:189-194.

Appendix 37. Sampling Levels for Calculation of Effective Population Size (Ne) Values in Orchard Seedlots of *Stream 2* Material

See Standards 33.4 and 33.4.1.

INTRODUCTION

Effective population size (Ne) (see Appendix 36 for calculation methods) is used as a surrogate for *genetic diversity* levels in seed and vegetative lots, and also reflects the degree of imbalance among *genotypes* contributing to a given lot. While genotypic representation in vegetative lots can be readily determined directly, in seedlots this is impossible, and an approximation must be made.

The orchard manager should be aware that *Ne* estimates will vary with the intensity of sampling. These estimates may be considerably lower than, or in some cases higher than, the actual *Ne*. Estimates based on assessment of only female flowers or cones will be less accurate than those including information from male flowers and reproductive phenology. Since the purpose of *Ne* estimation is to ensure that a threshold has been met, rather than to determine the actual value of *Ne*, the required intensity of sampling is higher where smaller numbers of *genotypes* contribute.

Simulations with actual orchard data showed that an orchard sample of 10% (as in Permanent Sample Trees [PSTs]) can yield a *Ne* estimate as low as one-fifth of the *Ne* calculated on a 100% orchard survey. On average, the ratio of the *Ne* estimate obtained with 10% sampling to the *Ne* estimate at 100% sampling [*Ne* (10%)/*Ne* (100%)] is expected to be approximately 0.5, depending on the distribution of genotypic frequencies. At a 50% sampling intensity, the average *Ne* (50%)/*Ne* (100%) ratio increased to approximately 0.9, but may, by chance, be below 0.7. Thus minimum requirements outlined below may not be adequate to demonstrate that *Ne* thresholds have been exceeded.

Estimates of female contributions may be based on flower, immature cone (pines) or mature cone counts.
Note that for pine species, if flower data is used for *Ne* estimation, it must be from the previous year, since cones mature over two years. Where *Ne* values are calculated based on cones collected by *clone* or family, males will also need to be assessed under some circumstances (see Tables A37.1-A37.5).

In orchards where the number of *genotype*s contributing to the crop is potentially low, PST assessments should be analyzed promptly to help guide sampling levels.

SAMPLING REQUIREMENTS

Sampling method and intensity (description of the data set upon which the calculation is based) must be included in the Annual Operations Report (see Appendix 35).

At the orchard manager's discretion, *Ne* may be estimated from PSTs alone (see Appendix 33 for PST requirements). PST-based estimates must be calculated in two ways: using female data alone, and using combined male and female data; the lower of these two estimates must be used. If PST based *Ne* estimates are not used, the following minimum sampling requirements apply.

CLONAL SEED ORCHARDS

Table A37.1 below outlines minimum sampling requirements for clonal *seed orchards.*

Table A37.1. Sampling requirements for Ne calculations in clonal seed orchards.

***Clone*s contributing**	**Minimum sampling requirement**	**Genders assessed**
100+	PSTs only	female
75+	15% including PSTs	male & female
	Alternative: 100%	female
50-74	25% including PSTs	male & female
	Alternative: 100%	female
25-49	50% including PSTs	male & female
< 25	100% - (all trees)	male & female

SEEDLING SEED ORCHARDS

A seedlot from a seedling *seed orchard* containing n families and an average of **t** trees per family (**t**>1) can be expected to have a higher *Ne* value than a seedlot from a clonal *seed orchard* with **n** *clone*s and an average of **t** *ramets* per *clone*. This is because there is considerable *genetic diversity* within families, but none within *clone*s. The ratio of the *Ne* from a seedling *seed orchard* with **n** families to that of a clonal orchard with **n** *clone*s is independent of **n**, and increases with increasing **t** (see example in Table A37.2 below; for simplicity, in this example it is assumed that all *clone*s or families have equal numbers of *ramets* or seedlings, and that all trees are equally productive).

Table A37.2. Ne comparison: open-pollinated seedling seed orchard with 40 families vs. clonal seed orchard with 40 clones.

	Number of seedlings per family or *ramets* per *clone* (t)										
	1	2	3	4	5	6	7	8	9	10	very large
Ne of open population seedling orchard	40	64	80	91.6	100	106.8	112	116.4	120	123.2	~160
Ne of clonal Orchard	40	40	40	40	40	40	40	40	40	40	40
Ratio of Ne (seedling orchard) to Ne (clonal orchard)	1.00	1.60	2.00	2.29	2.50	2.67	2.80	2.91	3.00	3.08	~4.00

Thus the numbers of trees to be sampled in a seedling *seed orchard* can be lower than in a clonal orchard, for a given number of families or *clone*s.

If the mean family size in the orchard is less than five trees, sampling requirements are as for clonal orchards (see Table A37.3). If the mean family size exceeds five, sampling requirements are given in Table A37.4.

Sampling requirements for mixed clonal and seedling *seed orchard*s are given in Table A37.5.

Table A37.3. Sampling requirements for Ne calculations in open-pollinated seedling seed orchards with an average of fewer than five trees per family.

Families contributing	Minimum sampling requirement	Genders assessed
100+	PSTs only	female
75+	15% including PSTs	male & female
	Alternative: 100%	female
50-74	25% including PSTs	male & female
	Alternative: 100%	female
25-49	50% including PSTs	male & female
< 25	100% - (all trees)	male & female

Table A37.4. Sampling requirements for Ne calculations in open-pollinated seedling seed orchards with an average of at least five trees per family.

Families contributing	Minimum sampling requirement	Genders assessed
50+	PSTs only	female
37-49	15% including PSTs	male & female
	Alternative: 100%	female
25-36	25% including PSTs	male & female
	Alternative: 100%	female
12-24	50% including PSTs	male & female
< 12	100% - (all trees)	male & female

Mixed clonal and seedling *seed orchard*s

Table A37.5 outlines minimum sampling requirements for mixed clonal and seedling *seed orchards.*

Table A37.5. Sampling requirements for Ne calculations in mixed clonal and seedling seed orchards.

***Genotypes* (*clone*s or families) contributing**	Minimum sampling requirement	Genders assessed
100+	PSTs only	female
75+	15% including PSTs	male & female
	Alternative: 100%	female
50-74	25% including PSTs	male & female
	Alternative: 100%	female
25-49	50% including PSTs	male & female
< 25	100% - (all trees)	male & female

Appendix 38. Species Codes

Species codes are used to construct *unique identifiers* (U.I.s), which are used to identify *genotype*s in *production population*s and *Stream 1 seed orchards* (see Appendix 25).
For species not listed in Appendix 38 contact *Alberta*.

Table A38.1. contains a listing of native tree species and naturally occurring hybrids.
Table A38.2. contains a listing of shrub species found in Alberta.
Table A38.3. contains a listing of non-native trees (pure species and hybrids).
Table A38.4. lists clonal and reproductive characteristics of selected boreal shrubs.

Table A38.1. Native tree species (pure species and known natural hybrids).

Family	Genus	Species	Common name	2-letter[1]	7-letter
Aceraceae (Sapindaceae)	Acer	negundo	Manitoba maple		Acerneg
Betulaceae	Betula	neoalaskana	Alaska/resin birch		Betuneo
Betulaceae	Betula	occidentalis	water/black birch		Betuocc
Betulaceae	Betula	papyrifera	paper (white) birch	Bw	Betupap
Betulaceae	Betula	papyrifera x occidentalis	paper x water birch hybrid		Betupxo
Betulaceae	Betula	papyrifera x neoalaskana	paper x Alaska birch hybrid		Betupxn
Cupressaceae	Juniperus	scopulorum	Rocky Mountain juniper		Junisco
Cupressaceae	Thuja	plicata	western red cedar		Thujpli
Pinaceae	Abies	balsamea	balsam fir	Fb	Abiebal
Pinaceae	Abies	lasiocarpa	alpine fir	Fa	Abielas
Pinaceae	Larix	laricina	tamarack	Lt	Larilar
Pinaceae	Larix	lyallii	alpine larch	La	Larilya
Pinaceae	Larix	occidentalis	western larch	Lw	Lariocc
Pinaceae	Picea	engelmannii	Engelmann spruce	Se	Piceeng
Pinaceae	Picea	glauca	white spruce	Sw	Picegla
Pinaceae	Picea	engelmannii x glauca	Engelmann x white spruce hybrid		Piceexg
Pinaceae	Picea	mariana	black spruce	Sb	Picemar
Pinaceae	Pinus	albicaulis	whitebark pine	Pa	Pinualb
Pinaceae	Pinus	banksiana	jack pine	Pj	Pinuban
Pinaceae	Pinus	banksiana x contorta	jack x lodgepole pine hybrid		Pinubxc
Pinaceae	Pinus	contorta	lodgepole pine	Pl	Pinucon
Pinaceae	Pinus	flexilis	limber pine	Pf	Pinufle
Pinaceae	Pinus	monticola	western white pine		Pinumon
Pinaceae	Pseudotsuga	menziesii	Douglas-fir	Fd	Pseumen
Pinaceae	Tsuga	heterophylla	western hemlock		Tsughet
Salicaceae	Populus	angustifolia	narrow-leaf cottonwood		Popuang
Salicaceae	Populus	balsamifera	balsam poplar	Pb	Popubal
Salicaceae	Populus	balsamifera x trichocarpa	balsam x black poplar hybrid		Popubxt
Salicaceae	Populus	deltoides	cottonwood western/plains	De	Popudel
Salicaceae	Populus	deltoides x balsamifera	western/plains x balsam cottonwood hybrid		Popudxb
Salicaceae	Populus	deltoides x balsamifera x angustifolia	western/plains x balsam x narrow-leaf cottonwood hybrid		Popudba
Salicaceae	Populus	tremuloides	trembling aspen	Aw	Poputre
Salicaceae	Populus	trichocarpa	black poplar	Tr	Poputri
Salicaceae	Salix	amygdaloides	peachleaf willow		Saliamy
Salicaceae	Salix	scouleriana	Scouler's willow		Salisco
Taxaceae	Taxus	brevifolia	western yew		Taxubre

[1] Two-letter abbreviations are historical; seven-letter abbreviations are mandatory for *reclamation*.

Table A38.2. Shrub species.

The use of naturally occurring shrub hybrids must also follow FGRMS 2016.

Family	Genus	Species	Common name	2-letter	7-letter
Aceraceae	Acer	glabrum	mountain maple		Acergla
Anacardiaceae	Rhus	aromatica	fragrant sumac		Rhusaro
Anacardiaceae	Rhus	trilobata	See Rhus aromatica		
Apocynaceae	Apocynum	androsaemifolium	spreading dogbane		Apocand
Apocynaceae	Apocynum	cannabinum	Indian hemp		Apoccan
Araliaceae	Oplopanax	horridus	devil's club		Oplohor
Asteraceae (Compositae)	Artemisia	cana	silver sagebrush		Artecan
Asteraceae (Compositae)	Artemisia	tridentata	big sagebrush		Artetri
Berberidaceae	Berberis	repens	creeping mahonia (barberry)		Berbrep
Betulaceae	Alnus	crispa	See Alnus viridis		
Betulaceae	Alnus	incana	river alder		Alnuinc
Betulaceae	Alnus	tenuifolia	See Alnus incana		
Betulaceae	Alnus	viridis	green alder		Alnuvir
Betulaceae	Betula	nana (includes glandulosa)	bog birch		Betunan
Betulaceae	Betula	pumila	dwarf bog birch		Betupum
Betulaceae	Corylus	cornuta	beaked hazelnut		Corycor
Caprifoliaceae	Linnaea	borealis	twin-flower		Linnbor
Caprifoliaceae	Lonicera	caerulea	blue-fly honeysuckle		Lonicae
Caprifoliaceae	Lonicera	dioica	twining honeysuckle		Lonidio
Caprifoliaceae	Lonicera	involucrata	bracted honeysuckle		Loniinv
Caprifoliaceae	Lonicera	utahensis	red twinberry		Loniuta
Caprifoliaceae	Sambucus	racemosa	red elderberry		Samrac
Caprifoliaceae	Symphoricarpos	albus	common snowberry		Sympalb
Caprifoliaceae	Symphoricarpos	occidentalis	buckbrush		Sympocc
Caprifoliaceae	Viburnum	edule	low-bush cranberry		Vibuedu
Caprifoliaceae	Viburnum	opulus	high-bush cranberry		Vibuopu
Celastraceous	Paxistima (Pachistima)	myrsinites	mountain lover/boxleaf		Paximyr
Chenopodiaceae	Sarcobatus	vermiculatus	greasewood		Sarcver
Cistaceae	Hudsonia	tomentosa	sand heather		Hudstom
Cornaceae	Cornus	sericea	red-osier dogwood		Cornser
Cornaceae	Cornus	stolonifera	See Cornus sericea		
Cupressaceae	Juniperus	communis	ground juniper		Junicom
Cupressaceae	Juniperus	horizontalis	creeping juniper		Junihor
Elaeagnaceae	Elaeagnus	commutata	wolf willow		Elaecom
Elaeagnaceae	Shepherdia	argentea	silver buffaloberry		Sheparg
Elaeagnaceae	Shepherdia	canadensis	Canada buffaloberry		Shepcan
Empetraceae (Ericaceae)	Empetrum	nigrum	crowberry		Empenig
Ericaceae	Andromeda	polifolia	bog rosemary		Andrpol
Ericaceae	Arctostaphylos	rubra	See Arctous rubra		
Ericaceae	Arctostaphylos	uva-ursi	bearberry/ kinnikinnick		Arctuva
Ericaceae	Arctous	rubra	alpine bearberry		Arctrub
Ericaceae	Cassiope	mertensiana	western moss heather		Cassmer
Ericaceae	Cassiope	tetragona	white arctic mountain heather		Casstet

Family	Genus	Species	Common name	2-letter	7-letter
Ericaceae	Chamaedaphne	calyculata	leatherleaf		Chamcal
Ericaceae	Gaultheria	hispidula	creeping snowberry		Gaulhis
Ericaceae	Gaultheria	humifusa	alpine spicy wintergreen		Gaulhum
Ericaceae	Kalmia	microphylla	alpine laurel		Kalmmic
Ericaceae	Kalmia	polifolia	bog laurel		Kalmpol
Ericaceae	Kalmia	procumbens	alpine azalea		Kalmpro
Ericaceae	Ledum	glandulosum	See Rhododendron columbianum		
Ericaceae	Ledum	groenlandicum	See Rhododendron groenlandicum		
Ericaceae	Ledum	palustre	See Rhododendron tomentosum		
Ericaceae	Loiseleuria	procumbens	See Kalmia procumbens		
Ericaceae	Menziesia	ferruginea	mock azalea		Menzfer
Ericaceae	Oxycoccus	microcarpus	See Vaccinium oxycoccos		
Ericaceae	Oxycoccus	quadripetalus	See Vaccinium oxycoccos		
Ericaceae	Phyllodoce	empetriformis	red mountain heath		Phylemp
Ericaceae	Phyllodoce	glanduliflora	yellow mountain heath		Phylgla
Ericaceae	Rhododendron	albiflorum	white rhododendron		Rhodalb
Ericaceae	Rhododendron	columbianum	glandular Labrador tea		Rhodcol
Ericaceae	Rhododendron	groenlandicum	common Labrador tea		Rhodgro/ Ledugro
Ericaceae	Rhododendron	lapponicum	Lapland rose-bay		Rhodlap
Ericaceae	Rhododendron	tomentosum	marsh Labrador tea		Rhodtom
Ericaceae	Vaccinium	cespitosum	dwarf bilberry		Vaccces
Ericaceae	Vaccinium	membranaceum	tall bilberry		Vaccmem
Ericaceae	Vaccinium	myrtilloides	dwarf blueberry		Vaccmyr
Ericaceae	Vaccinium	myrtillus	low bilberry		Vaccmyt
Ericaceae	Vaccinium	ovalifolium	Alaskan blueberry		Vaccova
Ericaceae	Vaccinium	oxycoccos	small bog cranberry		Vaccoxy
Ericaceae	Vaccinium	scoparium	grouseberry		Vaccsco
Ericaceae	Vaccinium	uliginosum	bog bilberry		Vacculi
Ericaceae	Vaccinium	vitis-idaea	bog cranberry/ lingonberry		Vaccvit
Grossulariaceae	Ribes	americanum	wild black currant		Ribeame
Grossulariaceae	Ribes	aureum	golden currant		Ribeaur
Grossulariaceae	Ribes	glandulosum	skunk currant		Ribegla
Grossulariaceae	Ribes	hirtellum	hairy-stem gooseberry		Ribehir
Grossulariaceae	Ribes	hudsonianum	wild black currant		Ribehud
Grossulariaceae	Ribes	inerme	white stemmed gooseberry		Ribeine
Grossulariaceae	Ribes	lacustre	bristly black currant		Ribelac
Grossulariaceae	Ribes	laxiflorum	trailing black currant		Ribelax
Grossulariaceae	Ribes	oxyacanthoides	prickly currant		Ribeoxy
Grossulariaceae	Ribes	triste	wild red currant		Ribetri
Grossulariaceae	Ribes	viscosissimum	sticky currant		Ribevis
Hydrangeaceae	Philadelphus	lewisii	mock orange		Phillew
Myricaceae	Myrica	gale	sweet gale		Myrigal
Ranunculaceae	Clematis	ligusticifolia	white/western clematis		Clemlig

Family	**Genus**	**Species**	**Common name**	**2-letter**	**7-letter**
Rhamnaceae	Ceanothus	velutinus	snowbush		Ceanvel
Rhamnaceae	Rhamnus	alnifolia	alderleaf buckthorn		Rhamaln
Rosaceae	Amelanchier	alnifolia	Saskatoon		Amelaln
Rosaceae	Amelanchier	ovalis	round leaved hawthorn		Amelova
Rosaceae	Dasiphora	floribunda	See Dasiphora fruticosa		
Rosaceae	Dasiphora	fruticosa	shrubby cinquefoil		Dasifru/ Dasiflo
Rosaceae	Crataegus	douglasii	black/river hawthorn		Cratdou
Rosaceae	Crataegus	rotundifolia	See Amelanchier ovalis		
Rosaceae	Potentilla	fruticosa	See Dasiphora fruticosa		
Rosaceae	Prunus	pensylvanica	pin cherry		Prunpen
Rosaceae	Prunus	virginiana	chokecherry		Prunvir
Rosaceae	Rosa	acicularis	prickly rose		Rosaaci
Rosaceae	Rosa	arkansana	prairie rose		Rosaark
Rosaceae	Rosa	woodsii	Woods' rose		Rosawoo
Rosaceae	Rubus	idaeus	wild red raspberry		Rubuida
Rosaceae	Rubus	parviflorus	thimbleberry		Rubupar
Rosaceae	Sorbus	scopulina	Greene's mountain ash		Sorbsco
Rosaceae	Sorbus	sitchensis	western mountain ash		Sorbsit
Rosaceae	Spiraea	alba	narrow-leaved meadowsweet		Spiralb
Rosaceae	Spiraea	betulifolia	white meadowsweet		Spirbet
Rosaceae	Spiraea	densiflora	See Spiraea splendens		
Rosaceae	Spiraea	splendens	rose meadowsweet		Spirspl
Salicaceae	Salix	alaxensis	feltleaf willow		Saliala
Salicaceae	Salix	arbusculoides	little tree willow		Saliarb
Salicaceae	Salix	arctica	arctic willow		Saliarc
Salicaceae	Salix	athabascensis	Athabasca willow		Saliath
Salicaceae	Salix	barclayi	Barclay's willow		Salibar
Salicaceae	Salix	barrattiana	Barratt's willow		Salibat
Salicaceae	Salix	bebbiana	Bebb's willow/ beaked willow		Salibeb
Salicaceae	Salix	boothii	Booth's willow		Saliboo
Salicaceae	Salix	brachycarpa	sand dune willow		Salibra
Salicaceae	Salix	candida	sage leaf willow		Salican
Salicaceae	Salix	commutata	undergreen willow		Salicom
Salicaceae	Salix	discolor	pussywillow		Salidis
Salicaceae	Salix	drummondiana	Drummond's willow		Salidru
Salicaceae	Salix	exigua	coyote/sandbar willow		Saliexi
Salicaceae	Salix	farriae	Farr's willow		Salifar
Salicaceae	Salix	glauca	greyleaf willow		Saligla
Salicaceae	Salix	lanata	woolly willow		Salilan
Salicaceae	Salix	lucida	shining willow		Saliluc
Salicaceae	Salix	lutea	yellow willow		Salilut
Salicaceae	Salix	maccalliana	MacCalla's willow		Salimac
Salicaceae	Salix	melanopsis	dusky willow		Salimel
Salicaceae	Salix	myrtillifolia	blueberry willow		Salimyr
Salicaceae	Salix	pedicellaris	bog willow		Saliped

Family	Genus	Species	Common name	2-letter	7-letter
Salicaceae	Salix	petiolaris	meadow/slender willow		Salipet
Salicaceae	Salix	planifolia	diamondleaf willow		Salipla
Salicaceae	Salix	prolixa	MacKenzie's willow		Salipro
Salicaceae	Salix	pseudomonticola	false mountain willow		Salipse
Salicaceae	Salix	pyrifolia	balsam willow		Salipyr
Salicaceae	Salix	reticulata	netleaf willow		Saliret
Salicaceae	Salix	serissima	autumn willow		Saliser
Salicaceae	Salix	sitchensis	Sitka willow		Salisit
Salicaceae	Salix	stolonifera	sproutingleaf willow		Salisto
Salicaceae	Salix	vestita	rock willow		Salives

Table A38.3. Non-native trees (pure species and hybrids).

Species are listed in this table for historical identification. Use of these and other non-native species and hybrids is limited to *Alberta*-approved research programs.

Family	Genus	Species	Common name	2-letter[1]	7-letter
Salicaceae	Populus	alba	white poplar	Ab	Popualb
Salicaceae	Populus	davidiana	Chinese/Korean aspen	Da	Popudav
Salicaceae	Populus	grandidentata	bigtooth aspen	Gr	Popugra
Salicaceae	Populus	laurifolia	laurel-leaf poplar		Populau
Salicaceae	Populus	maximowiczii	Japan poplar	Ma	Popumax
Salicaceae	Populus	nigra	black poplar	Ni	Popunig
Salicaceae	Populus	sargentii	Sargent's poplar	Sa	Popusar
Salicaceae	Populus	tremula	European aspen	Ta	Poputrm
Salicaceae	Populus	deltoides x balsamifera	northwest poplar		Popudxb

[1] Two-letter abbreviations are historical; seven-letter abbreviations are mandatory for *reclamation*.

Table A38.4. Selected boreal shrubs: some clonal and reproductive characteristics.

Family	Species	Common name	Previous name	Clonal and other reproductive info C=clonal, N=not clonal, U=unknown	
Araliaceae	Oplopanax horridus	devil's club		U	Diploid, pollination, dispersal and vegetative reproduction unknown
Betulaceae	Alnus incana	river alder	Alnus tenuifolia	N	Diploid, wind pollinated, wind dispersed, not clonal†
Betulaceae	Alnus viridis	green alder	Alnus crispa	N	Diploid, wind pollinated, wind dispersed, not clonal†
Betulaceae	Betula nana	bog birch	includes B. glandulosa	N	Clonal in north, diploid, wind pollinated, wind dispersed‡
Betulaceae	Betula pumila	dwarf (bog) birch		N	Clonal in north, diploid, wind pollinated, wind dispersed‡
Betulaceae	Corylus cornuta	beaked hazelnut		N	Diploid, wind pollinated, wind dispersed, not clonal‡
Caprifoliaceae	Lonicera caerulea	blue-fly honeysuckle		N	Tetraploid, bee pollinated, wildlife dispersed, not clonal‡
Caprifoliaceae	Lonicera dioica	twining honeysuckle		N	Diploid, bee pollinated, wildlife dispersed, not clonal‡
Caprifoliaceae	Lonicera involucrata	bracted honeysuckle		N	Diploid, bee pollinated, wildlife dispersed, not clonal‡
Caprifoliaceae	Symphoricarpos albus	common snowberry		C	Polyploid, clonal (rhizome)† likely wind pollinated and wildlife dispersed
Caprifoliaceae	Symphoricarpos occidentalis	buckbrush		C	Insect pollinated, wildlife dispersed, clonal (rhizome)†
Caprifoliaceae	Viburnum edule	low-bush cranberry		U	Diploid, insect poll, wildlife disperse, possibly clonal (rhizomes)†
Caprifoliaceae	Viburnum opulus	high-bush cranberry		U	Diploid, insect pollinated*, bird dispersed[µ], clonal (rhizomes)
Cistaceae	Hudsonia tomentosa	sand heather		N	Diploid, pollination and dispersal unknown, not clonal‡
Cornaceae	Cornus sericea	red-osier dogwood	Cornus stolonifera	U	Diploid, insect pollinated, dispersed by wildlife, clonal (stolons)†
Cupressaceae	Juniperus communis	ground juniper		N	Diploid, pollination unknown, wildlife dispersed, not clonal‡
Elaeagnaceae	Elaeagnus commutata	wolf willow		U	Diploid, insect pollinated, bird dispersed, clonal (rhizome/stolon)†
Elaeagnaceae	Shepherdia canadensis	Canada buffaloberry		U	Diploid; insect pollinated, wildlife dispersed, clonal by roots†
Ericaceae	Andromeda polifolia	bog rosemary		N	Diploid, self-incompatible, insect pollinated, wind dispersed‡
Ericaceae	Arctostaphylos uva-ursi	bearberry, kinnikinnick		C	Diploid and tetraploid, clonal, self pollinated (stolon)†
Ericaceae	Arctous rubra	alpine bearberry	Arctostaphylos rubra	C	Diploid, wildlife dispersed, clonal (rhizome/stolon)‡
Ericaceae	Chamaedaphne calyculata	leatherleaf		U	Diploid, insect pollinated, wind dispersed, clonal (rhizome)‡
Ericaceae	Gaultheria hispidula	creeping snowberry		U	Diploid, pollination and dispersal unknown, clonal (rhizome)‡
Ericaceae	Kalmia microphylla	alpine laurel		U	Diploid, pollination unknown, wind dispersed, clonal (rhizome)‡
Ericaceae	Kalmia polifolia	bog laurel		U	Diploid, pollination unknown, wind dispersed, clonal (rhizome)‡
Ericaceae	Rhododendron groenlandicum	common Labrador tea	Ledum groenlandicum	N	Diploid, insect pollinated, self-incompatible wind dispersed, not clonal‡
Ericaceae	Rhododendron lapponicum	Lapland Rose-bay		U	Diploid

Family	**Species**	**Common name**	**Previous name**	**Clonal and other reproductive info C=clonal, N=not clonal, U=unknown**	
Ericaceae	Rhododendron tomentosa	northern Labrador tea	Ledum palustre	N	Tetraploid, likely insect pollinated, wind dispersed, not clonal‡
Ericaceae	Vaccinium caespitosum	dwarf bilberry		U	Diploid, likely insect pollinated and wind dispersed, clonal (rhizome)
Ericaceae	Vaccinium myrtilloides	dwarf blueberry		U	Diploid, insect pollinated, wildlife dispersed, clonal (rhizomes)†
Ericaceae	Vaccinium oxycoccos	small bog cranberry	Oxycoccus microcarpus	C	Diploid, insect pollinated, wind dispersed, clonal (rhizome)‡
Ericaceae	Vaccinium uliginosum	bog bilberry		U	Tetraploid, bird dispersed, clonal (rhizome)‡, likely insect pollinated
Ericaceae	Vaccinium vitis-idaea	bog cranberry, lingonberry		U	Diploid, wildlife dispersed, clonal (rhizome)‡, insect pollinated[€]
Grossulariaceae	Ribes americanum	wild black currant		N	Diploid, insect pollinated*, wildlife dispersed, not clonal‡
Grossulariaceae	Ribes glandulosum	skunk currant		N	Diploid, insect pollinated, wildlife dispersed, not clonal (RIBES)
Grossulariaceae	Ribes hirtellum	hairy-stem gooseberry		N	Diploid, insect pollinated, wildlife dispersed, not clonal (RIBES)
Grossulariaceae	Ribes hudsonianum	wild black currant		N	Insect pollinated, wildlife dispersed, not clonal (RIBES)
Grossulariaceae	Ribes lacustre	bristly black currant		N	Diploid, insect pollinated, wildlife dispersed, not clonal (RIBES)
Grossulariaceae	Ribes oxyacanthoides	prickly currant		N	Diploid, insect pollinated, wildlife dispersed, not clonal (RIBES)
Grossulariaceae	Ribes triste	wild red currant		N	Diploid, insect pollinated, wildlife dispersed, not clonal)‡
Myricaceae	Myrica gale	sweet gale		U	Tetraploid, clonal (rhizome), likely wind pollinated and wildlife dispersed‡
Rhamnaceae	Rhamnus alnifolia	alderleaf buckthorn		N	Insect pollinated, wildlife dispersed, not clonal‡
Rosaceae	Amelanchier alnifolia	Saskatoon		C	Clonal (stolons), insect pollinated, dispersed by wildlife†
Rosaceae	Dasiphora fruticosa	shrubby cinquefoil	Potentilla fruticosa / Dasiphora floribunda	N	Tetraploid, wind dispersed, not clonal‡, insect pollinated°
Rosaceae	Prunus pensylvanica	pin cherry		U	Tetraploid, self-incompatible, insect poll, wildlife dispersed†
Rosaceae	Prunus virginiana	chokecherry		U	Tetraploid,self-incompatible, insect poll, wildlife dispersed†
Rosaceae	Rosa acicularis	prickly rose		C	Tetraploid, clonal (10-20m^2), wildlife dispersed‡, polyploid, insect pollinated*
Rosaceae	Rosa woodsii	Woods' rose		N	Diploid, insect pollinated, wildlife dispersed, not clonal‡
Rosaceae	Rubus idaeus	wild red raspberry		C	Polyploid, clonal (rhizome/sucker), insect poll, wildlife dispersed‡
Rosaceae	Sorbus scopulina	Greene's mountain ash		N	Insect pollinated, wildlife dispersed, not clonal[£]
Salicaceae	Salix species	willows		C	many clonal, wind pollinated, wind dispersed

†Chai, S.L., B. Eaton, J. Woosaree, D. Rweyongeza and E. Fraser. 2013. Seed Transfer of Woody Shrubs in Alberta – Are current seed zones applicable? Prepared by Alberta Innovates Technology Futures, Vegreville, AB and Alberta Environment and Sustainable Resource Development, Edmonton, AB. 41 pp.

‡Species profile on FEIS. http://www.fs.fed.us/database/feis/plants/shrub/

€ Rook, E.J.S. Boundary Waters Compendium http://www.rook.org/earl/bwca/index.html

*Plants for a Future database.

°Elkington, T.T. and S.R.J. Woodell. 1963. *Potentilla fruticosa* L. (*Dasiphora fruiticosa* (L.) Rydb.). Journal of Ecology 51: 769-781.

±McGregor, S.E. 1976. Insect pollination of cultivated crop plants. U.S. Department of Agriculture, Washington, DC. 411 pages.

£Francis, J.K. 2004. Wildlands Shrubs of the United States and its Territories: Thamnic Descriptions: Volume 1. General Technical Report IITF-GTR-26. San Juan, PR. Department of Agriculture, Forest Service, Rocky Mountain Research Station. 830 pp.

µ USDA NRCS Plant Materials Program. 2002. American Cranberry bush *Viburnum opulus* L. var. *americanum* Ait. United States Department of Agriculture, Natural Resources Conservation Service. Available online: http://plants.usda.gov/factsheet/pdf/fs_viopa2.pdf

Devil's Club:
Clonal – Trevor C. Lantz and Joseph A. Antos (2002). "Clonal expansion in the deciduous understory shrub, devil's club". *Can. J. Bot.* **80** (10): 1052–1062.
Photo of bees (Wikipedia) implying insect pollination and "bugGuide" http://bugguide.net/node/view/898275 has a photo of a black and white fly.
Dispersed by wildlife. http://www.uaf.edu/files/ces/publications-db/catalog/anr/HGA-00232G.pdf

Lapland Rose-bay
Pollinated by insects (bees): http://www.wildflower.org/plants/result.php?id_plant=RHLA2 & PFAF
Likely not clonal, occupying limited areas
Likely wind dispersed, dry capsule similar to Kalmia, Andromeda and Chamaedaphne

Appendix 39. Operational Clonal Deployment Report of *Stream 2* Material

Standards 18.4.3.4.5, 18.4.3.4.6, 18.4.3.5.5 and 18.4.3.5.6.

Note: The objective of this report is to describe *deployment* outcomes including all signs of clonal success and/or failure. This report can be completed in conjunction with the required *reforestation* stand survey at year 7 and will require a second site visit to be completed for the year 14 report.

Introduction

- i) Proponent(s);
- ii) *CPP* plan;
- iii) Indicate report year (7 or 14);
- iv) Year of initial planting;
- v) Species & vegetative lot(s);
- vi) Site preparation method(s);
- vii) *Deployment* design (mixed or monoclonal blocks) and planting density; and
- viii) Block *opening*(*s*).

Assessments

- i) Provide site visit dates;
- ii) Provide general description of site performance based on a visual assessment including: presence of ingress (including conifers), level of natural suckering (aspen or balsam poplar), and general health of trees on the site;
- iii) Detail performance assessment method(s);
- iv) Provide measurements or assessments of performance in Excel;
- v) Does the stand meet the *Reforestation* Stocking Standard of Alberta (RSA)? (i.e., 80% stocking);
  - a. If yes: list what species are contributing to RSA requirements and approximate stand density;
  - b. If no: indicate pattern (if any) to explain lack of regeneration success (e.g., have individual clonal blocks failed, are there holes due to site conditions, is mortality dispersed);
- vi) Include any additional comments or concerns with the installation (e.g., nursery stock condition at time of planting, weather events in the area over the 7 or 14-year period, success or failure of site preparation methods, impact of snowshoe hares or other relevant outbreaks in the region such as forest tent caterpillar).

Related documents if relevant/available

- i) *Reforestation* standard (RSA) report for block *opening*;
- ii) Research plan.

Appendix 40. Age-age Correlations for Application to Conifer *Stream 2* Programs

Alberta tree improvement programs use the age-age correlation to adjust height breeding values at the measurement age to breeding values at the rotation age. The government-approved genetic gain and the genetic worth associated with all seedlots where genetic gain could potentially be claimed include the age-age correlation in the calculation. The correlation coefficients in Table 40.1 and 40.2 were developed using data from progeny and provenance trials of white spruce and lodgepole pine in Alberta, which had sufficient serial measurements for fitting regression equations (see Rweyongeza 2016). Although these correlation coefficients are based on white spruce and lodgepole pine data, they are applicable to all spruces and pines, respectively. It is assumed that the height growth modes of other conifers are similar to either spruces or pines. For these species, use the white spruce Table (Table 40.1) for larch (western larch and tamarack) and the lodgepole pine Table (Table 40.2) for Douglas-fir genetic gain and genetic worth calculations. These phenotypic correlation coefficient are considered adequate approximations of the corresponding genetic correlation coefficients which are currently not available. For deciduous programs consult with *Alberta*.

Reference

Rweyongeza, D.M (2016). A new approach to prediction of the age-age correlation for use in tree breeding. Annals of Forest Science. DOI 10.1007/s13595-016-0570-5.

Table A40.1. Age-age correlation coefficients for white spruce (<u>Picea glauca</u>).

Selection age (yrs)	White Spruce														
	Rotation age (yrs)														
	50	**55**	**60**	**65**	**70**	**75**	**80**	**85**	**90**	**95**	**100**	**105**	**110**	**115**	**120**
10	0.638	0.606	0.574	0.545	0.516	0.490	0.464	0.440	0.417	0.396	0.375	0.356	0.337	0.320	0.303
11	0.656	0.623	0.593	0.563	0.536	0.509	0.484	0.460	0.438	0.416	0.395	0.376	0.357	0.340	0.323
12	0.672	0.641	0.611	0.582	0.555	0.529	0.504	0.481	0.458	0.437	0.416	0.397	0.378	0.360	0.344
13	0.689	0.659	0.629	0.601	0.575	0.549	0.525	0.501	0.479	0.458	0.438	0.418	0.400	0.382	0.365
14	0.706	0.676	0.648	0.620	0.594	0.569	0.545	0.522	0.500	0.479	0.459	0.440	0.421	0.404	0.387
15	0.718	0.691	0.665	0.639	0.615	0.592	0.569	0.547	0.527	0.507	0.487	0.469	0.451	0.434	0.417
16	0.735	0.708	0.683	0.658	0.635	0.612	0.590	0.568	0.548	0.528	0.509	0.491	0.473	0.456	0.440
17	0.751	0.726	0.701	0.677	0.654	0.632	0.610	0.589	0.569	0.550	0.531	0.512	0.496	0.479	0.462
18	0.767	0.743	0.719	0.696	0.673	0.652	0.631	0.611	0.591	0.572	0.554	0.536	0.519	0.502	0.486
19	0.783	0.760	0.737	0.714	0.693	0.672	0.652	0.632	0.613	0.594	0.576	0.559	0.542	0.526	0.510
20	0.792	0.771	0.751	0.731	0.712	0.693	0.675	0.657	0.640	0.623	0.607	0.591	0.575	0.560	0.545
21	0.808	0.788	0.768	0.749	0.731	0.713	0.695	0.678	0.661	0.645	0.629	0.613	0.597	0.583	0.569
22	0.823	0.804	0.786	0.767	0.749	0.732	0.715	0.698	0.682	0.666	0.651	0.636	0.621	0.606	0.592
23	0.838	0.820	0.802	0.785	0.768	0.751	0.735	0.719	0.703	0.688	0.673	0.658	0.644	0.630	0.616
24	0.853	0.835	0.818	0.802	0.785	0.770	0.754	0.739	0.724	0.709	0.695	0.681	0.667	0.653	0.640
25	0.859	0.844	0.830	0.816	0.802	0.788	0.775	0.762	0.749	0.736	0.723	0.711	0.699	0.687	0.676
26	0.873	0.859	0.845	0.832	0.819	0.806	0.793	0.780	0.768	0.756	0.744	0.732	0.720	0.709	0.698
27	0.886	0.873	0.860	0.847	0.835	0.823	0.811	0.799	0.787	0.775	0.764	0.752	0.741	0.730	0.720
28	0.899	0.886	0.874	0.862	0.851	0.839	0.828	0.816	0.805	0.794	0.783	0.773	0.762	0.752	0.741
29	0.910	0.899	0.888	0.876	0.865	0.855	0.844	0.833	0.822	0.812	0.802	0.792	0.782	0.772	0.763
30	0.914	0.905	0.896	0.887	0.878	0.869	0.960	0.851	0.843	0.834	0.826	0.817	0.809	0.801	0.793
31	0.925	0.917	0.908	0.900	0.891	0.883	0.875	0.866	0.858	0.850	0.842	0.834	0.827	0.819	0.811
32	0.936	0.927	0.919	0.912	0.904	0.896	0.888	0.881	0.873	0.865	0.858	0.851	0.843	0.836	0.829
33	0.945	0.937	0.930	0.922	0.915	0.908	0.901	0.894	0.887	0.880	0.873	0.866	0.859	0.852	0.846
34	0.953	0.946	0.939	0.932	0.926	0.919	0.913	0.906	0.900	0.893	0.887	0.880	0.874	0.868	0.862
35	0.956	0.950	0.944	0.939	0.934	0.929	0.923	0.918	0.913	0.908	0.903	0.898	0.893	0.888	0.883
36	0.962	0.957	0.953	0.948	0.943	0.938	0.933	0.928	0.924	0.919	0.914	0.910	0.905	0.900	0.896
37	0.969	0.964	0.960	0.955	0.951	0.946	0.942	0.938	0.933	0.929	0.925	0.920	0.916	0.912	0.908
38	0.974	0.970	0.966	0.962	0.958	0.954	0.950	0.946	0.942	0.938	0.934	0.930	0.926	0.922	0.918
39	0.979	0.975	0.972	0.968	0.964	0.961	0.957	0.953	0.950	0.946	0.943	0.939	0.935	0.932	0.928
40	0.980	0.977	0.974	0.971	0.969	0.966	0.963	0.960	0.957	0.955	0.952	0.949	0.946	0.944	0.941
41	0.984	0.981	0.979	0.976	0.974	0.971	0.969	0.966	0.963	0.961	0.958	0.956	0.953	0.951	0.948
42	0.987	0.985	0.983	0.980	0.978	0.976	0.973	0.971	0.969	0.966	0.964	0.962	0.959	0.957	0.955
43	0.990	0.988	0.986	0.984	0.982	0.980	0.977	0.975	0.973	0.971	0.969	0.967	0.965	0.963	0.961
44	0.992	0.990	0.988	0.986	0.985	0.983	0.981	0.979	0.977	0.975	0.974	0.972	0.970	0.968	0.966
45	0.992	0.991	0.990	0.988	0.987	0.985	0.984	0.982	0.981	0.980	0.978	0.977	0.975	0.974	0.972
46	0.994	0.993	0.992	0.990	0.989	0.988	0.986	0.985	0.984	0.983	0.981	0.980	0.978	0.977	0.976
47	0.996	0.995	0.993	0.992	0.991	0.990	0.989	0.987	0.986	0.985	0.984	0.983	0.982	0.980	0.979
48	0.997	0.996	0.995	0.994	0.993	0.992	0.991	0.989	0.988	0.987	0.986	0.985	0.984	0.983	0.982
49	0.998	0.997	0.996	0.995	0.994	0.993	0.992	0.991	0.990	0.989	0.988	0.987	0.986	0.985	0.984
50	1.000	0.997	0.996	0.996	0.995	0.994	0.993	0.993	0.992	0.991	0.990	0.990	0.989	0.988	0.987

Table A40.2. Age-age correlation coefficients for lodgepole pine (Pinus contorta).

Selection age (yrs)	Lodgepole Pine														
	Rotation age (yrs)														
	50	**55**	**60**	**65**	**70**	**75**	**80**	**85**	**90**	**95**	**100**	**105**	**110**	**115**	**120**
10	0.418	0.370	0.328	0.291	0.258	0.229	0.203	0.180	0.159	0.141	0.125	0.111	0.098	0.087	0.077
11	0.448	0.401	0.360	0.322	0.289	0.259	0.232	0.207	0.186	0.166	0.149	0.134	0.120	0.107	0.096
12	0.478	0.433	0.391	0.354	0.320	0.290	0.262	0.237	0.214	0.194	0.175	0.159	0.144	0.130	0.117
13	0.508	0.464	0.423	0.387	0.353	0.322	0.294	0.268	0.245	0.224	0.204	0.186	0.170	0.155	0.142
14	0.538	0.495	0.456	0.419	0.386	0.355	0.327	0.301	0.277	0.255	0.235	0.216	0.199	0.183	0.168
15	0.565	0.526	0.489	0.455	0.423	0.393	0.366	0.340	0.316	0.294	0.274	0.254	0.237	0.220	0.205
16	0.594	0.556	0.521	0.487	0.456	0.427	0.400	0.375	0.351	0.329	0.308	0.288	0.270	0.253	0.237
17	0.622	0.586	0.552	0.520	0.490	0.462	0.435	0.410	0.387	0.364	0.343	0.323	0.305	0.287	0.271
18	0.650	0.616	0.584	0.553	0.524	0.497	0.471	0.446	0.423	0.401	0.380	0.630	0.341	0.323	0.306
19	0.678	0.646	0.615	0.586	0.559	0.532	0.507	0.483	0.460	0.439	0.418	0.398	0.379	0.361	0.344
20	0.695	0.668	0.642	0.618	0.594	0.571	0.550	0.528	0.508	0.489	0.470	0.452	0.435	0.418	0.402
21	0.722	0.697	0.673	0.650	0.627	0.606	0.585	0.564	0.545	0.526	0.508	0.490	0.473	0.457	0.441
22	0.749	0.726	0.703	0.681	0.660	0.639	0.620	0.600	0.582	0.563	0.546	0.529	0.512	0.496	0.481
23	0.775	0.753	0.732	0.712	0.692	0.673	0.654	0.636	0.618	0.601	0.584	0.568	0.552	0.536	0.521
24	0.800	0.780	0.761	0.742	0.723	0.705	0.688	0.671	0.654	0.638	0.622	0.606	0.591	0.577	0.562
25	0.811	0.796	0.781	0.766	0.752	0.738	0.724	0.710	0.697	0.684	0.671	0.658	0.646	0.634	0.622
26	0.835	0.821	0.807	0.794	0.781	0.767	0.755	0.742	0.729	0.717	0.705	0.693	0.682	0.670	0.659
27	0.858	0.845	0.832	0.820	0.808	0.796	0.784	0.772	0.760	0.749	0.738	0.727	0.716	0.705	0.695
28	0.878	0.867	0.855	0.844	0.833	0.822	0.811	0.800	0.790	0.779	0.769	0.759	0.749	0.739	0.729
29	0.897	0.887	0.876	0.866	0.856	0.846	0.836	0.926	0.817	0.807	0.798	0.789	0.779	0.770	0.761
30	0.904	0.897	0.889	0.882	0.875	0.867	0.861	0.853	0.846	0.839	0.832	0.825	0.818	0.812	0.805
31	0.921	0.914	0.907	0.901	0.894	0.887	0.881	0.874	0.868	0.862	0.855	0.849	0.843	0.837	0.830
32	0.935	0.929	0.923	0.917	0.911	0.905	0.899	0.893	0.888	0.882	0.876	0.871	0.865	0.859	0.854
33	0.947	0.942	0.936	0.931	0.926	0.921	0.915	0.910	0.905	0.900	0.895	0.890	0.885	0.880	0.875
34	0.957	0.953	0.948	0.943	0.939	0.934	0.930	0.925	0.921	0.916	0.912	0.907	0.903	0.898	0.894
35	0.961	0.957	0.954	0.951	0.948	0.945	0.942	0.939	0.936	0.933	0.930	0.927	0.924	0.921	0.918
36	0.969	0.966	0.963	0.961	0.658	0.955	0.952	0.950	0.947	0.944	0.942	0.939	0.936	0.933	0.931
37	0.756	0.973	0.971	0.968	0.966	0.964	0.961	0.959	0.956	0.954	0.952	0.949	0.947	0.945	0.942
38	0.981	0.979	0.977	0.975	0.973	0.971	0.690	0.967	0.965	0.962	0.960	0.958	0.956	0.954	0.952
39	0.985	0.984	0.982	0.980	0.978	0.977	0.975	0.973	0.971	0.970	0.968	0.966	0.964	0.963	0.961
40	0.986	0.985	0.984	0.983	0.982	0.981	0.980	0.979	0.978	0.976	0.975	0.974	0.973	0.972	0.971
41	0.990	0.989	0.988	0.987	0.986	0.985	0.984	0.983	0.982	0.981	0.980	0.979	0.978	0.977	0.976
42	0.992	0.991	0.991	0.990	0.989	0.988	0.987	0.986	0.986	0.985	0.984	0.983	0.982	0.982	0.981
43	0.994	0.994	0.993	0.992	0.991	0.991	0.990	0.989	0.988	0.987	0.987	0.987	0.986	0.985	0.984
44	0.996	0.995	0.994	0.994	0.993	0.993	0.992	0.992	0.991	0.990	0.990	0.989	0.989	0.988	0.988
45	0.996	0.996	0.995	0.995	0.995	0.994	0.994	0.994	0.993	0.993	0.993	0.992	0.992	0.991	0.991
46	0.997	0.997	0.996	0.996	0.996	0.996	0.995	0.995	0.995	0.994	0.994	0.994	0.994	0.993	0.993
47	0.998	0.998	0.997	0.997	0.997	0.997	0.996	0.996	0.996	0.996	0.995	0.995	0.995	0.995	0.994
48	0.998	0.998	0.998	0.998	0.998	0.997	0.997	0.997	0.997	0.997	0.996	0.996	0.996	0.996	0.996
49	0.999	0.999	0.999	0.998	0.998	0.998	0.998	0.998	0.998	0.997	0.997	0.997	0.997	0.997	0.997
50	1.000	0.999	0.999	0.999	0.999	0.998	0.998	0.998	0.998	0.998	0.998	0.998	0.998	0.998	0.998

Glossary

Term	Definition
Accession number	Four-digit number historically assigned by *Alberta* to research or conservation seedlots. These may include individual family collections or bulked seedlots. *Accession number* is one category of *genetic identity*.
Alberta	The government of Alberta, or the appropriate agency within the government of Alberta (e.g., Alberta Tree Improvement and Seed Centre [ATISC]).
Amplified family	An aggregate of multiple *vegetative propagules* from each of a number of members of a half- or full-sib family, without individual testing of the constituent clones.
Approved facility	A designation provided by *Alberta* to a facility that is qualified to produce, process, test or store material destined for *deployment*.
Artificial regeneration	The creation of a new stand by direct seeding or by planting seedlings or cuttings.
Artificially regenerated	Established through *artificial regeneration*.
Base population	The larger source population from which a *selected population* for a *controlled parentage program* is chosen. May include one or more *wild* populations, plantations, or genetic *tests* (e.g., a progeny or provenance *test*).
Breeding population	The population within which crosses are made to generate material for the next cycle of selection. *Breeding population*s are generally large, compared to the *production population*.
Breeding value (BV)	The genetic value of an individual for a given trait at a specified age. *BV* is usually expressed in relative terms, as a percent deviation from the population mean, but it may be expressed in terms of measurement units such as m or cm.
Checked dataset	A set of raw data that has been examined and corrected for format, unambiguous errors and omissions, and credibility. Checking is now largely conducted during the data collection phase by programming the data logger to detect anomalies such as shrinking trees, trees that are too tall for the given diameter at breast height (DBH), and live trees that were previously reported dead.
Clone	A population of individuals all originating asexually from the same single parent and, therefore, genetically identical. Clones are named with non-Latin names preceded by the abbreviation 'cl'.
Collections, public land	Genetic material gathered and removed from *public land* for the purposes of *reforestation*, breeding or research. It does not include collections from approved *production populations* or *production units*.
Comparison tree method	A method for selection of parent trees in which measurements of the candidate are compared to those of nearby dominant trees. See Appendix 11.
Contributing landbase (Operable area)	The area available for timber harvesting activities. In the forecasting model, it is the area available for timber harvest action(s). Also known as the net landbase, active landbase, AAC-contributing landbase, or timber harvesting landbase.
Controlled parentage program (CPP)	A program to produce *Stream 2* material for *deployment* within the associated *CPP region.*
CPP region	A geographic area, defined initially by adaptation criteria as indicated by ecological and geographical proximity, and to be confirmed by testing, for which *Stream 2* material is produced.

Term	Definition
Cumulative effective population size	See *effective population size*. The *effective population size (Ne)* of *deployment populations* aggregated across years, *production units*, or *production populations*. Can also refer to *deployed populations* aggregated across years. See Appendix 20 for calculation method.
Cumulative Ne	See *cumulative effective population size*.
Deployment	Establishment of plants through *artificial regeneration*; through physical movement from one site (e.g., a nursery) to the establishment site; or through planting or seeding designed to meet resource management objectives or obligations.
Deployment population	The collection of *propagules*, produced from a single *production population* or its associated *production unit(s)* and registered under a single *registered lot number* (e.g., a seedlot from a *seed orchard*; a collection of cuttings from a *stoolbed* or *stoolbeds*; a collection of *rootlings*; a collection of micropropagated plantlets).
Dioecious	Refers to a plant having distinct male and female reproductive structures on separate plants.
Effective population size (Ne)	The size of an ideal population, which when contrasted to the population under study, would possess the same rate of increase in inbreeding, or decrease in genetic diversity due to genetic drift. As used in FGRMS: *Effective population size (Ne)* is a measure of *genetic diversity* and relatedness in a seed or vegetative lot, and is a function of the number of *genotype*s (parents), the degree of relatedness among parents, and the degree of balance among parental contributions to the given lot.
Equilibrium relative humidity (eRH)	The relative humidity of the air in an enclosed environment containing seeds, at the point where seeds are no longer gaining or losing moisture from the surrounding air. The *eRH* measurement is non-destructive and is expressed as a percentage.
Ex situ conservation; Ex situ gene conservation	Transfer of organisms (plant or animal) from one site (e.g. in the wild) to another site (e.g., seed banks, zoos) for the purpose of maintenance or breeding as a means of conserving the organism.
Extensive	Artificial *reforestation* of a cutblock or cutblocks where there is minimal follow-up treatment that would impact re-establishment of native vegetation. (With respect to management intensity; see Appendix 9.)
Forest tenure holder	A person or institution with defined ownership rights and obligations for the management and use of forest resources.
Genetic class code	A code assigned to *Stream 1* and *Stream 2* materials, and used for *deployment* reporting in ARIS. See Appendix 5.
Genetic diversity	The genetic variability within a population or a species.
Genetic gain	The heritable change in the population mean for a specified trait as a result of selection and breeding.
Genetic identity	One of several unambiguous current or historical identifiers (e.g., *unique identifier*, *accession number, registered lot number*) of seed or vegetative material, that can be used to identify the genetic source of the material.
Genetic research planting	A planting associated with a research plan or *CPP* plan. All materials in *genetic research plantings* must be *Stream 1* materials, *Stream 2* materials, *local research materials* or *non-local research materials,* and must be registered or have a *genetic identity*.
Genetic test site	A field experimental area containing research *trial*s related to genetics and plant breeding.

Term	Definition
Genetic worth	For a seed or vegetative lot, the predicted difference in value of a given trait (e.g., height or volume) at a specified age from the value of that trait at that age in *wild* stand material. This difference is expressed as a percentage of the *wild* stand value.
Genetically modified organism (GMO)	An organism that, through human intervention in a laboratory, has had its genome, or genetic code, deliberately altered through the insertion of a specific identified sequence of genetic coding material (generally DNA) that has been either manufactured or physically excised from the genome of another organism. Genetic modification may be used to alter any of a wide range of traits, including insect and disease resistance, herbicide tolerance, tissue composition and growth rate. Substantially equivalent to *living modified organism*.
Genotype	The genetic makeup of an individual organism, usually with reference to a specific characteristic under consideration. May also refer to a specific individual plant or clone.
Green Area	The area outlined and colored green on a map annexed to the order Classifying *Public Lands* dated April 16, 1963, and published in The Alberta Gazette on April 30, 1963, as amended from time to time. The *Green Area* includes *public land* that is primarily forested and is managed for timber production, oil/gas development, watershed, wildlife and fisheries, recreation and other uses.
Hybrid orchard	An orchard including non-hybrid parents that is managed to produce hybrid seed. This term does not apply to orchards that include naturally occurring hybrid parents (e.g., white x Engelmann spruce).
In situ conservation; **In situ gene conservation**	Retention, conservation, and propagation of germ plasm resources on the site as a means of continuing the organism or ecosystem in its original habitat or location.
Intellectual property rights	The rights to intangible property that is the product of the human intellect. Intellectual property may be protected by copyright, trademark or patent. The holder of *intellectual property rights* is usually the person or persons who developed the product or the organization that funded it. In the context of Forest Genetic Policy, *intellectual property rights* apply to genetic data and to the *genotype*s to which they apply, either separately or in aggregate.
Intensive	Planting of an entire cutblock, or cutblocks across a large area, with recurrent near-complete control of native vegetation prior to canopy closure. Site is dominated by artificial regeneration material through use of vegetation management techniques. (With respect to management intensity; see Appendix 9.)
Living modified organism	Any living organism that possesses a novel combination of genetic material obtained through the use of modern biotechnology. (Definition from the Cartagena Protocol.) Substantially equivalent to *genetically modified organism.*
Local research material	See *research material, local*.
Locally adapted material	Material deemed to be adapted by virtue of origin or testing. *Locally adapted material* may be one of: 1. *Stream 1* material collected from within the *seed zone* in which *deployment* is planned, 2. *Stream 2* material from *genotypes* under test, or scheduled for testing, but accepted by *Alberta* as locally adapted, or 3. *Stream 2* material from *genotypes* confirmed as adapted on the basis of field testing.

Term	Definition
Lot number, registered	A number used to uniquely identify a seed or vegetative lot from the time of *registration* through storage, *deployment* and monitoring. The *registered lot number* is assigned by *Alberta* when material is registered.
Lot number, temporary	A number used to uniquely identify a seed or vegetative lot prior to *registration.*
Material transfer agreement (MTA)	*Material transfer agreements (MTAs)* are contractual legal agreements between two or more parties governing the transfer and subsequent use of genetic materials. MTAs specify which rights are conferred, and may contain clauses concerning such topics as record keeping, reclaim rights, liability disclaimers and prohibitions on use of the material for further breeding.
Material use rights	The right to use genetic materials (e.g., seeds, seedlings, somatic seedlings or rooted cuttings) for plantation purposes. The holder of *material use rights* does not usually have propagation or breeding rights.
Moisture content	A measurement of the quantity of water contained in seed. In the case of seed, it is a destructive method and is calculated on a wet weight basis. Moisture content is expressed as a percentage.
Moisture measurement	A measurement of the water status of a seedlot. Can refer to non-destructive *equilibrium relative humidity* (eRH) measurement or to the destructive *moisture content* measurement (MC).
Monoecious	Refers to a plant in which male and female reproductive structures occur on the same individual.
Natural regeneration	The renewal of a forest stand by natural rather than human means, such as seeding-in from adjacent stands, with the seeds being deposited by wind, birds, or animals. Regeneration may also originate from sprouting, suckering, or layering.
Ne	See *effective population size*.
Non-local material	Material of unknown adaptation. Either of: 1. *Wild* material collected from outside the *seed zone* in which *deployment* is proposed, 2. *Stream 2* material that is not deemed to be locally adapted.
Non-local research material	See *research material, non-local*.
Opening	An area created by timber harvest which is the unit for reforestation management (i.e., Regeneration surveys) and tracking of reforestation activities in the Alberta Regeneration Information System (ARIS). Openings have a unique administrative identification, contain one reforestation stratum, and a single timber disposition holder with reforestation responsibility.
Operable area	The total area of all stands included in the Annual Allowable Cut (AAC) calculation.
Orthodox seed	Seed which will survive drying to a low moisture content and subsequent freezing.
Pedigree	A record of parentage, sometimes also including data on the performance of parents and other relatives.
Phenotype	The visible, observable and measurable characteristics of an organism, such as morphology, physiology, biochemistry, and behavior, resulting from the influence of environmental conditions on its genetic constitution.
Point collection	Registerable *Stream 1* material collected within area and elevation limits, and diversity criteria, as defined in Appendix 4; compliance enables application for variance.
Production population	The population of *genotypes* used for *propagule* production, or the aggregate of *genotypes* represented in the *production unit(s)* for a given *CPP region*.

Term	Definition
Production site	The physical location or place where *propagules* are produced (e.g., a *seed orchard* site, *stoolbed* site, collection of pots at a nursery, or laboratory).
Production unit(s)	The direct physical source(s) of *Stream 2* seed or vegetative lots (e.g., the group of trees or other plants that is a *seed orchard*; individual or aggregate *stoolbeds*, or a collection of tissues used for *rootling* propagation or micro-propagation).
Propagule	Plant material (e.g., cutting, root segment, seed, or cultured callus tissue) from which a new individual can be grown.
Public land collections	See *collections, public land*.
Public land(s)	"Land of the Crown in right of *Alberta*" (definition from *Alberta*'s Public Lands Act). Includes *Green Area* (land managed primarily as forest land) and White Area (land managed primarily for agriculture and uses other than forestry).
Ramet	A genetically identical individual produced by vegetative propagation.
Ramet, grafted	A *ramet* created by grafting a twig or bud from the original plant onto a physically distinct rootstock. The portion of the *grafted ramet* above the graft union is genetically identical to the original plant (see also *ramet, rooted*.)
Ramet, rooted	A *ramet* created by rooting a twig or cutting from the original plant. The whole *ramet* is genetically identical to the original plant (see also *ramet, grafted*).
Rare species	A species belonging to either of these two categories: 1. Species that are ranked provincially as S1 or S2 (or any combination including either S1 or S2) by the Alberta Conservation Information Management System (ACIMS). 2. Species ranked nationally as N1, N2 or N3 or that have been designated in the Species at Risk Act (SARA) or listed as threatened and/or endangered by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC).
Reclamation	As used in FGRMS: A planned process to assist the ecological recovery of an ecosystem that has been disturbed. It does not require the recovery process to target the pre-disturbance system, but should return the specified land to an equivalent (but not necessarily identical) land capability.
Reforestation	The reestablishment of trees on denuded forest land by natural or human-mediated means such as planting and seeding.
Registered lot number	See *lot number, registered*.
Registration	Process that allows a seed or vegetative lot to be used for *deployment* within its *CPP region* or *seed zone*. Only *Stream 1* and *Stream 2* materials can be registered. *Registration* may be *restricted* or *unrestricted.* A registered seed or vegetative lot is one that has completed the *registration* process.
Regulated professional	A person regulated by a recognized professional body to be accountable and to provide competent and ethical services.
Rehabilitation	In reference to clonal standards *rehabilitation* refers to planting on road sides, landing and decking areas, and forest voids created by regeneration failures.
Remediation	The establishment of locally adapted material tested and employed for the purpose of re-establishing the biophysical capacity of a site.

Term	Definition
Research material, local	Seed or vegetative materials from within the target *CPP region* or an adjacent *CPP region* that may not be eligible for *registration* (e.g., an open-pollinated seedlot collected from a single plant). These materials may be included in a *CPP* leading to production of *Stream 2* material, and must have *U.I.*s assigned before being established in *genetic research plantings* or included in a *CPP*. Breeding, Testing and Verification Standards apply to this material.
Research material, non-local	Seed or vegetative materials of unknown adaptation (such as species, provenance, family or hybrid material from outside the *seed zone* or *CPP region* of origin). Untested *non-local research materials* are not eligible for *deployment* within the *Green Area*, or inclusion in *production populations* or *units* associated with *CPPs* (with some exceptions of material from adjacent *CPP regions*), but may be included in *genetic research plantings*. These materials must have *U.I.*s assigned before being established in *genetic research planting*s. Following testing and demonstration of adaptedness, these materials may be included in *CPP*s leading to production of *Stream 2* materials. Breeding, Testing and Verification Standards apply to this material.
Restricted registration	*Registration* of material not in compliance with one or more documentation, adaptation and diversity requirements, that allows a seed or vegetative lot to be used for *deployment* within its *CPP region* or *seed zone*. Restrictions on *deployment* may be imposed.
Rolling front orchard	A *seed orchard* in which individual plants or groups of plants of known *breeding value* are replaced on a more or less continuous basis as new material of higher *breeding value* becomes available.
Rootling	A plant generated from a root segment.
Seed orchard	A plantation, usually several hundred to several thousand plants in number, established and managed primarily for early and abundant production of seed for *deployment*. Plants in the orchard are derived and propagated from selected parents, usually by grafting or by seed.
Seed zone	A geographic area, defined on the basis of ecological characteristics and genetic information, within which *Stream 1* material meeting *unrestricted registration* requirements may be collected and freely deployed. (*Seed zones* may apply to group of species, or *species-specific seed zones* may be developed).
Seed zone collection	Registerable *Stream 1* material collected within a single *seed zone*, not otherwise subject to constraints of area or elevation range; not eligible for variance (see Appendix 4).
Selected population	A population of plants, chosen from a *base population*, from which *breeding population*s and *production population*s are chosen or derived by breeding or propagation.
Serial propagation	The propagation of multiple clonal copies of a plant through repeated cycles of collection of vegetative units (e.g., scions or cuttings), creation of new plants from these units, and vegetative growth of the derived plants, without returning to the original plant. Also known as "bulking up" or multiplication.
Serotinous cones	Cones that after seed maturity remain closed on the tree and open to release seed following fire or excessive heat (e.g., lodgepole and jack pine cones).
Species-specific seed zone	A *seed zone*, delineated for a single species or group of species on the basis of adaptation as assessed from genetic *trials*, within which *Stream 1* material may be collected and freely deployed.
Species-specific target strata	The area to be regenerated to the species produced by the *production unit(s)* for a given *CPP*.
Stoolbed	An aggregation of closely spaced stumps, or stools, managed for the production of vegetative sprouts (whips). Harvested whips are used for operational planting stock and can be pre-rooted prior to *deployment*.

Term	Definition
Stream 1	*Stream 1* material refers to seed or vegetative material collected from *wild* or artificially regenerated stands (including *Stream 1 seed orchards*) of native species within a given *seed zone*, having *restricted* or *unrestricted registration* for *deployment* in that *seed zone*.
Stream 2	*Stream 2* material refers to registered or registerable seed or vegetative material produced from an approved *production population* or *production unit(s)*.
Stream 1 seed orchard	A *seed orchard* established to produce seed for a single *seed zone.*
Temporary lot number	See *lot number, temporary*.
Test	A *genetic research planting* designed to address a given genetic issue. May stand alone or may be one planting of a series including the same or overlapping material (e.g., a single progeny *test* site). Used interchangeably with *trial*.
Test series	A group of *genetic research plantings* of the same or overlapping material, on one or several sites, designed to address a given genetic issue (e.g., a progeny *test* established on four sites). Used interchangeably with *trial series*.
Trial	A *genetic research planting* designed to address a given genetic issue. May stand alone or may be one planting of a series including the same or overlapping material (e.g., a single progeny *trial* site). Used interchangeably with *test*.
Trial series	A group of *genetic research plantings* of the same or overlapping material, on one or several sites, designed to address a given genetic issue (e.g., a progeny *trial* established on four sites). Used interchangeably with *test series*.
Unique identifier (U.I.)	An alphanumeric code of 7 to 18 characters assigned to genetic material. The first seven characters of the *U.I.* are essential, and uniquely identify the *genotype* by agency and sequence number. Subsequent characters may be included as applicable, and specify material type (e.g., scions, pollen), individual number (e.g., cutting 103), and species (e.g., Sw, Picegla). A *U.I.* is required for all unregistered material included in research *trials* related to *CPPs*, and for all material in *Stream 1 seed orchard*s. See Appendix 25 for details of variables, structure and agency codes.
Unrestricted registration	*Registration* based on compliance with documentation, adaptation and diversity requirements that allow a seed or vegetative lot to be used for *deployment* within its *CPP region* or *seed zone*. Restrictions on *deployment* may be imposed (see Appendices 4, 9 and 21).
Vegetative propagule	A part of a plant used for vegetative propagation (e.g., a root, a stem, or somatic embryonic tissue).
White Area	Private and *public land* in the settled portion of the province, managed primarily for agriculture use, but not excluding other uses such as timber, oil/gas development, recreation, soil and water conservation, and fish and wildlife habitat.
Wild	Of natural origin; not derived from material established through *artificial regeneration.*

Acronyms

AAC	Annual Allowable Cut
AOP	Annual Operating Plan
ARIS	Alberta Regeneration Information System
ATISC	Alberta Tree Improvement and Seed Centre
BLP	Best Linear Prediction
BLUP	Best Linear Unbiased Prediction
BTV	Breeding, Testing and Verification (Section of FGRMS 2016)
BV	Breeding Value
CNT	Consultative Notation
CPP	Controlled Parentage Program
DBH	Diameter at Breast Height
DNA	Deoxyribonucleic acid
DRS	Disposition Reservation (see Standard 30.4.1)
eRH	Equilibrium Relative Humidity
FGRMS	Forest Genetic Resource Management and Conservation Standards (formerly STIA)
FMA	Forest Management Agreement
FMP	Forest Management Plan
FOIP	Freedom Of Information and Protection of Privacy Act
GAD	Green Area Deployment (Section of FGRMS 2016)
GMO	Genetically Modified Organism
GW	Genetic Worth
ISP	Industrial Sample Plot Designation
LMO	Living Modified Organism
MCHRS	Material Collection, Handling, Registration and Storage (Section of FGRMS 2016)
MLL	Miscellaneous Lease
MTA	Material Transfer Agreement
Ne	Effective Population Size
PCPM	Production of Controlled Parentage Material (Section of FGRMS 2016)
PNT	Protective Notation (see Standard 30.4.1)
PST	Permanent Sample Tree
RP	Research Program
SMP	Supplemental Mass Pollination
SSSZ	Species-Specific Seed Zone
STIA	Standards for Tree Improvement in Alberta
U.I.	Unique Identifier