

Alberta Forest Genetic Resource Management and Conservation Standards

Second Revision of STIA

**Forestry Division
Alberta Sustainable Resource Development
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Harry Archibald	Hugh Lougheed
Colin Bamsey	Kent MacDonald
Leonard Barnhardt	Bruce Macmillan
Peter Blake	Scott Milligan
Jean Brouard	Dave Morgan
Lee Charleson	Florance Niemi
Daniel Chicoine	Donna Palamarek
John Edwards	Daryl Price
Dave Fox	Fred Radersma
Tim Gylander	Diane Renaud
Christine Hansen	Doug Sklar
Gary Harmata	Cliff Smith
Anita Jenkins	Harry Stelfox
Sally John	Barb Thomas
Chuck Kaiser	Pat Wearmouth
Don Lester	Ken Yackimec

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Steering Committee	Technical Committee	Contributors	Administrative and Technical Support
Leonard Barnhardt	Leonard Barnhardt	Jean Brouard	Tammy De Costa
Roger Butson	Sally John	Donna Palamarek	Pearl Gutknecht
Fred Radersma	Barb Thomas	Christine Hansen	Wanda Gruinheidt
Diane Renaud	Don Lester	Deogratias Rweyongeza	Karen Koo
Ken Greenway (Chair)	Ken Greenway (Chair)		

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GENERAL

1.0 Principles

The forest genetic resources of Alberta are crucial to the well being of the people of Alberta, to sustainable forest management, and to the long-term economic and ecological stability of the province.

The government of Alberta and the forest industry:

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

Forest managers have responsibilities for maintaining the value of the genetic resources of the province.

The role of the government of Alberta is to:

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

The role of the industry is to:

- respect the public interest by conforming to enacted policies, regulations and standards, and
- develop objectives and strategies that will increase the value derived from the forest genetic resource.

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. These standards were developed to allow for the possibility that all forests originating from *Stream 2 material* will be replaced through natural regeneration rather than planting. These standards will be adapted to evolving knowledge.

The standards were implemented in 2003, reviewed in 2004 and 2005 and revised in July, 2005. They were reviewed again in 2008 and 2009 with a revision in May of 2009. A future review is planned for 2013. Issues not resolved during the current review and to be addressed in the interim or during the next review include:

- acceptable *deployment* patterning of clonal material at both the stand and landscape scales;
- development of a methodology for determining landscape Ne requirements once the current landscape Ne *deployment* caps for seed-based *Stream 2 material* has been reached...i.e., what new Ne values would be and how would they be calculated;
- conservation requirements for *Controlled Parentage Program (CPP)* plans once the ongoing GAP analysis has determined to what extent *in situ* conservation requirements are currently met with existing reserves and where additional *in situ* conservation efforts are required;
- determination of gender ratios for *CPPs* for vegetatively propagated hardwood species where gender determination may be difficult due to delayed or infrequent expression. The 2009 FGRMS changed the required 50:50 gender ratio of deployed material to a requirement to document the gender of deployed material where possible, and added a requirement that the gender of at least 50% of deployed material be determined within five years of initial *deployment*. Once sufficient information has been accumulated, this issue will be re-addressed to assess the realized gender ratio, and to determine what gender ratio should be required.

3.0 Applicability

These standards apply to the *Green Area*. In addition, the standards for Material Collection, Handling, Registration and Storage (MCHRS) apply to all material collected from *public land* as well as all material intended for *deployment* on the *Green Area*, regardless of where the material is collected.

The two main users of the standards are those who:

- work primarily with *wild* material collected for normal *reforestation* activities (*Stream 1 material*), and
- have *CPP* (*Stream 2 material*).

Genetically Modified Organisms

Genetically 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. Genetic modification may be used to alter any of a wide range of traits, including insect and disease resistance, flowering, herbicide tolerance, tissue composition, and growth rate.

Though it is recognized that *GMO* material has a theoretical potential for *reforestation*, the performance and impacts on the forest ecosystem are poorly understood. In view of the potential risks associated with *reforestation* with *GMOs* and in accordance with the current position of the Alberta Forest Genetic Resources Council, *GMOs* are not approved for use on Crown 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, this manual outlines additional requirements for review, testing, and research from a provincial perspective (see Standards 23.5 and 25.3).

Submission and Approval of Documents

Plans and forms that are required to be submitted to the Department of Sustainable Resource Development or Alberta Tree Improvement and Seed Centre (hereinafter referred to as *Alberta*) as specified in the standards and appendices will receive one of four responses:

- approve;
- approve with conditions;
- requires additional information and
- reject with reasons.

4.0 Structure of the Document

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

The five sections are:

- Ownership and Data Access (ODA),
- Material Collection, Handling, Registration and Storage (MCHRS),
- Green Area Deployment (GAD),
- Breeding, Testing and Verification (BTV), and
- Production of Controlled Parentage Materials (PCPM).

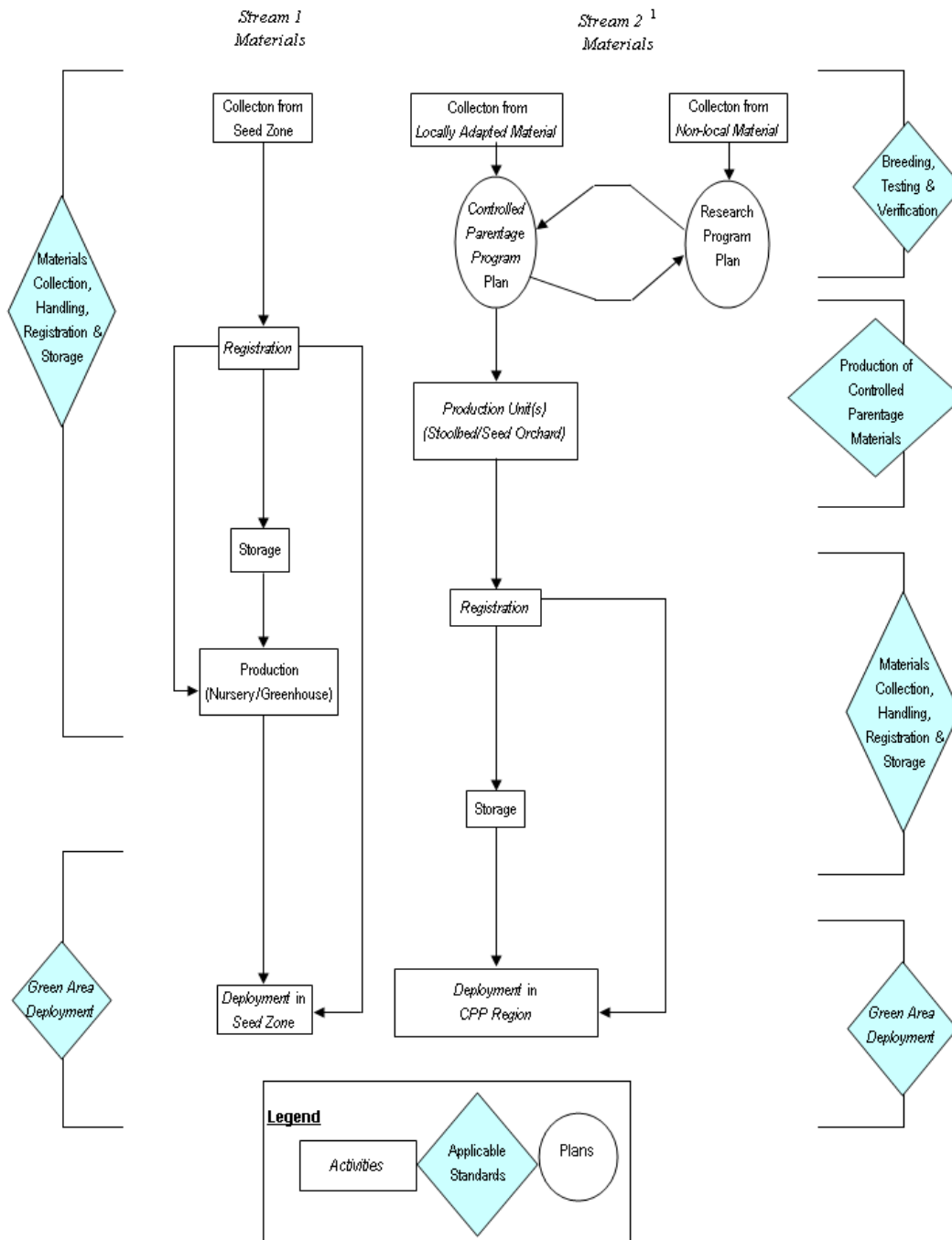
This document also contains a glossary, a list of acronyms and numerous appendices (tables, forms and other supplements to the standards). The glossary provides definitions of terms specific to their usage in this policy.

Notes about the format of this document:

1. To help separate which standards apply to each of the two streams of material, a double-lined box has been placed around standards that apply exclusively to the *CPP* (see Figure 1, Stream 2) or research programs (RP). Standards appearing outside the box may apply to both streams of material.
2. Terms found in the glossary appear in italics in the text to indicate that the use of the term has been defined.

5.0 Standards Framework

Figure 1 below illustrates a functional arrangement of the components of the FGRMS.



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

6.0 Effective Date and Retroactivity

These standards were enabled through Timber Management Regulation 144.2 and were effective as of May 01, 2003. This version is effective as of the 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 new standards through discussion with *Alberta* and the proponent(s). The intent is to capitalize on work in progress while phasing in new standards.

OWNERSHIP AND DATA ACCESS (ODA)

Preamble

The Government of Alberta has stewardship responsibility for the management of forest genetic resources on *public land* in Alberta.

Alberta, the forest industry, research organizations and tree improvement cooperatives:

- undertake research, conservation, genetic improvement and breeding programs jointly or individually, and
- are involved in the collection and *deployment* of genetically improved trees on *public land* in Alberta.

As genetic improvement programs in the province mature, information will accrue on the performance of genetically improved material. The value of such material, and ownership issues, will become of greater importance to government and industry. It is also possible that forest material collected from Alberta *public land* could be utilized for commercial purposes other than fiber production in Alberta. In such instances, benefits to the province must be retained.

Goals

The goals of this section are to:

- establish ownership and access rights to forest genetic resources, and
- state *Alberta's* requirements for access to data on genetically improved forest material to ensure stewardship of Alberta's forested *public land*.

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

ODA Standards

7.0 Ownership of Material

Trees and other plant material (physical material) on *public land* are the property of the province. This includes source materials (e.g., pollen, seed, graft materials and *vegetative propagules*) that have potential for collection through *reforestation*, and genetic improvement activities. Provincial ownership of material applies regardless of *deployment* method (natural regeneration, planting, seeding, etc.).

Once authorized by the province through licenses, permits or otherwise, an organization or person(s) owns the trees or plants that have been harvested or other physical material that is collected from *public land* for the purpose of genetic improvement. This ownership right remains until the material is deployed back on to *public land*, at which time the right transfers to the province.

Some exceptions apply:

- The province reserves the right to retain some collected material for conservation or research purposes. (See Standards 17.0, 29.2, 29.3 and 29.4 for more detail). Such material may be shared with research agencies, but the province will inform those recipients that they cannot distribute material or *genotype-specific* information on the material. The intent is to encourage use of material for knowledge creation and research, while establishing limits on the distribution of material.
- The province may reserve the right to *genotypes* and intellectual property (IP) wholly or in part developed from forest material collected from Alberta *public land* when such material is utilized for commercial means. This is outlined in more detail in the next section of this document, "Management of Intellectual Property."

- 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 genetically improved material that has been deployed on *public land*).

8.0 Management of Intellectual Property

For the purpose of these standards, IP is considered to be all genetic information that is attributable to specific forest plant material and associated *genotypes*, and associated rights to take out a patent on such *genotypes*. Intellectual property resulting from forest genetics and tree improvement research and development projects will be shared between the province, forest company, research organization and/or genetic improvement cooperative in accordance with the following principles.

- a) The province recognizes that ownership of IP rights should be based on the degree of effort by parties involved in a breeding or research program in which the province is a cooperator. Effort is generally considered to be financial investment, but may include in-kind contributions such as, but not limited to, facility use, provision of material and scientific support for a specific breeding program. The greater the level of effort, the greater should be the rights to IP. Respective rights to IP should be defined in an agreement between the province and other members of the cooperative.
- b) The province will endeavour to retain benefits in the form of revenue whenever material from *public land* is utilized for commercial means. However, the province will not seek to obtain revenue when material is used for the *deployment* or strengthening of genetic improvement programs in Alberta. Exchanges of material between Alberta and other jurisdictions will generally not be considered for royalties; as such exchanges benefit the province and provincial genetic improvement.

Implementation

For existing and future genetic improvement cooperatives involving the province, the province 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 and associated *reforestation* obligations in Alberta, a letter of authorization and collection plan is 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.

Rights Authorizations

The owner of material and IP may authorize another to exercise the owner's rights by way of agreement. The types of rights that might be addressed are *material use rights*, *breeding rights* or commercial sales rights. For example, other provinces in Canada have utilized an agreement called a *material transfer agreement (MTA)* to specify such rights.

Such agreements may be required between *Alberta* and any other entity – industrial, academic or research – involved in forest genetic improvement activities in Alberta, nationally or internationally. Some situations where these agreements may apply are:

- where a third party wishes to use materials and associated *genotypes* from a genetic improvement program involving *Alberta* or *public land* for propagation or further breeding for commercial or profit objectives, and
- where any member of a cooperative involving the Government of Alberta wishes to use material and associated *genotypes* for propagation or further breeding outside the cooperative(s) where they are participants.

9.0 Access to Data and Information

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

All information provided to Alberta, or in the custody or control of Alberta, can be potentially disclosed under Freedom of Information and Protection of Privacy (FOIP) legislation if a request for disclosure were made. It is recognized that cooperative genetic improvement programs with Alberta and any other party's information submissions to Alberta are subject to FOIP legislation, and that other parties may request access to 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:

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

MATERIAL COLLECTION, HANDLING, REGISTRATION AND STORAGE (MCHRS)

Goals

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

- ensure adaptation and diversity,
- maintain documented *genetic identity* and ensure materials are appropriately tracked, and
- 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 (Stream 1) and Appendix 3 (Stream 2).

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

10.3 Required *registration* information must be complete, accompanied by the signature of the owner or registrant 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 (e.g., insufficient number of parents). 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 Stream 2 lot with *unrestricted registration* under the following conditions:

- the Stream 1 lot has *unrestricted registration*;
- the Stream 2 lot has an *Ne* of at least 5;
- the *seed zone* of the Stream 1 lot and *CPP region* of the Stream 2 lot overlap;
and
- 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 the table below.

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

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

Stream 1 material

- 10.6 For *registration* of *Stream 1 material* the material collection criteria defined in Appendix 4 must be met.
- 10.7 For *registration* of *Stream 1 material* the information requested in Appendix 2 is required including : owner, species, type of material, source location, horizontal extent of collection, the elevations of the highest and lowest collection point, *seed zone*, collection dates, number of parents, material genetics class code (see Appendix 6), amount being registered, storage location and signature of a *regulated professional*.
- 10.7.1 For *registration* of Stream 1 seed, the following additional information is required: *temporary lot number*, volume of cones collected (conifer), yield, viability or germination %, purity, moisture content and 1000 seed weight. Refer to 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 the table in 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.

Stream 2 material

- 10.9 For *registration* of *Stream 2 material* (see Appendix 3), the *effective population size* (N_e) criteria contained in Appendix 5 must be met.
- 10.10 *Stream 2 material* must originate from an *Alberta approved production site and production unit or production population* (see Standards 32.2 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, viability or germination %, purity, moisture content and 1000 seed weight. 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.

Restricted registration

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

- documentation standards of 10.7 have not been met, or
- collections (*Stream 1*) do not meet requirements for *unrestricted registration* (see Appendix 4), or
- documentation standards of 10.11 have not been met, or
- *effective population size* (*Stream 2*) is less than that required for *unrestricted registration* (see Appendix 5), or
- *Stream 2 material* is not derived from *locally adapted material* (e.g., non-local provenances, non-local species, non-local hybrids, *GMOs* as determined on a case-by-case basis), or
- genetic risks have been identified through the *Stream 2* risk assessment process (Appendix 9) leading to constraints on deployment dealt with through standards or deployment conditions in the FMP.

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

11.0 Collection

11.1 Collections from *public land*

- 11.1.1 All collections of seed and vegetative material intended for *reforestation* or for research supporting *reforestation* that is carried out on *public land* require an authorization from *Alberta* as per Timber Management Regulation 141.5.
- 11.1.2 *Forest tenure holders* responsible for *reforestation* will outline their intent to collect in their Annual Silviculture Schedule. *Alberta* is to be notified of the target species and general location of a collection no less than 2 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 a Government of Alberta field 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.
- 11.1.4 Native plant material collections not intended for *reforestation* also require authorization from the field office and must follow the Native Plant Revegetation Guidelines for Alberta. Details are available at:
<http://www.srd.gov.ab.ca/lands/managingpublicland/landinformation/nativeplantrevegetationguidelines/appendixg.aspx>.
- 11.1.5 For collections falling outside Sustainable Resource Development's jurisdiction (e.g., Provincial Parks, Federal Lands), those agencies' approval processes must be followed.

11.1.6 Genetic material collected from *public land* for research or *CPPs* will be documented on the appropriate form (Appendix 11A, 11B 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 disposition holder will maintain a minimum of one registered Stream 1 lot for each species, in each *seed zone* where artificial regeneration is planned using seedlings.
- 11.3 The maximum registered seedlot or vegetative lot size will depend on numerical restrictions on *deployment* from a single seedlot or vegetative lot. Maximum numbers deployable by *seed zone* size are shown in Appendix 14.
- 11.4 Stream 1 vegetative material may be multiplied in *stoolbeds* established from collections that contain the required minimum number of trees per collection for *Stream 1 material* (see Appendix 4 – Material Category D).

11.5 Genetic material collected outside Alberta will be documented on the appropriate form (Appendix 15) and submitted (in either hard copy or electronic format) to *Alberta* upon entry into 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.

12.0 Transportation of Material

12.1 A proper identification tag must accompany each container of material/cones from the time of collection to delivery to the processing and/or storage facility.

- Identification for *Stream 1 material* must include the *temporary lot number*; the material's owner name; Section, Township, Range and Meridian; year of collection and species.
- Identification for *Stream 2 material* must include the *temporary lot number*, the material's owner 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 *CPP* Material Transportation and Storage Form (Appendix 16) which lists all material by either the *accession number*, temporary or *registered lot number* or *unique identifier (U.I.)*. In addition, each genetic entity will also be labelled unequivocally with the *U.I.*, accession or temporary or *registered lot number* both inside and outside its container. Where material is documented on a parent tree selection form (Appendices 11A, 11B, 12 or 15) these forms meet the documentation requirements for transportation and storage.

12.3 Transportation of materials from *public land*

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

12.4 Transportation of materials from an approved *production site*

12.4.1 A completed Registration Request Form - Stream 2 (Appendix 3) must accompany all cone and material shipments.

12.5 Withdrawal and transportation

12.5.1 A completed Reforestation Seed and Vegetative Materials Withdrawal and Transportation Form (Appendix 17) must be received by *Alberta* (Provincial Seed Officer) 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 Reforestation Seed and Vegetative Materials Withdrawal and Transportation Form (Appendix 17) is to be used for tracking materials from withdrawal from storage through to nurseries or related facilities. *Alberta* (Provincial Seed Officer) is to be notified of any deviation from the 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 the Government of Alberta website <http://srd.alberta.ca/forests/managing/manuals.aspx>.

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

13.3 Seed shall be processed and delivered for storage within six months of collection.

13.4 The completed Registration Request Form (Appendix 2 or Appendix 3) must accompany the seed to Alberta Tree Improvement & Seed Centre (ATISC) or other approved storage facility for *registration*.

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

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

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 Government of Alberta website <http://srd.alberta.ca/forests/managing/manuals.aspx> or supplied by ATISC.
- 14.2 Seed testing must be conducted in an *approved facility* and an experienced seed testing technician or laboratory scientist responsible for the seed testing laboratory must sign seed test result reports.
- 14.3 Seed test results must be provided to *Alberta* (ATISC) within four months of receipt of seed for storage.

15.0 Storage

- 15.1 All registered seed must be stored at ATISC or another storage facility approved by *Alberta*.
- 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 labelled with the temporary 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 not originating on *public land*, or of seed or vegetative materials obtained from other agencies, the minimum information required is: date of collection; owner, species, seed source, moisture content, 1000 seed weight and total seed amount submitted for storage at ATISC or other approved storage facility.

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* (Provincial Seed Officer). An exchange of material between material owners does not require *Alberta* approval as long as all standards within this manual are followed when deploying the material.

17.0 Retention of Material for *Ex Situ* 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. *Alberta* will notify the owner of any withdrawals. Amounts greater than this will require written consent of the company.
 - 17.1.2 *Alberta* may retain *Stream 2* material with written consent from the company.
 - 17.1.3 For seed collections from *public land* intended for inclusion in research or *CPPs* in *Alberta*, *Alberta* may request that 5% of the seed be provided to *Alberta*.
 - 17.1.4 For all other *public land* seed or vegetative material collections not intended for *reforestation* or tree improvement in *Alberta*, *Alberta* may request that 10 % of harvested seed or vegetative material be provided 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:

- 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*,
- maintain or enhance forest productivity,
- be consistent with sustainable forest management principles (economic, social and environmental sustainability), and
- recognize that the Forest Management Plan (FMP) or plans of an equivalent level, guided by this and other related 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* sources 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* material collected as per requirements in Appendix 4 is eligible for application for *deployment* outside the *seed zone* of origin (see Appendices 8 and 13 for procedures). Without applying for a variance *deployment* may occur within 1 km of the *seed zone* boundary, provided 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*.

- Variances for *Stream 1* material may be requested by submitting a Request for Deployment Variance for *Stream 1* Material (see Appendix 8) to *Alberta* (Provincial Seed Officer).
- 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.
- Any three requests for the same variance, or a standing approval for variance, may initiate a request by 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 *restricted Stream 1* material, a determination is to be made by *Alberta* (ATISC) on the basis of a request for variance (see Appendix 8).

18.3 Seed zone development and amendment

18.3.1 Requests for review and amendment of *seed zone* boundaries will be decided by the director of the Forest Management Branch. Reviews will be based on ecological and genetic information.

18.3.2 Development of *species-specific seed zones* will require testing according to Standards 28.4 and 30.2.9.

18.4 Deployment of *Stream 2 materials*

Stream 2 materials originating from programs for *CPP regions* listed in Appendix 19 may be registered and deployed prior to *CPP* plan approval provided the following conditions are met:

- *Controlled parentage program production population* contains only *locally adapted material*;
- previous project planning and implementation schedules are being followed;
- *production population* or *production unit (s)* meet FGRMS monitoring and reporting standards; and
- *deployment populations* meet FGRMS 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:

- *Controlled parentage program* plan approval has been obtained;
- proponent complies with *CPP* plan implementation schedule;
- *Controlled parentage program production population* contains only *locally adapted material*;
- *production population* or *production unit(s)* meet FGRMS and monitoring and reporting standards; and
- *deployment populations* meet FGRMS diversity and documentation standards.

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

- a schedule for progeny/clonal *test* establishment;
- a reference to approved Parent Tree Selection Report(s); and
- a reference, using *Alberta* (ATISC) 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 associated orchard(s). The total *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 estimated for the target strata over a rotation. An orchard or orchards with estimated *cumulative Ne* of 30 or more may produce material for *deployment* on up to 50% of the total area estimated for target strata over a rotation (Appendix 21A provides the method for calculating these *cumulative Ne deployment* levels). For *deployment* on areas greater than 50% of the total area estimated for the target strata, over a rotation, an acceptable *cumulative Ne* for output from the orchard(s), must be approved by *Alberta*. Note: This standard does not imply an area cap for *Stream 2* seed material *deployment* to strata, but does require ensuring that output from *production units* and *production populations(s)* maintains an acceptable landscape level *Ne* for proposed *deployment* on greater than 50% of the stratum area.

18.4.3.2 Vegetative Materials: Following the risk management process outlined in Appendices 1 and 9, restricted *deployment* of vegetative materials as clonal mixtures or clonal blocks for planting roads, landings, decking areas, voids in cutblocks and for oil and gas well sites may occur subject to meeting the following standards:

18.4.3.2.1. Total *deployment* shall be capped at a maximum of one million *ramets* per clone.

18.4.3.2.2. A minimum *Ne* of 18 must be met for each *opening*.

18.4.3.2.3. The total area deployed must not exceed 15% of the cutblock or *opening*. For oil and gas well sites less than 2.0 ha in size, the 15% area standard does not apply.

All other *deployment* strategies (e.g., *conversion*) must be approved by *Alberta* prior to *deployment* (Appendix 9).

- 18.4.4 *Deployment* numbers by proponent are presented in the FMP or Annual Operating Plans (AOP) and identified 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 *production population-planning* and reporting under a *CPP* plan.
- 18.4.5 Existing *CPP region* boundaries may be periodically reviewed and revised (see Standard 28.0).
- 18.4.6 Minor changes to existing *CPP region* boundaries may be made with the mutual consent of the 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 tests 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* (Provincial Seed Officer).
- 18.4.9 Where a block or harvest *opening* is intersected by a *CPP region* boundary, *deployment* of the *CPP region* stock is allowed within the full *opening* as long as the highest or lowest elevation of the block/*opening* is within 50 m of the *CPP region* elevation limits.

19.0 Deployment of Unregistered Material

- 19.1 *Wild* transplants and cuttings from within 5 km and 100 m elevation of the target planting site may be deployed without *registration*. These transplants and cuttings may not be multiplied or serially propagated.
- 19.2 For a single clone, a maximum of 5000 *propagules* may be deployed within the *seed zone* of collection.

20.0 In Situ Gene Conservation

- 20.1 *In situ* conservation for *Stream 1 material* or other species not identified in a *CPP* for a specific *seed zone* will be accommodated through the provincial gene conservation plan <http://srd.alberta.ca/forests/default.aspx>.

20.2 Between two and four areas of *wild* forest populations (as represented by species and stratum class, e.g., timber productivity rating, timber type) are required to be designated for gene conservation for each species included in a *CPP* plan, in each *seed zone* for which at least 15% of its gross area lies within the cooperators' areas of influence in the *CPP region* for that *CPP* plan. A single area may provide conservation for more than one species. The number of gene conservation areas required will depend on the area of *seed zone* contained within the cooperators' areas of influence in the *CPP region*-as follows:

Area of Seed Zone Within Cooperators' Areas of Influence in <i>CPP Region</i>	Number of Conservation Areas Required
> 1.0 million ha	4
0.5 – 1.0 million ha	3
< 0.5 million ha	2

Where less than 15% of a *seed zone* lies within the cooperators' areas of influence in the specified *CPP region*, gene conservation areas are not the responsibility of the cooperators.

For sizes of specific *seed zones*, see Appendix 7.

These 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 specifically from the core conservation area (see 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 from biological and non-biological threats. A consultative notation (CNT) is recommended for these areas.

20.7.3 Areas will be large enough to meet a reasonable expectation of 5000 trees of the target species (at rotation) in a core area with an additional buffer of 500 m around it.

20.7.4 The target species as identified in the *CPP* plan will be managed as per the options specified in Standards 20.2 and 21.1.3.

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* standards are being met. 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.

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 gene conservation will be described in the FMP, which will also include a statement of intended management on a time horizon of two rotations.

21.2 Reporting

21.2.1 Compliance monitoring of *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/type of material will be reported.

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

21.2.2 *Deployment* of all registered material will be reported annually to *Alberta* in the Alberta Regeneration Information System (ARIS).

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

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

21.2.3.2 *deployment of unrestricted registration Stream 2 seed material* from a given *production population* exceeds 50% of the total area (Stream 1 and 2) reforested by stratum and species in a five year period.

21.2.3.3 clonal *deployment* of vegetative materials occurs on roads, landings, well sites and voids in harvest blocks as per Standard 18.4.3.2.

21.2.4 This 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 format.

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 (G&Y) monitoring will be as per FMP and FMA requirements.

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

23.0 Genetic Research Plantings

23.1 Research *tests* maybe 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 cumulative area of 85 ha must be addressed 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 (see Appendices 1, 18 and 24).

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

23.6 A standing approval can be requested for planting material from subsequent collections from the same source.

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, 24).

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

BREEDING, TESTING AND VERIFICATION (BTV)

Goals

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

- use testing, analysis and documentation protocols that are effective, efficient and scientifically sound, and
- be designed to ensure long-term flexibility in direction and development of *CPPs*, and
- produce reliable estimates of *genetic gain* when gain is included as an objective of the *CPP* plan.

BTV Standards

24.0 Controlled Parentage Programs (CPPs)

24.1 Proponent(s) of *CPPs* 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 wholly 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 *CPPs* 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 6 months of receipt.

24.2.1 For establishment of *CPP* plans and *CPP* regions 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 the director of the Forest Management Branch 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 intended to produce *Stream 2 material* will identify the following for all *CPP* materials (see Appendices 21A and 21B):

- the total area (ha) by participating tenure holder within the target *CPP* region,
- the total operable area (ha) by tenure holder within the *CPP* region,
- the target strata (species by *CPP* region, not necessarily yield stratum) for which the *Stream 2 production population(s)* is designed,
- the total area (ha) of target strata by tenure holder.

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

- estimated plants required for 100% planting of target strata area per rotation for each participating tenure holder,
- estimated annual number of seedlings from a *production population* allocated to each participating tenure holder, and
- provide 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.

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

24.5 Revisions to CPP Plans

24.5.1 When significant changes occur, revised *CPP* plans will be submitted to *Alberta* (ATISC) for review. *Alberta* will respond within three months of submission.

25.0 Research Programs

25.1 All genetic testing 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 and 24).

25.1.1 Proponents of RP plans will submit plans for *Alberta's* (ATISC) 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.

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" (see Appendix 29).

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

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

- will review all relevant scientific information on a case-by-case basis to evaluate the risks and benefits of *deployment*, and
- 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 standards in Standards 23.0 and 30.0.

25.5 All unregistered material destined for testing on *public land* or for inclusion in a breeding/*base population* to be deployed on *public land* will be labelled using *U.I.s* (see Appendix 25 for codes and Appendices 11A, 11B, 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 the director of the Forest Management Branch 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 Agencies and companies involved in *controlled parentage* and research programs with the intent of developing genetic material for *deployment* on *public land* will maintain and submit to *Alberta* (ATISC) 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*. This report(s) will include:

26.1.1.1 completed parent tree forms (see Appendices 11A, 11B, 12 and 15),

26.1.1.2 an introduction summarizing the objective, timing, participants, general location and any other information of interest, and

26.1.1.3 a map to scale with locations of parent trees plotted 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 plan, an electronic listing will be prepared, in ASCII or another previously agreed-upon format that will allow the unambiguous identification of each *test* tree in the field when accompanied by the appropriate map(s). This listing will contain:

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

27.2 This file will be submitted to *Alberta* (ATISC) 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* (ATISC) 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 *Alberta* requires submission of any edited data sets used to support claims of adaptation, diversity or performance of *tests* established under *CPP* or RP plans.

27.9 *Alberta* (ATISC) will provide upon request, cooperators with checked raw *test* data in ASCII format, along with required supporting documentation, contingent on the cooperator's right to such material and knowledge.

28.0 Planning, Delineation and Revision of Controlled Parentage Program Regions and Species-Specific Seed Zones

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 Establishment of *species-specific seed zones* will require an RP plan and genetic provenance testing for adaptation (see Standard 30.2.9).

28.5 Material originating from outside the *CPP region* shall, prior to inclusion in a *production population*, be tested for adaptation or approval obtained from *Alberta* for material to be deemed equivalent - to - local based on surrogates of 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 of genetic material. Documentation on genetic material identity will be made available to *Alberta*.

29.2 Samples of genetic tests – *public land*

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

29.3 Samples of genetic tests – private land

29.3.1 When genetic *tests* 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 it is destroyed. A *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 a *MTA* may be required.

29.4.2 Notification and access to the clonal material will be provided to SRD 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 for 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 plan 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:

- Follow procedures outlined in the example report “Genetic Analysis Report for Region E White Spruce Tree Improvement”. An example report is posted on the web at <http://srd.alberta.ca/forests/managing/manuals.aspx>;
- Submit a proposal to *Alberta* for alternate procedures. *Alberta* must approve any alternative procedures prior to analysis being initiated.

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 The period of adaptation testing required for *non-local material* included in the *CPP* will be determined through consultation with *Alberta*.
- 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 can 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 from 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) and through 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 regions* or *seed zone* boundaries, the number of *test sites* will be specified in the *CPP* or RP plan.
- 30.2.9 For establishment of *species-specific seed zones*, the number of *test sites* will be specified in the RP plan.
- 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:
- geographical and ecological proximity,
 - rotation length,
 - taxonomy and potential to hybridize with local material, and
 - *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 actual or proposed *CPP region* or *seed zone*.
- 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 (see Appendix 29) must be submitted for each *test site* at least six months prior to *test materials* being deployed in the *Green Area*. Approved *trials* will be issued a *trial number* by *Alberta* (ATISC) and completed Genetic Test Site Information Forms are to be submitted with *trial Establishment Reports* (see Appendices 26 and 29).

30.4 Site protection

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

30.5 Field marking

- 30.5.1 Field marking will be established and maintained that allows for identification of each *test* tree, complete with an establishment report map(s) and description 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. (available at FGRMS website <http://srd.alberta.ca/forests/managing/manuals.aspx>).

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 code 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 accurate 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 centimetre).
- 30.10.3 Height will be measured to within 5% of the check value 95% of the time across the *test series*, based on the use of standard measurement equipment, measurement procedures and sampling precision.
- 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 95% 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* (ATISC) 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* (ATISC) 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 an average value expected for specific traits. *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:

- associated RP plans,
- results of genetic *tests* (e.g., *genetic worth* calculation – Appendix 31),
- literature review,
- expert opinion,
- results from other programs, and
- other relevant information.

31.3 Any increase to the Annual Allowable Cut (AAC) attributable to *genetic gain* must be approved through the FMP process.

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:

$$\text{Minimum age in years} = 4 + 0.1 \times (\text{midpoint of rotation age class})$$

As shown in Table 1 below.

Table 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:

- performance for adaptive traits from field *tests*,
- geographic proximity,
- ecological compatibility,
- genetic distance, and
- 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:

- in *Alberta* approved *production sites*, *production units* and/or *production populations* using established procedures,
- 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
- 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* (ATISC). An application will include a risk assessment that will address the following where appropriate:

- pollen contamination for proposed orchard(s),
- infrastructure (e.g., roads, water source, labour supply, expansion capability, *production site* modification),
- environment,
- potential pest risks,
- security in space and time, and
- preconditioning/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 notation.

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

32.5 Production of controlled parentage materials must be integrated with an approved *CPP* plan. 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 production 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 units will provide *Alberta* with information supporting approval.

32.8 Continued compliance with approval conditions is required to maintain an 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 February 28 of the year following establishment as outlined (see Appendix 32). A sample establishment report is available on the *Alberta* website <http://srd.alberta.ca/forests/managing/manuals.aspx>.
- 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 protocol (see Appendix 34B) and reporting as required in Appendix 35A.
- 32.8.4 An annual operations report shall be submitted to *Alberta* (ATISC) by March 31 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* of 18.
- 33.2 Orchards must be designed using specialized design software (e.g., SOL32 or SOMAD).
- 33.3 *Deployment population genetic worth* is calculated according to the procedures outlined in Appendix 31.
- 33.4 *Effective population size* is calculated according to procedures outlined in Appendices 36 and 37.
- 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 and provided upon request for possible auditing.
- 33.4.3 Where the aggregate of *deployment populations* from *production unit(s)* (*seed orchard(s)*) with *cumulative Ne* of less than 30 has reached its limit for total production (see Standard 18.4.3 and Appendix 21A), a replacement *production population* will be required. The aggregate of the *production unit(s)* associated with both the new *production population* and the previous *production population* must be capable of producing *deployment populations* (orchard crops) with a *cumulative Ne* of at least 30. Appendix 20 provides details of methods for calculating *cumulative Ne*.
- 33.4.4 The aggregate *deployment populations* from a *rolling front orchard* (*production unit* representing a *production population*) must have a *cumulative Ne* of at least 30 by the time 50% of the target strata area has been regenerated with that material (see Appendix 21A). Appendix 20 provides details of methods for calculating *cumulative Ne*.
- 33.5 The *genetic identity*, and where available the *pedigree*, of *seed orchard* parents must be maintained.
- 33.6 Documentation for each *deployment population* (crop) must be submitted for *registration* (see Appendix 3).
- 33.7 *Alberta* (ATISC) will assign a *production unit* identifier for approved seed *production populations* and associated *production units* (see Appendix 35A for reporting).

34.0 Vegetative Materials Production

34.1 *Deployment population genetic worth* is calculated according to procedures in Appendix 31.

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*.

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 and provided upon request for possible auditing.

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

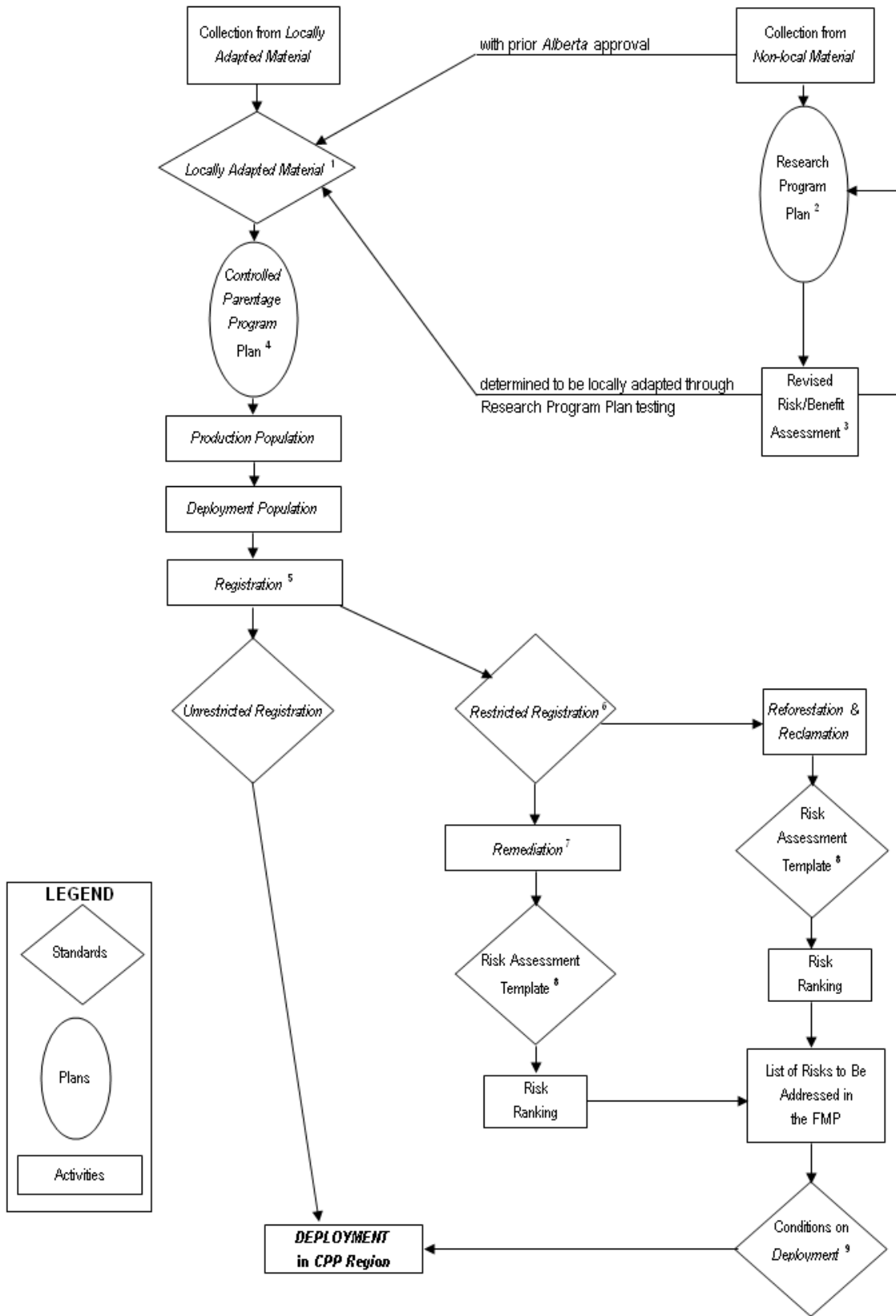
34.5 Documentation for each *deployment population* (crop) must be submitted for *registration* (see Appendix 3).

34.6 Alberta (ATISC) 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 *Ne* Requirements for Registration of *Stream 2 Material*; also, 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.

Appendix 2. Registration Request Form - Stream 1

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

All forest tree 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* (Provincial Seed Officer) assigns a *registered lot number* once *registration* is complete.



STREAM 1 REGISTRATION REQUEST (APPENDIX 2 FGRMS)

1. ADMINISTRATIVE INFORMATION				
OWNER/ADDRESS		(For Department Use Only)		
		SIMS INVENTORY NO.		
		REGISTRATION CATEGORY <input type="checkbox"/> UNRESTRICTED <input type="checkbox"/> RESTRICTED <input type="checkbox"/> PENDING REGISTRATION*		
REGISTERED LOT NUMBER (For Department Use Only)				
2. STAND AND SITE INFORMATION				
SPECIES			GENETIC CLASS 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	TO	max	SEED ZONE
LEGAL LOCATION				
PROVIDE LATITUDE & LONGITUDE INFORMATION BELOW. Record the four most outside collection points to the degrees/minutes/seconds. 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. (degrees° minutes' seconds" format style)				
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 <input type="checkbox"/>	Felled trees <input type="checkbox"/>	Slash <input type="checkbox"/>	Cuttings <input type="checkbox"/>	
Climbing/ladder/lift <input type="checkbox"/>		Squirrel cache <input type="checkbox"/>		Hand picked <input type="checkbox"/>
MECHANICALLY PICKED <input type="checkbox"/>				
COLLECTION DATES		NUMBER OF TREES FROM WHICH THE COLLECTION WAS MADE ³		
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	
REMARKS			COMPANY	
6. EXTRACTION AND CLEANING INFORMATION (TO BE COMPLETED BY PROCESSING FACILITY FOR SEED ONLY)				
DATE RECEIVED	DATE(S) EXTRACTED	AMOUNT CLEANED (KG)	SEED MOISTURE CONTENT	
Approval Decision (Department use only)				
Approved by			Date	

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

* Pending fulfillment of all requirements for registration such as adequate number of trees sampled.

² See code listing in Appendix 6 STIA.

³ Provide exact number of trees if minimum trees per collection for unrestricted registration (see table in Appendix 4) has not been exceeded; provide estimates if minimum number of trees has been exceeded.

Appendix 3. Registration Request Form - Stream 2

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



STREAM 2 REGISTRATION REQUEST (APPENDIX 3 FGRMS)

1. ADMINISTRATIVE INFORMATION			
TEMPORARY LOT NO.	(FOR DEPARTMENT USE ONLY)		
REGISTERED LOT NO. <small>(FOR DEPARTMENT USE ONLY)</small>	SIMS INVENTORY No.		
APPROVED PRODUCTION UNIT or PRODUCTION POPULATION NO.	REGISTRATION CATEGORY		
PRODUCTION SITE LOCATION(S)	<input type="checkbox"/> UNRESTRICTED <input type="checkbox"/> RESTRICTED <input type="checkbox"/> PENDING REGISTRATION		
2. OWNERSHIP			
COMPANY	% OF LOT ALLOCATED		
3. GENETIC INFORMATION			
SPECIES	OPP Region		
EFFECTIVE POPULATION SIZE	GENETIC WORTH	GENETIC CLASS CODE	
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 CONTENT
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)			
Approved by		Date	

Appendix 4. Collection Requirements for Registration of Stream 1 Material

See Standards 10.4, 10.6, 10.8, 10.12, 11.4, 18.2.4 and 20.6.

Point Collections: Where collections meet the number, area and elevation requirements as shown in the table and are 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. These 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).

Seed Zone Collections: Where collections do not meet the area and elevation requirements in the table but are collected within a *seed zone* and meet the minimum number requirements in the table below and *Stream 1 unrestricted registration* requirements, this collection is eligible for *registration*. *Deployment* is limited to a total of 5 million seedlings/*propagules* per lot. Variance requests for *deployment* outside the *seed zone* of origin will not be considered.

Restricted Registration Collections: Collections not fully meeting *Point* 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 trees specified below) may be collected and stored, pending fulfillment of *registration* requirements (including combining lots from the same *seed zone* to meet *registration* requirements).

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

Table of Requirements for Point Collections of Stream 1 Material

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

¹ Proponents are encouraged to make *Stream 1* collections from *wild* stands within *in situ* conservation areas (see Standard 20.2) and adjoining areas to ensure that *wild* genetic resources are preserved.

² Collections from trees fewer than listed in this column may be stored “pending registration” (see Appendix 2) and will only be registerable where combined to meet *unrestricted* or *restricted registration* requirements.

³ Must be collected from clones separated by at minimum of 500 m.

⁴ Must be collected from trees separated by at least 10 m.

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

See Standards 10.4, 10.9 and 10.12.

Effective population size (Ne) requirements for registration of Stream 2 reforestation seed or vegetative material destined for deployment on Green Area Public Land.

Stream 2 material	Ne (effective population size) ¹	Registration category	Maximum deployable numbers from a production population
Seedlots	$\geq 18^1$	Unrestricted	see Appendix 21A
Vegetative lots	$\geq 18^1$	Unrestricted	see FGRMS 18.4.3.2
Seedlots	$6 - 18^2$	Restricted	see Appendices 1, 9
Vegetative lots	$6 - 18^2$	Restricted	see Appendices 1, 9
Seedlots	$< 6^{2,3}$	pending registration	None
Vegetative lots	$< 6^{2,3}$	pending registration	None

¹See Appendix 36 for *Ne* calculation methods.

²Lots 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 *CPP region*. See Appendix 20 for calculation methods.

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

Appendix 6. Stream Categories and Genetic Class Codes for Genetic Material

See Standards 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 from wild stands		
1. Unselected parents from unselected stands	1	AIa1
2. Unselected parents from selected stands ²	1	AIa2
3. Selected parents ² from unselected stands	1	AIa3
4. Selected parents ² from selected stands ²	1	AIa4
b. Native seed collections from artificially regenerated stands		
5. Unselected parents from unselected stands	1	AIb5
6. Unselected parents from selected stands ²	1	AIb6
7. Selected parents ² from unselected stands	1	AIb7
8. Selected parents ² from selected stands ²	1	AIb8
c. Seed collections from <i>production units</i>³		
9. Improved orchard	2	AIc9
10. Unimproved orchard	2	AIc10
11. Seedlot with $N_e < 18$ (<i>registration restricted</i>) ⁴	2	AIc11
12. <i>Hybrid orchard</i> ⁵	2	AIc12
13. <i>Non-local material</i>	2	AIc13
14. <i>Genetically Modified Organisms GMOs</i>	2	AIc14

List of Potential Precursor Materials for Deployment on Provincial Public Land

a. Local seed		
15. Individual family	R	
16. Pollen	R	
17. <i>GMOs</i>	R	
b. Non-local seed		
18. Provenances	R	
19. Species	R	
20. Hybrids	R	
21. Individual family	R	
22. <i>GMOs</i>	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 Codes 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 from wild stands⁵		
1.	Unselected parents from unselected stands	1	BIa1
2.	Unselected parents from selected stands	1	BIa2
3.	Selected parents ² from unselected stands	1	BIa3
4.	Selected parents ² from selected stands	1	BIa4
b.	Native propagule collections from artificially regenerated stands		
5.	Unselected parents from unselected stands	1	BIb5
6.	Unselected parents from selected stands	1	BIb6
7.	Selected parents ² from unselected stands	1	BIb7
8.	Selected parents ² from selected stands	1	BIb8
c.	Propagules generated from production units or production populations³		
9.	Selected population	2	BIc9
10.	Tested population	2	BIc10
11.	Lot with $N_e < 18$ (<i>registration restricted</i>) ⁴	2	BIc11
12.	<i>Amplified family</i>	2	BIc12
13.	Hybrids	2	BIc13
14.	<i>Non-local material</i>	2	BIc14
15.	<i>GMOs</i>	2	BIc15

List of Potential Precursor Materials for Deployment on Provincial Public Land

a.	Local material	
16.	Individual family	R
17.	Individual clones	R
18.	Pollen	R
19.	<i>GMOs</i>	R
b.	Non-local material	
21.	Provenance material	R
22.	Species material	R
23.	Hybrid material ⁶	R
24.	Individual clones	R
25.	Pollen	R
26.	<i>GMOs</i>	R

Stream 1 = traditional *reforestation* stream (see glossary)

Stream 2 = controlled parentage stream (see glossary)

R = *research material* (see glossary)

¹ Genetic Class Codes 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 Production units and populations 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 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).

⁶ Hybrid with at least one non-local parent.

Appendix 7. Seed Zone Descriptions, Areas and Maps

See Standards 10.8, 18.2.1 and 20.2.

Populations of forest tree species exhibit genetic variation associated with differences in the 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 seed to *reforestation* sites on *public land* is regulated.

Seed Zones

A seed zonation system for Alberta has been developed for natural seed movement and will replace the existing 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 criteria. They limit seed movement to a conservative area where native trees of all species can be moved without risk of mal-adaptation or erosion of genetic integrity. Seed collections from natural stands of all species within a *seed zone* meeting *unrestricted registration* requirements can be moved without restriction. 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*.

The Forestry Seed Zones of Alberta are delineated for all areas of Alberta and are inclusive for 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, with emphasis on tree 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.

Seed zone labelling is structured so that:

- a. the designated alphabetic descriptor denotes the Natural Subregion which the *seed zone* falls in;
- b. the number preceding the decimal designates groupings of *seed zones* within a subregion that are more similar in climate; and
- c. the decimal portion designates the individual *seed zone* within a climate grouping and numbering generally follows a pattern of decreasing continentality.

The *seed zones* are listed in Table 1 and mapped in the three subsequent figures.

Seed zone delineation will be periodically reviewed and updated to incorporate any significant boundary changes to the Natural Regions, Natural Subregions or Ecodistricts.

For seed zone digital line work and maps contact the Alberta Tree Improvement and Seed Centre, Sustainable Resource Development at phone number (780) 656-5072.

Table 1. Seed Zone Numbers, Areas and Names

SEEDZONE LABEL	AREA IN HECTARES	NATURAL SUBREGION	SEED ZONE NAME
A 1.1	341810.8	Alpine	Kakwa-Athabasca Alpine
A 1.2	572905.6	Alpine	Athabasca-Kootenay Alpine
A 1.3	491421.7	Alpine	Kootenay-Bow Alpine
A 1.4	86943.2	Alpine	Bow-Crowsnest Alpine
A 1.5	15371.2	Alpine	Crowsnest-Waterton Alpine
AP 1.1	1352525.6	Athabasca Plain	Athabasca Plain
BSA 1.1	952530.5	Boreal Subarctic	Caribou Mountains Boreal Subarctic Uplands
BSA 1.2	229741.8	Boreal Subarctic	Cameron Hills Boreal Subarctic Uplands
CM 1.1	1675648.5	Central Mixedwood	Great Slave Central Mixedwood Plains
CM 1.2	1209779.7	Central Mixedwood	Vermillion Central Mixedwood Lowlands
CM 1.3	1739402.7	Central Mixedwood	Hay River Central Mixedwood Lowlands
CM 2.1	1243579.2	Central Mixedwood	Saskatchewan Central Mixedwood Plains
CM 2.2	1384867.1	Central Mixedwood	Mackay Central Mixedwood Lowlands
CM 2.3	1103601.7	Central Mixedwood	Loon Lake Central Mixedwood Lowlands
CM 2.4	1786122.0	Central Mixedwood	Wabasca Central Mixedwood Lowlands
CM 3.1	2524587.7	Central Mixedwood	Mostoos Hills Central Mixedwood Uplands
CM 3.2	1301522.9	Central Mixedwood	Swan Hills-Pelican Central Mixedwood Uplands
CM 3.3	1402207.2	Central Mixedwood	Swan Hills-Utikuma Central Mixedwood Uplands
CM 3.4	992845.8	Central Mixedwood	Wapiti-Smoky Central Mixedwood Uplands
CM 3.5	421437.0	Central Mixedwood	Drayton Central Mixedwood Plains
CP 1.1	3487578.3	Central Parkland	Northern Central Parkland Plains
CP 1.2	1883038.0	Central Parkland	Southern Central Parkland Plains
DM 1.1	1476414.8	Dry Mixedwood	Vermillion Dry Mixedwood Lowlands
DM 1.2	1736061.1	Dry Mixedwood	Peace River Dry Mixedwood Lowlands
DM 1.3	1704193.5	Dry Mixedwood	Smoky River Dry Mixedwood Lowlands
DM 2.1	1138703.2	Dry Mixedwood	Lac La Biche Dry Mixedwood Plains
DM 2.2	1951238.3	Dry Mixedwood	Edmonton Dry Mixedwood Plains
DM 2.3	525542.8	Dry Mixedwood	Red Deer Dry Mixedwood Plains
DMG 1.1	4693718.1	Dry Mixedgrass	Southeastern Dry Mixedgrass Plains
FF 1.1	1362344.8	Foothills Fescue	Southwestern Foothills Fescue
FP 1.1	355167.2	Foothills Parkland	Southwestern Foothills Parkland
FP 1.2	37001.8	Foothills Parkland	Waterton Foothills Parkland
KU 1.1	971879.6	Kazan Uplands	Kazan Upland
LBH 1.1	624397.6	Lower Boreal Highlands	Bistcho Lower Boreal Highlands
LBH 1.2	469631.8	Lower Boreal Highlands	Caribou Mountains Lower Boreal Highlands
LBH 1.3	1042175.7	Lower Boreal Highlands	Birch Mountains Lower Boreal Highlands
LBH 1.4	595418.8	Lower Boreal Highlands	Buffalo Head Hills Lower Boreal Highlands
LBH 1.5	665699.1	Lower Boreal Highlands	Stony Mountain Lower Boreal Highlands
LBH 1.6	1985730.4	Lower Boreal Highlands	Clear Hills Lower Boreal Highlands
LBH 2.1	178449.6	Lower Boreal Highlands	Cameron Hills Lower Boreal Highlands
LF 1.1	253335.0	Lower Foothills	Pelican Mountains Lower Foothills
LF 1.2	295218.4	Lower Foothills	Saddle Hills Lower Foothills
LF 1.3	952135.0	Lower Foothills	Swan Hills Lower Foothills
LF 1.4	779499.8	Lower Foothills	Wapiti-Athabasca Lower Foothills
LF 1.5	999586.3	Lower Foothills	McLeod-North Saskatchewan Lower Foothills
LF 2.1	663891.0	Lower Foothills	Athabasca-McLeod Lower Foothills

SEEDZONE LABEL	AREA IN HECTARES	NATURAL SUBREGION	SEED ZONE NAME
LF 2.2	335231.0	Lower Foothills	Brazeau-Clearwater Lower Foothills
LF 2.3	211005.0	Lower Foothills	Clearwater-Bow Lower Foothills
M 1.1	30947.5	Montane	Cypress Hills Montane
M 2.1	48420.3	Montane	Grande Cache Montane
M 2.2	33608.0	Montane	Jasper Lower Montane
M 3.2	94234.8	Montane	Jasper Upper Montane
M 4.1	17078.1	Montane	Kootenay Lower Montane
M 4.2	2170.1	Montane	Ya Ha Tinda Montane
M 4.3	71656.7	Montane	Bow Lower Montane
M 4.4	139315.8	Montane	Bow-Porcupine Lower Montane
M 4.5	137018.7	Montane	Crowsnest Lower Montane
M 5.1	25296.9	Montane	Kootenay Upper Montane
M 5.3	77028.8	Montane	Bow Upper Montane
M 5.4	102078.3	Montane	Bow-Old Man Upper Montane
M 5.5	20759.1	Montane	Porcupine Hills Upper Montane
M 5.6	77161.1	Montane	Crowsnest Waterton Upper Montane
MG 1.1	1719775.7	Mixedgrass	Western Mixedgrass Plains
MG 1.2	38335.2	Mixedgrass	Sweetgrass Mixedgrass Uplands
MG 1.3	249065.5	Mixedgrass	Cypress Hills Mixedgrass Uplands
NF 1.1	1493334.8	Northern Fescue	Northern Fescue Plains
NM 1.1	2380309.9	Northern Mixedwood	Great Slave Northern Mixedwood Plains
NM 2.1	571010.5	Northern Mixedwood	Bistcho Lake Northern Mixedwood Uplands
PAD 1.1	553545.0	Peace-Athabasca Delta	Peace-Athabasca Delta Plains
PRP 1.1	312042.3	Peace River Parkland	Peace River Parkland Lowlands
SA 1.1	574366.7	Subalpine	Wapiti-Athabasca Lower Subalpine
SA 1.2	307193.1	Subalpine	Athabasca-Kootenay Lower Subalpine
SA 2.1	385373.6	Subalpine	Wapiti-Athabasca Upper Subalpine
SA 2.2	333915.4	Subalpine	Athabasca-Kootenay Upper Subalpine
SA 3.1	270422.0	Subalpine	Kootenay-Bow Lower Subalpine
SA 3.2	172154.3	Subalpine	Bow-Crowsnest Lower Subalpine
SA 3.3	65628.1	Subalpine	Crowsnest-Waterton Lower Subalpine
SA 4.1	232365.2	Subalpine	Kootenay-Bow Upper Subalpine
SA 4.2	139366.3	Subalpine	Bow-Crowsnest Upper Subalpine
SA 4.3	41063.9	Subalpine	Crowsnest Waterton Upper Subalpine
UBH 1.1	601181.3	Upper Boreal Highlands	Birch Mountains Upper Boreal Highlands
UBH 1.2	168899.6	Upper Boreal Highlands	Buffalo Head Upper Boreal Highlands
UBH 1.3	415742.6	Upper Boreal Highlands	Clear Hills Upper Boreal Highlands
UF 1.1	215721.1	Upper Foothills	Swan Hills Upper Foothills
UF 1.2	85115.6	Upper Foothills	Mayberne Upper Foothills
UF 1.3	912816.1	Upper Foothills	Wapiti-Athabasca Upper Foothills
UF 1.4	471903.8	Upper Foothills	Athabasca-North Saskatchewan Upper Foothills
UF 1.5	196392.0	Upper Foothills	North Saskatchewan-Bow Upper Foothills
UF 2.4	75246.8	Upper Foothills	Brazeau Upper Foothills
UF 2.5	196549.1	Upper Foothills	Red Deer Upper Foothills

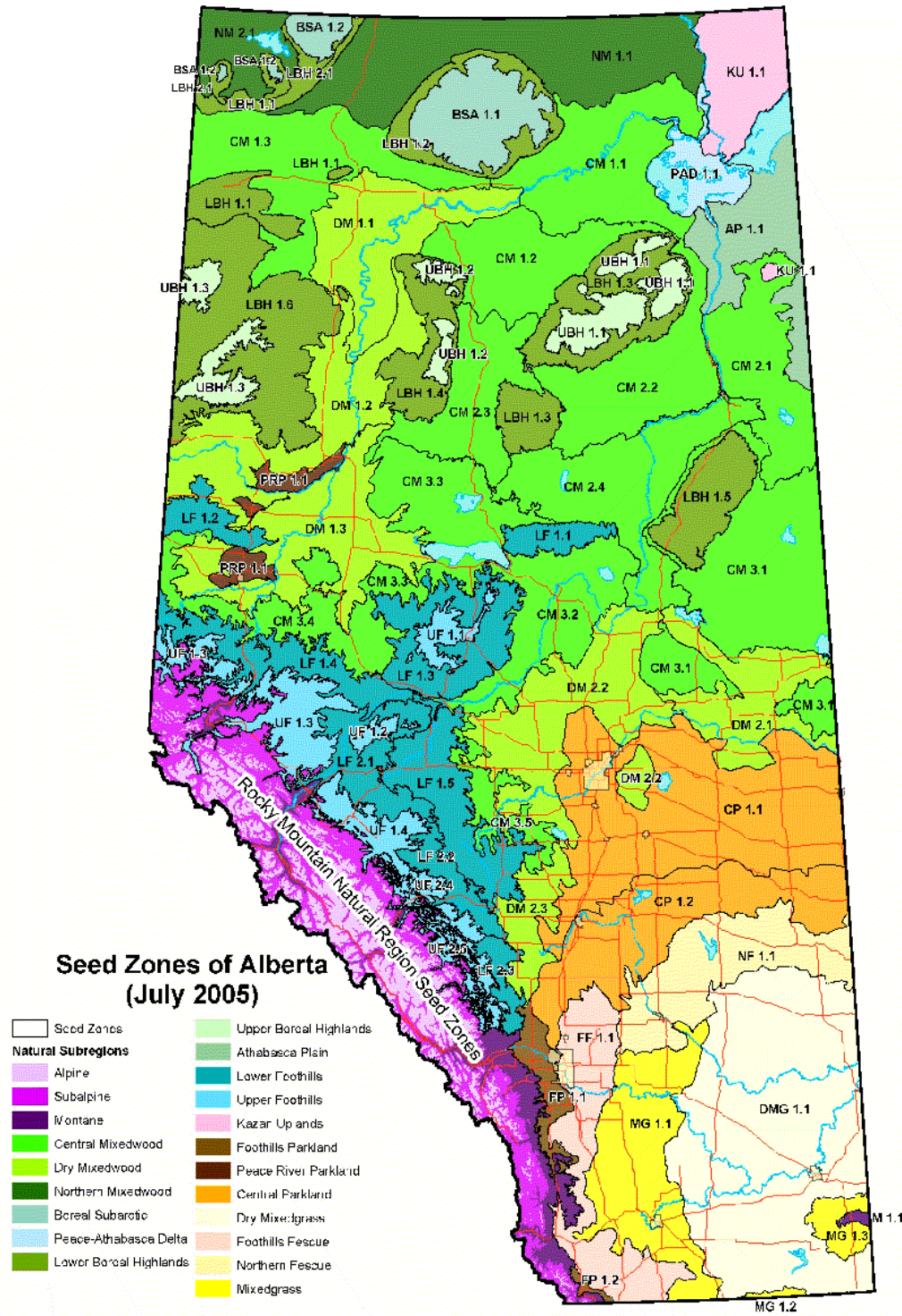


Fig. 1. Seed zones of Alberta, July, 2005.

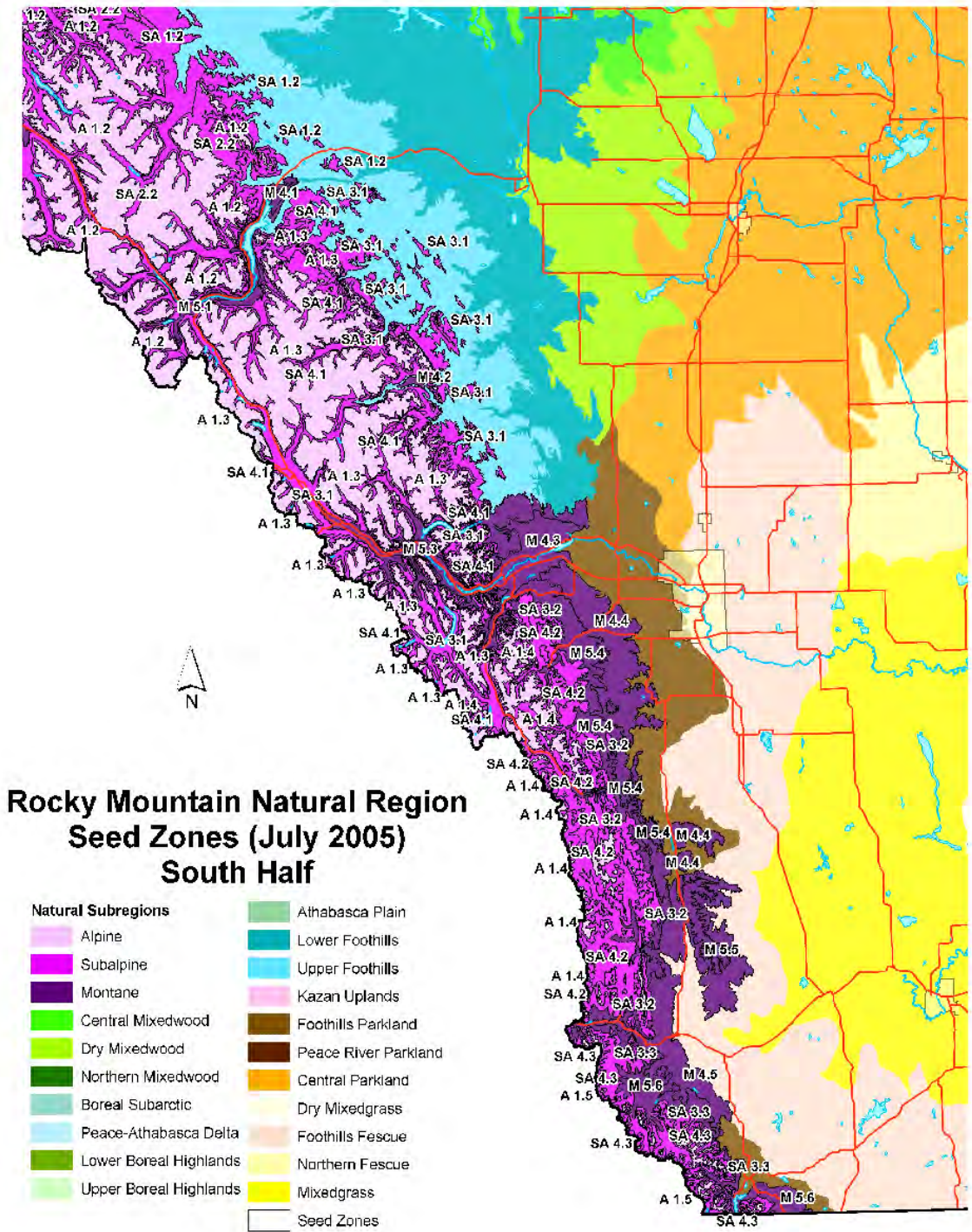


Fig. 2 Seed zones of Alberta, July, 2005: southern Rocky Mountains.

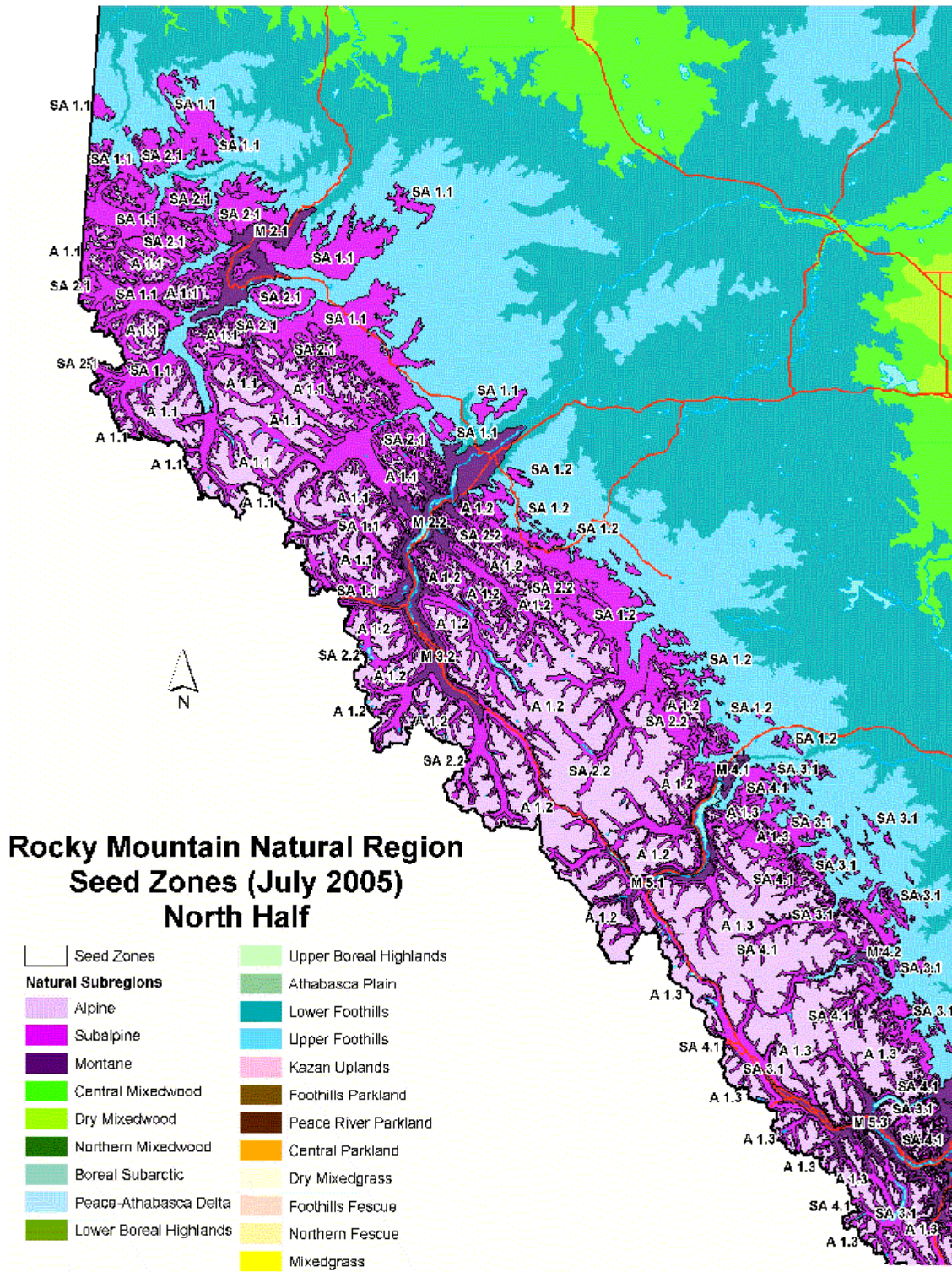


Fig. 3 Seed zones of Alberta, July, 2005: northern Rocky Mountains.

Appendix 8. Request for Deployment Variance for Stream 1 Material

See Standards 10.13, 18.2.4, 18.2.5 and 18.2.6.



STREAM 1 REQUEST FOR DEPLOYMENT VARIANCE (APPENDIX 8 F GRMS)

REQUESTING AGENCY		DATE _____	
Agency Name _____			
Mailing Address _____ _____			
Contact _____			
Phone _____		Fax _____	
E-mail _____			
REQUEST CATEGORY			
Lot has restricted registration <input type="checkbox"/>		and/or transfer outside of seed zone origin <input type="checkbox"/>	
TYPE OF VARIANCE REQUESTED			
<input type="checkbox"/> Annual		<input type="checkbox"/> Standing	
REASONS FOR REQUEST			
CROP DESCRIPTION			
Registered lot number _____	Species _____		
Seed Zone _____	Legal Location (to Section) _____	sec _____	twp _____ rge _____ W _____
Elevation Mean (m) _____	Elevation Range (m) _____	min _____	max _____
<input type="checkbox"/> Seed	<input type="checkbox"/> Seedling	<input type="checkbox"/> Vegetative	Crop size _____
PROPOSED DEPLOYMENT		ARIS Opening No(s) _____ Attach sheet for additional openings _____	
Seed Zone _____	Legal Location (to Section) _____	sec _____	twp _____ rge _____ W _____
Elevation Mean (m) _____	Elevation Range (m) _____	min _____	max _____
Years of Deployment (Standing Variance only) _____			
# of seedlings/propagules to be deployed in proposed deployment area _____			
PROPONENT/AGENCY			
Name _____		Position _____	
Signature _____		Date _____	
VARIANCE APPROVAL (DEPARTMENT USE ONLY)		Date _____	
<input type="checkbox"/> Approved		<input type="checkbox"/> Denied	
Approved with conditions <input type="checkbox"/>		Reviewed by _____	
Conditions _____		_____	
Variance No. _____			

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

See Standards 10.13, 18.4.1, 18.4.7, 22.2 and 24.4.1.

This risk assessment template is a generic form to be applied to *Stream 2 materials* and materials of *restricted registration*. It is to be applied at the stand and landscape levels as well as for plantings where seedlings or vegetative material are deployed as mixes or where materials are proposed for *deployment* as single clones or single-family blocks. Where a row in the matrix table is completed with “A”s, *deployment* risks and conditions for *registration* have been reviewed and addressed within the Forest Genetics Resource Management & Conservation Standards (FGRMS) review process. Where rows in the matrix are blank for a planned *CPP* plan 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.

Risk Assessment Template

Deployment objective ¹	Deployment Scenario						Landscape Level Risk ⁶			Stand Level Risk ⁶		
	Species/ Species Group	Seed or Veg	>18 Ne ²	Planting Strategy ³	Elk Size ⁴	Manage. Intensity ⁵	Genetic Sustainability ⁷	Ecosys Diversity ⁸	Ecosys Impact ⁹	Genetic Sustainability ⁷	Ecosys Diversity ⁸	Ecosys Impact ⁹
Reforestation	Conifer	Seed	>18	mixed	--	Non Conver	A	A	A	A	A	A
Reforestation	Conifer	Seed	>18	mixed	--	Plnt&VegMg	A	A	A	A	A	A
Reforestation	Conifer	Seed	>18	mixed	--	Plnt	A	A	A	A	A	A
Reforestation	Conifer	Seed	>18	family-blks	out	Non Conver						
Reforestation	Conifer	Seed	>18	family-blks	out	Plnt&VegMg						
Reforestation	Conifer	Seed	>18	family-blks	out	Plnt						
Reforestation	Conifer	Veg	>18	mixed	--	Non Conver	A	A	A	A	A	A
Reforestation	Conifer	Veg	>18	mixed	--	Plnt&VegMg						
Reforestation	Conifer	Veg	>18	mixed	--	Plnt						
Reforestation	Conifer	Veg	>18	clonal-blks	out	Non Conver						
Reforestation	Conifer	Veg	>18	clonal-blks	out	Plnt&VegMg						
Reforestation	Conifer	Veg	>18	clonal-blks	out	Plnt						
Reforestation	Conifer	Veg	>18	family-blks	out	Non Conver						
Reforestation	Conifer	Veg	>18	family-blks	out	Plnt&VegMg						
Reforestation	Conifer	Veg	>18	family-blks	out	Plnt						
Reforestation	Aspen	Seed	>18	mixed	--	Non Conver	A	A	A	A	A	A
Reforestation	Aspen	Seed	>18	mixed	--	Plnt&VegMg	A	A	A	A	A	A
Reforestation	Aspen	Seed	>18	mixed	--	Plnt	A	A	A	A	A	A
Reforestation	Aspen	Seed	>18	family-blks	out	Non Conver						
Reforestation	Aspen	Seed	>18	family-blks	out	Plnt&VegMg						
Reforestation	Aspen	Seed	>18	family-blks	out	Plnt						
Reforestation	Aspen	Veg	>18	mixed	--	Non Conver	A	A	A	A	A	A
Reforestation	Aspen	Veg	>18	mixed	--	Plnt&VegMg						
Reforestation	Aspen	Veg	>18	mixed	--	Plnt						
Reforestation	Aspen	Veg	>18	clonal-blks	in	Non Conver	A	A	A	A	A	A
Reforestation	Aspen	Veg	>18	clonal-blks	in	Plnt&VegMg						
Reforestation	Aspen	Veg	>18	clonal-blks	in	Plnt						
Reforestation	Aspen	Veg	>18	clonal-blks	out	Non Conver	A	A	A	A	A	A
Reforestation	Aspen	Veg	>18	clonal-blks	out	Plnt&VegMg						
Reforestation	Aspen	Veg	>18	clonal-blks	out	Plnt						
Reforestation	Aspen	Veg	>18	family-blks	out	Non Conver						
Reforestation	Aspen	Veg	>18	family-blks	out	Plnt&VegMg						
Reforestation	Aspen	Veg	>18	family-blks	out	Plnt						
Reforestation	Balsam Poplar	Seed	>18	mixed	--	Non Conver	A	A	A	A	A	A
Reforestation	Balsam Poplar	Seed	>18	mixed	--	Plnt&VegMg	A	A	A	A	A	A
Reforestation	Balsam Poplar	Seed	>18	mixed	--	Plnt	A	A	A	A	A	A
Reforestation	Balsam Poplar	Seed	>18	family-blks	out	Non Conver						
Reforestation	Balsam Poplar	Seed	>18	family-blks	out	Plnt&VegMg						
Reforestation	Balsam Poplar	Seed	>18	family-blks	out	Plnt						
Reforestation	Balsam Poplar	Veg	>18	mixed	--	Non Conver	A	A	A	A	A	A
Reforestation	Balsam Poplar	Veg	>18	mixed	--	Plnt&VegMg						
Reforestation	Balsam Poplar	Veg	>18	mixed	--	Plnt						
Reforestation	Balsam Poplar	Veg	>18	clonal-blks	in	Non Conver	A	A	A	A	A	A
Reforestation	Balsam Poplar	Veg	>18	clonal-blks	in	Plnt&VegMg						
Reforestation	Balsam Poplar	Veg	>18	clonal-blks	in	Plnt						
Reforestation	Balsam Poplar	Veg	>18	clonal-blks	out	Non Conver	A	A	A	A	A	A
Reforestation	Balsam Poplar	Veg	>18	clonal-blks	out	Plnt&VegMg						
Reforestation	Balsam Poplar	Veg	>18	clonal-blks	out	Plnt						
Reforestation	Balsam Poplar	Veg	>18	family-blks	out	Non Conver						
Reforestation	Balsam Poplar	Veg	>18	family-blks	out	Plnt&VegMg						
Reforestation	Balsam Poplar	Veg	>18	family-blks	out	Plnt						
Other ¹⁰												

Explanatory Notes for Risk Assessment Template:

- ¹Deployment Objective a) *Reforestation* – deploy a broad range of genetic material on largely intact (unaltered) substrate; includes roads and well site reclamation;
 b) *Remediation* – deploy a restricted range of genetic material on altered substrate to facilitate remediation (not included in current matrix).
- ²Effective Population Size (N_e) a) >18 - Current strategy/scenario matrix is for all *reforestation* material to have an N_e of 18 or greater;
 b) 12-18 - Only strategies/scenarios with N_e of 18 or greater are provided in the current matrix; proponent to propose a strategy/scenario line where one does not exist in the matrix table above;
 c) 6-12 - Only strategies/scenarios with N_e of 18 or greater are provided in the current matrix; proponent to propose a strategy/scenario line where one does not exist in the matrix table above.
- ³Planting Strategy a) Mixed – planting to occur as a 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.
- ⁴Block Size Refers to the size of blocks to be deployed
 a) “in” refers to sizes within the natural range of variability for a given region;
 b) “out” refers to sizes outside the natural range of variability for a given region.
- ⁵Management Intensity Refers to following management (silviculture) intensity categories:
 a) **Non Conver** – Stand “non-conversion” plantings including fill planting of small areas in cutblocks to remedy localized poor *reforestation* success due to natural site conditions as well as planting of in-block roads, landings and decking areas. Also includes oil and gas well sites where poor natural *reforestation* is expected due to site alteration;
 b) **Plnt&VegMg** – Planting of an entire cutblock or cutblocks across a large area with near-complete native vegetation control. Site is dominated by artificial regeneration material through use of vegetation management techniques;
 c) **Plnt** – Conventional artificial reforestation of a cutblock or cutblocks across large areas where there is minimal follow-up treatments to impact re-establishment of native vegetation. Site preparation is the only silvicultural management technique used.
- ⁶Stand and Landscape Risks a) Landscape – deals with risks associated with *deployment* with aggregate effects at the 10,000 ha scale;
 b) Stand – deals with risks at the cutblock level, 30-100 ha scale.
- ⁷Sustainability Can it persist through natural regeneration without needed management interventions or risk to sustained productivity due to inbreeding potential from reduced number of parents.
- ⁸Genetic Diversity Risks due to reduced genetic diversity enabling increased vulnerability to pests, weather, genetic recombination in hybrids and reduced evolutionary potential.
- ⁹Ecosystem Impacts Potential for deployed material to serve as centres for pest dispersal, weediness, gene flow and impacts on non-target species.
- Risk Ratings “A” in the matrix represents risks Accounted for with no additional conditions placed on *deployment* or monitoring as they have been accounted for through existing FGRMS standards.
- Other¹⁰ Other reforestation materials not currently covered in the matrix

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 11A. Parent Tree Selection Form – Wild Stand Comparison Tree Method

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* and is not appropriate for selecting and comparing putative clones which may be difficult to identify in the field and are often too dispersed to gather meaningful information on individual phenotype performance.



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 (dms)	degree	min	sec	SEED ZONE		
LONGITUDE (dms)	degree	min	sec	*LEGAL LOCATION	tpw range meridian	
ELEVATION (m)		STAND OR SITE TYPE				
*Stand Comments						
PARENT TREE AND MATERIALS COLLECTION INFORMATION						
SEX	MALE	<input type="checkbox"/>	FEMALE	<input type="checkbox"/>	UNKNOWN <input type="checkbox"/> MONOECIOUS <input type="checkbox"/>	
WOOD SAMPLE	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	COLLECTION DATE	
VEGETATIVE SAMPLE	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	COLLECTION DATE SCIONS <input type="checkbox"/> OTHER <input type="checkbox"/>	
OPEN POLLINATED SEED	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	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/disease/climate)						
Parent Tree Location and Access Information						
Parent Tree Location Map			Access Information			
Photo Attached Yes <input type="checkbox"/> No <input type="checkbox"/>			Map Attached Yes <input type="checkbox"/> No <input type="checkbox"/>		*Tree Marking	
Agency Representative		Signature		Date		
Approved for entry into Alberta Tree Improvement & Seed Centre Parent Tree Registry Yes <input type="checkbox"/> No <input type="checkbox"/> (Department use only)						
Approved by				Date		

¹Optional fields
¹ Trait coding as per the Superior Tree Selection/Collection Project – Comparison Tree Method manuals

Appendix 11B. Parent Tree Selection Form – Wild Stand Non-Comparison Tree Method

See Standards 11.1.6, 12.2, 25.5 and 26.1.1.1.



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 (dms)	degree	min	sec	SEED ZONE					
LONGITUDE (dms)	degree	min	sec	*LEGAL LOCATION	twp	range meridian			
ELEVATION (m)				STAND OR SITE TYPE					
*Stand Comments									
PARENT TREE AND MATERIALS COLLECTION INFORMATION									
SEX	MALE	<input type="checkbox"/>	FEMALE	<input type="checkbox"/>	UNKNOWN	<input type="checkbox"/>	MONOECIOUS	<input type="checkbox"/>	
WOOD SAMPLE	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	COLLECTION DATE				
VEGETATIVE SAMPLE	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	COLLECTION DATE	SCIONS	<input type="checkbox"/>	OTHER	<input type="checkbox"/>
OPEN POLLINATED SEED	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	COLLECTION DATE				
Trait [†]	Data/Score	Comments		Trait [†]	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)									
*Lat 11-20 yrs (mm)									
*Other Trait									
Parent Tree Location and Access Information									
Parent Tree Location Map				Access Information					
*Tree Marking									
Photo Attached	Yes	<input type="checkbox"/>	No	<input type="checkbox"/>	Map Attached	Yes	<input type="checkbox"/>	No	<input type="checkbox"/>
Agency Representative			Signature			Date			
Approved for entry into Alberta Tree Improvement & Seed Centre Parent Tree Registry Yes <input type="checkbox"/> No <input type="checkbox"/> (Department use only)									
Approved by				Date					

*Optional fields
† Trait coding as per the Superior Tree Selection Project Standards and Code Sheet for Field Use

Appendix 12. Parent Tree Selection Form – Genetic Test Materials

See Standards 11.1.6, 12.2, 25.5 and 26.1.1.1.



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 (dms)	degree	min	sec				
TRIAL CODE		LONGITUDE (dms)	degree	min	sec				
*LEGAL LOCATION	sec.	township	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	<input type="checkbox"/>	FEMALE	<input type="checkbox"/>	UNKNOWN	<input type="checkbox"/>	MONOECIOUS	<input type="checkbox"/>	
WOOD SAMPLE	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	COLLECTION DATE				
VEGETATIVE SAMPLE	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	COLLECTION DATE	SCIONS	<input type="checkbox"/>	OTHER	<input type="checkbox"/>
OPEN POLLINATED SEED	YES	<input type="checkbox"/>	NO	<input type="checkbox"/>	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		degree	min	sec.	Latitude		degree	min	sec
Longitude		degree	min	sec.	Longitude		degree	min	sec
Elevation (m)				Elevation (m)					
GENERAL REMARKS:									
Agency Representative			Signature			Date			
Photo of selected tree attached			<input type="checkbox"/> Yes			<input type="checkbox"/> No			
Approved for entry into Alberta Tree Improvement & Seed Centre Parent Tree Registry: Yes <input type="checkbox"/> No <input type="checkbox"/> (Department use only)									
Approved by					Date				

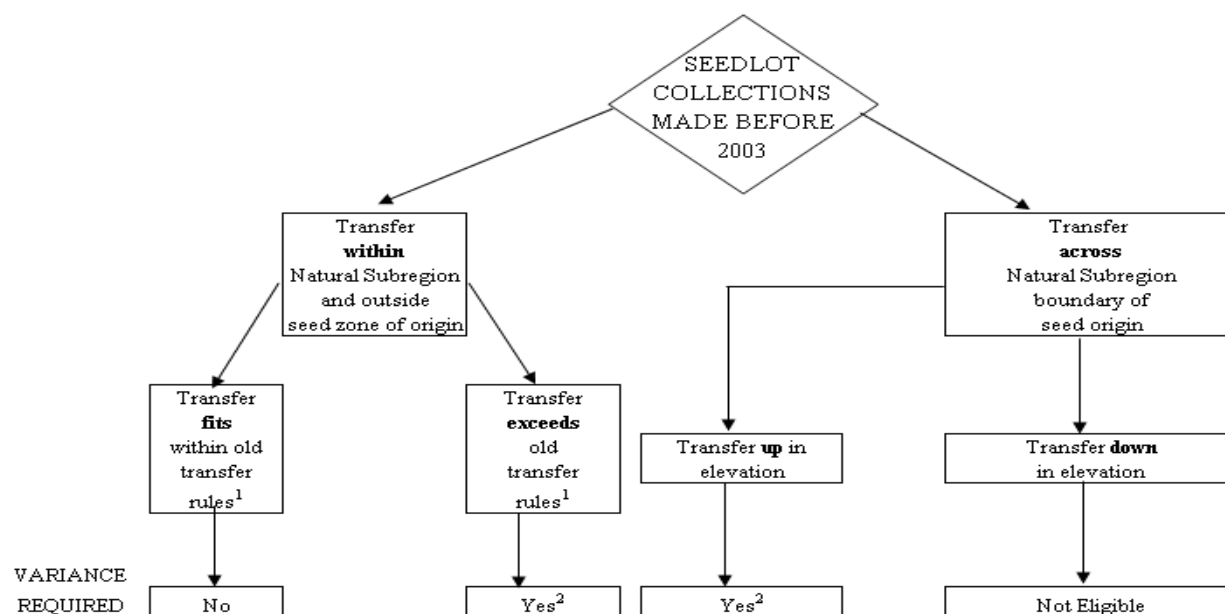
*Optional fields

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

See Standards 10.8, 18.2.2 and 18.2.4.

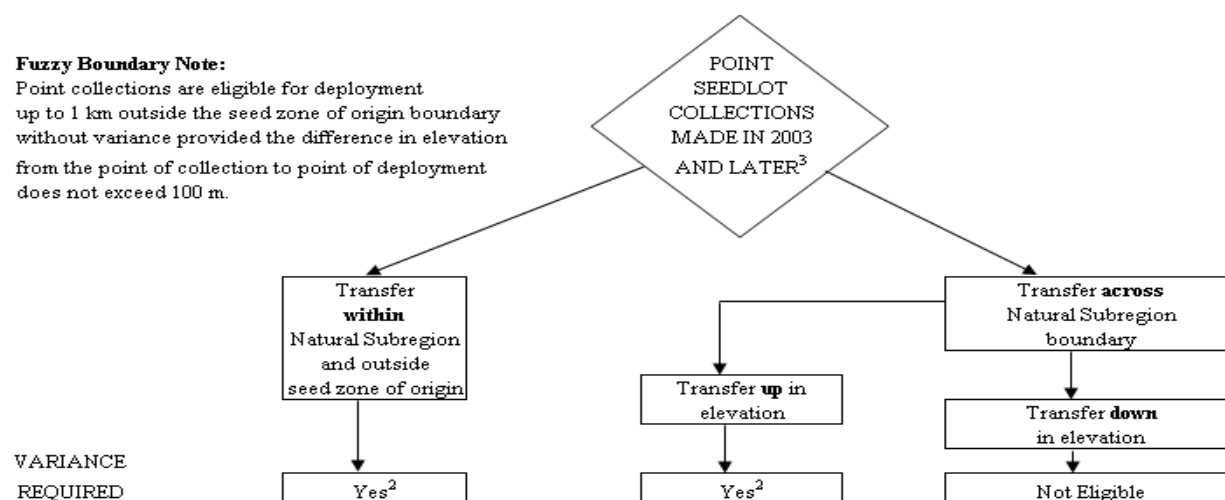
This transfer decision tree is based on seedlot type, seed collection and use history, ecological classification and results from Alberta conifer provenance tests and climate transfer analyses which show:

- moderate movement up in elevation is neutral or can increase growth without adversely effecting survival or pest damage;
- downward movement in the mountains and hill systems can seriously reduce growth and lead to increased pest damage;
- transfer sensitive populations of high genetic growth potential generally originate from mid elevations and latitudes in the province;
- hardy populations of low genetic growth potential typically originate at low elevations in the north and high elevations in the southwest foothills and mountains.



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.



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.

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.

Size Category	Seed Zone Area (ha) ¹	Maximum Number Deployable per Lot ²		Approximate kg Seed ³			Approximate Coverage in ha (@1800/ha)	
		Seedlings	Vegetative Propagules	Sw	Aw	PI	Seedlings	Vegetative Propagules
1	> 1 million	25 million	20 million	150	6.1	250	13,888	11,110
2	500,000 to 1 million	20 million	16 million	120	4.9	200	11,111	8,889
3	100,000 to 500,000	15 million	12 million	90	3.7	150	8,333	4,167
4	< 100,000	10 million	8 million	60	2.4	100	5,555	2,778

¹ Refer to Appendix 7 for *seed zone* sizes.

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

³ Assumes two seeds per cavity.

Appendix 16. Research, Conservation or Controlled Parentage Program Material Transportation and Storage Form

See Standard 12.2.



RESEARCH, CONSERVATION OR CPP MATERIAL TRANSPORTATION AND STORAGE FORM (APPENDIX 16 FGRMS)¹

UNIQUE IDENTIFIER <hr/> <small>(or other genetic identifier including accession, temporary or registered lot number)</small>									
DESTINATION FACILITY Mailing Address <hr/> <hr/>									
<table style="width: 100%; border: none;"> <tr> <td style="width: 30%; border: none;">Contact</td> <td style="width: 30%; border: none;">Phone</td> <td style="width: 30%; border: none;">Fax</td> </tr> <tr> <td style="border: none;"><hr/></td> <td style="border: none;"><hr/></td> <td style="border: none;"><hr/></td> </tr> <tr> <td style="border: none;">E-mail</td> <td colspan="2" style="border: none;"><hr/></td> </tr> </table>	Contact	Phone	Fax	<hr/>	<hr/>	<hr/>	E-mail	<hr/>	
Contact	Phone	Fax							
<hr/>	<hr/>	<hr/>							
E-mail	<hr/>								
COLLECTING AGENCY Representative <hr/> Phone <hr/> E-mail <hr/>									
DATE OF COLLECTION <hr/>									
DATE OF SHIPPING <hr/>									
MATERIAL DESCRIPTION Species <hr/> Type of Material <hr/> <small>(e.g. cones, fruit, seed, pollen, cuttings, roots)</small> Quantity of Material <hr/> <small>(specify measurements units: e.g. grams of seed, metres of roots, number or volume of cones)</small>									

¹This form is to accompany any genetic material (seed, pollen, cuttings, etc.) to be included in or as part of a *controlled parentage*, research or conservation program. 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.

Appendix 18. Controlled Parentage Program Plan – Contents

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 *CPP* plan is posted on the Government of Alberta website
<http://srd.alberta.ca/forests/managing/manuals.aspx>.

INTRODUCTION

History

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

Program Objectives

- Target species (a brief description of the species, its taxonomy and geographic range);
- Ecology (information on its successional role, site, climate and soil preferences common plant community associates, geographic range etc.);
- 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);
- Objectives (genetic improvement, seed production, seed supply or *propagule* production targets etc.);
- Improvement traits (traits to be considered for improvement, improvement targets and any information on selected traits such as heritabilities and variation);
- Similar programs in other regions where available (review of other programs working with genetic improvement of the same species).

CPP Region Description and Delineation

- Ecological information (ecological classification at various scales and general biome description);
- Forest types and plant communities (e.g., general description of ecosite types and plant communities);
- Topography (general description of terrain and surface expression);
- Parent materials;
- Climate (e.g., precipitation, frost-free-period, growing degree days, average July and average January mean daily temperatures, wind patterns, chinooks);
- Information on adaptive genetic variation that is pertinent to the description and delineation of the *CPP region*;
- Administration and land use information (land management jurisdiction, main land use activities and planning objectives for the area);
- Process used to delineate the *CPP region* (see Standard 28.1);
- 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);
- Location description (latitude, longitude, elevation, range).

Parent Selection Plan

- Selection traits (traits to be selected on and description of traits);
- Parent tree selection method (stand and parent tree selection procedure e.g., comparison, non-comparison, selection from genetic *trials*);
- Selection strategy, including consideration of correlated traits (e.g., wood density and growth);
- Materials collection (shoots, scions, root sections, seed, wood samples etc.).

Breeding/Clonal Plan

a) Seed-based programs

- First generation plan
 - Traits to be selected for;
 - *Base population* description and listing;
 - *Breeding population* description;
 - Description of planned *production populations*;
 - Schedule and predicted timelines for establishment of *production sites*, *production unit(s)*, establishment and measurement of progeny, provenance, or other *tests*, orchard roguings etc.;
 - Gain estimates where applicable;
 - Advanced generation/*pedigree* information (where available).

b) Clonal programs

- Traits to be selected for;
- *Base population* description and listing;
- *Breeding population* description where employed;
- Description of planned *production populations* (e.g., clonal turn over, stand level and landscape level *effective population size (Ne)* management, pest and disease screening program);
- 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;
- Gain estimates where applicable;
- Selection intensity and target *Ne* (stand and landscape).

Genetic Field Testing Plan

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

Field Test Area Justification and Risk/Benefit Assessment

- Where a *CPP* Program 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;

- 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:
 - Volume/growth expectations, benefit(s);
 - Genetic make-up (i.e., based on flowering, leaf morphology analysis, DNA analysis);
 - Gender;
 - Fertility (hybridization potential [phenology, viability, control]);
 - Gene flow;
 - Suckering potential (possible control, if a *genetically modified organism (GMO)* may be specific to type);
 - Planting location, design, timeline, size;
 - Buffer requirements, maintenance standards;
 - Harvesting method, clean-up and *reclamation*;
 - Potential for release of toxins;
 - Centre of insect and disease outbreaks;
 - Potential to ameliorate risk (e.g., silviculture practices);
 - Invasiveness;
 - Ecosystem impact;
 - Monitoring.

Production Plan

a) Seed-based programs

- *Production unit* (orchard) design
 - 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);
 - *Production unit* design and layout (e.g., seedling, clonal, *rolling front orchard*; number of trees, inbreeding control i.e. a general description that would be followed up in more detail in the orchard establishment report (see Appendix 32).
- *Production unit* establishment
 - *Production site*;
 - Establishment dates (planned or known initiation and completion dates);
 - *Alberta production unit* number when known issued by Alberta Tree Improvement & Seed Centre (ATISC).
- *Production unit* management
 - Pollen contamination;
 - Pollen management;
 - Weed, insect, and disease monitoring and control;
 - Tree management;
 - *Crop* management;
 - Permanent Sample Tree monitoring.

b) Clonal programs

- Where *production units* are employed such as *stoolbeds*, *stoolbed* design and production planning (program production needs, *production sites*, *stoolbed* design, size and number, production expectations and projections).
- *In vitro* micro-propagation
 - Production design including production needs, methods and systems, planned *production sites*, approach to *production population* assembly and *deployment population* production expectations and projections;
 - *Alberta* (ATISC) issued *production population* numbers when issued and available.

- *Production unit* establishment
 - *Production unit* (s) description (due to the variable nature of potential production systems for clonal material, description may vary particularly if *production units* are dispersed or ephemeral);
 - Proposed or existing *production site(s)*.
- *Production unit* or *production population* management
 - Weed, insect, and disease monitoring and control for *production units* (e.g., in *stoolbeds*);
 - 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

- All requirements met as per Standards 18.4.31, 18.4.4, 24.4 and Appendix 21A including:
 - Identification of target strata and landscape *deployment Ne* limits;
 - Stand based *Ne* planning and *deployment* strategies (e.g., proposed use of unrestricted or restricted *registration* materials, targeted ecosites, productivity classes);
 - Site/strata - specific *deployment* strategies.

b) Clonal Programs

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

Genetic Conservation Plan

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

Link to Supportive Research Plan(s)

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

Reference to Additional Relevant Reports

- Genetic *Test* Establishment Report;
- Genetic *Test* Measurement Report;
- Genetic *Test* Analysis Report;
- Parent Tree Selection Report.

Appendix 19. Current Controlled Parentage Program Regions and Associated Programs

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 agriculture 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 contained in the seedlot collection. *Controlled parentage program regions* are not necessarily coincident with *seed zones*, as they are based on a target *deployment* area for a single specified species and are generally accompanied by clonal, provenance and progeny 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 prior or coincident testing for adaptiveness of the proposed genetic material.

Seed and *vegetative propagule* movement and *deployment* from *CPPs* and *production populations* and associated *production units* are generally unrestricted within their specific *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 21 currently approved *CPP regions* in *Alberta* include nine white spruce, three black spruce, six lodgepole pine, one jack pine, one Douglas-fir and one western larch (see below). It is recognized that there are other breeding programs (hardwood and softwood) under development in *Alberta*.

Figures 1 through 4 are for conceptual use only. For *CPP region* digital boundary line work, contact the *Alberta Tree Improvement and Seed Centre*, Sustainable Resource Development at phone number (780) 656-5072.

Description of CPP Regions by Tree Species

Species	CPP Region	Description
Lodgepole pine (Fig. 3)	A	West-central lower foothills <i>CPP region</i> represented by mixedwood forest types at lower elevations and conifer dominated forest types at upper elevations. Approved operational elevations are 1050 m to 1350 m.
Lodgepole pine (Fig. 3)	B1	Northern lower foothills <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 metres.
Lodgepole pine (Fig. 3)	B2	Northern upper foothills <i>CPP region</i> dominated by conifer forest types. Approved operational elevations are 1200 to 1600 metres.
Lodgepole pine (Fig. 3)	C	Swan Hills area outlier foothills <i>CPP region</i> dominated by pure and mixed conifer forest types. Approved operational elevations are 800 to 1200 metres. Area of lodgepole and jack pine hybridization.
Lodgepole pine (Fig. 3)	K1	Southern upper foothills <i>CPP region</i> dominated by conifer forest types. Approved operational elevations are 1100 to 1500 metres.
Lodgepole pine (Fig. 3)	J	Clear Hills area outlier foothills <i>CPP region</i> dominated by mixedwood and conifer forest types, including areas of lodgepole and jack pine hybridization. Approved operational elevations are 600 to 1000 metres except for an area on the north slope of Zama Ridge which follows the NM to LBH Natural Subregion boundary.
Jack pine (Fig. 3)	P1	Northeastern lowlands boreal <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 250 to 600 metres.
Western larch (Fig. 3)	M	Southern lower subalpine <i>CPP region</i> dominated by conifer forest types. This species is rare in Alberta. The main project objectives are conservation and restricted use for <i>CPP region deployment</i> . Approved operational elevations are 1450 to 1700 metres.
White spruce (Fig. 1)	D	Swan Hills area outlier lower foothills <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 650 to 1050 metres.
White spruce (Fig. 1)	D1	Slave Lake area boreal <i>CPP region</i> dominated by boreal lowland and upland mixedwood forest types. Approved operational elevations are 500 to 800 metres.
White spruce (Fig. 1)	E	Northeastern boreal lowland <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 300 to 650 metres.
White spruce (Fig. 1)	E1	Northeastern boreal lowland <i>CPP region</i> dominated by mixedwood forest types. Northern extension of <i>CPP Region E</i> . Approved operational elevations are 250 to 600 metres.
White spruce (Fig. 1)	E2	East central sub-boreal and parkland <i>CPP region</i> dominated by mixedwood and parkland forest types. Project objectives include conservation and restricted <i>Deployment</i> . Approved operational elevations are 550 to 750 metres.
White spruce (Fig. 1)	G1	Northern lower foothills <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 650 to 1050 metres except along the Smoky River where the lower elevation limit is 600 metres.
White spruce (Fig. 1)	G2	Northwestern outlier foothills <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 500 to 900 metres.
White spruce (Fig. 1)	H	Northwestern boreal lowlands <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 250 to 550 metres elevation.
White spruce (Fig. 1)	I	North-central lower foothills <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 in the south and 700 to 1050 metres in the north.

Description of CPP Regions By Tree Species (cont'd)

Species	CPP Region	Description
Interior Douglas-fir (Fig. 4)	F1	Southern montane <i>CPP region</i> dominated by montane mixedwood forest types. Approved operational elevations are 1300 to 1550 metres (up to 1700 m in the Porcupine Hills).
Black spruce (Fig. 2)	L1	North-central lower foothills <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 metres.
Black spruce (Fig. 2)	L2	Northern lower foothills <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 800 to 1200 metres.
Black spruce (Fig. 2)	L3	Northeastern boreal lowlands <i>CPP region</i> dominated by mixedwood forest types. Approved operational elevations are 300 to 650 metres.



Fig. 1 Controlled parentage program regions for white spruce.



Fig. 2 Controlled parentage program regions for black spruce.

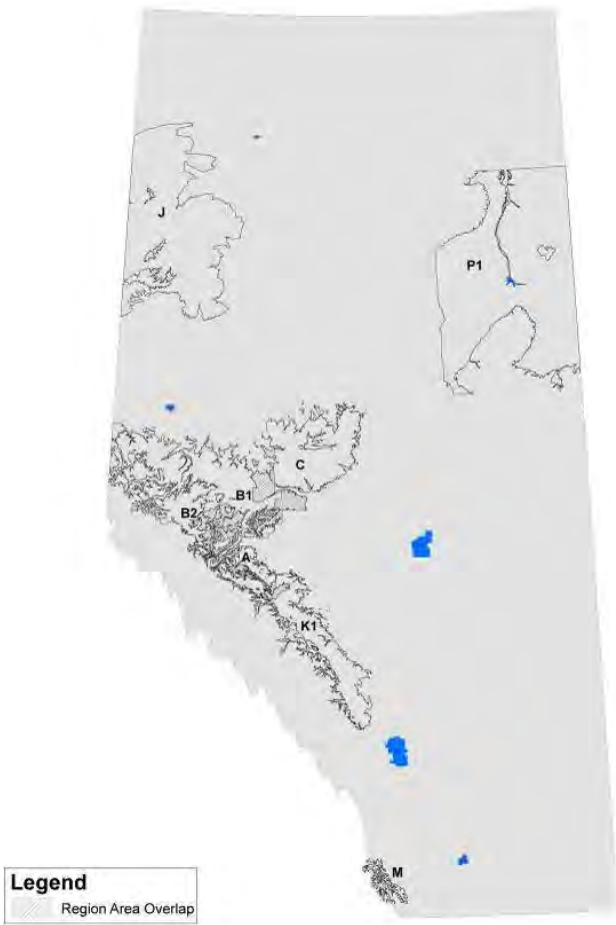


Fig. 3 Controlled parentage program regions for lodgepole pine, jack pine and western larch.



Fig. 4 Controlled parentage program region for interior Douglas-fir.

Appendix 20. Calculation of Cumulative Effective Population Size (N_e) of Deployed Populations

See Standards 18.4.4, 21.2.1.1, 32.6, 33.4.3 and 33.4.4.

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

STEPS IN CALCULATING CUMULATIVE N_e

See below for an example, including three populations with subsets of 60 unrelated and non-inbred *genotypes*. Columns in Table 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 \mathbf{i} by *genotype* \mathbf{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 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* ($\sum \mathbf{pc}_j^2$; table row 61, column 13).

And finally:

6. *Cumulative N_e* = $1/\sum \mathbf{pc}_j^2$ (table row 62, column 13).

Note: For an orchard containing related and/or inbred *genotypes*, *cumulative N_e* would be calculated as outlined in Appendix 36, using \mathbf{pc}_j values (e.g., column 12, rows 1-60) as the \mathbf{p} vector, and generating the covariance matrix \mathbf{C} (defined in Appendix 36); then *cumulative N_e* = $0.5/\mathbf{p}'\mathbf{C}\mathbf{p}$.

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

EXAMPLE

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

Table 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 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
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

	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
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 j th *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 j th *genotype* in the second population
- P_{3j} = proportional contribution of the j th *genotype* in the third population
- n_{1j} = total contribution of the j th *genotype* in the first population
- n_{2j} = total contribution of the j th *genotype* in the second population
- n_{3j} = total contribution of the j th *genotype* in the third population
- $ntot_j$ = total contribution of the j th *genotype*, summed over populations
- pc_j = proportional contribution of the j th *genotype*, over populations

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

See Standards 18.4.3.1, 18.4.4, 24.4, 24.4.1, 32.6, 33.4.3 and 33.4.4.

To maintain forest genetic diversity and associated sustainability, a limit is placed on the total number of *controlled parentage program (CPP)* seedlings to be deployed from a *production population*. This limit 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:

- total area of target strata in the region/zone and;
- the number of seedlings required per hectare (trees per ha).

SEEDLING *production population* limits are calculated as follows.

- Where the *Ne* is <30 (cumulative over the life of the *production population*, see Appendix 20):
Planned Total Production Limit (e.g., column 6) = Area of Target Strata (e.g., column 4) x Trees per ha x 0.25;
- Where the *cumulative Ne* is ≥30, these limits are doubled:
Planned Total Production Limit (e.g., column 7) = Area of Target Strata (e.g., column 4) x Trees per ha x 0.50.

The following example illustrates how the size of *production populations* may be planned to meet the landscape level cumulative limits as calculated above.

Stream 2 CPP Production Population Planning - Seedling Example

1	2	3	4	5	6	7
Tenure Holder(s) (including unallocated CPP Region area)	Total CPP Region Area by Tenure Holder	Operable Area Within CPP Region	Area of Target Strata ¹	Estimated Plants Required for 100% Planting of Target Strata	Planned Total Production Limit, one or more production units (cumulative Ne<30)	Planned Total Production Limit, one or more production units (cumulative Ne≥30)
(ha)	(ha)	(ha)	(ha)	(# seedlings)	(# seedlings)	(# seedlings)
TI Coop Member X	1,595,000	1,096,250	150,000	270,000,000	67,500,000	135,000,000
TI Coop Member Y	957,000	817,750	87,000	156,000,000	39,000,000	78,000,000
Non Coop Member Z ²	638,000	478,500	50,000	90,000,000	22,500,000	45,000,000
Unallocated ²	445,000	310,000	35,000	63,000,000	15,750,000	31,500,000
Totals	3,635,000	2,702,500	322,000	579,000,000	144,750,000	289,500,000

¹ Target strata refers to the area to be regenerated to the species produced by the *production population* unit which may, or may not, be the regenerated yield strata.

² Data are to be provided by Sustainable Resource Development. Where data are not available, a weighted average of cooperators holdings will be used for estimating values in columns 3 and 4.

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 table in Appendix 21A, the following table 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.

Stream 2 CPP Production Population Planning – Vegetative Propagule Example

1	2	3	4
Tenure Holder(s) (including unallocated <i>CPP Region</i> area)	Total CPP Region Area by Tenure Holder	Operable Area Within CPP Region	Area of Target Strata ¹ by Tenure Holder
	(ha)	(ha)	(ha)
TI Coop Member X	1,595,000	1,096,250	150,000
TI Coop Member Y	957,000	817,750	87,000
Non Coop 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 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 Sustainable Resource Development. Where data are not available, a weighted average of cooperators holdings will be used for estimating values in columns 3 and 4.

Appendix 22. Request for Deployment Variance for Stream 2 Material

See Standard 18.4.8.

Variance request to be submitted for emergencies only.



STREAM 2 REQUEST FOR DEPLOYMENT VARIANCE (Appendix 22 F GRMS)

REQUESTING AGENCY		DATE	
Agency Name	_____	Contact	_____
Mailing Address	_____		
Phone	_____	Fax	_____
E-mail	_____		
REQUEST CATEGORY <input type="checkbox"/> Lot has restricted registry <input type="checkbox"/> and/or transfer outside of CPP Region			
REASON(S) FOR EMERGENCY REQUEST			
DEPLOYMENT POPULATION (CROP) DESCRIPTION			
Registered Lot Number	_____	<input type="checkbox"/> Seed	<input type="checkbox"/> Seedling <input type="checkbox"/> Vegetative
CPP Region	_____		
Production Unit Number (seed)	_____	Species	_____
Production Population Number (vegetative)	_____		
Production Population Origins if not a fixed Production Unit (Additional pages added <input type="checkbox"/> [attach as necessary])	_____		
Latitude	degree	min	sec
Longitude	degree	min	sec
*Legal Location	tpw	range	meridian
Deployment Population Effective Population Size	_____		
PROPOSED DEPLOYMENT			
CPP Region	_____	ARIS Opening No(s)	_____
		Attach sheet for additional openings	_____
*Latitude	degree	min	sec
Elevation: Mean (m)	_____		
*Longitude	degree	min	sec
Elevation: Range (m)	min	max	
Legal Location	sec	tpw	range meridian
PROPONENT/AGENCY			
NAME		POSITION	
SIGNATURE		DATE	
VARIANCE APPROVAL (DEPARTMENT USE ONLY)			
<input type="checkbox"/> Approved <input type="checkbox"/> Denied		Date	_____
Approved with conditions <input type="checkbox"/>		Reviewed by	_____
Conditions		_____	
Variance No		_____	

*Optional fields

Appendix 23. Request for Planting Variance for Research Material

See Standards 23.1 and 23.7.

REPEALED

Appendix 24. Research Program Plan – Contents

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

The following topics are to be addressed in a research program (RP) plan. A proponent is advised to submit a letter of intent to *Alberta* prior to developing a program plan.

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

Introduction

- Project title;
- Research proponents;
- Research problem;
- Traits of interest;
- Research objective(s);
- Hypothesis test(s);
- *Deployment* objectives where applicable;
- Link to *controlled parentage program*, if relevant.

Field Test Area Justification and Risk/Benefit Assessment

- 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.
- 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:
 - Volume/growth expectations, benefit(s);
 - Genetic make-up (i.e., based on flowering, leaf morphology analysis, DNA analysis);
 - Gender;
 - Fertility (hybridization potential [phenology, viability, control]);
 - Gene flow;
 - Suckering potential (possible control, if a *genetically modified organism (GMO)* may be specific to type);
 - Planting location, design, timeline, size;
 - Buffer requirements, maintenance standards;
 - Harvesting method and clean-up;
 - Potential for release of toxins;
 - Centre of insect and disease outbreaks;
 - Potential to ameliorate risk (e.g., silviculture practices);
 - Invasiveness;
 - Ecosystem impact;
 - Monitoring.

Materials

- Target species;
- Genetic *test* material (provenances, populations, families, etc.);
- Genetic *test* material origin;
- Physical *test* material (seedling, seed, rooted cuttings, stock type, etc.);
- Controls;
- Physical *test* environment (e.g., lab, green house, field *test*);
- *Test* environment conditions (field *test* site location climate, soils, etc.; lab or greenhouse *test* environment conditions).

Methods

- Research hypothesis *test(s)*;
- Experimental design;
- Data collection;
- Criteria for selection and protection of *test* site(s) if applicable;
- Description of assessment methods and procedures;
- Analysis procedures.

Anticipated Deliverables

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

References

- Citation of pertinent literature.

Appendix 25. Unique Identifier Codes

See Standard 25.5.

Where agencies do not have a code in the table below, contact *Alberta* (Alberta Tree Improvement & Seed Centre) to have one issued.

UNIQUE IDENTIFIER (U.I.)

Field Number	1	2	3	4	5	6	7	8	9	10	11	12	13
Example	D	M	0	0	0	4	5	A	W	0	0	1	S

Fields 1 - 7 provide the unique *genotype* and are compulsory fields.
Fields 8 - 13 provide the material description and are optional fields.

FIELD DESCRIPTION WITH EXAMPLE

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

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

All alpha fields are in uppercase letters only.

CODES

Type of Material (field 13):

<i>grafted ramet</i>	(G)
<i>rooted ramet</i>	(C)
seedlot	(S)
scion	(N)
root	(R)
flower buds	(B)
pollen	(P)
whole tree/seedling	(T)
other	(X)

AGENCY CODES (fields 1 - 2):

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
LAND AND FOREST DIVISION, CLEARWATER AREA	LC
LAND AND FOREST DIVISION, FOOTHILLS AREA	LF
LAND AND FOREST DIVISION, LAC LA BICHE AREA	LL
LAND AND FOREST DIVISION, LESSER SLAVE AREA	LS
LAND AND FOREST DIVISION, PEACE AREA	LP
LAND AND FOREST DIVISION, SMOKY AREA	LG
LAND AND FOREST DIVISION, SOUTHERN ROCKIES AREA	LR
LAND AND FOREST DIVISION, UPPER HAY AREA	LU
LAND AND FOREST DIVISION, WATERWAYS AREA	LW
LAND AND FOREST DIVISION, WOODLANDS AREA	LO
LAND AND FOREST 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
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
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

AGENCY CODES (cont'd)

Agency Name	Code
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

SPECIES CODES (Fields 8-9):

Section 1: Pure Species

Species Code	Family	Genus	Species	Common Name
BW	Betulaceae	<i>Betula</i>	<i>papyrifera</i>	paper (white) birch
PL	Pinaceae	<i>Pinus</i>	<i>contorta</i>	lodgepole pine
PJ	Pinaceae	<i>Pinus</i>	<i>banksiana</i>	Jack pine
PW	Pinaceae	<i>Pinus</i>	<i>albicaulis</i>	whitebark pine
PF	Pinaceae	<i>Pinus</i>	<i>flexilis</i>	limber pine
LA	Pinaceae	<i>Larix</i>	<i>lyallii</i>	alpine larch
LT	Pinaceae	<i>Larix</i>	<i>laricina</i>	tamarack
LW	Pinaceae	<i>Larix</i>	<i>occidentalis</i>	western larch
SW	Pinaceae	<i>Picea</i>	<i>glauca</i>	white spruce
SE	Pinaceae	<i>Picea</i>	<i>engelmannii</i>	Engelmann spruce
SB	Pinaceae	<i>Picea</i>	<i>mariana</i>	black spruce
FD	Pinaceae	<i>Pseudotsuga</i>	<i>menziesii</i>	Douglas-fir
FB	Pinaceae	<i>Abies</i>	<i>balsamea</i>	balsam fir
FA	Pinaceae	<i>Abies</i>	<i>lasiocarpa</i>	alpine fir
AB	Salicaceae	<i>Populus</i>	<i>alba</i>	white poplar
PB	Salicaceae	<i>Populus</i>	<i>balsamifera</i>	balsam poplar
DA	Salicaceae	<i>Populus</i>	<i>dauriana</i>	Chinese/Korean aspen
DE	Salicaceae	<i>Populus</i>	<i>deltooides</i>	plains cottonwood
GR	Salicaceae	<i>Populus</i>	<i>grandidentata</i>	bigtooth aspen
LA	Salicaceae	<i>Populus</i>	<i>laurifolia</i>	—
MA	Salicaceae	<i>Populus</i>	<i>maximowiczii</i>	poplar (Japan)
NI	Salicaceae	<i>Populus</i>	<i>nigra</i>	poplar
SA	Salicaceae	<i>Populus</i>	<i>sargentii</i>	sargentii poplar
TA	Salicaceae	<i>Populus</i>	<i>tremula</i>	European aspen
AW	Salicaceae	<i>Populus</i>	<i>tremuloides</i>	trembling aspen
TR	Salicaceae	<i>Populus</i>	<i>trichocarpa</i>	black cottonwood

Section 2: Hybrids

Species Code	Family	Genus	Species	Common Name
Codes to be developed				

¹ For all parent materials collected prior to May 1, 2003 and documented at Alberta Tree Improvement & Seed Centre (ATISC), a *U.I.* will be assigned for each unique *genotype* as outlined in the standards and Appendix 25. This would allow for filling in of all compulsory fields and optional fields if desired. The only change to standards in order to accomplish this would be the assignment of a suitable Agency Code. The problem of a suitable Agency Code could be solved by adding “XX” to the agency codes of Appendix 25 and under “Agency Name” identifying this “XX” agency code as “Parent Material Collections made prior to May 1, 2003”.

Appendix 26. Genetic Test Establishment Report – Contents

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

- Program;
- Agency/cooperators;
- *Trial* code;
- Site name;
- Reference to associated *Controlled Parentage Program (CPP)* or Research Plan;
- List of associated *trials* (i.e., *tests* containing the same genetic material).

Test Material

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

Controls

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

Planting Stock

- Description and location of sowing/striking and growing, including nursery, sowing/striking date, lift date and stock type; also any relevant descriptive details relating to growing, lifting, packing and delivery.

Experimental and Field Design

- Type (e.g., alpha, randomized complete block);
- Number of replicates;
- Number of blocks/rep;
- Plot size and shape;
- Include outputs from design generation program showing treatment randomizations and replicate/block assignments;
- Border row(s) description;
- Spacing.

Test Site

- Include the completed Genetic Test Site Information Form (see Appendix 29) and access map.

Field Marking

- Description;
- Percent of trees marked.

Planting

- Names of contractors and supervisors;
- Dates;
- Planter allocation description (e.g., one planter/rep).

Map or Maps

- Must unambiguously define genetic and experimental design identity of each tree.

Test Content File

- Attach electronic listing as per Standard 27.1.

References

- List of citations.

Appendix 27. Genetic Test Measurement Report – Contents

See Standards 27.5, 30.8.1 and 30.12.2.

For recommended field *trial* measurement equipment, measurement procedures and quality control procedures, refer to the Forest Genetic Resource Management & Conservation Standards (FGRMS) at the Government of Alberta's website <http://srd.alberta.ca/forests/managing/manuals.aspx>.

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

Introduction

- *Trial* description and objective(s);
- Applicable *Controlled Parentage Program* or Research Program Plan;
- Measurement objectives;
- Measurement schedule;
- Measuring agency and personnel.

Methods

- Variables assessed and measured;
- Assessment and measurement methods, procedures and equipment;
- Quality control procedures (e.g., measurement procedures, data handling and verification procedures, field measurement spot checking and sampling intensity, measurement instrument calibration).

Results

- Data dictionary containing variable listing, description of values of variables, position in file and file format;
- Data format (ASCII standard);
- Measurement start and completion dates;
- Data summaries;
- Tree counts by site, replicate and treatment;
- Appropriate site means and ranges for assessed traits;
- Trait means by replicate;
- Trait means by treatment;
- Attach verified raw data set to be submitted electronically with report and in accordance with data handling standards outlined in Standard 27.0.
- Quality control summary results (see attached form).

Notes

- Significant items of interest or concern relating to assessment or data.

DATE: June 30, 2009

- ▶ Replace Site 1 ID*, 2 ID*, 3 ID*, 4 ID* with actual test site names in the trial series
- ▶ 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	2090	2040	2040	3200	3200	2900	2900	10230	10230
b number of test trees living and measured	count	2014	1978	1971	2867	2864	2846	2831	9805	9768
c number of living trees checked	count	105	105	105	160	160	150	150	520	520
d number of checked trees included	count	105	104	104	159	159	148	149	516	517
e number exceeding tolerance	count	4	2	4	6	8	7	10	19	29
f % sample [= d/b]	ratio	5.2%	5.3%	5.3%	5.4%	5.4%	5.2%	5.3%	5.3%	5.3%
g % exceeding tolerance [= e/d]	ratio	3.8%	1.9%	3.8%	3.8%	5.0%	4.7%	6.7%	3.7%	5.6%
h reason for exclusion (include all applicable; see codes below) ²	list	N/A	2	2	1	1	1,3	1	1,2,3	1,2

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]

³ actual site name to be inserted in cell(s)

example

Appendix 28. Genetic Test Analysis Report – Contents

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 Relevant *Controlled Parentage Program* or Research Program Plan

Genetic Test Analysis Report

- *Trial* identity;
- Filename of checked dataset (submitted with Genetic Test Measurement Report; see Appendix 27 for contents);
- Objective(s) of analyses;
- Editing procedure used to convert checked dataset, to analyzed dataset (e.g., treatment of outliers, values deleted, reasoning);
- Analytical procedure:
 - Method (e.g., Analysis of Variance [ANOVA], Best Linear Predictor [BLP]);
 - Model;
 - Expected mean squares where appropriate.

Summary Statistics for Traits of Interest (e.g., height and survival)

Estimates of Genetic Parameters (e.g., *breeding values*, heritability and genetic correlations)

- Showing method and formulae used.

Standard Errors

- Calculated for parameter estimates used to calculate heritability and genetic correlations;
- Calculation methods to be shown.

Dataset Analyzed

- Submitted in electronic format with this analysis report.

Reference to Additional Relevant Reports

- Research program plan or *controlled parentage program* plan;
- Establishment report;
- Measurement report.

Appendix 29. Genetic Test Site Information Form

See Standard 25.1.2 and 30.3.2. See also Appendix 26.

Minimum required information for initial submission is identified by asterisks for *Alberta* (Alberta Tree Improvement & Seed Centre) assignment of a *trial* code. A completed form is to be included in the *trial* establishment report.



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)		
Site location	Latitude*	degree min sec
	Longitude*	degree min sec
	Legal	two 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)		
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	

*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.

Appendix 30. Example of Data Collection Form and Corresponding Map

See Standard 27.1, 27.3 and 30.5.1.

EXAMPLE OF DATA COLLECTION FORM (Excel Sheet)

This form may be used as a template for any *trial*. Therefore, not all columns will be relevant to all *trials*. For silvicultural *trials* there will be a treatment column; for genetics *trials* there may be a provenance and clone column. 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 a new column for the trait being measured. For example: FHt99|FHt00|FHt01|FCp99|FCp00|FCp01|, etc. It is very 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 directly onto a computer.

(Fall Height 1999 : FHt99)

Location _____ Trial Code _____ Measurement Date _____ Contractor _____								Page: __ of __ Year of Planting _____ Recorders' Names _____
Excel line	Site Code	Replicate	Clone or Family	Tree	Height (cm or m) Indicate fall /spring and the year (e.g., FHt99)	RCD (cm) or DBH (cm) Indicate fall /spring and the year (e.g., FCp99)	Survival 0=dead 1=alive	COMMENTS
9		1	100	1				
10		1	100	2				
11		1	405	1				
12		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_____

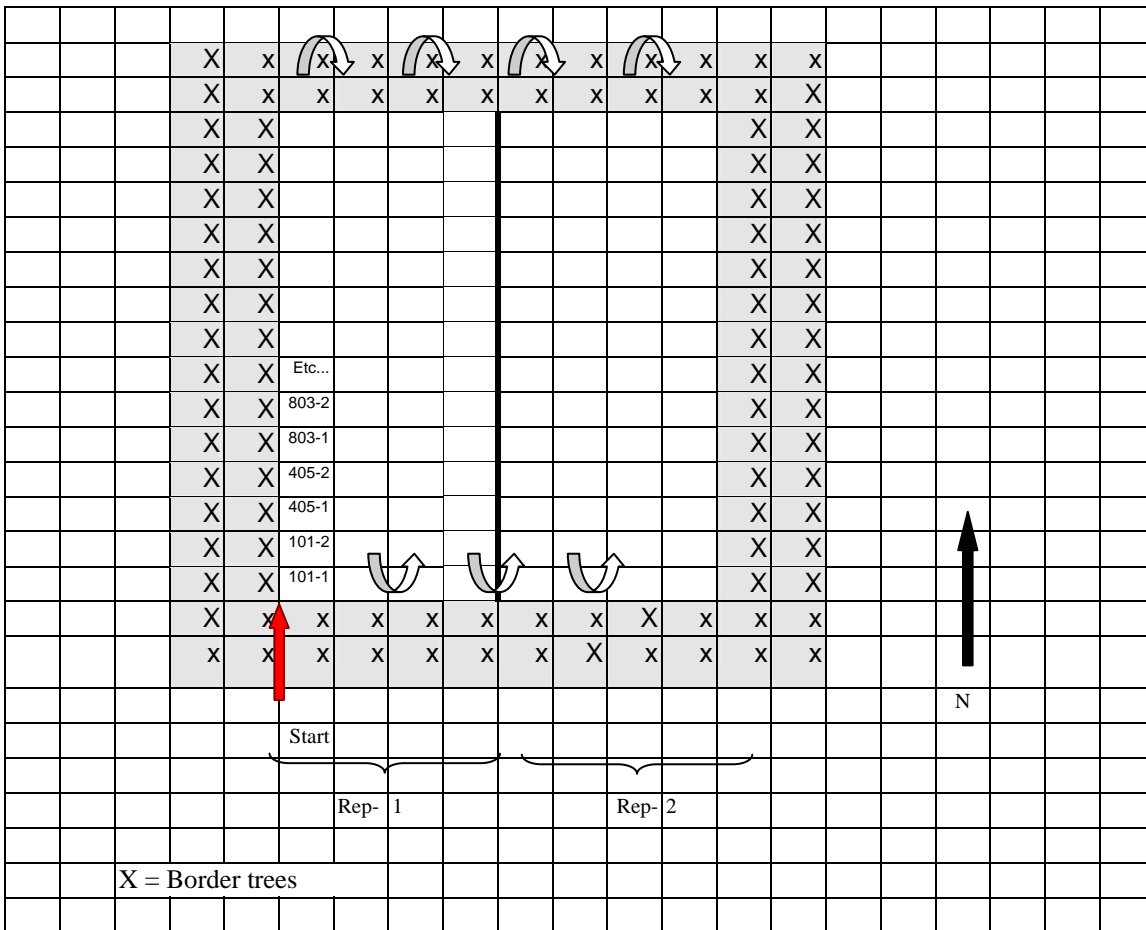
Year of planting_____

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

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 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 may need to be adjusted for genetic (pollen) contamination and supplemental mass pollination (SMP).

APPLICABILITY

Where application or 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 here. Where no claim for *genetic gain* applies, *GW*, for the purpose of lot *registration*, can be considered to be 0.

ASSUMPTIONS AND CALCULATIONS

1. It is assumed that phenotypic selection from *wild* stands will yield, on average, a 2% gain in height, where selections have been made intensively (using the *comparison tree method*, Appendix 11A) and there is documented height over age superiority. This figure may be used as a *BV* for selected clones until reliable test results are available (see Table 1, Standard 31.5). Individuals in seedling *seed orchards* will be assigned a *BV* of 1% until reliable test results are available.
2. *Breeding values* for height, estimated from genetic *test* data, are calculated relative to unselected or operational lot controls appropriate to the given *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 intensively (*comparison tree method*) as described in Item 1 above, 2% may be added to the calculated *BV* for clonal orchards and 1% for open-pollinated seedling orchards.
3. The genetic correlation between height at rotation age and height at assessment age is estimated using the following equation:

$$r_a(j,m) = 1.02 + 0.308\text{Ln}(j/m)$$

where

$r_a(j,m)$ = the additive genetic correlation between performance at ages j and m , assessment (juvenile) and rotation (mature) ages respectively; and

$\text{Ln}(j/m)$ = the natural logarithm of the age ratio j/m .

j = age at selection; m = age at rotation

4. It will be assumed that the *genetic worth* of contaminating pollen is 0, unless evidence to the contrary exists.
5. p_i , the proportion of gametes produced by *genotype* i , will be estimated as follows.

Other options will be considered by *Alberta* on a case-by-case basis.

A. Seedlots from clonal and/or uneven-aged seed orchards

Method of estimation will depend on the number of *genotypes* contributing to the *deployment population* (see Table 1). 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 *genotype i* are both assumed to equal p_i .

Table 1. Method of genotypic contribution estimation for clonal and/or uneven aged orchards

Number of genotypes contributing	Method of estimation of genotypic contribution
Fewer than 50	As per Table 1, Appendix 37. Alternatively, if collections are made on a clonal basis, cone volume per clone may be used to estimate 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 p_i .
75 or more	Genotypic frequency in the cone-bearing population may be used to estimate p_i . Example: Clone x has 15 <i>ramets</i> that bear cones out of an orchard total of 250 cone-bearing <i>ramets</i> . $p_i = 15/250 = 0.06$. Alternatively, if collections are made on a clonal basis, cone volume per clone may be used to estimate p_i .

B. Seedlots from even-aged half-sibling family orchards

Method of estimation will depend on number of families contributing to the *deployment population* (see Table 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 p_i .

Table 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 1, Appendix 37. Alternatively, if collections are made on a family basis, cone volume per family may be used to estimate 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 p_i .
38 or more	$p_i =$ proportion of orchard trees of family <i>i</i> .

C. Vegetative lots

p_i = proportion of *vegetative propagules* produced by *genotype i*

SEVERAL CASES ARE CONSIDERED BELOW.

CASE 1. Seed or vegetative lot produced with no genetic contamination or supplemental mass pollination (SMP)

$$GW = \sum(p_i BV_i)$$

where

GW = *genetic worth* of the seed or vegetative lot;

BV_i = *breeding value* of *genotype* (clone or family) *i*

Example 1: *Breeding values* and genotypic contributions as shown in table below.

Genotype	p _i	BV _i	p _i *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

$$GW = 0.10, \text{ or } 10\%$$

CASE 2. Seedlot produced where pollen contamination exists

$$GW = 0.5 \sum [(1-PC) \cdot BVM + PC \cdot BVC + BV_i] \cdot p_i$$

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

$$\begin{aligned} GW &= 0.5 \sum \{ (1-PC) \cdot BVM + BV_i \} \cdot p_i \\ &= 0.5 [(1-PC) \cdot BVM + \sum (BV_i) \cdot p_i] \end{aligned}$$

Example 2: *Breeding values* and genotypic contributions as in Table 1.

$$PC = 0.23$$

BVC is assumed to be 0.

Thus

$$\begin{aligned} GW &= 0.5 \cdot [(1-0.23) \cdot 0.1003 + 0.1003] \\ &= 0.5 \cdot [0.0772 + 0.1003] \\ &= 0.09, \text{ or } 9\% \end{aligned}$$

CASE 3. Seedlot produced with supplemental mass pollination (SMP), where pollen contamination exists

$$GW = 0.5 \sum [PSMP_i \cdot BVSMP_i + (1-PSMP_i) [(1-PC) \cdot BVM + PC \cdot BVC] + BV_i] \cdot p_i$$

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

See Standard 32.8.1.

Establishment reports are due March 31st in the year following the establishment of the *production unit*. Establishment reports for seed *production units* must contain the following information (for details, refer to the sample establishment report on the Government of Alberta website <http://srd.alberta.ca/forests/managing/manuals.aspx>. For vegetative *production units*, complete as appropriate. Contact *Alberta* (ATISC) for information.

Project Title

Location

- Site name;
- Legal land description;
- Latitude and longitude;
- Elevation.

Site Information

- Physical description;
- History of site use.

Description of Orchard Parental Material

- List of material (identified by Unique Identifier (U.I.) comprising the orchard population.

Orchard Stock

- Description of rearing regime;
- Rootstock provenance.

Orchard Design

- Design software used;
- Constraints on spacing of related clones.

Planting Report

- Planting date;
- Temperature, precipitation and soil moisture status during plant (e.g., wet, moist, dry).

Table of Origin of Clones

- *Unique Identifier (U.I.)*. (and clone or family number, if different);
- Collection site;
- Latitude and longitude;
- Elevation.

Distribution of Clones

- *Ramets* per clone in the clone bank;
- Inventory of potted grafts per clone;
- List of grafts planted in the current year including clone and *ramet* number and planting position in the orchard.

Orchard Layout Map

- Showing orchard design and positions with planted positions keyed to *genetic identity*.

Site Layout Map

- Showing position of orchard in relation to other plantations on site.

Access Map

- 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* as outlined in Appendix 35.

Appendix 33. Permanent Sample Tree (PST) Protocols

See Standard 32.8.2.

PST System for Flowering and Seed Production Monitoring in Seed Orchards

PURPOSE

- To provide orchard-specific local data for monitoring *seed orchard* development, flowering, cone and seed production, and seed quality, and
- To provide an estimate of reproductive contribution and a tool for cone crop forecasting.

SAMPLE SIZE AND DISTRIBUTION

- For orchards with fewer than 600 trees planned, a minimum of 60 PSTs will be designated;
- For orchards with 600-2000 trees planned, a minimum of 10% of trees will be designated as PSTs;
- For orchards with more than 2000 trees planned, a minimum of 200 PSTs will be designated;
- PSTs will proportionately represent each planting year (with a tolerance of 5 trees or 20%, whichever is greater (see excel spreadsheet at <http://srd.alberta.ca/forests/managing/manuals.aspx> to calculate yearly PST additions and tolerances);
- All clones or families with five or more trees will be represented in PSTs;
- Mortality in the PST population will be replaced to ensure continued compliance with these rules;
- 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, ALL ORCHARDS

- Height to the nearest centimetre to tip of terminal bud;
- Crown width at widest part of crown to nearest centimetre;
- Diameter at breast height (DBH) to nearest centimetre, once grafts reach breast height;
- Number of male and female flowers (actual count, or estimate if flowering is prolific);
- Number of immature cones (pine species only) (actual count, or estimate if numbers are large);
- Number of mature cones (actual count, or estimate if numbers are large). If an orchard crop is collected in the given year, this information need not be collected; an average will be calculated from operational cone collection data;
- Where data or material collection is incompatible with orchard operations (e.g., sanitation picking), such data and/or material need not be collected.

MATERIAL COLLECTION, SEED YIELD CALCULATIONS AND GERMINATION TESTING

In years when no operational crop is collected from the orchard, ripe cones will be collected from PSTs (5 cones per tree, where available) and bulked into a single PST collection for extraction and testing. In years when a crop is collected, information from operational cone collections may be used; PST cones need not be collected separately.

The following information shall be reported:

- Mean number of cones per litre;
- Seed production (g);
- Number of seeds per cone;
- 1000 seed weight;
- Seed germination %.

ASSESSMENT SCHEDULE

Assessments are completed annually except for growth trait measurements, i.e., height, crown width and DBH. These are done 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 and 35A) as shown in Tables 1 and 2.

In Table 1, where an orchard has a collectable crop in the given year:

- lines 31 and 34–38 may be completed from operational crop data;
- lines 30, 32 and 33 may be left blank.

Table 1. Template: Annual Summary of Seed Production and Monitoring Information for Region Seed Orchard, Year 2_____

Line	Orchard Characteristics	Result	Line	Immature Cone Production (pine spp. only)	Result
1	Orchard design capacity		23	Date assessed	
2	Total no. of seed trees established		24	No. of PSTs producing cones	
3	Total no. of clones/families established		25	Mean no. of cones/PST	
4	Average age		26	Standard error of (line 25)	
5	Age range		27	Range of cones/PST	
6	Average height (cm ± SE)		28	Cone crop estimate (# of cones)¹	
7	Height range		29	Cone crop estimate (hectolitres)²	
8	Average crown width (cm ± SE)		Cone Production		
9	Crown width range		30	No. of PSTs producing cones	
10	Average DBH (cm ± SE)		31	Mean no. of cones/tree	
11	DBH range		32	Range of cones/PST	
12	Total no. of PSTs		33	Total no. of cones collected from all PSTs (max. 5/tree; developing orchards only)	
Reproductive Balance			34	Mean no. of cones/litre	
13	No. of PSTs flowering		Seed Production		
Male Flowering			35	Seed production (g)	
14	No. of PSTs with male flowers		36	No. of seeds/cone	
15	Mean no. of male flowers/PST		37	1000 seed weight	
16	Standard error of (line 15)		38	Germination %	
17	Range of male flowers/PST				
Female Flowering					
18	No. of PSTs with female flowers				
19	Mean no. of female flowers/PST				
20	Standard error of (line 19)				
21	Range female flowers/PST				
22	Mean male-female flower production ratio				

Table 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

¹ For all species except pine, cone crop estimate equals (line 2) x (line 19); for pine species it equals (line 2) x (line 25)

² To estimate hectoliters, divide (line 28) by the appropriate factor:

- For white spruce – 15,000 cones/hl
- For black spruce – 24,000 cones/hl
- For lodgepole pine – 38,000 cones/hl

Appendix 34A. Pollen Contamination Monitoring

See Standard 32.8.3.

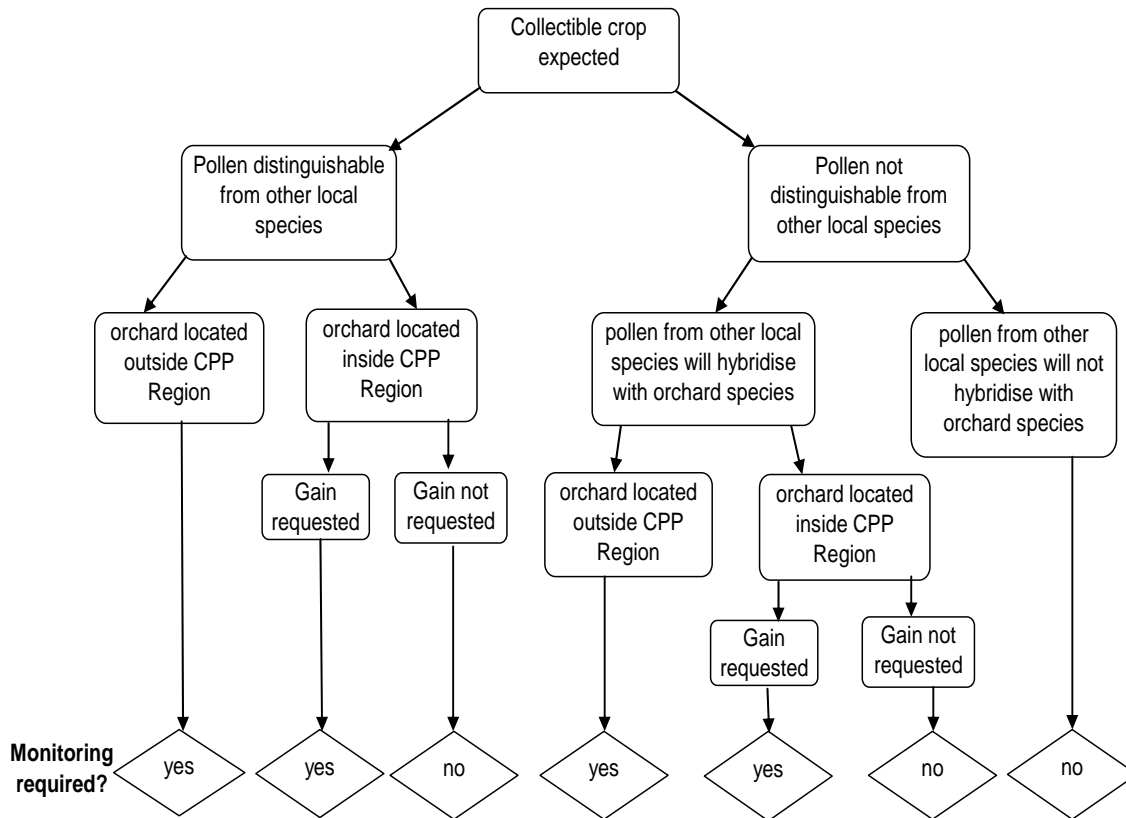
Note: A re-assessment of monitoring requirements will be undertaken at the scheduled 2013 review.

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, or aspen from balsam poplar.

In years when no collectible crop is anticipated in the given orchard, pollen monitoring is not required in that orchard. The flowchart below will be used to determine pollen monitoring requirements in each orchard.

Where pollen monitoring is not required, the orchard manager must demonstrate to *Alberta's* satisfaction that pollen contamination will not significantly compromise the adaptation of seed produced, and, if gain is requested, how pollen contamination will be factored into gain estimates.



Part 1. Pollen Contamination Estimation Using Pollen Flight Monitoring

PROCEDURES FOR POLLEN FLIGHT MONITORING

- The orchard manager will monitor pollen flight within each orchard at a minimum of two locations.
- 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.
- 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.
- 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.
- Traps are to be changed at least every two days.
- 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 mm² 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).
- All traps will be installed several days before pollen flight (locally or in the orchard) is expected to begin and pollen trapping will continue until the orchard manager has determined that pollen flight has ended.
- For pine orchards, within-orchard monitors should be located at a height of one-half of the average crown height of the orchard.
- 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

$$ct = R * xt$$

where

$$R = \min (ws/xs, 1)$$

and the proportion of contaminant pollen, **pc**, within the orchard can be estimated as

$$pc = ct/wt$$

$$= \mathbf{R} * \mathbf{xt}/\mathbf{wt}$$

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 the table below. 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**).

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

$$\begin{aligned}
 xs &= (30.5+33.5)/2 = 32.0 \\
 ws &= (14.1+16.9+12.6)/3 = 14.5 \\
 xt &= (179.4+175.3)/2 = 177.4 \\
 wt &= (415.3+395.1+404.0)/3 = 404.8 \\
 ct &= 14.5/32.0 = 80.5 \\
 pc &= 80.5/404.8 = 0.20
 \end{aligned}$$

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 as well. 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 clones 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 specific to the species. Each marker is a segment of chloroplast DNA from a unique 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 and 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 depending upon 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 seed embryos only.

In addition to pollen contamination estimates, cpDNA markers can provide information on orchard pollen dynamics and its 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* (N_e).

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 clones. 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 Tree Improvement & Seed Centre (ATISC) by ATG Genetics Inc. (Craig Newton, PhD.), Nanaimo, British Columbia (www.atggenetics.com). In 2008, the cost of haplotyping per tree using bud samples was \$75-\$100, 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 clones represented by 14 cpDNA 5-locus haplotypes (Table 1). 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 2). Fifty seeds from the 2008 seed crop were haplotyped and 41 of these seeds matched haplotypes found in the orchard (Table 1). Nine seeds did not match any of the 14 orchard haplotypes (Table 2).

The expected proportion of orchard ovules fertilized by background pollen with a haplotype unique to the background stands is

$$\mathbf{b} = \mathbf{m}\mathbf{d}$$

where

\mathbf{m} = the probability that an orchard ovule is fertilized by a pollen grain from the background stand, and
 \mathbf{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

$$\mathbf{m} = \mathbf{b}/\mathbf{d}$$

The fraction of seeds not matching any orchard haplotypes, $9/50 = 0.18$, is \mathbf{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 \mathbf{d} . Therefore, pollen contamination in the 2008 seedlot is estimated as $0.18/0.44 = 41\%$.

The variance of \mathbf{m} is calculated as follows:

$$\mathbf{Var}(\mathbf{m}) = (\mathbf{b}(1 - \mathbf{b}))/\mathbf{n}\mathbf{d}^2$$

where

\mathbf{n} = the number of embryos sampled to estimate \mathbf{b} .

This must be considered a minimum variance because it does not take into account the fact that both \mathbf{b} and \mathbf{d} are estimated, or the possibility of failure of assumptions.

For this example, the variance of \mathbf{m} is 0.015 giving a standard error of 0.12. Pollen contamination is therefore estimated as $41\% \pm 12\%$.

Table 1. Orchard haplotypes

Haplotype Number	Haplotype (cpDNA size in basepairs) ¹					Clones 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 2. 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

¹ bold and italicized haplotypes are also found in the background stands and plantations² bold and italicized haplotypes are also found in the orchard parental clones³ numbers in brackets are included in the Table 1 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 clones 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 clones 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:

- each clone or family will be assessed for a minimum of five years after operational production begins;
- measurement years for individual clones must overlap sufficiently that an accurate assessment of relative phenology can be made;
- each clone must have overlapping data from at least 10 other clones.

Phenology monitoring is not required in orchards where:

- pollen contamination estimation is not required (see flowchart, Part 1), and
- actual (or anticipated, if orchard not yet in full production) *cumulative Ne* levels are >30.

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 below) until stage 7, at intervals of two days or less.

White spruce female bud and 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

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

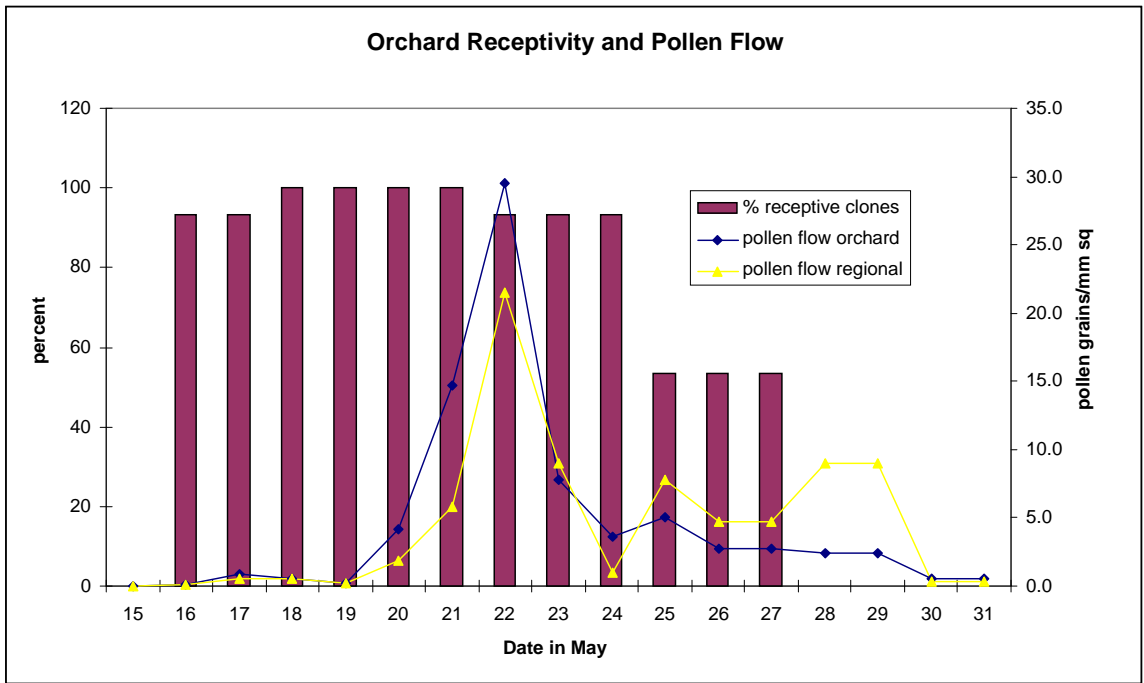
- A clone is considered receptive when 20% of the cones are fully receptive (stage 6).
- A clone is considered to have completed receptivity when 80% of the cones are post-receptive (stage 7).
- The orchard is considered receptive when 20% of clones are receptive, and to have completed receptivity when 80% of clones are post-receptive.

EXAMPLE

A 30-clone white spruce orchard is receptive from May 16 to 27. A summary of the phenology and pollen monitoring data is tabulated and shown graphically below.

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



REFERENCES

Owens, J.N. 1984. The reproductive cycle of lodgepole pine. BC Ministry of Forests. 29p.
 Owens, J.N. and Molder, M. 1984. The reproductive cycle of interior spruce. BC Ministry of Forests. 31p.

Appendix 35. Annual Operations Report

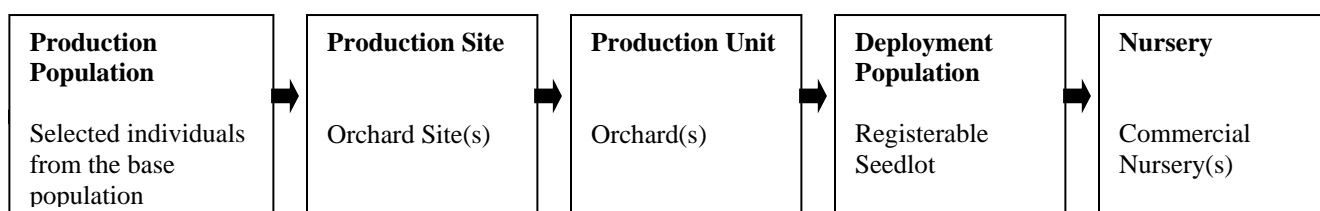
See Standard 32.1.

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 *Production Population* are taken from a *base population* which can include materials collected from *wild* stands, plantations, genetic *tests*, clone banks, or germplasm archives etc.

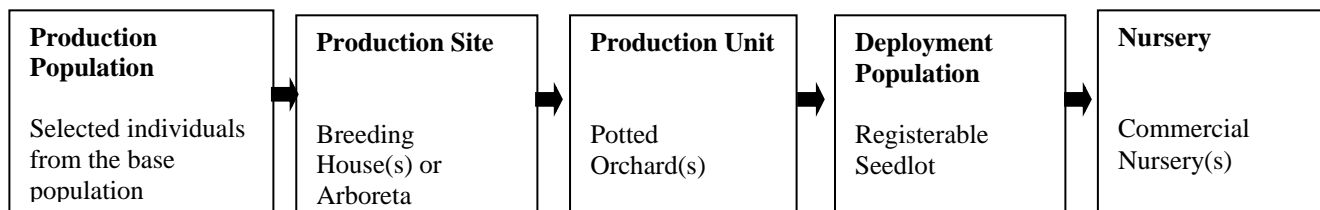
A. Sexual Production

Alberta (Alberta Tree Improvement & Seed Centre) will assign *Production Unit* identifiers.

1. Fixed Seed Orchards



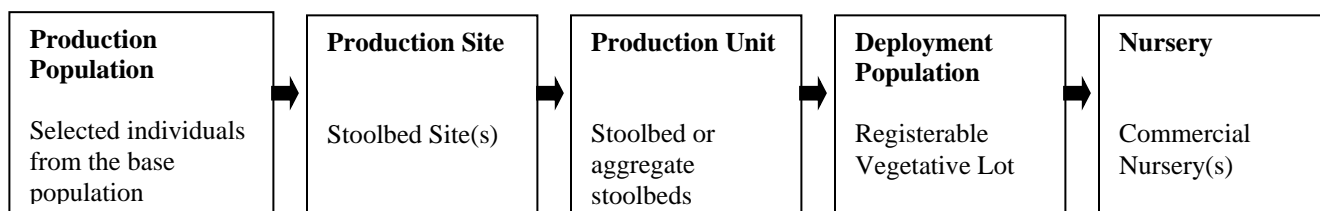
2. Potted Seed Orchards



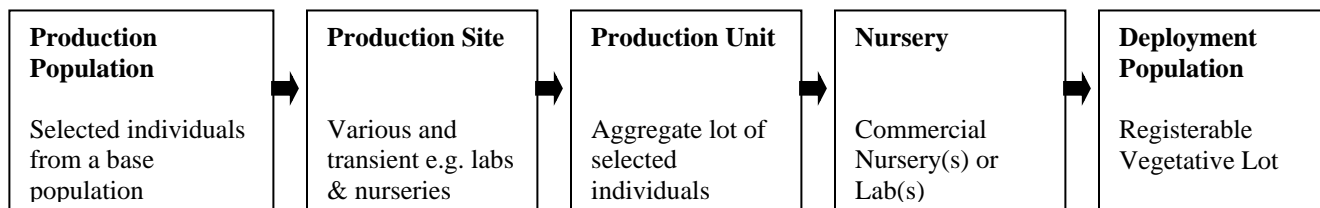
B. Vegetative Production

Alberta (Alberta Tree Improvement & Seed Centre) will assign *Production Population* identifiers.

1. Vegetative Stoolbeds



2. Vegetative Collections



Appendix 35A. Production Population and Unit Annual Operations Report for Sexual Production Systems

See Standards 32.8.3, 32.8.4 and 33.7.

Annual operations reports are due March 31 in the year following the year in which the operations took place. Annual operations reports for seed facilities must contain the following information (for details, refer to the sample report located on the Government of Alberta website <http://srd.alberta.ca/forests/managing/manuals.aspx>).

Name of the Relevant Controlled Parentage Program (CPP) Plan

Base Population

- Population type (e.g., *wild* stands, plantations, genetic *tests*);
- *Trial series* name(s), numbers(s).

Production Site Description

- Site Name/Location;
- Manager(s);
- Area occupied (ha).

Production Population and Unit

- *Production Unit* Identifier (assigned by *Alberta*);
- Design capacity (planned final number of clones, families, trees);
- Current number of trees in *production unit*.

Cultural Activities

- Cultural activities including irrigation, fertilization, mowing, herbicide applications, crown management, flower induction, root pruning, girdling, supplemental pollination.

Insect and Disease Incidence

- Monitoring methods;
- Control measures.

Other Activities

- Activities that may not occur annually but have an impact on orchard composition, e.g., roguing, thinning, tree moving.

Orchard Monitoring

- Permanent Sample Tree (PST) report (see Appendix 33);
- Pollen density and phenology of orchard receptivity (see Appendix 34).

Deployment Population (cone and seed production)

- Timing and method of cone collection;
- Total cone production (hectoliters);
- Total seed production (grams);
- 1000 seed weight;
- Germination %;
- *Effective population size* (see Appendix 36);
- *Genetic worth*.

Subsequent Years' Planning

- Report on items that may affect *registration* of *crops* or licensing of *production sites* or *production units* planned for the subsequent production season.

Annual Establishment Summary

- Report on planting including:
 - List trees planted in the current year including family id. clone id or *Unique Identifier (U.I.)* and planting position in the orchard;
 - Planters;
 - Planting date;
 - Planting conditions (temperature and soil moisture).
- Report on mortality including:
 - Listing of trees with family, clone or *U.I.* designation which died in the previous winter and over the past growing season along with its orchard position;
 - Known or suspected causes of mortality.
- Report on distribution of families/clones 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 Population, Site and Unit Annual Operations Report for Vegetative Production Systems

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

- Population type (e.g., *wild* stands, *provenance trial*, *clonal trial*);
- *Trial series* name(s), number(s), location.

Production Population

- *Alberta* assigned *production population* identifier number;
- *Genotypes* selected from *base population*;
- Gender of *production population* clones¹.

Production Site(s) Description

- Name(s), location(s);
- Manager(s).

Production Unit (each production site) (*production unit* numbers to be assigned by the proponent)

- Type (e.g., field, lab based production or greenhouse pots);
- Physical capacity (e.g., square meters of *stoolbed*, number of beds, number of mother pots per clone);
- Design capacity (number of clones, number of *ramets* of each clone² or number of cultures of each clone).

Cultural Activities (each production site)

- Silviculture management (example, mowing, cultivation, irrigation, fertilization, CO₂ enhancement, herbicide applications, root pruning, etc.).

Insect and Disease Incidence (each production site)

- Monitoring methods;
- Control methods.

Other Activities (each production site)

- Activities that may not occur annually but 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).

¹ Minimum of 50% of clones identified in the *production population*, 5-year target after 1st year of *deployment population* production.

² If number of ramets 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 *deployment 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 *deployment population* can be registered after the design capacity of the *production unit* has been determined, prior to nursery propagation.

Propagule Production (across all production sites)

- Timing of harvest (e.g., *stoolbed* or potted mother plant);
- Number of cuttings/*propagules*/root sections collected by clone/bed, culture, pot;
- Total number of clones in *deployment population* and total number of cuttings/plantlets;
- Storage location and method; and
- *Effective population size* (N_e) (see Appendix 36).

Subsequent Years' Planning

- Report on items that may affect *registration of deployment population* or approval.

Appendix 36. Calculation of Effective Population Size (N_e) for Deployment Populations

See Standards 33.4, 34.3 and 34.3.1.

INTRODUCTION

Calculation methods presented here for *effective population size* (N_e) 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 N_e 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

$$N_e = 0.5 / (\sum \sum p_i p_j c_{ij}) \quad (i, j = 1, 2, \dots, n) \quad \text{equation 1}$$

or, in matrix notation

$$N_e = 0.5 / \mathbf{p}'\mathbf{C}\mathbf{p} \quad \text{equation 2}$$

where

- N_e = *effective population size*
- p_i = the proportional genetic contribution of clone or *genotype* i
- p_j = the proportional genetic contribution of *genotype* j
- c_{ij} = coancestry between *genotypes* i and j
- n = number of *genotypes*
- \mathbf{p} = the $n \times 1$ vector of gametic proportions for *genotypes* $i = 1, 2, \dots, n$
- \mathbf{C} = the $n \times n$ coancestry matrix for *genotypes* $i = 1, 2, \dots, n$

The proportional genetic contribution, p_i , of *genotype* i is calculated as follows:

- $p_i = f_i / \sum f_i$ for proportions based only on samples of female “flower” or cone counts
- $p_i = (f_i / \sum f_i + m_i / \sum m_i) / 2$ for proportions based on samples of both female and male “flower” counts
- $p_i = n_i / \sum n_i$ for proportions based on total counts of cuttings per clone

where

- f_i = the number of female “flowers” occurring on *genotype* i (alternatively, cone counts can be used)
- m_i = the number of male “flowers” occurring on *genotype* i
- n_i = the number of cuttings taken from *genotype* i

Where *genotypes* are unrelated and not inbred, formula (1) simplifies to

$$N_e = 1 / \sum p_i^2 \quad \text{equation 3}$$

COANCESTRIES

Coancestry values for some common relationships between non-inbred individuals are shown below.

Common coancestry values

Relationship between genotypes	Coancestry
Identical (tree with itself or with <i>ramet</i> 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 clones;
2. *production populations* producing vegetative lots of related clones (amplified full-sib or half-sib families).

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 clones).

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 the 1 and 3 categories 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*. For *production units* or *production populations* including a very large number of *genotypes* (e.g., seedling *seed orchards*), SAS or the ACCESS program noted below can be used.

An ACCESS program developed for calculation of N_e 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 through the Forest Genetics Program, Alberta Sustainable Resource Development, Edmonton. The contributions of BC Ministry of Forests geneticist Michael Stoehr are gratefully acknowledged.

WORKED EXAMPLES

A. VEGETATIVE MATERIAL

Note: *Effective population size* (N_e) 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 clones

EXAMPLE 1: A vegetative lot containing 2360 individuals of 10 unrelated clones

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)

$$\begin{aligned}
 N_e &= 1/\sum p_i^2 \\
 &= 1/0.1218 = 8.21
 \end{aligned}$$

A.2. Vegetative lots of related clones (amplified full-sib or half-sib families)

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* (ATISC).

EXAMPLE 2: A vegetative lot containing five clones, with two clones 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 clones 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:

$$\sum \sum p_i p_j c_{ij} = 0.181175$$

and using equation (1)

$$N_e = 0.5 / (\sum \sum p_i p_j c_{ij}) = 2.76$$

EXAMPLE 2 reworked using matrices

$$\mathbf{p} = \begin{bmatrix} 0.13 \\ 0.28 \\ 0.41 \\ 0.15 \\ 0.03 \end{bmatrix} \quad \mathbf{C} = \begin{bmatrix} 0.5 & 0.25 & 0 & 0 & 0 \\ 0.25 & 0.5 & 0 & 0 & 0 \\ 0 & 0 & 0.5 & 0.125 & 0.125 \\ 0 & 0 & 0.125 & 0.5 & 0.125 \\ 0 & 0 & 0.125 & 0.125 & 0.5 \end{bmatrix}$$

$$\mathbf{p}'\mathbf{C}\mathbf{p} = 0.181175$$

and using equation (2)

$$N_e = 0.5 / \mathbf{p}'\mathbf{C}\mathbf{p} = 2.76, \text{ as above.}$$

B. SEED ORCHARD DEPLOYMENT POPULATIONS

(See Appendix 37 for sampling levels required for N_e determination.)

B.1. Seedlots from orchards of unrelated and non-inbred *genotypes* (e.g., most first generation clonal orchards)

The value of 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 ramets of 10 clones

Count of female and male “flowers” for each ramet

Clone	Ramet	Females	Males
x123	1	50	500
x123	2	50	600
x123	3	0	100
x123	4	75	660
x123	5	85	1000
x123	6	80	450
x123	7	0	120
x123	8	230	1860
x354	1	0	20
x354	2	0	0
x354	3	25	300
x354	4	0	50
x354	5	0	0
x465	1	50	430
x465	2	350	1980
x466	1	225	2100
x466	2	125	1490
x466	3	425	3580
x466	4	0	0
x466	5	900	7500
x466	6	100	900
x466	7	1450	9800
x466	8	85	400
x487	1	0	50
x487	2	20	200

Clone	Ramet	Females	Males
x487	3	125	980
x487	4	75	640
x699	1	475	3200
x699	2	575	6000
x699	3	275	1300
x699	4	375	2900
x699	5	0	50
x732	1	0	170
x732	2	0	50
x732	3	0	60
x732	4	60	590
x732	5	0	0
x732	6	80	680
x744	1	50	370
x744	2	0	210
x744	3	35	250
x744	4	175	1500
x798	1	225	1900
x798	2	30	290
x798	3	450	5400
x798	4	0	60
x798	5	75	650
x900	1	80	870
x900	2	0	50
x900	3	0	110

Summarize by clone and calculate proportions:

- for proportions based only on female counts: $p_i = f_i / \sum f_i$
- for proportions based on both female and male counts: $p_i = (f_i / \sum f_i + m_i / \sum m_i) / 2$

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
$Ne = 1/\sum(p_i^2)$					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 clones (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 orchards and advanced generation clonal orchards with related clones)

EXAMPLE 4: a half-sib seedling orchard containing two families with three and two individuals respectively

$$\mathbf{p} = \begin{bmatrix} 0.24 \\ 0.32 \\ 0.09 \\ 0.20 \\ 0.15 \end{bmatrix} \quad \mathbf{C} = \begin{bmatrix} 0.5 & 0.125 & 0.125 & 0 & 0 \\ 0.125 & 0.5 & 0.125 & 0 & 0 \\ 0.125 & 0.125 & 0.5 & 0 & 0 \\ 0 & 0 & 0 & 0.5 & 0.125 \\ 0 & 0 & 0 & 0.125 & 0.5 \end{bmatrix}$$

$$\mathbf{p}'\mathbf{C}\mathbf{p} = 0.1546$$

and using equation (2)

$$Ne = 0.5/\mathbf{p}'\mathbf{C}\mathbf{p} = 3.23.$$

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Appendix 37. Sampling Levels for Calculation of Effective Population Size (N_e) Values in Orchard Seedlots

See Standards 33.4 and 33.4.1.

INTRODUCTION

Effective population size (N_e) (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 N_e estimates will vary with the intensity of sampling. These estimates may be considerably lower than, or in some cases higher than, the actual N_e . 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 N_e estimation is to ensure that a threshold has been met, rather than to determine the actual value of N_e , 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 N_e estimate as low as one-fifth of the N_e calculated on a 100% orchard survey. On average, the ratio of the N_e estimate obtained with 10% sampling to the N_e estimate at 100% sampling [$N_e(10\%)/N_e(100\%)$] is expected to be approximately 0.5, depending on the distribution of genotypic frequencies. At a 50% sampling intensity, the average $N_e(50\%)/N_e(100\%)$ 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 N_e thresholds have been exceeded.

Note that for pine species, if flower data is used for N_e estimation, it must be from the previous year, since cones mature over two years.

SAMPLING REQUIREMENTS

At the orchard manager's discretion, N_e 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. Estimates of female contributions may be based on flower, immature cone (pines) or mature cone counts.

If PST based N_e estimates are not used, the following minimum sampling requirements apply.

CLONAL SEED ORCHARDS

Table 1 below outlines minimum sampling requirements for clonal *seed orchards*.

Table 1. Sampling requirements for N_e calculations in clonal seed orchards

Clones 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 N_e value than a seedlot from a clonal *seed orchard* with n clones and an average of t ramets per clone. This is because there is considerable genetic diversity within families, but none within clones. The ratio of the N_e from a seedling *seed orchard* with n families to that of a clonal orchard with n clones is independent of n , and increases with increasing t (see example in Table 2 below; for simplicity, in this example it is assumed that all clones or families have equal numbers of ramets or seedlings, and that all trees are equally productive).

Table 2. N_e 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 clones.

If the mean family size in the orchard is less than five trees, sampling requirements are as for clonal orchards (see Table 3). If the mean family size exceeds five, sampling requirements are given in Table 4.

Table 3. Sampling requirements for N_e 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 4. Sampling requirements for N_e 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

GLOSSARY OF TERMS

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. <i>Accession number</i> is one category of <i>genetic identity</i> .
Afforestation	The establishment of a tree crop on an area from which forest cover has always been absent, or absent for a very long time.
Alberta	A designation meaning the Government of Alberta to be interpreted as Alberta Sustainable Resource Development or the Alberta Tree Improvement & Seed Centre.
Amplified family	An aggregate of multiple <i>vegetative propagules</i> from each of several to many 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 or store material for <i>deployment</i> .
Base population	The population of trees from which individuals are chosen to establish the <i>breeding population</i> and/or <i>production population</i> for a <i>controlled parentage program</i> . May refer to a <i>wild</i> population, or to a plantation or a genetic <i>test</i> , such as a progeny or provenance <i>test</i> .
Breeding population	A set of trees within which crosses are made to generate material for the next cycle of selection. <i>Breeding populations</i> are generally large, as compared to the <i>production population</i> .
Breeding rights	The right to use genetic materials for one or more generations of crossing, genetic testing and selection. These rights are usually exercised by tree breeders to produce successive generations of improved materials.
Breeding value (BV)	The genetic value of an individual for a given trait, based on the mean performance of its offspring or other relatives. <i>BV</i> may be expressed in terms of measurement units such as m or cm; it is more commonly expressed in relative terms, as a percent deviation from the population mean.
Checked data	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 such anomalies as shrinking trees, trees that are too tall for the given diameter at breast height (DBH), and live trees that were previously reported dead.
Collections, public land	Genetic material gathered and removed from <i>public land</i> for the purposes of <i>reforestation</i> , breeding or research. It does not include collections from approved <i>production populations</i> or <i>production units</i> .
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).
Controlled parentage program (CPP)	A program to produce <i>Stream 2 material</i> for <i>deployment</i> within the associated <i>CPP region</i> .
Conversion	Stand replacement through planting of <i>Stream 2 material</i> . Removal of original stand may have been either through natural (e.g., fire) or artificial (e.g., logging) causes.
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 <i>Stream 2 material</i> is produced.

Term	Definition
Cumulative effective population size	The <i>effective population size (Ne)</i> of <i>deployment populations</i> aggregated across years, <i>production units</i> , or <i>production populations</i> . See Appendix 20 for calculation method.
Cumulative Ne	See “ <i>Cumulative effective population size.</i> ”
Deployment	Establishment of a new stand through artificial regeneration; through physical movement from one site (e.g., a nursery) to the <i>deployment</i> site; or through planting or seeding designed to meet resource management objectives or obligations.
Deployment population	The collection of <i>propagules</i> , produced from a single <i>production population</i> or its associated <i>production unit(s)</i> and registered under a single <i>registered lot number</i> that will be deployed (e.g., a seedlot from a <i>seed orchard</i> ; a collection of cuttings from a <i>stoolbed</i> or <i>stoolbeds</i> ; a collection of <i>rootlings</i> ; a collection of micropropagated plantlets).
Dioecious	Refers to a species in which male and female “flowers” generally occur on different plants; each plant is usually either male or female, but not both (e.g., aspen (<i>Populus tremuloides</i>)).
Effective population size (Ne)	<i>Effective population size (Ne)</i> is one measure of genetic diversity and relatedness in a seed or vegetative lot, and reflects both the degree of relatedness among parents and the degree of balance among parental contributions to the given lot.
Effective population size, cumulative	See “ <i>Cumulative effective population size.</i> ”
Forest tenure holder	A person or institution with defined ownership rights and obligations for the management and use of forest resources.
Genetic gain	The average heritable change attributable to selection in a given trait, from one generation to the next.
Genetic identity	One of several unambiguous current or historical identifiers of seed or vegetative material lots that can be used to identify the genetic source of material. The <i>unique identifier</i> ., <i>accession number</i> or <i>registered lot number</i> may be used.
Genetic research planting	A planting associated with a research plan or <i>controlled parentage</i> plan. All materials in <i>genetic research plantings</i> must be <i>Stream 1 materials</i> , <i>Stream 2 materials</i> , <i>local research materials</i> or <i>non-local research materials</i> , and must be registered or have a <i>genetic identity</i> .
Genetic test site	A field experimental area containing genetics and tree improvement research <i>trials</i> .
Genetic worth	For a seed or vegetative lot, the predicted difference in value of a given trait (e.g., height or volume) from the value of that trait in <i>wild</i> stand material.
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.
Genotype	The <i>genetic identity</i> or constitution of an individual. Physical material, in the form of plant tissue, provides the medium for storage and transmission of a <i>genotype</i> .
Green area	The area outlined and colored green on a map annexed to the order <i>Classifying Public Lands</i> dated April 16, 1963, and published in <i>The Alberta Gazette</i> on April 30, 1963, as amended from time to time. The <i>Green Area</i> includes <i>public land</i> that is primarily forested, and is managed for timber production, oil/gas development, watershed, wildlife and fisheries, recreation and other uses.

Term	Definition
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., Sw x Se).
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 <i>intellectual property rights</i> is usually the person or persons who developed the product or the organization that funded it. In the context of Forest Genetic Policy, <i>intellectual property rights</i> apply to genetic data and to the <i>genotypes</i> to which they apply, either separately or in aggregate.
Local research material	See “Research material, local.”
Locally adapted material	Material deemed to be adapted by virtue of origin or testing. Locally <i>adapted material</i> may be one of: <ol style="list-style-type: none"> 1. <i>Stream 1 material</i> collected from within the <i>seed zone</i> in which <i>deployment</i> is planned, 2. <i>Stream 2 material</i> from <i>genotypes</i> under test, or scheduled for testing, but accepted by Alberta as locally adapted, or 3. <i>Stream 2 material</i> from <i>genotypes</i> confirmed as adapted on the basis of field testing.
Lot number, registered	A number used to uniquely identify a seed or vegetative lot through to storage, <i>deployment</i> and monitoring. The <i>registered lot number</i> is assigned by Alberta when material is registered.
Lot number, temporary	A number used to uniquely identify a seed or vegetative lot prior to <i>registration</i> .
Material transfer agreement (MTA)	<i>Material transfer agreements (MTAs)</i> 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 <i>material use rights</i> does not usually have propagation or <i>breeding rights</i> .
Monoecious	Refers to a species in which male and female “flower” parts generally occur on the same plant, either within a single “flower” or separately; thus each plant is usually both male and female; (e.g., white spruce { <i>Picea glauca</i> }).
Ne	See “ <i>Effective population size</i> .”
Non-local material	Material of unknown adaptation. Either of: <ol style="list-style-type: none"> 1. <i>Wild material</i> collected from outside the <i>seed zone</i> in which <i>deployment</i> is proposed, 2. <i>Stream 2 material</i> that is not deemed to be locally adapted.
Non-local research material	See “Research material, non-local.”
Opening	An administrative area created as a result of planned or actual harvesting activities and formally designated with a unique “opening identification number” in the Alberta Regeneration Information System. A cutblock will have one or more openings within it.
Pedigree	A record of parentage, sometimes also including data on the performance of parents and other relatives.

Term	Definition
Plant with novel traits (PNT)	<p>A plant variety/<i>genotype</i> possessing characteristics that demonstrate neither familiarity nor substantial equivalence to those present in a distinct, stable population of a cultivated species of seed in Canada and that have been intentionally selected, created or introduced into a population of that species through a specific genetic change.</p> <p>In this definition, familiarity means, the knowledge of the characteristics of a plant species and experience with the use of that plant species in Canada; substantial equivalence means, the equivalence of a novel trait within a particular plant species, in terms of its specific use and safety to the environment and human health, to those in that same species, that are in use and generally considered as safe in Canada, based on valid scientific rationale.</p> <p>All <i>GMO</i> plants are PNTs, but not all PNTs are <i>GMOs</i>.</p>
Point collection	Registerable <i>Stream 1 material</i> collected within area and elevation limits as defined in Appendix 4; compliance enables application for variance.
Production population	The population of <i>genotypes</i> used for <i>propagule</i> production, or the aggregate of <i>genotypes</i> represented in the <i>production unit(s)</i> for a given <i>CPP region</i> .
Production site	The physical location or place where <i>propagules</i> are produced (e.g., a <i>seed orchard</i> site, <i>stoolbed</i> site, collection of pots at a nursery, or laboratory).
Production unit(s)	The direct physical source(s) of <i>Stream 2</i> seed or vegetative lots (e.g., the group of trees that is a <i>seed orchard</i> ; individual or aggregate <i>stoolbeds</i> , or a collection of tissues used for <i>rootling</i> propagation or micro-propagation).
Propagule	Plant material from which a new individual or individuals may be developed (e.g., cutting, root segment, seed, or cultured callus tissue).
Public land	Alberta “ <i>public lands</i> ” as defined in the <i>Public Lands Act</i> . Includes <i>Green Area</i> (land managed primarily as forest land) and <i>White Area</i> (land managed primarily for agriculture and uses other than forestry).
Public land collections	See “ <i>Collections, public land.</i> ”
Ramet	An individual that has been vegetatively reproduced from the original plant, or ortet, and is thus genetically identical to it.
Ramet, grafted	A <i>ramet</i> created by grafting a twig or bud from the original plant onto a physically distinct rootstock. The portion of the grafted <i>ramet</i> above the graft union is genetically identical to the original plant (see also “ <i>Ramet, rooted.</i> ”)
Ramet, rooted	A <i>ramet</i> created by rooting a twig or cutting from the original plant. The whole <i>ramet</i> is genetically identical to the original plant (see also, “ <i>Ramet, grafted.</i> ”)
Reclamation	A planned series of activities designed to recreate the biophysical capacity of an ecosystem.
Reforestation	The reestablishment of trees on denuded forest land by natural or artificial means such as planting and seeding.
Registered lot number	See “ <i>Lot number, registered.</i> ”
Registration	Process that allows a seed or vegetative lot to be used for <i>deployment</i> within its <i>CPP region</i> or <i>seed zone</i> . Only <i>Stream 1</i> and <i>Stream 2 materials</i> can be registered. <i>Registration</i> may be <i>restricted</i> or <i>unrestricted</i> . A registered seed or vegetative lot is one that has completed the <i>registration</i> process.
Regulated professional	A person regulated by a recognized professional body to be accountable and provide competent and ethical services.
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 <i>CPP region</i> or an adjacent <i>CPP region</i> that may not be eligible for <i>registration</i> (e.g., an open-pollinated seedlot collected from a single tree). These materials may be included in a <i>controlled parentage program</i> leading to production of <i>Stream 2 material</i> . These materials must have an assigned <i>U.I.</i> before being established in <i>genetic research plantings</i> or a <i>CPPs</i> . The 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 <i>seed zone</i> or <i>CPP region</i> of origin). Untested <i>non-local research materials</i> are not eligible for <i>deployment</i> within the <i>Green Area</i> , or inclusion in <i>production populations</i> or <i>units</i> associated with <i>CPPs</i> (with some exceptions of material from adjacent <i>CPP regions</i>), but may be included in <i>genetic research plantings</i> . These materials must have an assigned <i>U.I.</i> before being established in <i>genetic research plantings</i> . Following testing and demonstration of adaptedness, these materials may be included in <i>CPPs</i> leading to production of <i>Stream 2 materials</i> . The Breeding, Testing and Verification Standards apply to this material.
Restricted registration	<i>Registration</i> 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 <i>deployment</i> within its <i>CPP region</i> or <i>seed zone</i> . Restrictions on <i>deployment</i> may be imposed.
Rolling front orchard	A <i>seed orchard</i> in which individual trees or groups of trees of known <i>breeding value</i> are replaced on a more or less continuous basis as new material of higher <i>breeding value</i> becomes available.
Rootling	Plant generated from root segment.
Seed orchard	A stand of trees, usually several hundred to several thousand in number, established and managed primarily for early and abundant production of seed for <i>deployment</i> . Trees in the orchard are derived and propagated from selected parent trees, usually by grafting or by seed.
Seed zone	A geographic area, defined on the basis of ecological characteristics and genetic information, within which <i>Stream 1 material</i> meeting <i>unrestricted registration</i> requirements may be collected and freely deployed. (<i>Seed zones</i> may apply to group of species, or <i>species-specific seed zones</i> may be developed).
Seed zone collection	Registerable <i>Stream 1 material</i> collected within a single <i>seed zone</i> , not otherwise subject to constraints of area or elevation range; not eligible for variance (see Appendix 4).
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.
Species-specific seed zone	A <i>seed zone</i> , delineated for a single species on the basis of adaptation as assessed from genetic <i>trials</i> , within which <i>Stream 1 material</i> may be collected and freely deployed.
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 <i>deployment</i> .
Stream 1 material	Seed or vegetative material collected from <i>wild</i> or artificially regenerated stands of native species within a given <i>seed zone</i> , having <i>restricted</i> or <i>unrestricted registration</i> for <i>deployment</i> in that <i>seed zone</i> .
Stream 2 material	Registered or registerable seed or vegetative material produced from an approved <i>production population</i> or <i>production unit(s)</i> .

Term	Definition
Temporary lot number	See “ <i>Lot number, temporary.</i> ”
Test	A <i>genetic research planting</i> 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 <i>test</i> site). Used interchangeably with <i>trial</i> .
Test series	A group of <i>genetic research plantings</i> of the same or overlapping material, on one or several sites, designed to address a given genetic issue (e.g., a progeny <i>test</i> established on four sites). Used interchangeably with <i>trial series</i> .
Trial	A <i>genetic research planting</i> 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 <i>trial</i> site). Used interchangeably with <i>test</i> .
Trial series	A group of <i>genetic research plantings</i> of the same or overlapping material, on one or several sites, designed to address a given genetic issue (e.g., a progeny <i>trial</i> established on four sites). Used interchangeably with <i>test series</i> .
Unique Identifier (U.I.)	An alphanumeric code of 7 to 13 characters assigned to genetic material. The first seven characters of the <i>U.I.</i> are essential, and uniquely identify the <i>genotype</i> by agency and sequence number. Subsequent characters may be included as applicable, and specify material type (e.g., scions or pollen), individual number (e.g., cutting 103), and species (e.g., Sw). A <i>U.I.</i> is required for all unregistered material included in research <i>trials</i> related to <i>CPPs</i> . See Appendix 25 for details of variables, structure and agency codes.
Unrestricted registration	<i>Registration</i> based on compliance with documentation, adaptation and diversity requirements that allow a seed or vegetative lot to be used for <i>deployment</i> within its <i>CPP region</i> or <i>seed zone</i> . Restrictions on <i>deployment</i> may be imposed (see Appendices 4, 9 and 21).
Vegetative propagule	A part of a plant used for regenerating a plant by vegetative propagation techniques such as a root, a stem, or somatic embryonic tissue.
White area	Private and <i>public land</i> 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 artificially regenerated material.

LIST OF ACRONYMS

AAC	Annual Allowable Cut
AFGF	Alberta Forest Genetics Framework
ANOVA	Analysis of Variance
AOP	Annual Operating Plan
ARIS	Alberta Regeneration Information System
ATISC	Alberta Tree Improvement and Seed Centre
BLP	Best Linear Predictor
BTV	Breeding, Testing and Verification
BV	Breeding Value
CNT	Consultative Notation
CPP	Controlled Parentage Program
DBH	Diameter at Breast Height
FGRMS	Forest Genetic Resource Management and Conservation Standards (formerly STIA)
FHt	Fall Height measurement
FMP	Forest Management Plan
FOIP	Freedom Of Information and Protection of Privacy Act
FMA	Forest Management Agreement
GAD	Green Area Deployment
GMO	Genetically Modified Organism
GW	Genetic Worth
G&Y	Growth and Yield
IP	Intellectual Property
ISP	Industrial Sample Plot Designation
MCHRS	Material Collection, Handling, Registration and Storage Section of the Standards
MLL	Miscellaneous Lease
MTA	Material Transfer Agreement
Ne	Effective Population Size
ODA	Ownership and Data Access
OGR	Operating Ground Rules
PCPM	Production of Controlled Parentage Material
PNT	Plants with Novel Traits
PST	Permanent Sample Tree
RP	Research Program
SRD	Sustainable Resource Development