USDA FOREST SERVICE
NATIONAL FOREST GENETICS LABORATORY
(NFGEL)

Annual Report 2004 – 2005
(FY05)

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INTRODUCTION

This report covers laboratory activities and accomplishments during Fiscal Year 2005.
October 1, 2004 through September 30, 2005

Background

NFGEL was established in 1988 as part of the National Forest System of the USDA-Forest Service. The focus of the lab is to address genetic conservation and management of all plant species using a variety of laboratory techniques including DNA analyses. NFGEL services are provided to managers within the Forest Service, other government agencies, and non-government organizations for assessing and monitoring genetic diversity.

Purpose of Laboratory

The purpose of the Laboratory is to analyze molecular genetic markers (protein and DNA) in plant material submitted by Forest Service employees and those from other cooperating entities. NFGEL provides baseline genetic information, determines the effect of management on the genetic resource, supports genetic improvement program, and contributes information in the support of conservation and restoration programs, especially those involving native and TES (threatened, endangered, and sensitive) species.

Alignment to National Strategic Plan for FY04-08

NFGEL's work aligns to the following National Strategic Plan measures:

1. Goal 1 (Reduce risks from catastrophic wildland fire)
2. Goal 2 (Reduce the impacts from invasive species).
3. Goal 4 (Help meet energy resource needs)
4. Goal 5 (Improve watershed condition)
5. Goal 6 (Mission related work in addition to that which supports the agency goals)

NFGEL Projects

NFGEL projects were processed to meet a variety of management objectives. Project results were used to guide restoration and conservation projects, and assist in silviculture and tree improvement activities. During FY 2005, NFGEL continued to follow its mission to "provide state-of-the-art molecular genetic information to the National Forests and other cooperating agencies for the evaluation and protection of our nation's genetic resource". Nine project reports are included in this Annual Report.

Valerie Hipkins
NFGEL Director
December 2005

Overview

NFGEL projects were processed to meet a variety of management objectives. Project results were used to guide restoration and conservation projects, and assist in silviculture and tree improvement activities. During FY 2005, NFGEL continued to follow its mission to "provide state-of-the-art molecular genetic information to the National Forests and other cooperating agencies for the evaluation and protection of our nation's genetic resource". Fourteen project reports follow.

Silviculture and Tree Improvement

1. **Ponderosa pine (*Pinus ponderosa*) source identification using molecular genetics**
   (NFGEL Project #103)
2. **Identification of ten unknown seedlings as *Pinus echinata* (Shortleaf pine) or *P. virginiana* (Virginia pine) through genetic testing**
   (NFGEL Project #168)
3. **Assessment of SMP success in Douglas-fir using three SSR markers**
   (NFGEL Project #187)
4. **Ramet identification in Douglas-fir using SSR markers**
   (NFGEL Project #190)
5. **Polymix breeding with paternity analysis in *Populus***
   (NFGEL Project #182)
6. **DNA extraction from Douglas-fir seed: SNP testing panels**
   (NFGEL Project #199)
7. **DNA Extraction from Douglas-fir Needles: Association Studies**
   (NFGEL Project #189)
8. **Identifying unknown seedlings as being Douglas-fir or Bigcone Douglas-fir using isozymes**
   (NFGEL Project #191)
9. **Estimation of population structure in a Douglas-Fir association mapping study**
   (NFGEL Project #184)

Conservation and Restoration

1. **Genetic structure of stands of quaking aspen (*Populus tremuloides*) on the Lassen National Forest**
   (NFGEL Project #150)
2. **Genetic evidence of hybridization between *Oenothera wolfii* (Wolf's evening primrose) and *O. glazioviana*, a garden escape**
   (NFGEL Project #158)
3. **Genetic diversity in *Bromus carinatus* from western Oregon: implications for seed collection and propagation**
   (NFGEL Project #185)
4. **Genetic analysis of intermountain plants: progress report**
   (NFGEL Project #s139, 140, 141, 142, 151, 152, 153, 159, 175, 176, 177, 178, 179)
5. ***Salix* and *Populus* species diversity on the Hopi Reservation**
   (NFGEL Project #149)

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Photo provided by Mary Frances Mahalovich

Ponderosa Pine (*Pinus ponderosa*) Source Identification using Molecular Genetics

NFGEL Project #103

Report prepared by: Valerie D. Hipkins and Konstantin Krutovsky

Project submitted by: Mary Frances Mahalovich, Regional Geneticist, USDA Forest Service, Northern, Rocky Mountain, Southwestern, and Intermountain Regions, Moscow, ID

May 27, 2005

OBJECTIVE

Concern over dieback of Ponderosa pine in plantations from the Rocky Mountain Region was noted in the report, "Dieback of Ponderosa Pine in Plantations Established ca. 1970; Gunnison Service Center, Forest Health Management, Rocky Mountain, Region, USDA Forest Service, 9/22/2000". Suspicion that off-site seed was used to plant these stands led to the development of this genetic study. The objective of this project is to characterize the genetic diversity in ponderosa pine seed sources to identify offsite plantings. The main project goal is to build a DNA database characterizing known ponderosa pine sources, using molecular genetic markers capable of distinguishing populations. Plantations of unknown source can then be compared against the database for possible source identification.

The DNA database created in this project is a collection of DNA profiles from selected ponderosa pine individuals that represent known sources. The strength of the database largely relies on the adequate representative sampling of known sources. If the source of a plantation is left out of the database, an accurate identification of the plantation origin is not possible. Assignment analyses will look for the 'best match' between the plantation and the existing known populations in the database. This match is still made even if the 'true' plantation source is not incorporated in the database. A plantation match to an incorrect source (which would happen if the plantations 'true' source was not in the database) usually has a moderate to low likelihood of occuring.

An additional factor influencing the strength of the database is the variability and appropriateness of the genetic markers used to profile individuals. Three genetic markers were used to create this ponderosa pine database: isozymes (a nuclear marker), a nuclear microsatellite, and a mitochondrial minisatellite. The nuclear markers represent the genetic information that an individual receives from both its maternal and paternal parents. The mitochondrial marker is inherited only through the maternal parent in pines. Therefore, the mitochondrial data is an excellent marker for tracking seed movement. The nuclear markers reflect not only seed movement, but also the contribution of pollen through the paternal parent. When making determinations of source identification in this study, more weight was given to the mitochondrial data over the nuclear data.

Finally, source determination can be obscured when and if the plantation is made up of more than one source. Several plantations in this study appear to consist of two or more sources. We have made determinations of the percent of a given source in a plantation, as well as the origin of each component source.

Because of the complexity of the data in this project, we include the full analysis for future reference and review. Following the detailed results section, we present a table, "Identification of Ponderosa Pine Planting Sources", that gives the final source determination of each plantation.

MATERIALS AND METHODS

Samples. One to two branch tips per individual (target of 30 individuals per source or stand) were received from the field during the period 5/10/2001 through 4/21/2004. Branches from a total of 1,049 trees per stand were submitted. Seed source, location, sample sizes, and abbreviations for 34 stands of *Pinus ponderosa* used in the study are presented in Table 1. Spatial coordinates for the stands are presented in Table 2.

Isozyme Analysis. All samples containing a healthy, dormant, vegetative bud were prepared for isozyme analysis following NFGEL Standard Operating Procedures (SOPs). A total of 1,036

samples (those containing a dormant vegetative bud) were prepared for isozyme analysis during the period 5/22/2001 through 4/23/2004. All samples were genotyped for 30 isozyme loci using 22 enzyme stains on four buffer systems (USDA Forest Service 2003). Based on resolution of samples, a total of 21 loci remained for analysis: PGI-1, PGI-2, PGM-1, LAP-1, LAP-2, ADH, GOT-1, GOT-2, SOD-1, UGPP, CAT-1, CAT-2, DIA-1, MDH-1, MDH-2, MDH-3, 6PGD-1, IDH-1, SKD-1, SKD-2, and FDP-1. Isozyme data was obtained during the period 1/8/2002 – 8/10/2004

DNA Extraction. DNA was extracted from all 1,049 samples submitted following NFGEL SOPs, using a combination of Bio101 FastPrep and Qiagen DNeasy chemistry. Concentration readings for all samples were determined by fluorometry (to provide DNA quantity information). DNA quality was verified by running an aliquot of each sample on an agarose gel, staining with ethidium bromide, and visualizing the samples under UV light.

Nuclear Microsatellite Analysis. Development of microsatellite markers began 5-13-04 using primers that were identified in a recent publication (Liewlaksaneeyanawin et al. 2004). Eight primer pairs were screened on a group of six samples spanning the range of the study (Bitterroot NF; Black Hills NF; Wasatch Cache NF; Ukiah, OR; Rio Grande NF; and Apache-Sitgreaves NF), following PCR conditions outlined in the publication. PCR products were analyzed on an Applied Biosystems ABI-3100 instrument. Results of the screening identified two primer pairs (LOP-8 AND LOP-9) to be monomorphic (one allele observed), and five other primer pairs (LOP-1, LOP-3, LOP-5, LOP-11, LOP-12) to have low variation (2 – 6 alleles observed). The final primer pair (PtTX2146) was determined to be more variable, and data was collected for all samples.

Mitochondrial Minisatellite Analysis. The minisatellite region in the second intron in the *nad1* mitochondrial genome gene was used as a mitochondrial DNA (mtDNA) marker (often referred to as an SSR marker). The pine sequences available for this region in Genbank (*Pinus cembra* AF160261, *P. densata* AF440388, *P. pinaster* AJ509804-AJ509806, *P. ponderosa* AF231325, *P. pumila* AF227463, *P. sibirica* AF160260, *P. sylvestris* AJ223312, *P. tabuliformis* AF440384, and *P. yunnanensis* AF440385-AF440387) were downloaded and aligned using the GeneDoc software (Nicholas et al. 1997; http://www.psc.edu/biomed/genedoc). These alignments were used to design forward and reverse PCR primers GGGGCTTATGGGTGAGCAAT (nad1-in2_F2) and CTCTGAATTGACGAATGCCG (nad1-in2_R2), respectively, using the computer program GeneRunner v3.04 (Hastings Software, Hudson, NY; http://www.generunner.com/).

A typical PCR reaction volume was 25 µl and included 10 mm TRIS HCl pH 8.3, 50 mm KCl, 1.5 mm MgCl2, 200 µm of each dNTP, 1 µm of each primer, 1 ng of DNA template, and 0.5 units of HotStart *Taq* DNA Polymerase from QIAGEN (Valencia, CA). Following HotStart *Taq* activation (94º for 15 min), PCR amplification involved denaturation at 94º for 20 sec, annealing for 30 sec, and extension for 2 min. The annealing temperature during the initial 10 cycles was lowered from 65º to 60º by 0.5º every second cycle. An additional 30 cycles of amplification were performed upon reaching the final annealing temperature (60º) followed by a final extension at 72º for 10 min. PCR products were visualized on 1.5%, 1X TBE, agarose gels stained with ethidium bromide under UV light.

Statistical Analysis. Analysis was performed on a combination of all three data types. Isozyme genotypes (21 loci) and the single nuclear microsatellite marker were combined into a single 22-locus dataset for analysis. The mitochondrial minisatellite data was analyzed as a separate dataset.

Pairwise *P*-values for allele distribution difference between 34 populations of *Pinus ponderosa* (Fisher exact test) were calculated using the GenePop v.3.4 software (Raymond & Rousset 1995a). Global differentiation (overall 34 populations) was calculated as Θ (which is Weir & Cockerham (1984) estimation of F_{ST}) using the FSTAT v. 2.9.3 software (Goudet 1995, 2001). Estimates of observed (H_o) and expected (H_e) heterozygosities, Nei's (1987) genetic differentiation (G_{ST}), and testing of natural vs. planted populations in terms of differentiation (F_{ST}), allelic richness and heterozygosity were conducted using FSTAT v. 2.9.3 software.

SPAGeDi v.1.2 software (Hardy & Vekemans 2002) was used to analyze whether genetic differentiation between populations correlates with geographic distance between them. Spatial analysis was conducted on UTM coordinates reflecting longitude, latitude, and elevation. The correlation between genetic differentiation (calculated as $F_{ST}/(1-F_{ST})$) and geographic isolation (calculated as Euclidian distance) was estimated. Both matrixes of pairwise genetic differentiation ($F_{ST}/(1-F_{ST})$ and geographic isolation (Euclidian distance) between 34 populations were used for Mantel-test using the PGMan software by Saúl Lozano-Fuentes (http://www.evolcafe.com/popgen/download.htm).

Principal Component Analysis (PCA) using PCA-GEN v.1.2 software by Jérôme Goudet (http://www2.unil.ch/popgen/softwares/pcagen.htm) was used to assess population relationships. Additionally, a Neighbor-Joining Tree of 34 populations of *Pinus ponderosa* based on Nei's (1978) genetic distance and 22 genetic markers was calculated using the PHYLIP software package (http://evolution.genetics.washington.edu/phylip.html). First, 1000 bootstrap data sets were generated using the "seqboot" program. Second, 1000 genetic matrices based on Nei's (1978) genetic distance were calculated from this set using the "gendist" program in the package. Third, 1000 Neighbor-Joining (NJ) Trees were inferred from this distance matrices set using the "neighbor" program in the package. Forth, the consensus tree was inferred from 1000 NJ trees using the "consense" feature. This tree was viewed and printed using the TreeView software (Page 1996; http://taxonomy.zoology.gla.ac.uk/rod/treeview.html).

The GeneClass2 v.2.0 software (Piry et al. 2004) was used to assign planted stands to natural populations that have been considered as reference populations. The population structure (number of potentially different clusters) and proportion of membership of each pre-defined population in each of the inferred clusters were inferred using the Structure v2.1 software (Pritchard et al. 2000; Pritchard & Wen 2004).

RESULTS

Isozyme Data. Genotypic data was generated at 21 loci for a total of 1036 individuals from 34 populations. The SD_BHNF-MV-P population was not genotyped for the FDP-1 locus (the alleles did not resolve at this locus in this population). This locus is practically monomorphic among all other 33 population. However, some analyses and software require all populations to be genotyped for the same set of loci. Therefore, to retain this locus and to keep consistency with other populations, we entered the most common FDP-1 allele for the SD_BHNF-MV-P population.

Nuclear Microsatellite Data. For the 1036 samples analyzed for this primer pair, 29 alleles were observed ranging in size from 130bp to 221bp.

Mitochondrial Minisatellite Data. The mtDNA primers have amplified fragments from ~570 to ~700 bp long. The relatively large fragment size difference allowed us to visually identify four fragments in the 1.5% TBE agarose gel. All four fragments have been sequenced in

both directions (forward and reverse) in two samples per each type using the same primers (data not shown). ABI chromatograms have been aligned and edited using the Sequencher v.4.5 software (http://www.genecodes.com/sequencher/; see the Ppond-nad1-in2-F2xR2.SPF file). Sequence analysis revealed the following four haplotypes that were differed by the number of repeats:

A: 569 bp R2+R1+R2+R1+R2+R1+R2+R1+R2,
B: 603 bp R2+R1+R1+R2+R1+R2+R1+R2+R1+R2,
C: 637 bp R2+R1+R1+R1+R2+R1+R2+R1+R2+R1+R2,
D: 701 bp R2+R1+R2+R1+R2+R1+R2+R1+R2+R1+R2+R1+R2,

where R1 and R2 correspond to two repeats described in Mitton et al. 2000. The four mtDNA haplotypes have been found in 34 populations in total. These haplotypes likely correspond to four haplotypes described earlier in Latta and Mitton (1999) and Johansen and Latta (2003): **A** in our study = **A** in Latta and Mitton 1999, **B** = **D**, **C** = **C**, and **D** = **B**, and it was also confirmed by Robert Latta in personal communications. The haplotypes **A** (Oregon, Cascade Mountains and Western Montana) and **D** (Washington, Cascade Mountains) characterize *P. ponderosa subsp. Ponderosa* (the 'North Plateau' group); the haplotype **B** characterizes *P. ponderosa subsp. brachyptera* (the 'South Rockies' group) and is fixed in all Arizona populations; the haplotype **C** characterizes *P. ponderosa subsp. scopulorum (Engelmann) E. Murray* (the 'North Rockies' group) and is fixed in the South Dakota population, while the Colorado and Wyoming populations contain either **B** or **C** haplotypes or both of them and may represent a transition zone between *subsp. brachyptera* and *subsp. scopulorum* (Table 13 and Fig. 5 in the report).

Genetic Diversity. Genetic diversity levels were typical for conifers (Table 3). Observed (H_o) and expected (H_e) heterozygosities equal 0.087 and 0.107 for 21 isozyme loci, respectively, and 0.117 and 0.138 for all 22 loci including the SSR marker. Nei's (1987) genetic differentiation (G_{ST}) was similar to Θ and also equals 0.135 based on all 22 markers. There was not much difference in levels of genetic diversity found between natural and planted populations (Table 4), but natural populations were more differentiated compared to planted (F_{ST} = 0.228 vs. 0.117, P = 0.06, respectively), and natural populations revealed more relatedness compared to planted (R = 0.335 vs. 0.179, P = 0.04, respectively). Allelic richness and heterozygosity were statistically heterogeneous across states with the highest allelic richness and heterozygosity observed for Utah and Montana populations, and lowest for Arizona populations (Table 4).

Population Differentiation and Source Identification. Global differentiation (overall 34 populations) was relatively high and statistically significant (Table 5), and was calculated as Θ = 0.135 ± 0.050 (which is Weir & Cockerham (1984) estimation of F_{ST}) using the FSTAT v. 2.9.3 software (Goudet 1995, 2001). This indicates that genetic differences do exist among the populations sampled.

Pairwise *P*-values for allele distribution difference between 34 populations of *Pinus ponderosa* are presented in Table 6. We tested the null hypothesis (Ho) whether the allele distribution is identical across populations. An unbiased estimate of the *P*-value of the probability test (or Fisher exact test) was performed as described by Raymond and Rousset (1995b) using the GenePop v.3.4 software (Raymond & Rousset 1995a). Pairs of populations with very highly significant difference in allele distributions are highlighted by red, significant difference are highlighted by pink, and insignificant difference by green. For instance, many populations from Colorado have a similar allele distribution between each other, and thus are shaded with green.

We have also calculated pairwise differentiation (F_{ST}) and *P*-values for all 34 populations (Table 7). Similar to data in Table 6 these data would allow to find out the most statistically similar or different pairs of populations. Population pairs shaded by red indicate statistically significant differences (populations are different from each other).

We used the SPAGeDi v.1.2 software (Hardy & Vekemans 2002) to analyze whether genetic differentiation between populations correlates with geographic distance between them. We found out that genetic differentiation ($F_{ST}/(1-F_{ST})$) significantly correlated with geographic isolation that was calculated as Euclidian distance from UTM coordinates X, Y, and Z in Table 2 (Figure 1, $F = 134.7$, $P = 5E\text{-}28$). Mantel-test was also highly significant over 10,000 permutation tests ($P = 0.0001$). The more geographically isolated the population, the more it was genetically differentiated.

Results of Principal Component Analysis (PCA) are presented in Figures 2 and 3. Inertia was 0.223, 0.171 and 0.047 per I, II, and III axis, respectively; percent inertia - 42.5%, 32.7% and 9.1%; percent cumulative inertia - 42.5%, 75.2% and 84.3%. The consensus unrooted Neighbor-Joining Tree of 34 populations of *Pinus ponderosa* based on Nei's 1978 genetic distance and 22 genetic markers and calculated using 1000 bootstraps is presented in Figure 4. All clades have low support (nodes are supported at < 59%).

The GeneClass2 v.2.0 software (Piry et al. 2004) has been used to assign planted (P) stands to natural (N) populations that have been considered as reference populations. Table 8 shows natural populations that are the most likely source of planted stands in terms of rank and score based on Bayesian methods by Rannala & Mountain (1997). Probabilities of individual planted (P) trees to be assigned to natural (N) populations are shown in Table 9.

We inferred 6 clusters among 34 populations (Table 10) using Structure v2.1 analysis (Pritchard et al. 2000; Pritchard & Wen 2004). Proportion of membership of each pre-defined population in each of the 6 clusters is presented in Table 11. Proportion of membership of each individual tree in each of the 6 clusters is presented in Table 12.

The minisatellite region in the second intron in the *nad1* mitochondrial genome gene was used as an mtDNA marker. The mitochondrial genome is maternally inheritance in pines and, therefore, represents strictly maternal lineages (Table 13 and Figure 5).

IDENTIFICATION OF PONDEROSA PINE PLANTING SOURCES

State	National Forest	Population	Abbreviation	Source as Determined by the Molecular Genetic Database
CO	BLM	Abyeta Mesa 1960s planting	CO-BLM-AM60P	About 90% of this plantation appears to have originated from the Wyoming area (93% likelihood). Ten percent of the stand shares the strongest similarity to the San Juan NF in Colorado (either the Pagosa RD or Sparks areas). This plantation shares very strong similarity to the Abyeta Mesa 1970s plantation.
CO	BLM	Abyeta Mesa 1970s planting	CO-BLM-AM70P	About 50% of this plantation appears to have originated from the Wyoming area (84% likelihood). The remainder of the stand shares moderate similarity to material from the San Juan NF in Colorado (either the Pagosa RD or Sparks areas). This plantation shares very strong similarity to the Abyeta Mesa 1960s plantation.
CO	BLM	Abyeta Mesa 1990s planting	CO-BLM-AM90P	Approximately 20% of this plantation is from the Pacific or Inland Northwest (Oregon or Montana area, respectively, based on the database). The remaining 80% of this plantation shows strong similarity to two other sources, and may be a mix of these sources: the Medicine Bow-Routt NF in Wyoming (>90% likelihood) and the San Juan NF, 8-mile area, in Colorado (~70% likelihood).
CO	BLM	Vigil Mesa 1960s planting	CO-BLM-VM60P	There is a 98% likelihood that this plantation originated from the GMUG NF in Colorado.
CO	BLM	Vigil Mesa 1970s planting	CO-BLM-VM70P	There is a 99% likelihood that the majority of this plantation (~90%) originated from the Wyoming area. The remaining 10% shares the greatest similarity to the Rio Grande NF in Colorado.
CO	GMUG	Delta/Nucla	CO-GMUG-DN-P	There is over a 90% likelihood that this plantation originated from the CO-GMUG-SM native stand.

State	National Forest	Population	Abbreviation	Source as Determined by the Molecular Genetic Database
CO	GMUG	Transfer	CO-GMUG-Tr-P	A small percentage of this plantation (~10%) is comprised of local material and shows the greatest similarity to the native stand sampled from the GMUG NF. Approximately 90% of the stand is from another Forest in Colorado. There is an 88% likelihood that this larger portion of the plantation originated from the Rio Grande National Forest in Colorado.
CO	San Juan	8-mile planted	CO-SJNF-8m-P	Over 90% of this plantation shows the greatest similarity to the material from the Medicine Bow-Routt NF in Wyoming (99% likelihood). The 8-mile natural stand is the likely origin of less than 10% of the sampled plantation.
CO	San Juan	Narraguinnep	CO-SJNF-Na-P	This plantation is made up of a mix of sources. Approximately 25% of the stand appears to be local in origin (sharing the greatest similarity to the CO-SJNF-BD plantation). The remaining 75% appears to be a mix of material from Wyoming (20% likelihood) and/or the GMUG NF (40% likelihood).
CO	San Juan	Sparks Planted	CO-SJNF-SP-P	This plantation is likely a mix of different source material. Approximately 5% of the plantation shows a strong similarity to the native material sampled from the Sparks Natural Area. The remainder of the plantation does not originate from the Sparks Natural Area, but instead shows moderate levels of similarity to material from South Dakota. With this moderate level of support, it is possible that the actual source of the majority of this stand was not sampled for inclusion in the database.

State	National Forest	Population	Abbreviation	Source as Determined by the Molecular Genetic Database
SD	Black Hills	McVey	SD-BHNF-MV-P	The source of this plantation is likely in the vicinity of Wyoming or South Dakota. However, this plantation does not appear to have originated from the native South Dakota stand sampled for the database. The plantation shows the strongest similarity to material sampled from Wyoming (>90%). This stand also shows some similarity to the material from the Rio Grande NF in Colorado. It is entirely possible that the exact source of the stand was not sampled for the database, though we can determine it is somewhere in the vicinity of Wyoming, South Dakota, or 'north-central' Colorado.
UT	Unita	Boy Scout Grove	UT-UNF-BSG-P	This is an offsite plantation. The source of this plantation is the Pacific Northwest. The plantation shows the greatest likelihood of originating from northeast Oregon (>99% likelihood) and, more specifically, from the Umatilla NF. This plantation shares strong genetic similarity to the UT-WCNF-YP-P (yellowpine) plantation.
UT	Unita	Ponderosa	UT-UNF-PoC-P	The majority of this plantation is from an offsite source(s). Approximately 70% of the sampled plantation is from the Pacific or Inland Northwest (Oregon, Washington, and/or Montana, the database is not able to narrow the source down more precisely). The remaining 30% shows the strongest similarity to sources from Wyoming, South Dakota, and the GMUG in Colorado (likelihood for each of these sources is 33%, 29%, and 26%, respectively). This stand appears to be planted with an extensive mix of sources.
UT	Wasatch-Cache	Shingle Creek	UT-WCNF-SC-Q	Approximately 12% of the sampled plantation is from Washington. The remainder of the plantation shares a strong genetic similarity (likelihood of 71%) to material from the San Juan NF in Colorado (specifically the Sparks area).

State	National Forest	Population	Abbreviation	Source as Determined by the Molecular Genetic Database
UT	Wasatch-Cache	Yellowpine	UT-WCNF-YP-P	This is an offsite plantation. The source of this plantation is the Pacific Northwest. We are likely missing in the database the precise native source from where this material originated. Data suggest that the source is likely in the vicinity of Oregon or Washington (likelihood >99% from some statistical tests). This plantation shares strong genetic similarity to the UT-UNF-BSG-P (boy scout grove) plantation.

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Table 1 Seed source and location, sample sizes, populations and their abbreviations used in the study.

Abbreviation	Seed Source	Collection Type	Collection Location	Total Number of Samples (# w/o buds)
AZ-ASNF-17-N	Apache-Sitgreaves NF	Natural	Apache-Sitgreaves NF, PP 6075, stand 17. T8N R29E Sec 32	70
AZ-CoNF-Co-N	Coconino NF	Natural	NAD 27 Conus datum: 12 S, 0457092 E, 3871463 N, New Mexico, R3	30
AZ-KaNF-Ka-N	Kaibab NF	Natural	NAD 27 Conus datum: 12 S, 0409467 E, 3903615 N, New Mexico, R3	27
CO-BLM-AM60P	Abeyta Mesa 1960s Planting	Plantation	BLM (collector's note: Hard to determine 60's from 70's plantations.)	30 (1)
CO-BLM-AM70P	Abeyta Mesa 1970s Planting	Plantation	BLM (collector's note: Hard to determine 60's from 70's plantations.)	30 (1)
CO-BLM-AM90P	Abeyta Mesa 1990s Planting	Plantation	BLM	30
CO-BLM-VM60P	Vigil Mesa 1960s Planting	Plantation	BLM (collector's note: Hard to determine 60's from 70's plantations.)	34
CO-BLM-VM70P	Vigil Mesa 1970s Planting	Plantation	BLM (collector's note: Hard to determine 60's from 70's plantations.)	32
CO-GMUG-DN-P	GMUG NF 1970s Planting	Plantation	Delta/Nucla Plantation (30 years old). Montrose County, CO. 38.51181N, 10834778W, NAD 27 Conus, ~8100ft elevation	30
CO-GMUG-SM-N	GMUG NF Native Stand	Natural	Sawmill Mesa, Montrose County, CO. 38.49462N, 108.40048W, NAD 27 Conus , ~8400ft elevation	30
CO-GMUG-Tr-P	GMUG NF 1920s Planting	Plantation	Transfer Plantation, planted circa 1920. 38.43297N, 108.16610W, NAD 27 Conus, ~7700ft elevation	30
CO-RGNF-LW-N	Rio Grande NF	Natural	Lower Willow Creek adjacent to Del Norte Peak Rd, Divide RD. T39N R3.5E, New Mexico Principal Meridean Section 1. 8750-8800 feet	33
CO-SJNF-8m-N	8-mile Natural Stand	Natural	San Juan NF	30
CO-SJNF-8m-P	8-mile Planted Stand	Plantation	San Juan NF	30
CO-SJNF-BD-N	San Juan NF, Boggy Draw SPA	Natural	Mancos-Dolores RD. T38N,R15W Sec 35, Montezuma Co, Colorado	31
CO-SJNF-Na-P	San Juan NF, Planted	Plantation	Narraguinnep Plantation, Dolores County, 37.72396N, 108.61905W, ~8300ft elevation	31
CO-SJNF-PR-N	San Juan NF	Natural	Pagosa Ranger District only	30 (1)
CO-SJNF-SN-N	Sparks Area Natural Stand	Natural	San Juan NF	30
CO-SJNF-SP-P	Sparks Area Planted Stand	Plantation	San Juan NF	30 (1)
MT-BiNF-BC-N	Bitterroot NF	Natural	Buck Creek T1N R21W sec32. 5500 ft	10
MT-BiNF-CC-N	Bitterroot NF	Natural	Camp Creek T1N R19W sec 34.5210 ft	10
MT-BiNF-PC-N	Bitterroot NF	Natural	Pierce Creek T2N R21W sec 29. 5600 ft	10
OR-OcNF-PF-N	Ochoco NF R6 eastern Oregon	Natural	Potato Flat, T21S,R27E,Sec 11,14. ~5300 feet	30
OR-UmNF-Um-N	Umatilla NF R6 eastern Oregon	Natural	North Fork-John Day Ranger District. 044° 58' 24.1"N, 118°52'22.6"W. ~3800 feet	30

Abbreviation	Seed Source	Collection Type	Collection Location	Total Number of Samples (# w/o buds)
OR-WWNF-LG-N	Wallowa-Whitman NF R6 eastern Oregon	Natural	LaGrande Ranger District. 045° 08'N, 117° 41'W. ~4000 feet	29
SD-BHNF-BS-N	Black Hills NF	Natural	Buskala SPA, T3N R2E sec24	35
SD-BHNF-MV-P	McVey Fire	Plantation	Black Hills NF, SD	30
UT-UNF-BSG-P	Boy Scout Grove	Plantation	Uinta NF, (lost 5 extra days in the mail, warm on arrival, samples may be compromised)	31
UT-UNF-PoC-P	Ponderosa Campground	Plantation	Uinta NF, (11/23/01 samples lost 2 extra days in the mail, warm on arrival, samples may be compromised). T12S, R2E, S21	36 (7)
UT-WCNF-SC-Q	Shingle Creek	Natural	Wasatch-Cache NF, (considered control if plant material is from native yellow pine trees)	41 (1)
UT-WCNF-YP-P	Yellowpine Plantation	Plantation	Wasatch-Cache NF, (considered treatment if plant material is from off-site trees)	47
WA-WeNF-We-N	Wenatchee NF	Natural	Entiat RD. PIPO-17-17004-105-3040-02	30
WY-MBNF-WC-N	Wyoming Casper District per Ft. Collins' Nursery Response	Natural	Medicine Bow NF, Brush Creek-Hayden RD, T12 N, R81 W, Section 10, 6th PM, Holroyd TS Area, Carbon County, WY	32
WY-MBNF-WR-N	Wyoming Rawlings District per Ft. Collins Nursery Response	Natural	Medicine Bow-Routt NF, SE Wyoming—Laramie RD, T28N R71W Sec27 SE1/4, Elev. 1930m	30

Table 2 Spatial coordinates for 34 populations of *Pinus ponderosa*

State	National Forest	Population	Abbreviation	Longitude (decimal degrees)	Latitude (decimal degrees)	Elevation, ft	X (UTM, WGS1984), m	Y (UTM, WGS1984), m	Z (elevation), m	trs
AZ	Apache-Sitgreaves	Apache-Sitgreaves	AZ-ASNF-17-N	-109.3098	34.0460	8020	656011	3768545	2444	T8N,R29E,S32
AZ	Coconino	Coconino	AZ-CoNF-Co-N	-111.6674	35.0003	7000	439099	3873280	2132	T19N,R7E,S29
AZ	Kaibab	Kaibab	AZ-KaNF-Ka-N	-112.0840	35.8333	6500	402095	3966002	1996	T28N,R3E,S4
CO	BLM	Abyeta Mesa 60	CO-BLM-AM60P	-106.8680	36.9981	8000	333781	4096293	2452	T32N,R1E,S20
CO	BLM	Abyeta Mesa 70	CO-BLM-AM70P	-106.8680	36.9981	8000	333781	4096293	2452	T32N,R1E,S20
CO	BLM	Abyeta Mesa 90	CO-BLM-AM90P	-106.8502	36.9981	8300	335365	4096262	2526	T32N,R1E,S21
CO	BLM	Vigil Mesa 60	CO-BLM-VM60P	-106.8502	37.0124	7600	335396	4097848	2335	T32N,R1E,S16
CO	BLM	Vigil Mesa 70	CO-BLM-VM70P	-106.8680	37.0124	7800	333812	4097879	2383	T32N,R1E,S17
CO	GMUG	Delta/Nucla	CO-GMUG-DN-P	-108.3478	38.5118	8100	731247	4265937	2494	T49N,R13W,S17
CO	GMUG	Sawmill Mesa	CO-GMUG-SM-N	-108.4005	38.4946	8400	726706	4263896	2560	T49N,R14W,S23
CO	GMUG	Transfer	CO-GMUG-Tr-P	-108.1661	38.4330	7700	747362	4257663	2347	T48N,R12W,S11
CO	Rio Grande	Rio Grande, Lower Willow Creek	CO-RGNF-LW-N	-106.5952	37.6559	8775	359289	4168834	2656	T39N,R3.5E,S1, NMM
CO	San Juan	8-mile natural	CO-SJNF-8m-N	-106.9752	37.1700	8000	324637	4115558	2438	T34N,R1W,S20
CO	San Juan	8-mile planted	CO-SJNF-8m-P	-106.9930	37.1700	8000	323057	4115591	2438	T34N,R1W,S19
CO	San Juan	Boggy Draw	CO-SJNF-BD-N	-108.4768	37.5084	7580	723020	4154264	2310	T38N,R15W,S35
CO	San Juan	Narraguinnep	CO-SJNF-Na-P	-108.6190	37.7240	8300	709842	4177861	2560	T40N,R16W,S16
CO	San Juan	San Juan	CO-SJNF-PR-N	-107.1002	37.2990	7900	313856	4130110	2421	T35N,R2W,S6
CO	San Juan	Sparks Natural	CO-SJNF-SN-N	-106.9038	37.2703	7800	331200	4126557	2395	T35N,R1W,S13
CO	San Juan	Sparks Planted	CO-SJNF-SP-P	-106.8859	37.2703	8300	332788	4126525	2554	T35N,R1E,S18
MT	Bitterroot	Buck Creek	MT-BiNF-BC-N	-114.2362	45.7936	5500	714800	5074830	1800	T1N,R21W,S32
MT	Bitterroot	Camp Creek	MT-BiNF-CC-N	-113.9466	45.7936	5210	270994	5075338	1463	T1N,R19W,S34
MT	Bitterroot	Pierce Creek	MT-BiNF-PC-N	-114.2319	45.8998	5600	714724	5086641	1805	T2N,R21W,S29
OR	Ochoco	Potato Flat	OR-OcNF-PF-N	-119.4473	43.7657	5300	303016	4848761	1585	T21S,R27ES11
OR	Umatilla	Umatilla	OR-UmNF-Um-N	-118.8729	44.9734	3800	352318	4981702	1099	T7S,R32E,S9
OR	Wallowa-Whitman	Wallowa-Whitman	OR-WWNF-LG-N	-117.6754	45.1306	4400	446270	4997986	1340	T5S,R41E,S15
SD	Black Hills	Black Hills	SD-BHNF-BS-N	-103.8217	44.2020	6380	594148	4894978	1944	T3N,R2E,S24

State	National Forest	Population	Abbreviation	Longitude (decimal degrees)	Latitude (decimal degrees)	Elevation, ft	X (UTM, WGS1984), m	Y (UTM, WGS1984), m	Z (elevation), m	trs
SD	Black Hills	McVey	SD-BHNF-MV-P	-103.5633	44.0518	5400	615088	4878631	1653	T1N,R5E,S18
UT	Unita	Boy Scout Grove	UT-UNF-BSG-P	-111.7005	39.9752	6000	440184	4425240	1746	T10S,R2E,S3,SLM
UT	Unita	Ponderosa	UT-UNF-PoC-P	-111.7046	39.7609	6200	439646	4401457	1962	T12S,R2E,S21,SLM
UT	Wasatch-Cache	Shingle Creek	UT-WCNF-SC-Q	-111.1173	40.6172	7300	490078	4496270	2432	T2S,R7E,S26,SLM
UT	Wasatch-Cache	Yellowpine	UT-WCNF-YP-P	-111.1735	40.6317	7200	485327	4497888	2194	T2S,R7E,S20,SLM
WA	Wenatchee	Wenatchee	WA-WeNF-We-N	-120.4278	47.5986	3400	693352	5274894	1032	T24N,R19E,S2
WY	Medicine Bow	WY Casper	WY-MBNF-WC-N	-106.4820	41.0239	8100	375404	4542468	2493	T12N,R81W,S10
WY	Medicine Bow-Routt	WY Rawlings	WY-MBNF-WR-N	-105.3512	42.3696	6400	471084	4690873	1955	T28N,R71W,S27

Table 3. Nei's (1987) estimation of observed (H_o), expected (H_e), and total (H_T) heterozygosity and differentiation (G_{ST}) based on 21 isozyme loci and one SSR marker.

Locus	H_o	H_e	H_T	D_{ST}	D_{ST}'	H_T'	G_{ST}	G_{ST}'	G_{IS}
PGI-1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PGI-2	0.082	0.171	0.299	0.128	0.132	0.302	0.429	0.436	0.519
PGM-1	0.221	0.258	0.267	0.009	0.009	0.267	0.033	0.034	0.145
LAP-1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
LAP-2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ADH	0.203	0.246	0.316	0.070	0.072	0.318	0.221	0.226	0.174
GOT-1	0.140	0.159	0.164	0.005	0.005	0.164	0.032	0.033	0.119
GOT-2	0.021	0.028	0.028	0.000	0.000	0.028	0.010	0.010	0.257
SOD-1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
UGPP	0.424	0.445	0.510	0.064	0.066	0.512	0.126	0.130	0.048
CAT-1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
CAT-2	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
DIA-1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
MDH-1	0.006	0.014	0.014	-0.000	-0.000	0.014	-0.008	-0.008	0.579
MDH-2	0.108	0.146	0.149	0.003	0.003	0.149	0.022	0.023	0.261
MDH-3	0.033	0.078	0.079	0.001	0.001	0.079	0.013	0.013	0.583
6PGD-1	0.033	0.051	0.051	-0.000	-0.000	0.051	-0.002	-0.002	0.350
IDH-1	0.151	0.147	0.226	0.079	0.081	0.228	0.349	0.355	-0.026
SKD-1	0.408	0.489	0.550	0.061	0.063	0.552	0.111	0.114	0.166
SKD-2	0.002	0.002	0.002	-0.000	-0.000	0.002	-0.002	-0.003	0.002
FDP-1	0.007	0.015	0.015	0.000	0.000	0.015	0.004	0.004	0.561
Overall for 21 isozyme loci	0.087	0.107	0.130	0.023	0.023	0.131	0.175	0.179	0.186
PtTX21	0.731	0.792	0.847	0.055	0.057	0.849	0.065	0.067	0.077
Overall for all 22 loci	0.117	0.138	0.160	0.022	0.022	0.160	0.135	0.139	0.155

Table 4. Genetic variation in natural vs. planted populations.
21 isozyme loci (without questionable population UT-WCNF-SC-Q and population SD-BHNF-MV-P with missing data for the FDP1 locus). *P*= two-sided *P*-values obtained after 100 permutations.

Populations (N)	Allelic richness	H_o	H_e	F_{is}	F_{ST}	R	Rc
Natural (19)	1.494	0.085	0.103	0.173	0.228	0.335	-0.419
Planted (13)	1.516	0.086	0.110	0.216	0.117	0.179	-0.552
P	0.38	0.85	0.36	0.22	**0.06**	**0.04**	0.22

21 isozyme loci and one SSR marker. *P*= two-sided *P*-values obtained after 100 permutations.

Populations (N)	Allelic richness	H_o	H_e	F_{is}	F_{ST}	R	Rc
Natural (19)	1.757	0.116	0.135	0.141	0.179	0.277	-0.329
Planted (15)	1.742	0.112	0.137	0.181	0.083	0.132	-0.441
P	0.73	0.62	0.81	0.14	0.09	0.09	0.14

21 isozyme loci and one SSR marker (without questionable population UT-WCNF-SC-Q). *P*= two-sided *P*-values obtained after 100 permutations.

Populations (N)	Allelic richness	H_o	H_e	F_{is}	F_{ST}	R	Rc
Natural (19)	1.757	0.116	0.135	0.141	0.179	0.277	-0.329
Planted (14)	1.736	0.111	0.136	0.183	0.085	0.135	-0.449
P	0.64	0.54	0.85	0.16	0.17	0.15	0.16

21 isozyme loci and one SSR marker (without questionable population UT-WCNF-SC-Q). *P*= two-sided *P*-values obtained after 100 permutations.

State (N of populations)	Allelic richness	H_o	H_e	F_{is}	F_{ST}	R	Rc
AZ (3)	**1.716**	**0.114**	**0.130**	0.122	0.157	0.249	-0.278
CO (16)	1.729	0.108	0.131	0.181	0.021	0.035	-0.442
MT (3)	**1.818**	**0.164**	**0.178**	0.079	0.001	-0.002	-0.171
OR (3)	1.802	0.123	0.145	0.153	0.256	0.374	-0.360
SD (2)	1.523	0.082	0.094	0.132	0.041	0.069	-0.304
UT (4)	**1.911**	0.134	0.162	0.169	0.103	0.165	-0.406
WA (1)	1.815	0.117	0.138	0.148	na	-0.035	-0.348
WY (2)	1.759	0.113	0.131	0.132	0.002	0.003	-0.305
P	**0.01**	**0.02**	**0.01**	0.87	0.41	0.31	0.90

Allelic richness is a measure of the number of alleles independent of sample size, hence allowing the comparison of this quantity between different sample sizes. The observed number of alleles in a sample is highly dependant on sample size. To bypass this problem, El Mousadik & Petit (1996) suggested to adapt the rarefaction index of Hurlbert (1971) to population genetics (see also Petit et al. 1998). The principle is to estimate the expected number of alleles in a sub-sample of 2n genes, given that 2N genes have been sampled. In FSTAT, n is fixed as the smallest number of individuals typed for a locus in a sample. **R** is relatedness estimated following Queller & Goodnight (1989). **Rc** is relatedness inbreeding corrected following Pamilo (1984, 1985).

Table 5. Weir & Cockerham (1984) estimation of F_{IT} (*F*), F_{ST} (Θ) and F_{IS} (*f*), and relatedness (R) estimated following Queller & Goodnight (1989)

21 isozyme loci

F ± SE	95% CI	99% CI	Θ ± SE	95% CI	99% CI	*f* ± SE	95% CI	99% CI	R ± SE	95% CI	99% CI
0.339 ± 0.092	0.214-0.526	0.191-0.595	0.181 ± 0.076	0.070-0.334	0.046-0.391	0.193 ± 0.051	0.117-0.310	0.095-0.366	0.270 ± 0.101	0.111-0.442	0.074-0.496

21 isozyme loci and one SSR marker

F ± SE	95% CI	99% CI	Θ ± SE	95% CI	99% CI	*f* ± SE	95% CI	99% CI	R ± SE	95% CI	99% CI
0.267 ± 0.071	0.183-0.436	0.166-0.504	0.135 ± 0.050	0.067-0.254	0.050-0.303	0.151 ± 0.043	0.102-0.267	0.088-0.315	0.216 ± 0.069	0.110-0.356	0.082-0.411

Standard error (SE) was calculated via Jackknifing over loci.
Confidence interval (CI) was calculated via Bootstrapping over loci.

Table 6. Unbiased pairwise estimates of the *P*-value of the probability test (Fisher exact test) for allele distribution difference between 34 populations of *Pinus ponderosa*

Population	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-BLM-AM60P	CO-BLM-AM70P	CO-BLM-AM90P	CO-BLM-VM60P	CO-BLM-VM70P	CO-GMUG-DN-P
AZ-CoNF-Co-N	0.0000								
AZ-KaNF-Ka-N	0.0000	0.0000							
CO-BLM-AM60P	0.0000	0.0009	0.0034						
CO-BLM-AM70P	0.0000	0.0241	0.0000	0.9825					
CO-BLM-AM90P	0.0000	0.0028	0.0000	0.0155	0.1805				
CO-BLM-VM60P	0.0000	0.5945	0.0000	0.0000	0.0129	0.0002			
CO-BLM-VM70P	0.0000	0.0070	0.0000	0.0118	0.2079	0.3963	0.0120		
CO-GMUG-DN-P	0.0000	0.0164	0.0000	0.0003	0.0326	0.0666	0.1610	0.0222	
CO-GMUG-SM-N	0.0000	0.1407	0.0000	0.0008	0.0729	0.0139	0.5480	0.0034	0.3893
CO-GMUG-Tr-P	0.0000	0.0000	0.0000	0.0000	0.0001	0.0000	0.0093	0.0000	0.4950
CO-RGNF-LW-N	0.0000	0.1062	0.0000	0.0006	0.0092	0.0042	0.0644	0.0239	0.0014
CO-SJNF-8m-N	0.0000	0.0061	0.0000	0.0000	0.0847	0.7022	0.0000	0.0067	0.0000
CO-SJNF-8m-P	0.0000	0.0000	0.0000	0.1879	0.1783	0.0505	0.0000	0.0001	0.0001
CO-SJNF-BD-N	0.0000	0.1616	0.0000	0.0007	0.0206	0.0777	0.2166	0.0317	0.2060
CO-SJNF-Na-P	0.0000	0.0016	0.0000	0.0000	0.0213	0.0000	0.1757	0.0072	0.5045
CO-SJNF-PR-N	0.0000	0.0536	0.0000	0.0472	0.2412	0.0175	0.0000	0.0634	0.0000
CO-SJNF-SN-N	0.0000	0.0000	0.0014	0.0795	0.0204	0.0000	0.0000	0.0000	0.0000
CO-SJNF-SP-P	0.0000	0.0000	0.0000	0.0000	0.0004	0.0000	0.0000	0.0000	0.0000
MT-BiNF-BC-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MT-BiNF-CC-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MT-BiNF-PC-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
OR-OcNF-PF-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
OR-UmNF-Um-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
OR-WWNF-LG-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SD-BHNF-BS-N	0.0000	0.0063	0.0000	0.0002	0.0096	0.1230	0.0000	0.0001	0.0000
SD-BHNF-MV-P	0.0000	0.0000	0.0000	0.0000	0.0005	0.0023	0.0000	0.0007	0.0049
UT-UNF-BSG-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UT-UNF-PoC-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UT-WCNF-SC-Q	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UT-WCNF-YP-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WA-WeNF-We-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WY-MBNF-WC-N	0.0000	0.0015	0.0000	0.0297	0.0385	0.0625	0.0001	0.1716	0.0362
WY-MBNF-WR-N	0.0000	0.0072	0.0000	0.0625	0.1504	0.4491	0.0002	0.4886	0.2433

Population	CO-GMUG-SM-N	CO-GMUG-Tr-P	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-8m-P	CO-SJNF-BD-N	CO-SJNF-Na-P	CO-SJNF-PR-N	CO-SJNF-SN-N
CO-GMUG-Tr-P	0.0153								
CO-RGNF-LW-N	0.0905	0.0005							
CO-SJNF-8m-N	0.0050	0.0000	0.0000						
CO-SJNF-8m-P	0.0001	0.0000	0.0001	0.0392					
CO-SJNF-BD-N	0.1142	0.0000	0.2176	0.0072	0.0004				
CO-SJNF-Na-P	0.1285	0.2688	0.0003	0.0001	0.0000	0.2269			
CO-SJNF-PR-N	0.0014	0.0000	0.0004	0.1890	0.0141	0.0396	0.0000		
CO-SJNF-SN-N	0.0077	0.0000	0.0002	0.0000	0.0135	0.0000	0.0000	0.0015	
CO-SJNF-SP-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0097	0.1965
MT-BiNF-BC-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MT-BiNF-CC-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
MT-BiNF-PC-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
OR-OcNF-PF-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
OR-UmNF-Um-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
OR-WWNF-LG-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
SD-BHNF-BS-N	0.0007	0.0000	0.0000	0.0026	0.0001	0.0001	0.0000	0.0621	0.0000
SD-BHNF-MV-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0251	0.0000	0.0000
UT-UNF-BSG-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UT-UNF-PoC-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0030	0.0000
UT-WCNF-SC-Q	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0001	0.0000
UT-WCNF-YP-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WA-WeNF-We-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WY-MBNF-WC-N	0.0026	0.0006	0.0097	0.0014	0.0001	0.0031	0.0107	0.0074	0.0000
WY-MBNF-WR-N	0.0164	0.0002	0.0070	0.1199	0.3878	0.0878	0.0067	0.4483	0.0008

Population	CO-SJNF-SP-P	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	SD-BHNF-MV-P
MT-BiNF-BC-N	0.0000								
MT-BiNF-CC-N	0.0000	0.9010							
MT-BiNF-PC-N	0.0000	0.2161	0.9889						
OR-OcNF-PF-N	0.0000	0.0000	0.0000	0.0000					
OR-UmNF-Um-N	0.0000	0.0078	0.0166	0.0155	0.0000				
OR-WWNF-LG-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.1583			
SD-BHNF-BS-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000		
SD-BHNF-MV-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	
UT-UNF-BSG-P	0.0000	0.0009	0.0080	0.0193	0.0000	0.8908	0.0922	0.0000	0.0000
UT-UNF-PoC-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UT-WCNF-SC-Q	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
UT-WCNF-YP-P	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0071	0.0000	0.0000
WA-WeNF-We-N	0.0000	0.0000	0.0000	0.0057	0.0000	0.0039	0.0026	0.0000	0.0000
WY-MBNF-WC-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
WY-MBNF-WR-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0003	0.0040

Population	UT-UNF-BSG-P	UT-UNF-PoC-P	UT-WCNF-SC-Q	UT-WCNF-YP-P	WA-WeNF-We-N	WY-MBNF-WC-N
UT-UNF-PoC-P	0.0000					
UT-WCNF-SC-Q	0.0000	0.0000				
UT-WCNF-YP-P	0.0001	0.0000	0.0000			
WA-WeNF-We-N	0.0000	0.0000	0.0000	0.6954		
WY-MBNF-WC-N	0.0000	0.0000	0.0000	0.0000	0.0000	
WY-MBNF-WR-N	0.0000	0.0000	0.0000	0.0000	0.0000	0.0169

Table 7 Pairwise estimates of the F_{ST} (above diagonal) and *P*-values (below diagonal) between 34 populations of *Pinus ponderosa*

Population	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-BLM-AM60P	CO-BLM-AM70P	CO-BLM-AM90P	CO-BLM-VM60P	CO-BLM-VM70P	CO-GMUG-DN-P
AZ-ASNF-17-N	*	0.2466	0.0527	0.1579	0.1834	0.2601	0.2319	0.248	0.2654
AZ-CoNF-Co-N	0.00009	*	0.1302	0.0211	0.0115	0.0132	-0.0068	0.0141	0.0162
AZ-KaNF-Ka-N	0.00009	0.00009	*	0.0547	0.0785	0.1465	0.1164	0.122	0.1208
CO-BLM-AM60P	0.00009	0.00027	0.00285	*	-0.0107	0.0152	0.0252	0.0096	0.0218
CO-BLM-AM70P	0.00009	0.02094	0.00214	0.89572	*	0.0022	0.0123	0.0019	0.0136
CO-BLM-AM90P	0.00009	0.00152	0.00009	0.01916	0.41275	*	0.0177	0.0057	0.0131
CO-BLM-VM60P	0.00009	0.16863	0.00009	0.00009	0.04287	0.00027	*	0.0157	0.0102
CO-BLM-VM70P	0.00009	0.00463	0.00009	0.04064	0.34768	0.43467	0.00428	*	0.0088
CO-GMUG-DN-P	0.00009	0.00437	0.00009	0.00152	0.0705	0.06373	0.1033	0.04421	*
CO-GMUG-SM-N	0.00009	0.01212	0.00009	0.00071	0.08547	0.00178	0.29563	0.00651	0.49724
CO-GMUG-Tr-P	0.00009	0.00036	0.00009	0.00009	0.0016	0.00009	0.00535	0.00018	0.43574
CO-RGNF-LW-N	0.00009	0.01399	0.00009	0.00187	0.01159	0.00143	0.00517	0.02032	0.00258
CO-SJNF-8m-N	0.00009	0.00098	0.00009	0.01132	0.06168	0.10633	0.00027	0.00642	0.00677
CO-SJNF-8m-P	0.00009	0.00018	0.00009	0.14617	0.16738	0.01604	0.00009	0.00053	0.00018
CO-SJNF-BD-N	0.00009	0.03262	0.00009	0.00053	0.02246	0.01453	0.07932	0.02602	0.09385
CO-SJNF-Na-P	0.00009	0.00018	0.00009	0.00027	0.01043	0.00009	0.01301	0.00517	0.35882
CO-SJNF-PR-N	0.00009	0.00686	0.00009	0.02023	0.05677	0.01827	0.00009	0.03128	0.00062
CO-SJNF-SN-N	0.00009	0.00009	0.00053	0.0516	0.00838	0.00009	0.00009	0.00107	0.00009
CO-SJNF-SP-P	0.00009	0.00009	0.00009	0.00036	0.00062	0.00009	0.00009	0.00009	0.00009
MT-BiNF-BC-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
MT-BiNF-CC-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
MT-BiNF-PC-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
OR-OcNF-PF-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
OR-UmNF-Um-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
OR-WWNF-LG-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
SD-BHNF-BS-N	0.00009	0.00027	0.00009	0.00036	0.00686	0.03164	0.00009	0.00018	0.00018
SD-BHNF-MV-P	0.00009	0.00009	0.00009	0.00009	0.00348	0.00071	0.00009	0.00401	0.00152
UT-UNF-BSG-P	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
UT-UNF-PoC-P	0.00009	0.00009	0.00009	0.00018	0.00009	0.00009	0.00009	0.00009	0.00009
UT-WCNF-SC-Q	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
UT-WCNF-YP-P	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
WA-WeNF-We-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
WY-MBNF-WC-N	0.00009	0.00027	0.00009	0.01586	0.03146	0.00722	0.00018	0.12754	0.03957
WY-MBNF-WR-N	0.00009	0.00045	0.00009	0.0492	0.25116	0.14697	0.00036	0.61729	0.05873

Population	CO-GMUG-SM-N	CO-GMUG-Tr-P	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-8m-P	CO-SJNF-BD-N	CO-SJNF-Na-P	CO-SJNF-PR-N	CO-SJNF-SN-N
AZ-ASNF-17-N	0.2224	0.2665	0.2305	0.246	0.1764	0.2429	0.2358	0.2351	0.1246
AZ-CoNF-Co-N	-0.0002	0.0333	-0.0025	0.0096	0.0163	0.0072	0.0228	0.0113	0.0342
AZ-KaNF-Ka-N	0.1129	0.1129	0.1066	0.1397	0.0796	0.1127	0.1092	0.1111	0.0366
CO-BLM-AM60P	0.0198	0.05	0.0154	0.017	-0.0035	0.0184	0.0187	0.0112	0.0006
CO-BLM-AM70P	0.0045	0.0465	0.0107	0.0097	-0.0035	0.0152	0.0046	0.0101	0.0131
CO-BLM-AM90P	0.0112	0.0702	0.021	-0.0036	0.0127	0.011	0.0282	0.0182	0.042
CO-BLM-VM60P	-0.0069	0.0274	0.0034	0.0149	0.0237	0.0065	0.0107	0.0252	0.0341
CO-BLM-VM70P	0.0152	0.0368	0.0057	0.0175	0.0267	0.0118	0.0073	0.0038	0.0295
CO-GMUG-DN-P	0.0049	0.0081	0.0117	0.0185	0.0303	0.0088	0.0028	0.0218	0.0454
CO-GMUG-SM-N	*	0.0329	0.0044	0.0071	0.0156	0.0139	0.0103	0.022	0.0299
CO-GMUG-Tr-P	0.00802	*	0.0176	0.0692	0.0666	0.0337	0.0174	0.046	0.0629
CO-RGNF-LW-N	0.03948	0.00089	*	0.0228	0.0187	0.0076	0.0163	0.0062	0.0262
CO-SJNF-8m-N	0.00169	0.00009	0.00009	*	0.0094	0.0134	0.0347	0.0164	0.0386
CO-SJNF-8m-P	0.00009	0.00009	0.00018	0.00258	*	0.0257	0.035	0.017	0.0167
CO-SJNF-BD-N	0.11756	0.0016	0.14652	0.00241	0.00018	*	0.0126	0.0073	0.0305
CO-SJNF-Na-P	0.12139	0.24153	0.00009	0.00009	0.00009	0.05321	*	0.0249	0.0449
CO-SJNF-PR-N	0.00152	0.00009	0.00009	0.06061	0.02602	0.0705	0.00045	*	0.0237
CO-SJNF-SN-N	0.00481	0.00009	0.00018	0.00009	0.00205	0.00392	0.00009	0.00152	*
CO-SJNF-SP-P	0.00009	0.00009	0.00009	0.00009	0.00018	0.00018	0.00009	0.00793	0.05125
MT-BiNF-BC-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
MT-BiNF-CC-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
MT-BiNF-PC-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
OR-OcNF-PF-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
OR-UmNF-Um-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
OR-WWNF-LG-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
SD-BHNF-BS-N	0.00071	0.00009	0.00009	0.00009	0.00018	0.00009	0.00009	0.06221	0.00009
SD-BHNF-MV-P	0.00009	0.00018	0.00009	0.00009	0.00009	0.00009	0.00731	0.00009	0.00009
UT-UNF-BSG-P	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
UT-UNF-PoC-P	0.00009	0.00009	0.00009	0.00018	0.00009	0.00009	0.00009	0.00071	0.00009
UT-WCNF-SC-Q	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00036	0.00009
UT-WCNF-YP-P	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
WA-WeNF-We-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
WY-MBNF-WC-N	0.00365	0.00027	0.00178	0.00062	0.00027	0.00107	0.01854	0.00089	0.00009
WY-MBNF-WR-N	0.00098	0.00027	0.00348	0.00455	0.14563	0.04492	0.00089	0.15463	0.00027

Population	CO-SJNF-SP-P	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	SD-BHNF-MV-P
AZ-ASNF-17-N	0.1409	0.3145	0.2339	0.2771	0.3128	0.2993	0.3257	0.261	0.3036
AZ-CoNF-Co-N	0.0429	0.2796	0.2397	0.2555	0.4358	0.1597	0.1584	0.0157	0.0657
AZ-KaNF-Ka-N	0.0556	0.2071	0.1384	0.1835	0.2196	0.1888	0.2135	0.1654	0.1928
CO-BLM-AM60P	0.0084	0.24	0.1893	0.2206	0.3574	0.1502	0.1559	0.0262	0.0583
CO-BLM-AM70P	0.0153	0.2765	0.2263	0.2512	0.4024	0.1643	0.1649	0.0074	0.0319
CO-BLM-AM90P	0.0461	0.3002	0.2655	0.2911	0.4634	0.1516	0.1489	0.0116	0.0641
CO-BLM-VM60P	0.0451	0.2567	0.2137	0.2311	0.4139	0.1488	0.1469	0.0251	0.0604
CO-BLM-VM70P	0.03	0.2827	0.2456	0.2709	0.4142	0.1677	0.1585	0.0204	0.0336
CO-GMUG-DN-P	0.0589	0.2805	0.2448	0.2747	0.407	0.1577	0.1602	0.0377	0.0526
CO-GMUG-SM-N	0.041	0.263	0.2223	0.2417	0.4179	0.1508	0.1539	0.0155	0.0535
CO-GMUG-Tr-P	0.0708	0.2741	0.2356	0.2611	0.3696	0.182	0.1823	0.0837	0.0731
CO-RGNF-LW-N	0.0322	0.277	0.2327	0.2538	0.4033	0.1695	0.1681	0.0264	0.053
CO-SJNF-8m-N	0.0479	0.2727	0.2363	0.2563	0.4479	0.1438	0.1391	0.0204	0.0861
CO-SJNF-8m-P	0.0262	0.2667	0.2152	0.2436	0.4048	0.1571	0.1672	0.018	0.0743
CO-SJNF-BD-N	0.0303	0.2562	0.2184	0.2481	0.4049	0.142	0.1421	0.0379	0.0739
CO-SJNF-Na-P	0.0439	0.2891	0.2406	0.2665	0.4001	0.1697	0.1689	0.0334	0.0157
CO-SJNF-PR-N	0.0153	0.2727	0.2314	0.2567	0.3973	0.1676	0.1686	0.0189	0.0617
CO-SJNF-SN-N	-0.0035	0.2072	0.16	0.1977	0.3219	0.1487	0.1598	0.0541	0.1029
CO-SJNF-SP-P	*	0.2262	0.1788	0.2185	0.3399	0.1588	0.1674	0.0497	0.0915
MT-BiNF-BC-N	0.00009	*	0.0001	0.0206	0.2807	0.0548	0.0827	0.3583	0.4094
MT-BiNF-CC-N	0.00009	0.29813	*	-0.0256	0.2261	0.0558	0.0884	0.3104	0.3577
MT-BiNF-PC-N	0.00009	0.01943	0.61925	*	0.2864	0.061	0.0805	0.3305	0.3819
OR-OcNF-PF-N	0.00009	0.00009	0.00009	0.00009	*	0.3287	0.3724	0.4886	0.4969
OR-UmNF-Um-N	0.00009	0.00472	0.06275	0.02041	0.00009	*	0.0042	0.202	0.2453
OR-WWNF-LG-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.09037	*	0.2026	0.2452
SD-BHNF-BS-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	*	0.0405
SD-BHNF-MV-P	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	*
UT-UNF-BSG-P	0.00009	0.00053	0.01239	0.01381	0.00009	0.82068	0.10624	0.00009	0.00009
UT-UNF-PoC-P	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
UT-WCNF-SC-Q	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00018	0.00009
UT-WCNF-YP-P	0.00009	0.00027	0.00045	0.02032	0.00009	0.00463	0.00918	0.00009	0.00009
WA-WeNF-We-N	0.00009	0.00009	0.0008	0.00205	0.00009	0.00285	0.00107	0.00009	0.00009
WY-MBNF-WC-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009
WY-MBNF-WR-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00009	0.00018	0.00125

Population	UT-UNF-BSG-P	UT-UNF-PoC-P	UT-WCNF-SC-Q	UT-WCNF-YP-P	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N
AZ-ASNF-17-N	0.2841	0.2256	0.2608	0.3282	0.3746	0.2378	0.2436
AZ-CoNF-Co-N	0.157	0.029	0.0256	0.1635	0.2241	0.0139	0.0079
AZ-KaNF-Ka-N	0.1836	0.1117	0.1365	0.213	0.2589	0.1077	0.1104
CO-BLM-AM60P	0.1426	0.0269	0.044	0.1718	0.2254	0.011	0.008
CO-BLM-AM70P	0.154	0.0309	0.0453	0.1839	0.2449	0.0067	-0.0003
CO-BLM-AM90P	0.1419	0.0292	0.0395	0.1748	0.2378	0.0123	0.008
CO-BLM-VM60P	0.1472	0.0306	0.0312	0.1558	0.2079	0.0137	0.0122
CO-BLM-VM70P	0.1594	0.0259	0.0279	0.1767	0.2385	-0.0022	-0.0034
CO-GMUG-DN-P	0.159	0.0328	0.0411	0.1692	0.2243	0.0018	-0.0009
CO-GMUG-SM-N	0.1484	0.0282	0.0391	0.1634	0.2194	0.012	0.0083
CO-GMUG-Tr-P	0.1902	0.0607	0.0569	0.1737	0.2286	0.0241	0.0267
CO-RGNF-LW-N	0.168	0.0326	0.0282	0.1719	0.231	0.0053	0.0009
CO-SJNF-8m-N	0.1349	0.0249	0.0369	0.1568	0.2131	0.0174	0.0143
CO-SJNF-8m-P	0.1511	0.0359	0.0525	0.1771	0.2349	0.023	0.0099
CO-SJNF-BD-N	0.14	0.0218	0.0221	0.1576	0.2054	0.0137	0.0043
CO-SJNF-Na-P	0.1671	0.0376	0.0587	0.1788	0.2359	0.0046	0.0052
CO-SJNF-PR-N	0.1652	0.0153	0.0178	0.1761	0.2355	0.0083	-0.0042
CO-SJNF-SN-N	0.139	0.0315	0.0343	0.1711	0.218	0.0346	0.0301
CO-SJNF-SP-P	0.1514	0.0251	0.0334	0.1801	0.2329	0.0383	0.0308
MT-BiNF-BC-N	0.0672	0.1821	0.2512	0.0464	0.0597	0.2649	0.283
MT-BiNF-CC-N	0.0635	0.1518	0.2227	0.05	0.058	0.2189	0.2393
MT-BiNF-PC-N	0.0656	0.1744	0.2478	0.0348	0.0491	0.2416	0.2697
OR-OcNF-PF-N	0.3376	0.3553	0.4019	0.3382	0.3771	0.3883	0.4073
OR-UmNF-Um-N	-0.0077	0.089	0.1585	0.0304	0.0412	0.1499	0.1671
OR-WWNF-LG-N	-0.0003	0.0903	0.1524	0.0261	0.0402	0.1447	0.1697
SD-BHNF-BS-N	0.1943	0.0335	0.0495	0.2151	0.2868	0.0268	0.0148
SD-BHNF-MV-P	0.2408	0.0878	0.1129	0.2462	0.3274	0.0426	0.0312
UT-UNF-BSG-P	*	0.0859	0.1558	0.041	0.0548	0.1463	0.1656
UT-UNF-PoC-P	0.00009	*	0.0191	0.1105	0.155	0.0241	0.028
UT-WCNF-SC-Q	0.00009	0.00009	*	0.1609	0.209	0.0357	0.0325
UT-WCNF-YP-P	0.00134	0.00009	0.00009	*	-0.0008	0.1603	0.1752
WA-WeNF-We-N	0.00009	0.00009	0.00009	0.38494	*	0.2152	0.2329
WY-MBNF-WC-N	0.00009	0.00009	0.00009	0.00009	0.00009	*	0.0016
WY-MBNF-WR-N	0.00009	0.00009	0.00009	0.00009	0.00009	0.01203	*

Table 8. Natural (N) populations that are likely the source of planted (P) stands based on Bayesian method by Rannala and Mountain (1997).

Assigned stands	Rank 1	Score, %	Rank 2	Score, %	Rank 3	Score, %	Rank 4	Score, %	Rank 5	Score, %
CO-BLM-AM60P	WY-MBNF-WC-N	76.7	WY-MBNF-WR-N	15.8	CO-SJNF-SN-N	3.8	CO-SJNF-8m-N	2.4	CO-RGNF-LW-N	0.8
CO-BLM-AM70P	WY-MBNF-WR-N	64.3	WY-MBNF-WC-N	20.8	CO-GMUG-SM-N	12.3	AZ-CoNF-Co-N	1.7	CO-SJNF-8m-N	0.6
CO-BLM-AM90P	WY-MBNF-WR-N	94.1	CO-RGNF-LW-N	4.3	SD-BHNF-BS-N	0.8	CO-SJNF-8m-N	0.6	WY-MBNF-WC-N	0.2
CO-BLM-VM60P	CO-GMUG-SM-N	98.2	AZ-CoNF-Co-N	0.9	CO-SJNF-BD-N	0.8	CO-RGNF-LW-N	0.0	CO-SJNF-8m-N	0.0
CO-BLM-VM70P	WY-MBNF-WR-N	76.5	WY-MBNF-WC-N	23.5	CO-RGNF-LW-N	0.0	CO-GMUG-SM-N	0.0	CO-SJNF-BD-N	0.0
CO-GMUG-DN-P	CO-GMUG-SM-N	99.9	WY-MBNF-WC-N	0.1	CO-SJNF-BD-N	0.0	WY-MBNF-WR-N	0.0	CO-RGNF-LW-N	0.0
CO-GMUG-Tr-P	CO-RGNF-LW-N	87.7	CO-GMUG-SM-N	7.2	AZ-CoNF-Co-N	2.7	WY-MBNF-WC-N	2.1	CO-SJNF-BD-N	0.3
CO-SJNF-8m-P	WY-MBNF-WR-N	100.0	CO-SJNF-SN-N	0.0	CO-RGNF-LW-N	0.0	CO-SJNF-PR-N	0.0	AZ-CoNF-Co-N	0.0
CO-SJNF-Na-P	CO-GMUG-SM-N	72.3	WY-MBNF-WC-N	20.3	CO-SJNF-BD-N	7.4	CO-RGNF-LW-N	0.0	AZ-CoNF-Co-N	0.0
CO-SJNF-SP-P	CO-SJNF-SN-N	99.9	CO-SJNF-PR-N	0.1	SD-BHNF-BS-N	0.0	WY-MBNF-WR-N	0.0	WY-MBNF-WC-N	0.0
SD-BHNF-MV-P	WY-MBNF-WR-N	92.5	CO-RGNF-LW-N	3.4	WY-MBNF-WC-N	2.8	SD-BHNF-BS-N	1.2	CO-SJNF-BD-N	0.1
UT-UNF-BSG-P	OR-UmNF-Um-N	100.0	OR-WWNF-LG-N	0.0	WA-WeNF-We-N	0.0	MT-BiNF-CC-N	0.0	MT-BiNF-PC-N	0.0
UT-UNF-PoC-P	WY-MBNF-WC-N	32.8	SD-BHNF-BS-N	29.2	CO-GMUG-SM-N	25.8	CO-SJNF-PR-N	8.9	CO-SJNF-BD-N	3.2
UT-WCNF-SC-Q	CO-SJNF-SN-N	70.8	CO-SJNF-8m-N	19.0	CO-GMUG-SM-N	8.3	SD-BHNF-BS-N	1.7	CO-SJNF-BD-N	0.1
UT-WCNF-YP-P	WA-WeNF-We-N	100.0	OR-WWNF-LG-N	0.0	OR-UmNF-Um-N	0.0	MT-BiNF-PC-N	0.0	MT-BiNF-BC-N	0.0

Criterion: Rannala & Mountain (1997)

Threshold: 0.05

Table 9. Probabilities of individual planted (P) trees to be assigned to natural (N) populations based on Bayesian method and 22 genetic markers. Colors used to shade Natural Stand ID's correspond to mitochondrial haplotypes (see Table 13).

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COBLMAM60P_2452	**0.263**	**0.707**	**0.419**	**0.798**	**0.751**	**0.278**	**0.631**	**0.354**	**0.440**	0.002	**0.016**	0.002	0.000	**0.050**	**0.147**	**0.255**	0.002	**0.667**	**0.124**	**C**
COBLMAM60P_2453	**0.027**	0.001	0.000	**0.012**	0.000	0.003	0.000	0.002	0.003	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	**B**
COBLMAM60P_2454	**0.423**	**0.946**	**0.875**	**0.943**	**0.930**	**0.957**	**0.982**	**0.957**	**0.983**	**0.217**	**0.209**	**0.020**	0.000	**0.309**	**0.792**	**0.795**	**0.083**	**0.968**	**0.929**	**C**
COBLMAM60P_2455	**0.093**	**0.422**	**0.224**	**0.286**	**0.492**	**0.389**	**0.639**	**0.770**	**0.747**	**0.062**	**0.057**	0.000	0.000	**0.029**	**0.015**	**0.191**	0.002	**0.530**	**0.565**	**C**
COBLMAM60P_2456	**0.187**	0.005	**0.115**	**0.013**	0.006	0.001	0.001	**0.030**	**0.088**	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	**0.015**	0.004	**C**
COBLMAM60P_2457	**0.643**	**0.193**	**0.899**	**0.581**	**0.467**	**0.341**	**0.674**	**0.672**	**0.951**	**0.592**	**0.657**	**0.097**	0.005	**0.662**	**0.324**	**0.237**	**0.155**	**0.656**	**0.572**	**C**
COBLMAM60P_2458	**0.036**	0.000	**0.044**	**0.039**	0.009	0.009	0.004	0.002	**0.055**	0.000	0.001	0.000	0.000	0.004	0.000	0.000	0.000	**0.019**	**0.043**	**C**
COBLMAM60P_2459	**0.249**	**0.774**	**0.892**	**0.869**	**0.883**	**0.716**	**0.944**	**0.865**	**0.878**	**0.167**	**0.164**	0.011	0.001	**0.205**	**0.604**	**0.343**	**0.060**	**0.964**	**0.909**	**C**
COBLMAM60P_2460	**0.179**	**0.694**	**0.571**	**0.594**	**0.781**	**0.532**	**0.573**	**0.669**	**0.756**	**0.033**	**0.044**	**0.019**	0.000	**0.316**	**0.394**	**0.433**	**0.074**	**0.889**	**0.771**	**C**
COBLMAM60P_2462	**0.353**	**0.945**	**0.695**	**0.733**	**0.887**	**0.896**	**0.812**	**0.867**	**0.969**	**0.189**	**0.141**	**0.093**	0.000	**0.692**	**0.816**	**0.886**	**0.282**	**0.932**	**0.853**	**C**
COBLMAM60P_2463	**0.101**	**0.372**	**0.119**	**0.203**	**0.262**	**0.436**	**0.208**	**0.318**	**0.620**	0.009	0.003	0.001	0.000	**0.012**	**0.020**	**0.159**	0.000	**0.372**	**0.176**	**C**
COBLMAM60P_2464	**0.371**	**0.823**	**0.639**	**0.890**	**0.636**	**0.926**	**0.790**	**0.815**	**0.941**	0.004	**0.018**	0.005	0.000	**0.015**	**0.172**	**0.573**	0.001	**0.887**	**0.579**	**C**
COBLMAM60P_2465	**0.052**	**0.307**	**0.041**	**0.230**	**0.301**	**0.388**	**0.220**	**0.606**	**0.345**	0.000	0.000	0.000	0.000	0.000	0.000	**0.140**	0.000	**0.295**	**0.393**	**C**
COBLMAM60P_2466	**0.045**	0.001	0.005	0.009	0.001	0.005	0.000	0.003	**0.017**	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	**0.022**	0.002	**C**
COBLMAM60P_2467	**0.061**	0.007	**0.022**	**0.030**	**0.013**	**0.037**	**0.030**	**0.059**	**0.139**	0.001	0.000	0.000	0.000	0.001	0.000	0.003	0.000	**0.018**	**0.043**	**C**
COBLMAM60P_2468	**0.407**	**0.977**	**0.752**	**0.803**	**0.932**	**0.935**	**0.804**	**0.871**	**0.974**	**0.048**	**0.031**	**0.093**	0.000	**0.176**	**0.589**	**0.907**	**0.029**	**0.939**	**0.857**	**C**
COBLMAM60P_2469	**0.714**	**0.040**	**0.498**	**0.086**	**0.174**	**0.066**	**0.105**	**0.274**	**0.732**	**0.024**	**0.026**	0.008	0.003	**0.036**	0.001	**0.037**	0.000	**0.191**	**0.179**	**C**
COBLMAM60P_2470	**0.261**	**0.717**	**0.383**	**0.571**	**0.473**	**0.774**	**0.425**	**0.594**	**0.847**	0.001	0.001	0.004	0.000	0.011	**0.121**	**0.571**	0.000	**0.738**	**0.408**	**C**
COBLMAM60P_2471	**0.045**	0.003	**0.032**	**0.162**	**0.020**	**0.213**	**0.025**	**0.042**	**0.222**	**0.037**	0.006	0.000	0.000	**0.173**	**0.028**	**0.012**	0.003	**0.118**	**0.132**	**C**
COBLMAM60P_2472	**0.267**	**0.805**	**0.775**	**0.929**	**0.923**	**0.705**	**0.804**	**0.830**	**0.821**	0.004	**0.031**	0.008	0.000	**0.030**	**0.158**	**0.474**	0.002	**0.963**	**0.909**	**C**
COBLMAM60P_2473	**0.383**	**0.921**	**0.785**	**0.931**	**0.925**	**0.928**	**0.973**	**0.963**	**0.981**	**0.187**	**0.440**	**0.048**	0.000	**0.756**	**0.850**	**0.879**	**0.350**	**0.973**	**0.952**	**C**
COBLMAM60P_2474	**0.027**	0.008	**0.018**	**0.061**	0.006	**0.016**	0.004	**0.091**	**0.026**	**0.026**	**0.025**	**0.021**	0.000	**0.040**	**0.018**	0.008	0.007	**0.019**	**0.037**	**C**
COBLMAM60P_2475	**0.158**	**0.035**	**0.802**	**0.213**	**0.117**	**0.126**	**0.193**	**0.327**	**0.335**	**0.246**	**0.278**	**0.024**	0.003	**0.102**	**0.120**	0.010	**0.021**	**0.335**	**0.399**	**C**
COBLMAM60P_2476	**0.209**	**0.774**	**0.628**	**0.662**	**0.838**	**0.589**	**0.561**	**0.675**	**0.772**	0.005	0.006	**0.019**	0.000	**0.051**	**0.230**	**0.458**	0.005	**0.901**	**0.780**	**C**
COBLMAM60P_2477	**0.761**	**0.040**	**0.913**	**0.186**	**0.201**	**0.049**	**0.113**	**0.190**	**0.680**	**0.024**	**0.025**	**0.046**	0.003	**0.021**	0.006	**0.021**	0.000	**0.269**	**0.215**	**B**
COBLMAM60P_2478	**0.860**	**0.029**	**0.800**	**0.232**	**0.080**	**0.086**	**0.175**	**0.220**	**0.797**	**0.036**	**0.046**	0.001	0.001	0.009	0.005	**0.020**	0.000	**0.195**	**0.100**	**C**
COBLMAM60P_2479	**0.203**	**0.772**	**0.716**	**0.624**	**0.837**	**0.607**	**0.714**	**0.736**	**0.836**	**0.147**	**0.109**	**0.057**	0.001	**0.525**	**0.634**	**0.421**	**0.208**	**0.925**	**0.821**	**B**
COBLMAM60P_2480	**0.385**	**0.029**	**0.800**	**0.576**	**0.526**	**0.178**	**0.273**	**0.143**	**0.924**	0.003	**0.017**	0.001	0.000	**0.011**	0.000	**0.103**	0.000	**0.514**	**0.464**	**C**
COBLMAM60P_2481	**0.031**	**0.034**	0.007	**0.039**	**0.018**	**0.076**	**0.020**	**0.052**	**0.129**	0.001	0.000	0.000	0.000	0.000	0.000	0.003	0.000	**0.041**	**0.011**	**C**
COBLMAM70P_2482	**0.309**	**0.110**	**0.488**	**0.352**	**0.324**	**0.080**	**0.258**	**0.458**	**0.879**	0.001	0.007	0.000	0.000	0.000	0.000	**0.131**	0.000	**0.291**	**0.380**	**B**
COBLMAM70P_2483	**0.126**	**0.503**	**0.789**	**0.756**	**0.784**	**0.393**	**0.768**	**0.692**	**0.609**	**0.015**	**0.050**	0.002	0.002	**0.063**	**0.243**	**0.144**	0.011	**0.935**	**0.845**	**B**
COBLMAM70P_2484	**0.301**	**0.685**	**0.598**	**0.785**	**0.481**	**0.866**	**0.751**	**0.720**	**0.888**	**0.037**	**0.029**	0.010	0.000	**0.021**	**0.208**	**0.371**	0.001	**0.784**	**0.457**	**B**
COBLMAM70P_2485	**0.170**	**0.029**	**0.189**	**0.181**	**0.070**	**0.063**	**0.086**	**0.152**	**0.324**	0.008	**0.078**	0.004	0.000	**0.075**	0.010	**0.040**	0.002	**0.435**	**0.434**	**B**
COBLMAM70P_2486	**0.995**	**0.071**	**0.972**	**0.454**	**0.296**	**0.141**	**0.274**	**0.393**	**0.920**	**0.023**	**0.116**	**0.040**	0.000	**0.021**	0.007	**0.099**	0.000	**0.365**	**0.323**	**B**
COBLMAM70P_2487	**0.362**	**0.946**	**0.606**	**0.775**	**0.887**	**0.883**	**0.663**	**0.815**	**0.941**	0.007	0.010	**0.033**	0.000	**0.088**	**0.359**	**0.920**	0.007	**0.908**	**0.810**	**B**
COBLMAM70P_2488	**0.028**	0.000	**0.043**	**0.022**	0.002	0.002	0.001	0.000	**0.013**	0.004	0.004	0.000	0.004	0.006	0.000	0.000	0.000	0.011	0.006	**B**
COBLMAM70P_2489	**0.056**	**0.239**	**0.119**	**0.192**	**0.111**	**0.205**	**0.269**	**0.284**	**0.331**	0.003	0.001	0.000	0.000	0.003	0.003	**0.055**	0.000	**0.132**	**0.179**	**B**
COBLMAM70P_2490	**0.027**	0.000	0.002	0.007	0.000	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	**B**

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COBLMAM70P_2491	0.086	0.183	0.284	0.376	0.121	0.640	0.194	0.443	0.349	0.001	0.008	0.003	0.000	0.004	0.068	0.119	0.000	0.425	0.328	B
COBLMAM70P_2492	0.225	0.736	0.802	0.852	0.877	0.659	0.924	0.875	0.868	0.146	0.362	0.028	0.002	0.591	0.680	0.416	0.262	0.970	0.932	C
COBLMAM70P_2493	0.452	0.962	0.750	0.978	0.958	0.950	0.885	0.937	0.963	0.005	0.043	0.016	0.000	0.051	0.257	0.934	0.003	0.967	0.929	B
COBLMAM70P_2494	0.107	0.346	0.420	0.672	0.432	0.274	0.360	0.276	0.600	0.278	0.488	0.028	0.001	0.274	0.305	0.133	0.073	0.551	0.399	B
COBLMAM70P_2495	0.091	0.251	0.208	0.429	0.265	0.385	0.409	0.452	0.471	0.029	0.100	0.004	0.000	0.497	0.501	0.257	0.035	0.438	0.392	B
COBLMAM70P_2496	0.476	0.018	0.502	0.068	0.080	0.018	0.021	0.070	0.397	0.023	0.034	0.105	0.003	0.044	0.002	0.011	0.001	0.110	0.091	B
COBLMAM70P_2497	0.748	0.007	0.370	0.151	0.024	0.058	0.035	0.163	0.548	0.063	0.032	0.008	0.000	0.009	0.003	0.009	0.000	0.085	0.100	C
COBLMAM70P_2498	0.089	0.044	0.050	0.235	0.031	0.369	0.073	0.315	0.321	0.026	0.004	0.001	0.000	0.012	0.089	0.049	0.001	0.162	0.191	B
COBLMAM70P_2499	0.301	0.870	0.898	0.950	0.957	0.784	0.908	0.885	0.891	0.025	0.080	0.028	0.000	0.066	0.305	0.460	0.009	0.980	0.941	B
COBLMAM70P_2500	0.267	0.840	0.731	0.812	0.829	0.716	0.911	0.903	0.976	0.105	0.097	0.002	0.000	0.049	0.174	0.576	0.005	0.845	0.839	B
COBLMAM70P_2502	0.339	0.861	0.636	0.912	0.878	0.875	0.899	0.931	0.952	0.045	0.230	0.016	0.000	0.513	0.607	0.895	0.125	0.954	0.921	C
COBLMAM70P_2503	0.090	0.173	0.172	0.331	0.239	0.212	0.264	0.353	0.104	0.054	0.120	0.037	0.000	0.244	0.482	0.114	0.071	0.453	0.069	C
COBLMAM70P_2504	0.047	0.076	0.032	0.365	0.044	0.128	0.085	0.158	0.157	0.002	0.003	0.000	0.000	0.025	0.013	0.072	0.001	0.096	0.144	C
COBLMAM70P_2505	0.456	0.975	0.786	0.982	0.977	0.961	0.947	0.971	0.983	0.007	0.059	0.003	0.000	0.130	0.475	0.979	0.013	0.985	0.975	C
COBLMAM70P_2506	0.044	0.146	0.033	0.083	0.146	0.104	0.196	0.073	0.206	0.001	0.000	0.000	0.000	0.008	0.001	0.029	0.000	0.096	0.091	C
COBLMAM70P_2507	0.096	0.465	0.145	0.250	0.615	0.564	0.624	0.878	0.628	0.006	0.025	0.001	0.000	0.038	0.024	0.234	0.003	0.656	0.631	C
COBLMAM70P_2508	0.065	0.230	0.080	0.264	0.105	0.281	0.109	0.253	0.196	0.001	0.000	0.001	0.000	0.011	0.030	0.136	0.002	0.284	0.060	C
COBLMAM70P_2509	0.181	0.651	0.373	0.437	0.418	0.550	0.408	0.565	0.895	0.003	0.001	0.001	0.000	0.002	0.020	0.361	0.000	0.587	0.362	C
COBLMAM70P_2510	0.327	0.832	0.567	0.938	0.809	0.783	0.663	0.684	0.927	0.015	0.077	0.003	0.000	0.067	0.285	0.768	0.005	0.838	0.716	C
COBLMAM70P_2511	0.866	1.000	0.795	1.000	1.000	1.000	1.000	1.000	0.976	0.713	0.886	0.439	0.931	0.999	1.000	1.000	1.000	1.000	1.000	C
COBLMAM90P_2512	0.054	0.177	0.123	0.355	0.125	0.141	0.416	0.352	0.333	0.008	0.029	0.010	0.000	0.050	0.087	0.144	0.002	0.386	0.388	C
COBLMAM90P_2513	0.137	0.210	0.146	0.447	0.330	0.273	0.198	0.219	0.387	0.002	0.042	0.000	0.000	0.024	0.106	0.367	0.000	0.679	0.226	C
COBLMAM90P_2514	0.257	0.901	0.594	0.625	0.832	0.672	0.644	0.790	0.967	0.019	0.011	0.010	0.000	0.023	0.096	0.704	0.001	0.789	0.746	A
COBLMAM90P_2515	0.170	0.228	0.210	0.670	0.689	0.379	0.810	0.433	0.833	0.043	0.117	0.005	0.000	0.233	0.258	0.201	0.042	0.413	0.568	B
COBLMAM90P_2516	0.069	0.215	0.354	0.420	0.298	0.415	0.632	0.385	0.364	0.034	0.035	0.001	0.000	0.038	0.140	0.079	0.005	0.491	0.605	C
COBLMAM90P_2517	0.155	0.178	0.156	0.287	0.142	0.566	0.219	0.520	0.664	0.375	0.042	0.021	0.000	0.478	0.618	0.234	0.158	0.431	0.403	B
COBLMAM90P_2518	0.155	0.407	0.370	0.650	0.355	0.440	0.411	0.306	0.744	0.797	0.707	0.079	0.000	0.478	0.523	0.240	0.162	0.442	0.331	B
COBLMAM90P_2519	0.136	0.133	0.053	0.172	0.161	0.233	0.158	0.304	0.234	0.001	0.007	0.000	0.000	0.001	0.002	0.086	0.000	0.230	0.538	A
COBLMAM90P_2520	0.080	0.034	0.040	0.287	0.023	0.205	0.054	0.174	0.184	0.047	0.003	0.001	0.000	0.015	0.081	0.026	0.000	0.095	0.111	B
COBLMAM90P_2521	0.371	0.894	0.712	0.956	0.861	0.855	0.804	0.751	0.967	0.079	0.186	0.011	0.000	0.139	0.497	0.751	0.020	0.882	0.765	B
COBLMAM90P_2522	0.339	0.861	0.636	0.912	0.878	0.875	0.899	0.931	0.952	0.045	0.230	0.016	0.000	0.513	0.607	0.895	0.125	0.954	0.921	B
COBLMAM90P_2523	0.887	1.000	0.871	1.000	1.000	1.000	1.000	1.000	0.987	0.920	0.966	0.648	0.988	1.000	1.000	1.000	1.000	1.000	1.000	B
COBLMAM90P_2524	0.028	0.003	0.003	0.027	0.001	0.027	0.004	0.042	0.183	0.017	0.001	0.000	0.000	0.002	0.001	0.002	0.000	0.010	0.022	B
COBLMAM90P_2525	0.048	0.133	0.134	0.378	0.021	0.463	0.049	0.569	0.516	0.020	0.025	0.001	0.000	0.333	0.103	0.036	0.012	0.375	0.121	B
COBLMAM90P_2526	0.188	0.621	0.588	0.863	0.750	0.485	0.561	0.545	0.750	0.009	0.059	0.002	0.000	0.039	0.178	0.323	0.003	0.828	0.687	C
COBLMAM90P_2527	0.070	0.075	0.345	0.516	0.523	0.253	0.290	0.151	0.772	0.001	0.002	0.000	0.000	0.003	0.000	0.136	0.000	0.459	0.479	B
COBLMAM90P_2528	0.081	0.038	0.476	0.650	0.533	0.517	0.299	0.078	0.619	0.166	0.162	0.079	0.000	0.605	0.077	0.102	0.027	0.661	0.450	C
COBLMAM90P_2529	0.250	0.771	0.484	0.629	0.650	0.668	0.480	0.510	0.897	0.278	0.186	0.093	0.000	0.477	0.589	0.626	0.132	0.702	0.544	C
COBLMAM90P_2530	0.201	0.613	0.317	0.497	0.607	0.513	0.357	0.589	0.397	0.007	0.022	0.031	0.000	0.247	0.436	0.589	0.043	0.757	0.276	A
COBLMAM90P_2531	0.507	0.994	0.906	0.992	0.992	0.989	0.992	0.991	0.997	0.048	0.141	0.011	0.000	0.251	0.722	0.972	0.047	0.995	0.993	B
COBLMAM90P_2532	0.452	0.962	0.750	0.978	0.958	0.950	0.885	0.937	0.963	0.005	0.043	0.016	0.000	0.051	0.257	0.934	0.003	0.967	0.929	B

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COBLMAM90P_2533	**0.125**	**0.472**	**0.753**	**0.746**	**0.737**	**0.378**	**0.665**	**0.619**	**0.537**	0.009	**0.036**	0.008	0.001	**0.022**	**0.113**	**0.121**	0.002	**0.890**	**0.764**	**A**
COBLMAM90P_2534	**0.035**	**0.053**	**0.061**	**0.084**	**0.151**	**0.080**	**0.043**	**0.068**	**0.366**	0.004	0.002	0.006	0.000	**0.015**	**0.019**	0.009	0.001	**0.119**	**0.048**	**B**
COBLMAM90P_2535	**0.199**	**0.782**	**0.373**	**0.344**	**0.743**	**0.770**	**0.623**	**0.795**	**0.831**	**0.040**	0.006	**0.019**	0.000	**0.031**	**0.117**	**0.425**	0.003	**0.742**	**0.635**	**C**
COBLMAM90P_2536	**0.027**	0.001	0.001	0.005	0.000	0.010	0.000	0.010	0.009	0.001	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.003	0.000	**C**
COBLMAM90P_2537	**0.130**	**0.506**	**0.332**	**0.712**	**0.363**	**0.178**	**0.528**	**0.547**	**0.779**	**0.393**	**0.609**	**0.093**	0.000	**0.694**	**0.551**	**0.373**	**0.224**	**0.731**	**0.457**	**C**
COBLMAM90P_2538	**0.084**	**0.162**	**0.137**	**0.185**	**0.209**	**0.262**	**0.258**	**0.425**	**0.300**	0.008	**0.048**	0.002	0.000	**0.131**	**0.136**	**0.130**	**0.012**	**0.300**	**0.301**	**B**
COBLMAM90P_2539	**0.087**	**0.188**	**0.183**	**0.345**	**0.123**	**0.393**	**0.309**	**0.318**	**0.433**	0.007	0.006	0.000	0.000	**0.032**	**0.208**	**0.108**	0.000	**0.324**	**0.167**	**B**
COBLMAM90P_2540	**0.223**	**0.576**	**0.382**	**0.740**	**0.652**	**0.563**	**0.578**	**0.742**	**0.429**	0.007	**0.105**	**0.015**	0.000	**0.290**	**0.478**	**0.583**	**0.055**	**0.848**	**0.372**	**A**
COBLMAM90P_2541	**0.106**	**0.472**	**0.171**	**0.255**	**0.576**	**0.594**	**0.561**	**0.803**	**0.566**	0.004	0.004	0.001	0.000	0.001	0.006	**0.158**	0.000	**0.558**	**0.522**	**A**
COBLMVM60P_0846	**0.035**	**0.309**	**0.234**	**0.399**	**0.035**	**0.337**	**0.050**	**0.444**	**0.400**	0.005	**0.043**	**0.016**	0.000	**0.224**	**0.023**	**0.030**	0.003	**0.370**	**0.071**	**B**
COBLMVM60P_0847	**0.030**	0.006	0.003	**0.024**	0.004	0.003	0.004	0.002	**0.026**	0.003	0.002	**0.016**	0.000	0.005	0.007	0.000	0.000	0.004	0.001	**B**
COBLMVM60P_0848	**0.407**	**0.977**	**0.752**	**0.803**	**0.932**	**0.935**	**0.804**	**0.871**	**0.974**	**0.048**	**0.031**	**0.093**	0.000	**0.176**	**0.589**	**0.907**	**0.029**	**0.939**	**0.857**	**B**
COBLMVM60P_0849	**0.027**	**0.020**	0.008	**0.066**	0.008	0.002	**0.053**	**0.012**	**0.020**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	**0.017**	**B**
COBLMVM60P_0850	**0.121**	**0.383**	**0.213**	**0.580**	**0.226**	**0.509**	**0.544**	**0.516**	**0.392**	0.000	0.001	0.000	0.000	0.002	**0.019**	**0.143**	0.000	**0.336**	**0.358**	**B**
COBLMVM60P_0851	**0.029**	**0.020**	0.006	**0.099**	0.004	**0.144**	**0.028**	**0.045**	**0.043**	0.002	0.000	0.000	0.000	0.002	0.002	0.003	0.000	**0.022**	**0.023**	**B**
COBLMVM60P_0852	**0.031**	**0.016**	0.007	**0.052**	0.005	0.007	**0.036**	0.006	**0.044**	0.001	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.002	**0.027**	**B**
COBLMVM60P_0853	**0.110**	**0.133**	**0.068**	**0.157**	**0.161**	**0.242**	**0.228**	**0.348**	**0.674**	**0.049**	**0.024**	0.007	0.000	**0.036**	**0.144**	**0.077**	0.002	**0.254**	**0.577**	**B**
COBLMVM60P_0854	**0.175**	**0.684**	**0.255**	**0.493**	**0.757**	**0.321**	**0.768**	**0.490**	**0.773**	0.008	**0.031**	0.001	0.000	**0.093**	**0.029**	**0.207**	0.005	**0.597**	**0.342**	**B**
COBLMVM60P_0855	**0.328**	**0.947**	**0.775**	**0.913**	**0.948**	**0.801**	**0.937**	**0.959**	**0.995**	**0.019**	**0.063**	0.001	0.000	**0.036**	**0.144**	**0.800**	0.002	**0.932**	**0.940**	**B**
COBLMVM60P_0856	**0.301**	**0.773**	**0.670**	**0.872**	**0.708**	**0.775**	**0.764**	**0.650**	**0.927**	**0.315**	**0.265**	**0.020**	0.000	**0.177**	**0.563**	**0.529**	**0.037**	**0.778**	**0.639**	**B**
COBLMVM60P_0857	**0.040**	0.008	0.002	**0.128**	0.005	**0.028**	0.009	0.003	**0.016**	0.000	0.000	0.002	0.000	0.003	**0.014**	0.000	0.000	**0.074**	0.000	**B**
COBLMVM60P_0858	**0.500**	**0.988**	**0.881**	**0.989**	**0.980**	**0.983**	**0.964**	**0.967**	**0.988**	**0.034**	**0.108**	**0.048**	0.000	**0.109**	**0.461**	**0.923**	**0.013**	**0.982**	**0.959**	**B**
COBLMVM60P_0859	**0.252**	**0.155**	**0.463**	**0.324**	**0.162**	**0.269**	**0.584**	**0.765**	**0.325**	0.007	**0.059**	0.003	0.000	**0.130**	**0.107**	**0.163**	**0.013**	**0.303**	**0.254**	**B**
COBLMVM60P_0860	**0.090**	**0.257**	**0.157**	**0.206**	**0.211**	**0.211**	**0.183**	**0.277**	**0.462**	0.003	0.001	0.001	0.000	0.003	0.008	**0.156**	0.000	**0.237**	**0.237**	**B**
COBLMVM60P_0861	**0.065**	**0.045**	**0.130**	**0.152**	**0.020**	**0.076**	**0.161**	**0.215**	**0.123**	**0.074**	**0.054**	0.002	0.000	**0.026**	0.010	**0.016**	0.009	**0.041**	**0.049**	**B**
COBLMVM60P_0862	**0.107**	**0.406**	**0.607**	**0.711**	**0.672**	**0.316**	**0.529**	**0.555**	**0.460**	0.001	**0.012**	0.003	0.000	0.009	**0.048**	**0.125**	0.001	**0.846**	**0.714**	**B**
COBLMVM60P_0863	**0.137**	**0.397**	**0.423**	**0.635**	**0.415**	**0.464**	**0.569**	**0.599**	**0.652**	0.004	**0.034**	0.001	0.000	**0.073**	**0.159**	**0.187**	0.008	**0.806**	**0.494**	**B**
COBLMVM60P_0864	**0.048**	**0.041**	**0.013**	**0.388**	**0.013**	**0.285**	**0.111**	**0.068**	**0.254**	0.000	0.000	0.000	0.000	0.000	0.000	**0.018**	0.000	**0.029**	**0.061**	**B**
COBLMVM60P_0865	**0.338**	**0.800**	**0.606**	**0.887**	**0.833**	**0.765**	**0.693**	**0.815**	**0.535**	0.005	**0.044**	**0.043**	0.000	**0.048**	**0.338**	**0.617**	0.004	**0.912**	**0.415**	**B**
COBLMVM60P_0866	**0.094**	**0.405**	**0.431**	**0.504**	**0.525**	**0.087**	**0.587**	**0.229**	**0.601**	**0.016**	**0.014**	0.000	0.000	0.007	0.007	**0.039**	0.000	**0.404**	**0.227**	**B**
COBLMVM60P_0867	**0.028**	**0.044**	**0.027**	**0.071**	**0.049**	0.002	**0.050**	0.005	**0.027**	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	**0.015**	0.011	**C**
COBLMVM60P_0868	**0.061**	**0.182**	**0.125**	**0.184**	**0.153**	**0.075**	**0.126**	**0.109**	**0.269**	0.002	0.002	0.001	0.000	**0.046**	**0.013**	**0.127**	0.001	**0.124**	**0.097**	**B**
COBLMVM60P_0869	**0.350**	**0.882**	**0.509**	**0.921**	**0.867**	**0.454**	**0.747**	**0.431**	**0.864**	0.001	0.010	0.004	0.000	**0.020**	**0.040**	**0.445**	0.000	**0.705**	**0.382**	**B**
COBLMVM60P_0870	**0.116**	**0.409**	**0.289**	**0.602**	**0.379**	**0.274**	**0.320**	**0.309**	**0.803**	**0.174**	**0.340**	0.005	0.000	**0.070**	**0.059**	**0.245**	0.006	**0.369**	**0.342**	**B**
COBLMVM60P_0871	**0.061**	0.000	**0.026**	**0.052**	0.003	0.000	0.000	0.000	**0.063**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	**B**
COBLMVM60P_0872	**0.116**	**0.409**	**0.289**	**0.602**	**0.379**	**0.274**	**0.320**	**0.309**	**0.803**	**0.174**	**0.340**	0.005	0.000	**0.070**	**0.059**	**0.245**	0.006	**0.369**	**0.342**	**B**
COBLMVM60P_0873	**0.083**	**0.199**	**0.227**	**0.384**	**0.226**	**0.076**	**0.289**	**0.108**	**0.155**	0.001	0.002	0.000	0.000	0.004	**0.023**	**0.012**	0.000	**0.345**	**0.023**	**B**
COBLMVM60P_0874	**0.206**	**0.782**	**0.555**	**0.497**	**0.672**	**0.581**	**0.605**	**0.691**	**0.927**	**0.105**	**0.020**	**0.019**	0.000	**0.031**	**0.117**	**0.482**	0.003	**0.670**	**0.618**	**B**
COBLMVM60P_0875	**0.094**	**0.087**	**0.072**	**0.177**	**0.054**	**0.444**	**0.104**	**0.156**	**0.283**	0.001	0.001	0.001	0.000	0.000	**0.017**	**0.031**	0.000	**0.406**	**0.074**	**B**
COBLMVM60P_0876	**0.028**	0.008	0.004	**0.025**	0.001	**0.050**	**0.015**	**0.016**	**0.015**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.005	**B**
COBLMVM60P_0877	**0.058**	**0.040**	**0.016**	**0.105**	**0.035**	0.007	**0.025**	0.006	**0.086**	0.001	0.000	0.004	0.000	0.000	0.007	0.002	0.000	**0.018**	0.003	**B**

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COBLMVM60P_0878	0.338	0.800	0.606	0.887	0.833	0.765	0.693	0.815	0.535	0.005	0.044	0.043	0.000	0.048	0.338	0.617	0.004	0.912	0.415	B
COBLMVM60P_0911	0.027	0.003	0.057	0.112	0.048	0.076	0.019	0.007	0.046	0.001	0.002	0.000	0.000	0.018	0.000	0.001	0.000	0.115	0.081	C
COBLMVM70P_0879	0.228	0.840	0.460	0.594	0.776	0.589	0.510	0.726	0.927	0.003	0.003	0.003	0.000	0.009	0.039	0.721	0.000	0.737	0.696	C
COBLMVM70P_0880	0.088	0.045	0.391	0.749	0.631	0.526	0.242	0.087	0.619	0.005	0.043	0.016	0.000	0.311	0.023	0.183	0.003	0.728	0.527	C
COBLMVM70P_0881	0.030	0.047	0.026	0.055	0.008	0.005	0.012	0.021	0.168	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.040	0.029	C
COBLMVM70P_0882	0.222	0.641	0.697	0.812	0.624	0.678	0.787	0.750	0.833	0.004	0.018	0.000	0.000	0.025	0.216	0.245	0.002	0.925	0.627	C
COBLMVM70P_0883	0.050	0.011	0.121	0.223	0.107	0.107	0.044	0.029	0.124	0.001	0.010	0.001	0.000	0.170	0.053	0.029	0.001	0.490	0.096	C
COBLMVM70P_0884	0.033	0.031	0.082	0.112	0.034	0.019	0.026	0.030	0.206	0.103	0.127	0.000	0.000	0.019	0.015	0.004	0.001	0.133	0.089	C
COBLMVM70P_0885	0.081	0.268	0.506	0.547	0.548	0.185	0.430	0.467	0.168	0.002	0.018	0.001	0.000	0.026	0.169	0.061	0.004	0.814	0.306	C
COBLMVM70P_0886	0.028	0.015	0.005	0.038	0.004	0.031	0.016	0.066	0.041	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.007	0.063	B
COBLMVM70P_0887	0.151	0.211	0.084	0.374	0.266	0.646	0.270	0.800	0.642	0.001	0.000	0.000	0.000	0.005	0.022	0.287	0.000	0.567	0.596	C
COBLMVM70P_0888	0.066	0.017	0.009	0.051	0.013	0.118	0.025	0.145	0.107	0.018	0.004	0.000	0.000	0.001	0.003	0.007	0.000	0.055	0.223	C
COBLMVM70P_0889	0.048	0.133	0.134	0.378	0.021	0.463	0.049	0.569	0.516	0.020	0.025	0.001	0.000	0.333	0.103	0.036	0.012	0.375	0.121	B
COBLMVM70P_0890	0.029	0.018	0.007	0.041	0.005	0.038	0.026	0.079	0.049	0.001	0.000	0.000	0.000	0.001	0.000	0.003	0.000	0.008	0.071	B
COBLMVM70P_0891	0.057	0.097	0.020	0.068	0.107	0.349	0.068	0.485	0.325	0.001	0.000	0.000	0.000	0.000	0.003	0.068	0.000	0.219	0.251	C
COBLMVM70P_0892	0.125	0.114	0.397	0.527	0.765	0.705	0.532	0.280	0.748	0.006	0.006	0.002	0.000	0.031	0.009	0.179	0.000	0.771	0.635	C
COBLMVM70P_0893	0.371	0.894	0.712	0.956	0.861	0.855	0.804	0.751	0.967	0.079	0.186	0.011	0.000	0.139	0.497	0.751	0.020	0.882	0.765	C
COBLMVM70P_0894	0.306	0.894	0.919	0.954	0.976	0.801	0.962	0.935	0.931	0.034	0.109	0.006	0.000	0.161	0.538	0.538	0.035	0.993	0.982	C
COBLMVM70P_0895	0.143	0.114	0.125	0.497	0.106	0.522	0.515	0.221	0.894	0.105	0.151	0.028	0.000	0.041	0.159	0.051	0.010	0.725	0.159	C
COBLMVM70P_0896	0.423	0.946	0.875	0.943	0.930	0.957	0.982	0.957	0.983	0.217	0.209	0.020	0.000	0.309	0.792	0.795	0.083	0.968	0.929	C
COBLMVM70P_0897	0.251	0.652	0.502	0.775	0.716	0.639	0.720	0.803	0.508	0.046	0.235	0.043	0.000	0.495	0.726	0.569	0.158	0.892	0.407	C
COBLMVM70P_0898	0.156	0.333	0.210	0.538	0.299	0.449	0.354	0.516	0.316	0.001	0.017	0.001	0.000	0.052	0.182	0.275	0.004	0.658	0.134	C
COBLMVM70P_0899	0.031	0.053	0.130	0.178	0.048	0.129	0.068	0.203	0.042	0.007	0.015	0.002	0.000	0.009	0.056	0.007	0.009	0.191	0.110	C
COBLMVM70P_0900	0.230	0.719	0.347	0.558	0.624	0.855	0.755	0.885	0.886	0.001	0.002	0.000	0.000	0.004	0.035	0.386	0.000	0.842	0.566	C
COBLMVM70P_0901	0.724	0.040	0.422	0.095	0.174	0.063	0.068	0.242	0.657	0.001	0.001	0.003	0.000	0.001	0.000	0.044	0.000	0.170	0.162	C
COBLMVM70P_0902	0.194	0.657	0.659	0.828	0.828	0.578	0.820	0.820	0.793	0.033	0.183	0.008	0.000	0.368	0.435	0.427	0.093	0.948	0.899	C
COBLMVM70P_0903	0.123	0.573	0.336	0.390	0.274	0.237	0.291	0.654	0.756	0.001	0.003	0.000	0.000	0.003	0.012	0.204	0.000	0.503	0.580	C
COBLMVM70P_0904	0.052	0.164	0.170	0.399	0.242	0.084	0.146	0.151	0.414	0.022	0.098	0.000	0.000	0.013	0.007	0.057	0.001	0.255	0.230	C
COBLMVM70P_0905	0.134	0.497	0.235	0.352	0.332	0.421	0.310	0.493	0.812	0.003	0.002	0.000	0.000	0.010	0.019	0.352	0.000	0.512	0.322	C
COBLMVM70P_0906	0.043	0.146	0.358	0.348	0.222	0.040	0.459	0.396	0.289	0.417	0.358	0.032	0.068	0.513	0.331	0.023	0.247	0.690	0.415	C
COBLMVM70P_0907	0.031	0.045	0.125	0.154	0.081	0.052	0.120	0.114	0.095	0.015	0.050	0.002	0.002	0.063	0.039	0.006	0.011	0.690	0.159	C
COBLMVM70P_0908	0.027	0.001	0.013	0.053	0.006	0.018	0.015	0.002	0.026	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.015	C
COBLMVM70P_0909	0.199	0.155	0.581	0.892	0.856	0.772	0.584	0.292	0.874	0.007	0.059	0.003	0.000	0.451	0.107	0.529	0.013	0.916	0.804	C
COBLMVM70P_0910	0.159	0.249	0.137	0.472	0.639	0.326	0.425	0.266	0.734	0.001	0.001	0.004	0.000	0.011	0.052	0.226	0.000	0.298	0.408	C
COGMUGDNP_5699	0.318	0.922	0.942	0.966	0.989	0.837	0.978	0.957	0.965	0.343	0.656	0.123	0.004	0.841	0.891	0.585	0.583	0.999	0.995	C
COGMUGDNP_5700	0.420	0.988	0.789	0.824	0.955	0.955	0.838	0.905	0.991	0.415	0.326	0.693	0.000	0.865	0.927	0.946	0.516	0.971	0.896	?
COGMUGDNP_5701	0.054	0.133	0.211	0.780	0.186	0.180	0.240	0.608	0.248	0.066	0.142	0.057	0.000	0.204	0.447	0.241	0.042	0.352	0.269	C
COGMUGDNP_5702	0.152	0.414	0.361	0.752	0.524	0.563	0.435	0.594	0.394	0.012	0.022	0.001	0.000	0.074	0.280	0.102	0.008	0.740	0.454	B
COGMUGDNP_5703	0.199	0.155	0.124	0.324	0.523	0.630	0.675	0.765	0.325	0.007	0.059	0.003	0.000	0.130	0.107	0.163	0.013	0.303	0.254	C
COGMUGDNP_5704	0.048	0.041	0.217	0.438	0.440	0.046	0.203	0.025	0.392	0.001	0.002	0.000	0.000	0.014	0.000	0.017	0.000	0.318	0.157	C
COGMUGDNP_5705	0.454	1.000	0.722	0.992	0.978	1.000	0.993	0.978	0.622	0.702	0.552	0.292	0.885	0.898	1.000	0.896	0.985	0.993	0.980	C

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COGMUGDNP_5706	0.043	0.090	0.158	0.144	0.073	0.116	0.093	0.117	0.218	0.008	0.003	0.007	0.000	0.014	0.027	0.007	0.001	0.324	0.083	C
COGMUGDNP_5707	0.183	1.000	0.372	0.976	0.916	1.000	0.912	0.905	0.150	0.308	0.340	0.269	0.614	0.739	1.000	0.779	0.992	0.965	0.736	C
COGMUGDNP_5708	0.102	0.535	0.506	0.774	0.494	0.512	0.683	0.685	0.714	0.329	0.304	0.031	0.003	0.347	0.296	0.195	0.358	0.761	0.742	B
COGMUGDNP_5709	0.038	0.017	0.329	0.425	0.411	0.129	0.142	0.040	0.387	0.006	0.025	0.002	0.000	0.049	0.001	0.017	0.000	0.473	0.370	C
COGMUGDNP_5710	0.087	0.072	0.109	0.258	0.073	0.357	0.292	0.100	0.572	0.493	0.242	0.517	0.003	0.560	0.674	0.015	0.522	0.713	0.108	C
COGMUGDNP_5711	0.027	0.005	0.002	0.041	0.001	0.002	0.004	0.004	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.013	C
COGMUGDNP_5712	0.030	0.084	0.039	0.359	0.007	0.166	0.021	0.236	0.239	0.000	0.001	0.000	0.000	0.012	0.000	0.009	0.000	0.085	0.030	C
COGMUGDNP_5713	0.301	0.870	0.898	0.950	0.957	0.784	0.908	0.885	0.891	0.025	0.080	0.028	0.000	0.066	0.305	0.460	0.009	0.980	0.941	C
COGMUGDNP_5714	0.616	1.000	0.825	1.000	1.000	1.000	0.999	0.999	0.740	0.317	0.644	0.382	0.820	0.978	1.000	0.996	1.000	1.000	1.000	C
COGMUGDNP_5715	0.042	0.086	0.080	0.624	0.114	0.033	0.107	0.150	0.130	0.003	0.016	0.004	0.000	0.042	0.038	0.069	0.001	0.118	0.049	C
COGMUGDNP_5716	0.281	0.762	0.512	0.892	0.750	0.721	0.675	0.678	0.918	0.076	0.291	0.003	0.000	0.379	0.475	0.741	0.075	0.823	0.709	B
COGMUGDNP_5717	0.333	0.900	0.711	0.676	0.803	0.878	0.764	0.785	0.941	0.217	0.052	0.147	0.000	0.222	0.662	0.699	0.050	0.857	0.730	C
COGMUGDNP_5718	0.333	0.900	0.711	0.676	0.803	0.878	0.764	0.785	0.941	0.217	0.052	0.147	0.000	0.222	0.662	0.699	0.050	0.857	0.730	C
COGMUGDNP_5719	0.027	0.024	0.029	0.122	0.025	0.025	0.023	0.047	0.043	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.247	0.316	C
COGMUGDNP_5720	0.312	0.803	0.743	0.837	0.792	0.869	0.955	0.909	0.952	0.564	0.563	0.079	0.001	0.829	0.901	0.664	0.539	0.918	0.857	C
COGMUGDNP_5721	0.125	0.114	0.397	0.527	0.765	0.705	0.532	0.280	0.748	0.006	0.006	0.002	0.000	0.031	0.009	0.179	0.000	0.771	0.635	B
COGMUGDNP_5722	0.146	0.532	0.432	0.714	0.692	0.169	0.660	0.303	0.616	0.007	0.058	0.002	0.000	0.182	0.090	0.135	0.015	0.663	0.353	C
COGMUGDNP_5723	0.122	0.329	0.313	0.504	0.306	0.683	0.635	0.446	0.500	0.034	0.034	0.012	0.000	0.024	0.107	0.215	0.001	0.436	0.559	C
COGMUGDNP_5724	0.197	0.323	0.473	0.514	0.308	0.484	0.396	0.442	0.744	0.031	0.057	0.016	0.000	0.071	0.397	0.227	0.005	0.815	0.579	?
COGMUGDNP_5725	0.030	0.038	0.077	0.139	0.023	0.016	0.100	0.113	0.121	0.004	0.009	0.000	0.000	0.015	0.012	0.003	0.001	0.279	0.055	C
COGMUGDNP_5726	0.222	0.641	0.697	0.812	0.624	0.678	0.787	0.750	0.833	0.004	0.018	0.000	0.000	0.025	0.216	0.245	0.002	0.925	0.627	B
COGMUGDNP_5727	0.259	0.693	0.611	0.815	0.647	0.713	0.774	0.645	0.918	0.703	0.657	0.020	0.001	0.695	0.792	0.499	0.342	0.762	0.633	C
COGMUGDNP_5728	0.178	0.444	0.196	0.666	0.310	0.206	0.299	0.117	0.657	0.001	0.002	0.000	0.000	0.003	0.009	0.127	0.000	0.315	0.078	C
COGMUGTrP_5759	0.094	0.305	0.176	0.446	0.146	0.054	0.414	0.169	0.532	0.023	0.015	0.005	0.000	0.030	0.042	0.047	0.001	0.359	0.062	B
COGMUGTrP_5760	0.350	0.882	0.509	0.921	0.867	0.454	0.747	0.431	0.864	0.001	0.010	0.004	0.000	0.020	0.040	0.445	0.000	0.705	0.382	C
COGMUGTrP_5761	0.235	0.789	0.707	0.875	0.902	0.289	0.864	0.428	0.805	0.008	0.031	0.001	0.000	0.070	0.126	0.175	0.004	0.815	0.461	B
COGMUGTrP_5762	0.137	0.397	0.423	0.635	0.415	0.464	0.569	0.599	0.652	0.004	0.034	0.001	0.000	0.073	0.159	0.187	0.008	0.806	0.494	C
COGMUGTrP_5763	0.030	0.090	0.091	0.339	0.080	0.080	0.097	0.155	0.119	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.170	0.248	C
COGMUGTrP_5764	0.042	0.013	0.049	0.331	0.099	0.058	0.029	0.005	0.090	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.134	0.014	C
COGMUGTrP_5765	0.306	0.894	0.919	0.954	0.976	0.801	0.962	0.935	0.931	0.034	0.109	0.006	0.000	0.161	0.538	0.538	0.035	0.993	0.982	C
COGMUGTrP_5766	0.315	0.913	0.511	0.682	0.827	0.425	0.639	0.347	0.889	0.012	0.006	0.025	0.000	0.077	0.150	0.417	0.003	0.643	0.316	C
COGMUGTrP_5767	0.125	0.472	0.753	0.746	0.737	0.378	0.665	0.619	0.537	0.009	0.036	0.008	0.001	0.022	0.113	0.121	0.002	0.890	0.764	C
COGMUGTrP_5768	0.125	0.472	0.753	0.746	0.737	0.378	0.665	0.619	0.537	0.009	0.036	0.008	0.001	0.022	0.113	0.121	0.002	0.890	0.764	C
COGMUGTrP_5769	0.142	0.596	0.313	0.692	0.457	0.079	0.706	0.370	0.751	0.103	0.234	0.025	0.000	0.627	0.248	0.210	0.099	0.660	0.252	C
COGMUGTrP_5770	0.065	0.292	0.300	0.464	0.301	0.027	0.560	0.210	0.441	0.314	0.264	0.024	0.001	0.545	0.186	0.029	0.121	0.520	0.169	C
COGMUGTrP_5771	0.179	0.694	0.571	0.594	0.781	0.532	0.573	0.669	0.756	0.033	0.044	0.019	0.000	0.316	0.394	0.433	0.074	0.889	0.771	B
COGMUGTrP_5772	0.079	0.072	0.532	0.408	0.546	0.357	0.292	0.100	0.536	0.167	0.038	0.091	0.001	0.481	0.109	0.080	0.036	0.690	0.481	C
COGMUGTrP_5773	0.094	0.391	0.546	0.631	0.647	0.098	0.604	0.223	0.442	0.003	0.012	0.000	0.000	0.025	0.037	0.032	0.001	0.629	0.309	B
COGMUGTrP_5774	0.032	0.071	0.092	0.096	0.027	0.008	0.062	0.177	0.057	0.047	0.070	0.012	0.000	0.201	0.158	0.004	0.027	0.254	0.053	C
COGMUGTrP_5775	0.027	0.003	0.017	0.071	0.034	0.003	0.027	0.000	0.046	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.008	C
COGMUGTrP_5776	0.038	0.083	0.364	0.261	0.154	0.177	0.139	0.281	0.116	0.002	0.019	0.004	0.000	0.007	0.042	0.013	0.001	0.430	0.474	C

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COGMUGTrP_5777	0.027	0.002	0.002	0.009	0.000	0.004	0.006	0.004	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.021	C
COGMUGTrP_5778	0.089	0.448	0.359	0.360	0.541	0.231	0.357	0.496	0.641	0.008	0.011	0.001	0.000	0.038	0.031	0.212	0.003	0.616	0.575	B
COGMUGTrP_5779	0.452	0.962	0.750	0.978	0.958	0.950	0.885	0.937	0.963	0.005	0.043	0.016	0.000	0.051	0.257	0.934	0.003	0.967	0.929	C
COGMUGTrP_5780	0.027	0.005	0.008	0.027	0.001	0.024	0.005	0.056	0.015	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	C
COGMUGTrP_5781	0.072	0.045	0.463	0.510	0.327	0.361	0.354	0.103	0.520	0.037	0.030	0.001	0.000	0.157	0.042	0.034	0.004	0.674	0.323	C
COGMUGTrP_5782	0.041	0.020	0.105	0.297	0.255	0.014	0.086	0.003	0.064	0.001	0.002	0.000	0.000	0.040	0.001	0.002	0.000	0.142	0.008	C
COGMUGTrP_5783	0.117	0.538	0.466	0.633	0.682	0.110	0.629	0.285	0.694	0.002	0.007	0.000	0.000	0.005	0.005	0.077	0.000	0.522	0.310	B
COGMUGTrP_5784	0.882	0.055	0.912	0.321	0.251	0.068	0.242	0.376	0.944	0.012	0.068	0.001	0.001	0.005	0.001	0.066	0.000	0.265	0.301	C
COGMUGTrP_5785	0.050	0.152	0.116	0.187	0.100	0.017	0.066	0.072	0.076	0.000	0.000	0.000	0.000	0.001	0.003	0.006	0.000	0.191	0.029	B
COGMUGTrP_5786	0.035	0.032	0.021	0.086	0.017	0.105	0.012	0.040	0.039	0.003	0.000	0.000	0.000	0.001	0.012	0.001	0.000	0.058	0.010	B
COGMUGTrP_5787	0.068	0.241	0.387	0.294	0.283	0.221	0.254	0.276	0.369	0.002	0.000	0.002	0.000	0.004	0.046	0.039	0.000	0.593	0.276	B
COGMUGTrP_5788	0.040	0.120	0.259	0.189	0.091	0.044	0.100	0.159	0.214	0.024	0.067	0.000	0.003	0.072	0.069	0.006	0.006	0.302	0.266	C
COSJNF8mP_8244	0.735	0.035	0.727	0.284	0.106	0.019	0.180	0.295	0.762	0.057	0.197	0.078	0.002	0.074	0.010	0.042	0.001	0.297	0.183	C
COSJNF8mP_8245	0.111	0.300	0.572	0.463	0.272	0.760	0.418	0.634	0.469	0.225	0.216	0.123	0.000	0.115	0.486	0.160	0.042	0.556	0.618	C
COSJNF8mP_8246	0.031	0.044	0.022	0.076	0.014	0.056	0.030	0.056	0.083	0.001	0.000	0.000	0.000	0.008	0.006	0.011	0.001	0.054	0.119	C
COSJNF8mP_8247	0.107	0.373	0.479	0.318	0.301	0.739	0.272	0.574	0.499	0.069	0.046	0.143	0.000	0.145	0.552	0.260	0.045	0.564	0.606	B
COSJNF8mP_8248	0.807	0.319	0.905	0.812	0.677	0.447	0.556	0.720	0.962	0.006	0.059	0.020	0.000	0.028	0.033	0.447	0.000	0.750	0.660	C
COSJNF8mP_8249	0.047	0.288	0.090	0.470	0.157	0.067	0.278	0.521	0.548	0.004	0.024	0.000	0.000	0.022	0.004	0.221	0.003	0.388	0.397	C
COSJNF8mP_8250	0.155	0.632	0.664	0.748	0.774	0.410	0.692	0.728	0.798	0.006	0.025	0.002	0.000	0.005	0.019	0.227	0.000	0.803	0.765	C
COSJNF8mP_8251	0.507	0.994	0.906	0.992	0.992	0.989	0.992	0.991	0.997	0.048	0.141	0.011	0.000	0.251	0.722	0.972	0.047	0.995	0.993	C
COSJNF8mP_8252	0.301	0.870	0.898	0.950	0.957	0.784	0.908	0.885	0.891	0.025	0.080	0.028	0.000	0.066	0.305	0.460	0.009	0.980	0.941	C
COSJNF8mP_8253	0.027	0.009	0.004	0.010	0.040	0.022	0.007	0.036	0.123	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.041	0.031	C
COSJNF8mP_8254	0.038	0.387	0.171	0.146	0.073	0.395	0.078	0.505	0.468	0.040	0.006	0.019	0.000	0.119	0.014	0.027	0.003	0.365	0.094	C
COSJNF8mP_8255	0.233	0.805	0.429	0.612	0.877	0.840	0.900	0.966	0.911	0.035	0.109	0.005	0.000	0.206	0.214	0.608	0.037	0.914	0.886	C
COSJNF8mP_8256	0.235	0.186	0.142	0.379	0.187	0.308	0.222	0.296	0.338	0.007	0.059	0.003	0.000	0.016	0.050	0.174	0.005	0.315	0.628	C
COSJNF8mP_8257	0.027	0.014	0.024	0.008	0.001	0.085	0.000	0.075	0.029	0.050	0.007	0.029	0.000	0.047	0.004	0.000	0.004	0.021	0.011	C
COSJNF8mP_8258	0.238	0.545	0.248	0.820	0.524	0.790	0.406	0.669	0.515	0.003	0.010	0.000	0.000	0.057	0.236	0.333	0.003	0.697	0.439	C
COSJNF8mP_8259	0.761	0.345	0.906	0.537	0.630	0.421	0.462	0.624	0.974	0.054	0.044	0.111	0.000	0.105	0.132	0.419	0.005	0.695	0.572	C
COSJNF8mP_8260	0.035	0.014	0.003	0.092	0.037	0.057	0.013	0.022	0.048	0.001	0.000	0.000	0.000	0.010	0.006	0.003	0.000	0.015	0.015	C
COSJNF8mP_8261	0.079	0.028	0.170	0.568	0.202	0.266	0.178	0.061	0.325	0.025	0.024	0.001	0.000	0.336	0.054	0.073	0.002	0.320	0.255	C
COSJNF8mP_8262	0.111	0.469	0.447	0.440	0.286	0.229	0.265	0.535	0.488	0.001	0.004	0.001	0.000	0.007	0.039	0.089	0.000	0.627	0.581	C
COSJNF8mP_8263	0.051	0.128	0.172	0.318	0.197	0.287	0.191	0.579	0.511	0.001	0.002	0.000	0.000	0.001	0.007	0.129	0.000	0.316	0.272	B
COSJNF8mP_8264	0.195	0.728	0.431	0.843	0.585	0.308	0.724	0.845	0.843	0.015	0.077	0.033	0.000	0.164	0.327	0.655	0.014	0.925	0.716	C
COSJNF8mP_8265	0.212	0.839	0.361	0.392	0.837	0.795	0.676	0.873	0.888	0.035	0.024	0.010	0.000	0.171	0.189	0.614	0.029	0.842	0.755	C
COSJNF8mP_8266	0.049	0.091	0.029	0.257	0.254	0.173	0.301	0.209	0.385	0.001	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.089	0.231	C
COSJNF8mP_8267	0.757	0.037	0.617	0.095	0.107	0.054	0.050	0.128	0.697	0.142	0.116	0.352	0.002	0.153	0.014	0.050	0.004	0.133	0.109	B
COSJNF8mP_8268	0.044	0.337	0.438	0.496	0.063	0.373	0.123	0.465	0.486	0.001	0.002	0.000	0.000	0.011	0.013	0.014	0.000	0.595	0.093	C
COSJNF8mP_8269	0.653	0.206	0.826	0.683	0.480	0.283	0.472	0.485	0.960	0.301	0.611	0.014	0.002	0.433	0.193	0.274	0.054	0.580	0.479	C
COSJNF8mP_8270	0.188	0.003	0.113	0.023	0.013	0.011	0.014	0.044	0.151	0.004	0.006	0.001	0.000	0.000	0.000	0.006	0.000	0.018	0.021	C
COSJNF8mP_8271	0.189	0.679	0.426	0.323	0.492	0.628	0.411	0.495	0.788	0.564	0.162	0.529	0.000	0.605	0.694	0.482	0.256	0.603	0.450	C
COSJNF8mP_8272	0.519	0.194	0.588	0.373	0.560	0.314	0.579	0.782	0.910	0.038	0.144	0.006	0.001	0.125	0.025	0.208	0.006	0.648	0.602	C

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COSJNF8mP_8273	**0.997**	**0.076**	**0.984**	**0.463**	**0.323**	**0.149**	**0.342**	**0.461**	**0.956**	**0.033**	**0.153**	0.009	0.002	**0.057**	**0.021**	**0.122**	0.001	**0.426**	**0.380**	**C**
COSJNFNaP_5627	**0.111**	**0.469**	**0.447**	**0.440**	**0.286**	**0.229**	**0.265**	**0.535**	**0.488**	0.001	0.004	0.001	0.000	0.007	**0.039**	**0.089**	0.000	**0.627**	**0.581**	**C**
COSJNFNaP_5628	**0.048**	**0.038**	**0.395**	**0.255**	**0.160**	**0.121**	**0.154**	**0.080**	**0.350**	**0.039**	**0.038**	0.002	0.001	**0.281**	**0.041**	0.011	0.005	**0.458**	**0.381**	**C**
COSJNFNaP_5629	**0.339**	**0.861**	**0.636**	**0.912**	**0.878**	**0.875**	**0.899**	**0.931**	**0.952**	**0.045**	**0.230**	**0.016**	0.000	**0.513**	**0.607**	**0.895**	**0.125**	**0.954**	**0.921**	**C**
COSJNFNaP_5630	**0.090**	0.000	**0.018**	**0.021**	0.000	0.004	**0.016**	0.003	**0.051**	**0.037**	**0.094**	0.005	0.001	**0.012**	0.000	0.000	0.000	0.004	0.001	**C**
COSJNFNaP_5631	**0.225**	**0.736**	**0.802**	**0.852**	**0.877**	**0.659**	**0.924**	**0.875**	**0.868**	**0.146**	**0.362**	**0.028**	0.002	**0.591**	**0.680**	**0.416**	**0.262**	**0.970**	**0.932**	**C**
COSJNFNaP_5632	**0.087**	**0.052**	**0.067**	**0.409**	**0.045**	**0.368**	**0.285**	**0.112**	**0.554**	0.004	**0.057**	0.003	0.000	**0.077**	**0.186**	**0.013**	**0.020**	**0.763**	**0.081**	**B**
COSJNFNaP_5633	**0.091**	**0.414**	**0.336**	**0.699**	**0.298**	**0.481**	**0.477**	**0.559**	**0.659**	**0.015**	**0.043**	0.002	0.000	**0.050**	**0.074**	**0.140**	**0.024**	**0.685**	**0.457**	**B**
COSJNFNaP_5634	**0.230**	**0.679**	**0.733**	**0.832**	**0.667**	**0.717**	**0.825**	**0.792**	**0.893**	**0.094**	**0.224**	**0.018**	0.001	**0.299**	**0.514**	**0.277**	**0.081**	**0.964**	**0.671**	**C**
COSJNFNaP_5635	**0.521**	**0.998**	**0.928**	**0.997**	**0.997**	**0.997**	**0.999**	**0.998**	**1.000**	**0.415**	**0.743**	**0.191**	0.001	**0.947**	**0.982**	**0.994**	**0.713**	**1.000**	**0.999**	**C**
COSJNFNaP_5636	**0.302**	**0.090**	**0.907**	**0.482**	**0.420**	**0.092**	**0.350**	**0.368**	**0.536**	0.011	**0.050**	0.011	0.003	**0.011**	0.010	**0.026**	0.000	**0.607**	**0.484**	**C**
COSJNFNaP_5637	**0.028**	**0.048**	**0.054**	**0.140**	**0.024**	**0.013**	**0.235**	**0.125**	**0.039**	**0.012**	0.009	0.002	0.000	0.007	0.007	0.001	0.000	**0.058**	**0.122**	**C**
COSJNFNaP_5638	**0.158**	**0.663**	**0.699**	**0.758**	**0.819**	**0.427**	**0.794**	**0.798**	**0.858**	0.008	**0.034**	0.000	0.000	**0.015**	**0.057**	**0.274**	0.001	**0.862**	**0.847**	**C**
COSJNFNaP_5639	**0.507**	**0.994**	**0.906**	**0.992**	**0.992**	**0.989**	**0.992**	**0.991**	**0.997**	**0.048**	**0.141**	0.011	0.000	**0.251**	**0.722**	**0.972**	**0.047**	**0.995**	**0.993**	**C**
COSJNFNaP_5640	**0.034**	0.010	0.002	**0.112**	0.002	0.001	**0.012**	**0.029**	**0.020**	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	**0.011**	0.000	**B**
COSJNFNaP_5641	**0.440**	**1.000**	**0.415**	**0.998**	**0.984**	**1.000**	**0.989**	**0.862**	**0.634**	**0.142**	**0.254**	**0.120**	**0.084**	**0.767**	**0.971**	**0.982**	**0.944**	**0.950**	**0.856**	**C**
COSJNFNaP_5642	**0.355**	**0.858**	**0.678**	**0.913**	**0.906**	**0.819**	**0.833**	**0.911**	**0.685**	**0.125**	**0.481**	**0.177**	0.000	**0.756**	**0.922**	**0.747**	**0.384**	**0.978**	**0.532**	**C**
COSJNFNaP_5643	**0.050**	**0.058**	**0.080**	**0.172**	**0.055**	**0.267**	**0.164**	**0.121**	**0.065**	**0.020**	**0.070**	**0.120**	0.000	**0.056**	**0.209**	0.005	0.006	**0.301**	**0.146**	**C**
COSJNFNaP_5644	**0.132**	**0.020**	**0.160**	**0.154**	**0.181**	**0.040**	**0.045**	**0.062**	**0.686**	**0.086**	**0.237**	**0.014**	0.000	**0.082**	0.010	**0.016**	0.003	**0.070**	**0.061**	?
COSJNFNaP_5645	**0.156**	**0.333**	**0.210**	**0.538**	**0.299**	**0.449**	**0.354**	**0.516**	**0.316**	0.001	**0.017**	0.001	0.000	**0.052**	**0.182**	**0.275**	0.004	**0.658**	**0.134**	**C**
COSJNFNaP_5646	**0.045**	**0.095**	**0.130**	**0.258**	**0.136**	**0.125**	**0.180**	**0.208**	**0.194**	0.005	**0.044**	0.002	0.000	**0.080**	**0.058**	**0.044**	0.009	**0.815**	**0.235**	**C**
COSJNFNaP_5647	**0.191**	**0.252**	**0.215**	**0.695**	**0.175**	**0.597**	**0.482**	**0.523**	**0.738**	0.001	0.004	0.000	0.000	0.006	**0.063**	**0.158**	0.000	**0.413**	**0.219**	**B**
COSJNFNaP_5648	**0.235**	**0.789**	**0.707**	**0.875**	**0.902**	**0.289**	**0.864**	**0.428**	**0.805**	0.008	**0.031**	0.001	0.000	**0.070**	**0.126**	**0.175**	0.004	**0.815**	**0.461**	**B**
COSJNFNaP_5649	**0.050**	0.010	**0.171**	**0.215**	**0.080**	**0.172**	**0.080**	**0.054**	**0.190**	0.001	0.008	0.000	0.000	**0.021**	0.002	**0.013**	0.000	**0.241**	**0.100**	**B**
COSJNFNaP_5650	**0.148**	**1.000**	**0.191**	**0.887**	**0.672**	**1.000**	**0.966**	**0.852**	**0.110**	**0.028**	**0.126**	**0.024**	0.008	**0.506**	**0.938**	**0.675**	**0.584**	**0.617**	**0.886**	**C**
COSJNFNaP_5651	**0.149**	**0.616**	**0.526**	**0.476**	**0.649**	**0.189**	**0.540**	**0.220**	**0.673**	**0.454**	**0.141**	**0.320**	0.001	**0.526**	**0.303**	**0.090**	**0.139**	**0.584**	**0.243**	**C**
COSJNFNaP_5652	**0.072**	**0.379**	**0.275**	**0.380**	**0.343**	**0.089**	**0.327**	**0.471**	**0.489**	**0.057**	**0.059**	**0.140**	0.000	**0.384**	**0.265**	**0.188**	**0.080**	**0.753**	**0.470**	**C**
COSJNFNaP_5653	**0.070**	**0.309**	**0.200**	**0.636**	**0.350**	**0.240**	**0.267**	**0.452**	**0.180**	0.000	0.001	0.000	0.000	0.003	**0.018**	**0.144**	0.001	**0.583**	**0.259**	**C**
COSJNFNaP_5654	**0.169**	**0.607**	**0.562**	**0.748**	**0.757**	**0.208**	**0.801**	**0.352**	**0.708**	**0.047**	**0.140**	0.006	0.000	**0.336**	**0.193**	**0.131**	**0.053**	**0.719**	**0.385**	**B**
COSJNFNaP_5655	**0.456**	**0.975**	**0.786**	**0.982**	**0.977**	**0.961**	**0.947**	**0.971**	**0.983**	0.007	**0.059**	0.003	0.000	**0.130**	**0.475**	**0.979**	**0.013**	**0.985**	**0.975**	**C**
COSJNFNaP_5656	**0.082**	**0.443**	**0.223**	**0.720**	**0.427**	**0.131**	**0.399**	**0.212**	**0.466**	0.000	0.000	0.000	0.000	0.003	0.003	**0.088**	0.000	**0.401**	**0.263**	**C**
COSJNFNaP_5657	**0.234**	**1.000**	**0.551**	**0.986**	**0.987**	**0.729**	**0.972**	**0.731**	**0.321**	**0.057**	**0.212**	**0.055**	**0.882**	**0.703**	**0.960**	**0.619**	**0.795**	**0.971**	**0.819**	**C**
COSJNFSPP_8154	**0.050**	0.008	**0.045**	**0.043**	**0.017**	0.002	**0.021**	**0.020**	**0.305**	0.001	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.004	0.001	**C**
COSJNFSPP_8155	**0.696**	0.006	**0.236**	**0.171**	**0.025**	**0.014**	**0.090**	**0.267**	**0.556**	0.004	**0.048**	0.001	0.002	**0.019**	0.000	**0.061**	0.000	**0.046**	**0.054**	**C**
COSJNFSPP_8156	**0.117**	0.003	**0.061**	**0.025**	0.005	**0.013**	0.003	**0.072**	**0.346**	0.001	0.000	0.000	0.000	0.001	0.000	0.008	0.000	0.008	**0.018**	**C**
COSJNFSPP_8157	**0.092**	**0.250**	**0.289**	**0.397**	**0.262**	**0.632**	**0.445**	**0.836**	**0.878**	**0.040**	**0.039**	0.002	0.000	**0.049**	**0.174**	**0.343**	0.005	**0.400**	**0.355**	**C**
COSJNFSPP_8158	**0.168**	**0.155**	**0.124**	**0.324**	**0.162**	**0.721**	**0.584**	**0.292**	**0.325**	**0.046**	**0.402**	**0.058**	0.000	**0.695**	**0.764**	**0.163**	**0.205**	**0.303**	**0.254**	**C**
COSJNFSPP_8159	**0.133**	**0.454**	**0.307**	**0.615**	**0.258**	**0.240**	**0.612**	**0.685**	**0.784**	**0.073**	**0.153**	**0.012**	0.000	**0.337**	**0.385**	**0.298**	**0.058**	**0.803**	**0.372**	**C**
COSJNFSPP_8160	**0.052**	0.004	0.008	**0.041**	0.002	**0.012**	**0.017**	**0.050**	**0.079**	**0.032**	**0.059**	0.000	0.000	**0.022**	**0.013**	0.009	0.008	**0.021**	**0.061**	**C**
COSJNFSPP_8161	**0.038**	0.002	**0.024**	**0.092**	0.002	**0.019**	0.007	**0.188**	**0.166**	**0.013**	**0.036**	0.001	0.000	**0.030**	0.004	**0.019**	0.001	0.009	0.003	**C**
COSJNFSPP_8162	**0.030**	0.001	0.001	**0.022**	0.001	0.008	0.005	**0.043**	**0.031**	0.001	0.002	0.000	0.000	0.006	0.003	**0.017**	0.000	**0.029**	0.002	**C**

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
COSJNFSPP_8163	0.074	0.334	0.206	0.396	0.090	0.113	0.270	0.297	0.296	0.088	0.068	0.028	0.000	0.194	0.246	0.074	0.008	0.543	0.181	B
COSJNFSPP_8164	0.087	0.000	0.001	0.008	0.000	0.000	0.000	0.026	0.055	0.002	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.000	0.000	C
COSJNFSPP_8165	0.029	0.000	0.000	0.012	0.000	0.000	0.001	0.037	0.018	0.004	0.004	0.000	0.000	0.001	0.000	0.002	0.000	0.001	0.003	C
COSJNFSPP_8166	0.055	0.052	0.032	0.129	0.034	0.350	0.064	0.169	0.225	0.002	0.000	0.001	0.000	0.008	0.038	0.076	0.000	0.117	0.224	C
COSJNFSPP_8167	0.064	0.000	0.002	0.006	0.000	0.002	0.000	0.003	0.012	0.001	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.000	C
COSJNFSPP_8168	0.028	0.003	0.003	0.023	0.001	0.025	0.002	0.033	0.049	0.002	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.035	0.081	C
COSJNFSPP_8168	0.189	0.002	0.074	0.012	0.014	0.007	0.008	0.055	0.193	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.053	0.045	C
COSJNFSPP_8170	0.920	0.046	0.868	0.378	0.186	0.080	0.155	0.195	0.869	0.057	0.197	0.009	0.001	0.028	0.008	0.058	0.000	0.220	0.183	C
COSJNFSPP_8171	0.134	0.491	0.126	0.418	0.626	0.170	0.381	0.311	0.256	0.000	0.000	0.000	0.000	0.001	0.003	0.138	0.000	0.475	0.086	C
COSJNFSPP_8172	0.230	0.404	0.347	0.573	0.588	0.537	0.539	0.566	0.600	0.007	0.077	0.001	0.000	0.106	0.380	0.593	0.004	0.948	0.490	C
COSJNFSPP_8173	0.620	0.022	0.321	0.094	0.070	0.004	0.032	0.010	0.405	0.002	0.001	0.005	0.000	0.003	0.000	0.002	0.000	0.022	0.005	C
COSJNFSPP_8174	0.037	0.091	0.041	0.099	0.103	0.106	0.114	0.237	0.222	0.000	0.000	0.000	0.000	0.000	0.000	0.029	0.000	0.390	0.479	C
COSJNFSPP_8175	0.029	0.020	0.003	0.017	0.004	0.012	0.007	0.231	0.082	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.061	0.073	C
COSJNFSPP_8176	0.135	0.208	0.179	0.416	0.199	0.287	0.269	0.252	0.447	0.079	0.182	0.001	0.000	0.177	0.195	0.162	0.029	0.296	0.375	C
COSJNFSPP_8177	0.102	0.465	0.345	0.478	0.490	0.285	0.587	0.696	0.870	0.026	0.084	0.001	0.000	0.038	0.024	0.309	0.003	0.514	0.598	C
COSJNFSPP_8179	0.074	0.035	0.026	0.251	0.033	0.018	0.254	0.225	0.295	0.001	0.005	0.000	0.000	0.014	0.002	0.132	0.000	0.032	0.018	C
COSJNFSPP_8180	0.079	0.019	0.122	0.478	0.157	0.117	0.250	0.177	0.599	0.000	0.000	0.000	0.000	0.001	0.000	0.196	0.000	0.179	0.176	C
COSJNFSPP_8181	0.093	0.419	0.178	0.465	0.427	0.077	0.311	0.194	0.654	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.000	0.217	0.153	C
COSJNFSPP_8182	0.802	0.036	0.854	0.238	0.150	0.052	0.175	0.255	0.838	0.058	0.077	0.007	0.001	0.002	0.000	0.025	0.000	0.159	0.179	C
COSJNFSPP_8183	0.383	0.921	0.785	0.931	0.925	0.928	0.973	0.963	0.981	0.187	0.440	0.048	0.000	0.756	0.850	0.879	0.350	0.973	0.952	C
SDBHNFMVP_5892	0.141	0.504	0.324	0.682	0.423	0.171	0.510	0.693	0.364	0.015	0.080	0.086	0.000	0.154	0.424	0.349	0.020	0.849	0.253	C
SDBHNFMVP_5893	0.270	0.833	0.804	0.936	0.950	0.726	0.884	0.892	0.878	0.005	0.044	0.002	0.000	0.080	0.317	0.553	0.009	0.983	0.960	C
SDBHNFMVP_5894	0.105	0.507	0.526	0.707	0.522	0.152	0.767	0.772	0.699	0.222	0.442	0.057	0.002	0.746	0.591	0.227	0.348	0.940	0.729	C
SDBHNFMVP_5895	0.033	0.078	0.077	0.212	0.071	0.073	0.300	0.186	0.057	0.001	0.007	0.000	0.000	0.013	0.007	0.007	0.001	0.085	0.262	C
SDBHNFMVP_5896	0.028	0.011	0.011	0.116	0.007	0.003	0.017	0.036	0.031	0.008	0.007	0.000	0.000	0.051	0.013	0.002	0.001	0.044	0.030	C
SDBHNFMVP_5897	0.107	0.406	0.607	0.711	0.672	0.316	0.529	0.555	0.460	0.001	0.012	0.003	0.000	0.009	0.048	0.125	0.001	0.846	0.714	C
SDBHNFMVP_5898	0.099	0.135	0.258	0.327	0.214	0.256	0.276	0.521	0.290	0.006	0.106	0.001	0.001	0.087	0.076	0.136	0.009	0.399	0.351	C
SDBHNFMVP_5899	0.168	0.275	0.194	0.710	0.275	0.396	0.334	0.425	0.439	0.004	0.007	0.000	0.000	0.039	0.157	0.268	0.001	0.415	0.378	C
SDBHNFMVP_5900	0.267	0.805	0.775	0.929	0.923	0.705	0.804	0.830	0.821	0.004	0.031	0.008	0.000	0.030	0.158	0.474	0.002	0.963	0.909	C
SDBHNFMVP_5901	0.194	0.657	0.659	0.828	0.828	0.578	0.820	0.820	0.793	0.033	0.183	0.008	0.000	0.368	0.435	0.427	0.093	0.948	0.899	C
SDBHNFMVP_5902	0.179	0.694	0.571	0.594	0.781	0.532	0.573	0.669	0.756	0.033	0.044	0.019	0.000	0.316	0.394	0.433	0.074	0.889	0.771	C
SDBHNFMVP_5903	0.123	0.462	0.281	0.632	0.383	0.494	0.728	0.653	0.424	0.007	0.060	0.002	0.000	0.135	0.141	0.251	0.014	0.421	0.647	C
SDBHNFMVP_5904	0.128	0.114	0.585	0.712	0.693	0.522	0.515	0.221	0.867	0.022	0.020	0.002	0.000	0.031	0.009	0.207	0.000	0.702	0.618	C
SDBHNFMVP_5905	0.029	0.015	0.017	0.071	0.024	0.015	0.012	0.036	0.009	0.000	0.003	0.001	0.000	0.007	0.010	0.003	0.000	0.335	0.005	C
SDBHNFMVP_5906	0.312	0.803	0.743	0.837	0.792	0.869	0.955	0.909	0.952	0.564	0.563	0.079	0.001	0.829	0.901	0.664	0.539	0.918	0.857	C
SDBHNFMVP_5907	0.339	0.861	0.636	0.912	0.878	0.875	0.899	0.931	0.952	0.045	0.230	0.016	0.000	0.513	0.607	0.895	0.125	0.954	0.921	C
SDBHNFMVP_5908	0.225	0.736	0.802	0.852	0.877	0.659	0.924	0.875	0.868	0.146	0.362	0.028	0.002	0.591	0.680	0.416	0.262	0.970	0.932	C
SDBHNFMVP_5909	0.126	0.503	0.789	0.756	0.784	0.393	0.768	0.692	0.609	0.015	0.050	0.002	0.002	0.063	0.243	0.144	0.011	0.935	0.845	C
SDBHNFMVP_5910	0.209	0.774	0.628	0.662	0.838	0.589	0.561	0.675	0.772	0.005	0.006	0.019	0.000	0.051	0.230	0.458	0.005	0.901	0.780	C
SDBHNFMVP_5911	0.339	0.861	0.636	0.912	0.878	0.875	0.899	0.931	0.952	0.045	0.230	0.016	0.000	0.513	0.607	0.895	0.125	0.954	0.921	C
SDBHNFMVP_5912	0.267	0.805	0.775	0.929	0.923	0.705	0.804	0.830	0.821	0.004	0.031	0.008	0.000	0.030	0.158	0.474	0.002	0.963	0.909	C

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
SDBHNFMVP_5913	**0.235**	**0.186**	**0.637**	**0.938**	**0.903**	**0.830**	**0.573**	**0.296**	**0.886**	0.001	0.010	0.003	0.000	**0.088**	**0.050**	**0.555**	0.001	**0.925**	**0.810**	**C**
SDBHNFMVP_5914	**0.094**	**0.499**	**0.283**	**0.292**	**0.449**	**0.254**	**0.364**	**0.543**	**0.838**	**0.026**	**0.017**	0.001	0.000	**0.030**	**0.020**	**0.313**	0.002	**0.418**	**0.473**	**C**
SDBHNFMVP_5915	**0.383**	**0.921**	**0.785**	**0.931**	**0.925**	**0.928**	**0.973**	**0.963**	**0.981**	**0.187**	**0.440**	**0.048**	0.000	**0.756**	**0.850**	**0.879**	**0.350**	**0.973**	**0.952**	**C**
SDBHNFMVP_5916	**0.090**	**0.343**	**0.640**	**0.605**	**0.615**	**0.285**	**0.688**	**0.608**	**0.511**	**0.074**	**0.202**	0.008	**0.021**	**0.312**	**0.342**	**0.104**	**0.112**	**0.866**	**0.752**	**C**
SDBHNFMVP_5917	**0.156**	**0.620**	**0.193**	**0.308**	**0.463**	**0.197**	**0.233**	**0.143**	**0.609**	**0.011**	0.010	**0.060**	0.000	**0.149**	**0.072**	**0.271**	0.008	**0.337**	**0.137**	**C**
SDBHNFMVP_5918	**0.091**	**0.369**	**0.218**	**0.389**	**0.414**	**0.080**	**0.202**	**0.073**	**0.440**	**0.015**	**0.016**	0.004	0.000	**0.081**	**0.033**	**0.067**	0.004	**0.306**	**0.118**	**C**
SDBHNFMVP_5919	**0.257**	**0.295**	**0.211**	**0.711**	**0.301**	**0.770**	**0.365**	**0.792**	**0.800**	0.003	0.007	0.000	0.000	**0.051**	**0.258**	**0.508**	0.003	**0.703**	**0.689**	**C**
SDBHNFMVP_5920	**0.339**	**0.861**	**0.636**	**0.912**	**0.878**	**0.875**	**0.899**	**0.931**	**0.952**	**0.045**	**0.230**	**0.016**	0.000	**0.513**	**0.607**	**0.895**	**0.125**	**0.954**	**0.921**	**C**
SDBHNFMVP_5921	**0.115**	**0.112**	**0.281**	**0.552**	**0.801**	**0.648**	**0.457**	**0.300**	**0.731**	0.001	0.007	0.000	0.000	**0.086**	0.006	**0.298**	0.001	**0.818**	**0.707**	**C**
UTUNFBSGP_1556	**0.064**	0.000	0.009	0.001	0.000	0.000	0.000	0.000	**0.011**	**0.571**	**0.344**	**0.484**	**0.163**	**0.083**	**0.025**	0.000	0.002	0.000	0.000	**A**
UTUNFBSGP_1557	**0.027**	0.000	0.000	0.001	0.000	0.002	0.000	0.000	0.000	**0.253**	**0.482**	**0.364**	0.001	**0.350**	**0.296**	0.000	**0.270**	0.000	0.000	**A**
UTUNFBSGP_1558	**0.027**	0.000	0.004	0.004	0.000	**0.021**	0.000	0.001	**0.014**	**0.715**	**0.305**	**0.803**	0.000	**0.659**	**0.814**	0.000	**0.757**	0.006	0.000	**A**
UTUNFBSGP_1559	**0.027**	0.000	0.001	0.002	0.000	0.000	0.000	0.000	0.001	**0.539**	**0.165**	0.010	0.000	**0.502**	**0.286**	0.000	**0.079**	0.000	0.000	**A**
UTUNFBSGP_1560	**0.027**	0.000	0.000	0.001	0.000	0.001	0.000	0.000	0.001	**0.018**	**0.283**	**0.219**	0.000	**0.203**	0.007	0.000	**0.011**	0.000	0.000	**A**
UTUNFBSGP_1561	**0.027**	0.000	0.000	0.001	0.000	0.005	0.000	0.000	0.002	**0.210**	**0.165**	**0.068**	0.000	**0.403**	**0.243**	0.000	**0.059**	0.000	0.000	**A**
UTUNFBSGP_1562	**0.027**	0.002	**0.013**	**0.021**	0.000	**0.060**	0.001	0.008	**0.036**	**0.368**	**0.408**	**0.320**	0.000	**0.657**	**0.279**	0.000	**0.245**	**0.029**	0.000	**A**
UTUNFBSGP_1563	**0.643**	**0.193**	**0.899**	**0.581**	**0.467**	**0.341**	**0.674**	**0.672**	**0.951**	**0.592**	**0.657**	**0.097**	0.005	**0.662**	**0.324**	**0.237**	**0.155**	**0.656**	**0.572**	**A**
UTUNFBSGP_1564	**0.028**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	**0.157**	**0.180**	**0.057**	0.001	**0.107**	0.002	0.000	0.001	0.000	0.000	**A**
UTUNFBSGP_1565	**0.045**	**0.011**	**0.027**	**0.048**	0.006	**0.112**	**0.063**	**0.016**	**0.088**	**0.687**	**0.695**	**0.092**	0.000	**0.664**	**0.792**	0.003	**0.222**	**0.050**	**0.027**	**A**
UTUNFBSGP_1566	**0.053**	**0.016**	**0.033**	**0.059**	**0.013**	**0.126**	**0.082**	**0.039**	**0.023**	**0.067**	**0.437**	**0.165**	0.000	**0.753**	**0.925**	0.006	**0.313**	**0.037**	0.007	**A**
UTUNFBSGP_1567	**0.030**	0.006	0.007	**0.018**	0.001	0.002	0.002	0.006	0.011	**0.106**	**0.195**	**0.020**	0.000	**0.191**	**0.044**	0.000	**0.037**	0.011	**0.013**	**A**
UTUNFBSGP_1568	**0.027**	0.001	0.003	0.010	0.000	0.001	0.000	0.010	**0.025**	**0.189**	**0.081**	**0.027**	0.000	**0.478**	**0.266**	0.000	**0.061**	**0.019**	0.005	**A**
UTUNFBSGP_1569	**0.027**	0.001	0.003	0.003	0.000	**0.017**	0.004	0.000	0.007	**0.448**	**0.628**	**0.407**	0.000	**0.775**	**0.540**	0.000	**0.231**	0.002	0.000	**A**
UTUNFBSGP_1570	**0.027**	0.000	0.000	0.001	0.000	0.001	0.000	0.000	0.001	**0.052**	**0.178**	**0.088**	0.000	**0.483**	**0.483**	0.000	**0.056**	0.000	0.000	**A**
UTUNFBSGP_1571	**0.030**	**0.016**	**0.158**	**0.061**	**0.040**	**0.029**	**0.051**	**0.046**	**0.048**	**0.475**	**0.385**	**0.041**	0.002	**0.621**	**0.399**	0.003	**0.259**	**0.047**	**0.048**	**A**
UTUNFBSGP_1572	**0.029**	0.005	0.006	0.009	0.002	**0.067**	0.006	**0.012**	0.004	**0.012**	**0.054**	**0.494**	0.000	**0.182**	**0.400**	0.001	**0.067**	**0.011**	0.001	**A**
UTUNFBSGP_1573	**0.027**	0.000	0.001	0.007	0.001	**0.013**	0.008	0.000	0.009	**0.128**	**0.165**	0.010	0.000	**0.043**	**0.032**	0.000	0.008	0.000	0.001	**A**
UTUNFBSGP_1574	**0.027**	0.001	0.001	**0.013**	0.000	0.001	0.000	0.002	0.002	**0.423**	**0.280**	**0.034**	0.000	**0.240**	**0.071**	0.000	**0.074**	0.000	0.000	**A**
UTUNFBSGP_1575	**0.028**	0.000	0.001	0.007	0.000	**0.035**	0.008	0.000	**0.012**	**0.254**	**0.500**	**0.384**	0.001	**0.855**	**0.860**	0.000	**0.257**	0.004	0.000	**A**
UTUNFBSGP_1576	**0.027**	0.000	0.002	0.001	0.000	0.000	0.000	0.000	0.001	**0.052**	**0.198**	**0.018**	0.002	**0.066**	0.000	0.000	0.000	0.000	0.000	**A**
UTUNFBSGP_1577	**0.027**	0.000	0.001	0.002	0.000	0.000	0.000	0.000	0.000	**0.449**	**0.258**	**0.067**	0.000	**0.521**	**0.676**	0.000	**0.247**	0.000	0.000	**A**
UTUNFBSGP_1578	**0.027**	0.003	0.009	**0.017**	0.001	0.007	0.002	0.003	**0.046**	**0.391**	**0.137**	0.009	0.000	**0.139**	**0.115**	0.001	**0.015**	0.002	0.002	**A**
UTUNFBSGP_1579	**0.016**	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.004	**0.021**	0.004	0.000	**0.075**	**0.031**	0.000	0.005	0.000	0.000	**A**
UTUNFBSGP_1580	**0.045**	0.010	**0.012**	**0.048**	0.005	**0.156**	**0.034**	**0.025**	**0.022**	**0.119**	**0.285**	**0.036**	0.000	**0.752**	**0.804**	0.002	**0.237**	**0.015**	0.007	**A**
UTUNFBSGP_1581	**0.041**	**0.069**	**0.097**	**0.171**	**0.033**	**0.025**	**0.132**	**0.200**	**0.168**	**0.434**	**0.599**	**0.444**	0.000	**0.936**	**0.643**	**0.037**	**0.467**	**0.229**	**0.101**	**A**
UTUNFBSGP_1582	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	**0.016**	**0.092**	**0.065**	0.000	**0.070**	0.010	0.000	0.001	0.000	0.000	**A**
UTUNFBSGP_1583	**0.027**	0.001	0.002	0.006	0.000	0.001	0.000	0.001	**0.038**	**0.100**	**0.172**	**0.089**	0.000	**0.430**	**0.375**	0.000	**0.069**	**0.038**	0.001	**A**
UTUNFBSGP_1584	**0.027**	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.001	**0.878**	**0.608**	**0.452**	0.000	**0.738**	**0.783**	0.000	**0.729**	0.000	0.000	**A**
UTUNFBSGP_1585	**0.015**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.032**	**0.206**	**0.177**	0.000	**0.423**	**0.214**	0.000	**0.061**	0.000	0.000	**A**
UTUNFBSGP_1586	**0.062**	**0.029**	**0.045**	**0.042**	**0.016**	**0.208**	**0.084**	**0.038**	**0.067**	**0.254**	**0.291**	**0.659**	0.000	**0.863**	**0.929**	**0.013**	**0.430**	**0.034**	**0.030**	**A**
UTUNFPoCP_0201	**0.032**	0.010	0.006	0.010	0.009	**0.103**	**0.062**	**0.050**	**0.030**	0.009	**0.064**	0.004	0.001	**0.089**	**0.062**	0.001	0.008	**0.015**	**0.019**	**A**

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
UTUNFPoCP_0202	**0.033**	**0.130**	**0.026**	**0.044**	**0.050**	**0.026**	**0.097**	**0.471**	**0.213**	0.002	0.005	0.000	0.000	**0.017**	0.003	**0.014**	0.000	**0.235**	**0.196**	**A**
UTUNFPoCP_1524	**0.061**	**0.017**	**0.016**	**0.181**	0.010	**0.037**	**0.070**	**0.291**	**0.081**	0.000	0.000	0.000	0.000	0.000	0.000	**0.094**	0.000	**0.034**	0.002	**C**
UTUNFPoCP_1525	**0.081**	**0.085**	**0.234**	**0.777**	**0.427**	**0.530**	**0.285**	**0.162**	**0.632**	0.001	0.007	0.000	0.000	**0.092**	0.007	**0.290**	0.003	**0.587**	**0.582**	**C**
UTUNFPoCP_1526	**0.027**	0.002	0.001	0.003	0.000	**0.015**	0.003	0.000	0.009	0.001	0.001	0.006	0.000	**0.081**	0.007	0.000	0.000	0.001	0.000	**A**
UTUNFPoCP_1527	**0.318**	**0.344**	**0.318**	**0.830**	**0.353**	**0.468**	**0.836**	**0.959**	**0.902**	0.005	**0.024**	0.001	0.000	**0.036**	**0.144**	**0.869**	0.002	**0.518**	**0.453**	**D**
UTUNFPoCP_1530	**0.100**	0.008	**0.043**	**0.032**	**0.031**	**0.015**	0.010	**0.030**	**0.093**	0.001	**0.012**	0.001	0.000	**0.034**	0.004	**0.028**	0.000	**0.202**	**0.025**	**C**
UTUNFPoCP_1531	**0.119**	**0.062**	**0.052**	**0.415**	**0.063**	**0.102**	**0.318**	**0.717**	**0.441**	0.000	0.001	0.000	0.000	0.001	0.004	**0.557**	0.000	**0.109**	**0.114**	**C**
UTUNFPoCP_1532	**0.028**	0.009	**0.019**	**0.116**	0.003	**0.020**	**0.025**	**0.080**	**0.017**	**0.423**	**0.289**	**0.034**	0.000	**0.522**	**0.393**	0.006	**0.155**	0.004	**0.016**	**A**
UTUNFPoCP_1533	**0.391**	**0.054**	**0.186**	**0.375**	**0.089**	**0.196**	**0.065**	**0.205**	**0.335**	0.001	0.001	0.000	0.000	0.000	0.002	**0.025**	0.000	**0.204**	**0.065**	**D**
UTUNFPoCP_1534	**0.027**	0.002	0.003	**0.018**	0.000	0.006	0.000	0.010	0.009	**0.112**	0.010	**0.035**	0.000	**0.236**	**0.262**	0.002	0.007	0.001	0.000	**A**
UTUNFPoCP_1536	**0.051**	**0.095**	**0.070**	**0.260**	**0.087**	**0.145**	**0.087**	**0.112**	**0.233**	**0.015**	**0.077**	0.003	0.000	**0.067**	**0.225**	**0.083**	0.005	**0.144**	**0.114**	**D**
UTUNFPoCP_1537	**0.312**	**0.803**	**0.743**	**0.837**	**0.792**	**0.869**	**0.955**	**0.909**	**0.952**	**0.564**	**0.563**	**0.079**	0.001	**0.829**	**0.901**	**0.664**	**0.539**	**0.918**	**0.857**	**C**
UTUNFPoCP_1538	**0.027**	0.000	0.002	0.002	0.000	0.002	0.000	0.000	0.008	**0.035**	**0.105**	**0.016**	0.000	**0.296**	**0.172**	0.000	**0.044**	0.001	0.000	**A**
UTUNFPoCP_1539	**0.036**	**0.012**	**0.015**	**0.156**	0.007	**0.142**	**0.089**	**0.103**	**0.045**	**0.744**	**0.876**	**0.770**	0.002	**0.981**	**0.934**	**0.027**	**0.814**	**0.020**	**0.018**	**A**
UTUNFPoCP_1541	**0.028**	0.000	0.002	0.005	0.000	**0.015**	0.005	0.000	**0.013**	**0.187**	**0.552**	**0.317**	0.000	**0.663**	**0.822**	0.000	**0.410**	**0.014**	0.000	**A**
UTUNFPoCP_1542	**0.220**	0.002	**0.168**	**0.237**	**0.027**	**0.042**	**0.083**	**0.054**	**0.487**	0.001	0.000	0.000	0.000	0.001	0.000	**0.021**	0.000	**0.067**	**0.029**	**D**
UTUNFPoCP_1543	**0.027**	0.000	0.000	0.001	0.000	0.001	0.000	0.000	0.001	0.001	**0.046**	**0.027**	0.000	**0.036**	**0.012**	0.000	0.000	0.000	0.000	**A**
UTUNFPoCP_1544	**0.101**	**0.055**	**0.041**	**0.342**	**0.051**	**0.028**	**0.299**	**0.274**	**0.369**	0.000	0.000	0.000	0.000	0.001	0.001	**0.177**	0.000	**0.046**	**0.024**	**D**
UTUNFPoCP_1546	**0.080**	**0.428**	**0.190**	**0.628**	**0.305**	**0.300**	**0.334**	**0.422**	**0.763**	**0.025**	**0.065**	0.000	0.000	**0.018**	0.010	**0.276**	0.004	**0.336**	**0.435**	**B**
UTUNFPoCP_1547	**0.041**	0.003	0.003	**0.151**	0.001	0.006	**0.013**	**0.168**	**0.164**	0.002	0.005	0.000	0.000	0.010	0.003	**0.018**	0.000	**0.015**	**0.016**	**D**
UTUNFPoCP_1548	**0.027**	0.000	0.006	0.001	0.000	0.003	0.000	0.000	0.006	**0.581**	**0.047**	**0.157**	0.000	**0.249**	**0.437**	0.000	**0.069**	0.003	0.001	**A**
UTUNFPoCP_1549	**0.035**	0.003	**0.011**	**0.106**	0.001	**0.026**	**0.019**	**0.281**	**0.121**	**0.062**	**0.056**	0.003	0.000	**0.142**	**0.115**	0.006	0.009	**0.043**	**0.068**	**B**
UTUNFPoCP_1550	**0.090**	**0.093**	**0.048**	**0.488**	**0.038**	**0.196**	**0.230**	**0.490**	**0.469**	0.000	0.000	0.000	0.000	0.000	0.000	**0.229**	0.000	**0.104**	**0.081**	**D**
UTUNFPoCP_1551	**0.027**	0.000	0.003	0.004	0.000	0.000	0.000	0.003	0.001	**0.953**	**0.595**	**0.340**	0.001	**0.785**	**0.552**	0.000	**0.574**	0.001	0.000	**A**
UTUNFPoCP_1552	**0.062**	0.000	0.001	**0.024**	0.000	0.001	0.005	0.003	**0.048**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	**D**
UTUNFPoCP_1553	**0.027**	0.000	0.001	0.008	0.000	0.002	0.000	0.004	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**B**
UTUNFPoCP_1554	**0.110**	**0.134**	**0.114**	**0.529**	**0.104**	**0.063**	**0.568**	**0.816**	**0.645**	**0.061**	**0.144**	0.010	0.000	**0.301**	**0.168**	**0.479**	**0.052**	**0.360**	**0.228**	**B**
UTUNFPoCP_1555	**0.027**	0.002	0.002	**0.030**	0.002	0.001	**0.015**	0.006	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**D**
UTWCNFSCQ_2055	**0.054**	0.005	**0.014**	**0.359**	**0.029**	**0.364**	**0.038**	0.008	**0.215**	0.003	**0.018**	0.007	0.000	**0.215**	**0.032**	0.004	0.006	**0.391**	**0.026**	**B**
UTWCNFSCQ_2056	**0.030**	**0.020**	**0.043**	**0.047**	**0.015**	**0.019**	**0.024**	**0.050**	**0.204**	0.002	0.001	0.000	0.000	0.000	0.003	0.005	0.000	**0.104**	**0.087**	**B**
UTWCNFSCQ_2057	**0.041**	**0.033**	**0.023**	**0.209**	**0.015**	**0.051**	**0.253**	**0.259**	**0.068**	0.000	0.000	0.000	0.000	0.000	0.000	**0.025**	0.000	**0.013**	**0.065**	**B**
UTWCNFSCQ_2058	**0.044**	**0.084**	**0.026**	**0.176**	**0.074**	**0.019**	**0.081**	**0.023**	**0.119**	**0.016**	0.006	0.000	0.000	**0.012**	0.001	0.002	0.000	**0.028**	0.005	**B**
UTWCNFSCQ_2059	**0.054**	**0.051**	**0.066**	**0.128**	**0.033**	**0.415**	**0.025**	**0.285**	**0.206**	0.004	0.001	0.006	0.000	**0.026**	**0.165**	**0.074**	0.003	**0.188**	**0.285**	**B**
UTWCNFSCQ_2060	**0.210**	**0.552**	**0.333**	**0.654**	**0.405**	**0.316**	**0.646**	**0.288**	**0.791**	0.011	**0.035**	0.001	0.000	**0.107**	**0.099**	**0.169**	0.005	**0.522**	**0.155**	**B**
UTWCNFSCQ_2061	**0.031**	**0.036**	**0.268**	**0.127**	**0.091**	**0.123**	**0.055**	**0.137**	**0.064**	**0.023**	**0.071**	**0.032**	0.000	**0.033**	**0.072**	0.006	0.006	**0.129**	**0.180**	**B**
UTWCNFSCQ_2062	**0.106**	**0.176**	**0.168**	**0.371**	**0.081**	**0.387**	**0.214**	**0.175**	**0.522**	**0.020**	0.010	0.000	0.000	0.003	**0.046**	**0.061**	0.000	**0.257**	**0.076**	**B**
UTWCNFSCQ_2063	**0.099**	**0.056**	**0.029**	**0.390**	**0.059**	**0.124**	**0.118**	**0.422**	**0.084**	0.001	0.000	0.000	0.000	0.005	**0.030**	**0.109**	0.000	**0.116**	**0.019**	**B**
UTWCNFSCQ_2064	**0.054**	**0.021**	**0.039**	**0.135**	**0.014**	**0.108**	**0.024**	**0.085**	**0.290**	**0.111**	**0.064**	0.000	0.000	**0.188**	**0.321**	**0.021**	**0.024**	**0.182**	**0.132**	**B**
UTWCNFSCQ_2065	**0.080**	**0.139**	**0.152**	**0.227**	**0.138**	**0.165**	**0.300**	**0.311**	**0.404**	**0.104**	**0.093**	0.001	0.000	**0.051**	**0.033**	**0.080**	0.006	**0.212**	**0.364**	**B**
UTWCNFSCQ_2066	**0.107**	**0.373**	**0.479**	**0.318**	**0.301**	**0.739**	**0.272**	**0.574**	**0.499**	**0.069**	**0.046**	**0.143**	0.000	**0.145**	**0.552**	**0.260**	**0.045**	**0.564**	**0.606**	**B**
UTWCNFSCQ_2067	**0.250**	**0.771**	**0.484**	**0.629**	**0.650**	**0.668**	**0.480**	**0.510**	**0.897**	**0.278**	**0.186**	**0.093**	0.000	**0.477**	**0.589**	**0.626**	**0.132**	**0.702**	**0.544**	**B**

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
UTWCNFSCQ_2068	**0.195**	**0.177**	**0.131**	**0.701**	**0.183**	**0.229**	**0.388**	**0.593**	**0.697**	0.001	0.010	0.000	0.000	0.006	**0.026**	**0.624**	0.000	**0.244**	**0.206**	**B**
UTWCNFSCQ_2069	**0.276**	**0.851**	**0.391**	**0.650**	**0.770**	**0.361**	**0.504**	**0.299**	**0.819**	0.002	0.002	0.007	0.000	**0.036**	**0.066**	**0.428**	0.001	**0.584**	**0.284**	**B**
UTWCNFSCQ_2070	**0.054**	**0.059**	**0.024**	**0.181**	**0.053**	**0.023**	**0.079**	**0.043**	**0.296**	0.002	0.003	0.000	0.000	0.008	0.001	0.008	0.000	**0.046**	**0.026**	**B**
UTWCNFSCQ_2071	**0.028**	0.000	0.000	**0.029**	0.000	**0.017**	**0.017**	0.006	**0.088**	0.001	0.009	0.001	0.000	0.001	0.000	0.000	0.000	**0.012**	0.000	**B**
UTWCNFSCQ_2072	**0.027**	**0.022**	**0.033**	**0.041**	0.002	**0.012**	0.002	**0.056**	**0.061**	0.001	0.002	0.000	0.000	0.005	0.000	0.000	0.000	**0.076**	0.002	**B**
UTWCNFSCQ_2073	**0.222**	**0.839**	**0.539**	**0.552**	**0.776**	**0.607**	**0.655**	**0.784**	**0.961**	**0.091**	**0.063**	0.010	0.000	**0.171**	**0.189**	**0.676**	**0.029**	**0.774**	**0.740**	**B**
UTWCNFSCQ_2074	**0.088**	**0.439**	**0.294**	**0.256**	**0.367**	**0.239**	**0.324**	**0.451**	**0.777**	**0.031**	0.004	0.003	0.000	0.004	0.011	**0.195**	0.000	**0.328**	**0.374**	**B**
UTWCNFSCQ_2075	**0.029**	**0.015**	0.007	**0.044**	0.001	0.005	0.004	**0.026**	**0.068**	0.000	0.000	0.000	0.000	0.005	0.000	0.001	0.000	0.004	0.000	**B**
UTWCNFSCQ_2076	**0.027**	**0.015**	**0.016**	**0.024**	0.001	0.011	0.001	**0.036**	**0.054**	0.004	0.003	0.000	0.000	0.001	0.000	0.000	0.000	0.007	0.002	**B**
UTWCNFSCQ_2077	**0.084**	**0.012**	**0.082**	**0.458**	**0.098**	**0.337**	**0.233**	**0.029**	**0.589**	0.003	0.011	0.001	0.000	**0.023**	0.000	**0.020**	0.000	**0.134**	**0.123**	**B**
UTWCNFSCQ_2078	**0.111**	**0.012**	**0.015**	**0.265**	0.004	**0.162**	**0.223**	**0.118**	**0.366**	0.001	0.000	0.000	0.000	0.000	0.002	**0.020**	0.000	**0.020**	0.008	**B**
UTWCNFSCQ_2079	**0.056**	**0.162**	**0.164**	**0.517**	**0.028**	**0.226**	**0.147**	**0.742**	**0.566**	0.001	0.003	0.001	0.000	**0.017**	0.007	**0.122**	0.000	**0.223**	**0.056**	**B**
UTWCNFSCQ_2080	**0.035**	**0.129**	**0.052**	**0.094**	**0.080**	**0.018**	**0.133**	**0.044**	**0.162**	0.001	0.000	0.000	0.000	0.000	0.000	0.005	0.000	**0.019**	**0.036**	**D**
UTWCNFSCQ_2081	**0.161**	**0.708**	**0.325**	**0.492**	**0.774**	**0.575**	**0.658**	**0.868**	**0.855**	0.001	0.003	0.000	0.000	0.000	0.002	**0.363**	0.000	**0.691**	**0.700**	**B**
UTWCNFSCQ_2082	**0.053**	**0.020**	**0.018**	**0.088**	0.008	**0.044**	**0.088**	**0.267**	**0.238**	0.006	0.000	0.000	0.000	0.004	0.005	**0.109**	0.000	**0.023**	**0.012**	**B**
UTWCNFSCQ_2083	**0.029**	0.000	0.000	0.011	0.000	0.007	0.002	0.006	**0.038**	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	**B**
UTWCNFSCQ_2085	**0.035**	0.006	0.006	**0.085**	0.003	**0.016**	**0.037**	**0.151**	**0.245**	0.001	0.000	0.000	0.000	0.000	0.000	**0.046**	0.000	0.008	0.009	**D**
UTWCNFSCQ_2086	**0.033**	0.011	**0.055**	**0.161**	**0.121**	**0.034**	**0.025**	**0.026**	**0.056**	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	**0.130**	**0.021**	**D**
UTWCNFSCQ_2087	**0.030**	**0.085**	**0.094**	**0.132**	0.011	**0.086**	**0.030**	**0.189**	**0.219**	**0.022**	**0.019**	0.000	0.000	**0.031**	0.002	0.004	0.000	**0.094**	**0.051**	**B**
UTWCNFSCQ_2088	**0.027**	0.003	0.002	**0.055**	0.001	**0.015**	0.002	**0.097**	**0.055**	0.001	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.001	0.001	**B**
UTWCNFSCQ_2089	**0.128**	**0.114**	**0.042**	**0.195**	**0.108**	**0.551**	**0.298**	**0.199**	**0.546**	0.005	0.003	0.010	0.000	**0.023**	0.010	**0.058**	0.001	**0.152**	**0.129**	**D**
UTWCNFSCQ_2090	**0.066**	0.011	0.006	**0.131**	0.009	**0.113**	**0.244**	**0.177**	**0.278**	0.004	0.003	0.000	0.000	0.003	0.001	**0.017**	0.000	**0.018**	**0.021**	**D**
UTWCNFSCQ_2091	**0.087**	**0.137**	**0.110**	**0.262**	**0.155**	**0.124**	**0.135**	**0.241**	**0.132**	0.001	0.002	0.000	0.000	0.000	0.003	**0.070**	0.000	**0.207**	**0.119**	**B**
UTWCNFSCQ_2092	**0.057**	0.005	0.005	**0.108**	**0.013**	**0.013**	**0.068**	**0.051**	**0.337**	0.001	0.000	0.001	0.000	0.000	0.004	0.010	0.000	0.006	**0.062**	**B**
UTWCNFSCQ_2093	**0.035**	**0.079**	**0.058**	**0.287**	**0.011**	**0.068**	**0.044**	**0.500**	**0.389**	0.000	0.000	0.000	0.000	0.000	0.000	**0.050**	0.000	**0.083**	**0.025**	**B**
UTWCNFSCQ_2094	**0.108**	**0.053**	**0.071**	**0.336**	**0.047**	**0.099**	**0.391**	**0.682**	**0.441**	0.007	0.006	0.000	0.000	0.006	**0.018**	**0.346**	0.000	**0.091**	**0.094**	**B**
UTWCNFSCQ_2095	**0.383**	**0.921**	**0.785**	**0.931**	**0.925**	**0.928**	**0.973**	**0.963**	**0.981**	**0.187**	**0.440**	**0.048**	0.000	**0.756**	**0.850**	**0.879**	**0.350**	**0.973**	**0.952**	**B**
UTWCNFYPP_2096	**0.013**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.066**	0.004	0.008	0.000	**0.038**	**0.026**	0.000	**0.015**	0.000	0.000	**A**
UTWCNFYPP_2097	**0.027**	0.000	0.000	0.002	0.000	0.005	0.000	0.000	0.000	0.001	0.007	**0.093**	0.000	0.001	**0.026**	0.000	0.001	0.005	0.000	**A**
UTWCNFYPP_2098	**0.027**	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.001	**0.145**	**0.054**	0.000	0.000	**0.082**	**0.163**	0.000	**0.028**	0.000	0.000	**A**
UTWCNFYPP_2099	**0.027**	0.000	0.000	**0.023**	0.000	0.007	0.005	0.007	**0.050**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	**A**
UTWCNFYPP_2100	**0.027**	0.001	0.005	**0.040**	0.000	0.009	0.000	**0.030**	0.006	**0.216**	**0.438**	**0.317**	0.000	**0.689**	**0.485**	0.004	**0.321**	0.002	0.002	**A**
UTWCNFYPP_2101	**0.054**	**0.027**	**0.078**	**0.206**	**0.018**	**0.524**	**0.208**	**0.119**	**0.363**	**0.664**	**0.811**	**0.281**	0.001	**0.788**	**0.910**	0.009	**0.948**	**0.479**	**0.108**	**A**
UTWCNFYPP_2102	**0.027**	0.000	0.001	0.005	0.000	0.005	0.000	0.000	**0.055**	**0.739**	**0.197**	**0.093**	0.000	**0.236**	**0.262**	0.000	**0.082**	0.009	0.000	**A**
UTWCNFYPP_2103	**0.027**	0.000	0.000	0.001	0.000	0.002	0.000	0.000	0.000	**0.095**	**0.074**	**0.041**	0.000	**0.179**	**0.041**	0.000	**0.018**	0.000	0.000	**A**
UTWCNFYPP_2104	**0.018**	0.000	0.001	0.002	0.000	0.000	0.000	0.001	0.000	**0.951**	**0.696**	**0.643**	0.000	**0.781**	**0.487**	0.000	**0.786**	0.000	0.000	**A**
UTWCNFYPP_2105	0.011	0.000	0.000	0.001	0.000	0.000	0.000	0.001	0.000	0.004	**0.014**	0.006	0.000	**0.019**	0.001	0.000	0.001	0.000	0.000	**A**
UTWCNFYPP_2106	**0.027**	0.001	0.002	**0.016**	0.000	0.000	0.000	0.003	0.002	**0.148**	**0.176**	**0.104**	0.000	**0.727**	**0.285**	0.000	**0.069**	0.001	0.000	**A**
UTWCNFYPP_2107	**0.027**	0.000	0.001	0.002	0.000	0.002	0.000	0.000	0.002	**0.065**	**0.209**	**0.167**	0.000	**0.155**	**0.059**	0.000	**0.074**	0.001	0.000	**A**
UTWCNFYPP_2108	**0.179**	0.003	**0.064**	**0.112**	0.004	**0.039**	**0.027**	0.010	**0.305**	**0.387**	**0.783**	**0.180**	0.002	**0.462**	**0.225**	0.001	**0.110**	**0.089**	0.007	**A**
UTWCNFYPP_2109	**0.027**	0.001	0.008	0.006	0.000	**0.011**	0.009	0.010	0.006	**0.664**	**0.845**	**0.716**	0.002	**0.649**	**0.472**	0.000	**0.768**	0.006	0.010	**A**

Assigned tree	AZ-ASNF-17-N	AZ-CoNF-Co-N	AZ-KaNF-Ka-N	CO-GMUG-SM-N	CO-RGNF-LW-N	CO-SJNF-8m-N	CO-SJNF-BD-N	CO-SJNF-PR-N	CO-SJNF-SN-N	MT-BiNF-BC-N	MT-BiNF-CC-N	MT-BiNF-PC-N	OR-OcNF-PF-N	OR-UmNF-Um-N	OR-WWNF-LG-N	SD-BHNF-BS-N	WA-WeNF-We-N	WY-MBNF-WC-N	WY-MBNF-WR-N	mtDNA
UTWCNFYPP_2110	**0.016**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.513**	**0.344**	**0.283**	0.000	**0.455**	**0.160**	0.000	**0.278**	0.000	0.000	**A**
UTWCNFYPP_2111	**0.027**	0.000	0.005	0.003	0.000	0.000	0.000	0.003	0.001	**0.432**	**0.441**	**0.516**	0.000	**0.378**	**0.215**	0.000	**0.347**	0.003	0.000	**A**
UTWCNFYPP_2112	**0.027**	0.004	**0.048**	**0.013**	0.000	**0.021**	0.000	**0.021**	**0.012**	**0.065**	**0.139**	**0.017**	0.000	**0.483**	**0.064**	0.000	**0.043**	0.006	0.001	**A**
UTWCNFYPP_2113	**0.027**	0.000	0.001	0.006	0.000	0.001	0.000	0.004	0.000	**0.155**	**0.208**	**0.421**	0.000	**0.171**	**0.164**	0.000	**0.130**	0.000	0.000	**A**
UTWCNFYPP_2114	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.061**	**0.026**	**0.048**	0.000	**0.016**	0.003	0.000	0.002	0.000	0.000	**A**
UTWCNFYPP_2115	**0.012**	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.004	0.001	0.000	0.000	0.000	0.000	**A**
UTWCNFYPP_2116	**0.099**	**0.070**	0.000	**0.159**	**0.033**	**0.262**	**0.354**	0.005	0.007	**0.042**	**0.365**	**0.562**	0.009	**0.876**	**1.000**	**0.015**	**0.795**	**0.370**	0.005	**A**
UTWCNFYPP_2117	**0.027**	0.003	**0.013**	**0.017**	0.004	0.010	0.003	0.007	**0.014**	0.007	**0.041**	0.003	0.000	**0.109**	**0.029**	0.007	0.006	0.004	0.003	**A**
UTWCNFYPP_2118	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.150**	**0.180**	**0.202**	0.000	**0.271**	**0.262**	0.000	**0.121**	0.000	0.000	**A**
UTWCNFYPP_2119	**0.033**	0.011	**0.023**	**0.018**	0.003	**0.277**	**0.033**	**0.030**	**0.041**	**0.267**	**0.126**	**0.332**	0.000	**0.274**	**0.509**	0.002	**0.112**	**0.021**	**0.016**	**A**
UTWCNFYPP_2120	**0.027**	0.001	0.008	0.003	0.000	**0.046**	0.000	0.004	0.004	**0.322**	**0.257**	**0.180**	0.000	**0.179**	**0.677**	0.000	**0.131**	0.007	0.003	**A**
UTWCNFYPP_2121	**0.027**	0.000	0.000	0.002	0.000	0.002	0.000	0.000	0.001	0.008	**0.041**	0.002	0.000	**0.040**	**0.046**	0.000	**0.043**	0.002	0.000	**A**
UTWCNFYPP_2122	**0.027**	0.003	0.005	**0.028**	0.001	0.001	0.006	**0.051**	**0.021**	**0.249**	**0.093**	**0.022**	0.001	**0.172**	**0.050**	0.001	**0.027**	**0.035**	**0.012**	**A**
UTWCNFYPP_2123	**0.017**	0.000	0.000	0.001	0.000	0.001	0.000	0.000	0.000	**0.016**	**0.105**	0.008	0.000	**0.035**	0.008	0.000	0.001	0.000	0.000	**A**
UTWCNFYPP_2124	**0.036**	0.011	**0.021**	**0.058**	0.005	**0.195**	**0.025**	**0.031**	**0.061**	**0.278**	**0.197**	**0.831**	0.000	**0.405**	**0.679**	0.002	**0.488**	**0.211**	0.007	**A**
UTWCNFYPP_2125	**0.014**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.464**	**0.248**	**0.019**	0.000	**0.023**	**0.026**	0.000	**0.099**	0.000	0.000	**A**
UTWCNFYPP_2126	**0.018**	0.000	0.002	0.001	0.000	0.000	0.000	0.000	0.000	**0.148**	**0.036**	**0.281**	0.000	**0.154**	**0.020**	0.000	**0.043**	0.000	0.000	**A**
UTWCNFYPP_2127	**0.012**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.027**	**0.042**	0.004	0.000	**0.133**	0.010	0.000	0.002	0.000	0.000	**A**
UTWCNFYPP_2128	**0.025**	0.000	0.000	0.001	0.000	0.003	0.000	0.000	0.000	**0.039**	**0.136**	**0.074**	0.000	**0.182**	**0.109**	0.000	**0.028**	0.000	0.000	**A**
UTWCNFYPP_2129	**0.019**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.342**	**0.511**	**0.352**	0.000	**0.584**	**0.514**	0.000	**0.336**	0.000	0.000	**A**
UTWCNFYPP_2130	**0.027**	0.000	0.002	0.003	0.000	0.008	0.000	0.000	0.006	**0.430**	**0.619**	**0.554**	0.001	**0.230**	**0.138**	0.000	**0.630**	0.005	0.000	**A**
UTWCNFYPP_2131	**0.052**	**0.037**	**0.087**	**0.105**	**0.028**	**0.560**	**0.228**	**0.157**	**0.096**	**0.254**	**0.768**	**0.221**	0.000	**0.850**	**0.928**	**0.019**	**0.717**	**0.110**	**0.153**	**A**
UTWCNFYPP_2132	**0.052**	**0.015**	**0.019**	**0.068**	0.007	**0.043**	**0.044**	0.003	**0.176**	**0.353**	**0.121**	**0.370**	0.000	**0.524**	**0.374**	0.001	**0.192**	**0.070**	0.001	**A**
UTWCNFYPP_2133	**0.019**	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	**0.105**	**0.268**	**0.159**	0.000	**0.521**	**0.293**	0.000	**0.096**	0.000	0.000	**A**
UTWCNFYPP_2134	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.564**	**0.057**	**0.116**	0.000	**0.031**	**0.243**	0.000	**0.018**	0.000	0.000	**A**
UTWCNFYPP_2135	**0.039**	**0.023**	**0.047**	**0.032**	0.011	**0.368**	**0.078**	**0.059**	**0.057**	**0.664**	**0.463**	**0.906**	0.000	**0.812**	**0.888**	0.006	**0.730**	**0.044**	**0.061**	**A**
UTWCNFYPP_2136	**0.027**	0.000	0.000	0.002	0.000	0.004	0.000	0.000	**0.024**	**0.266**	**0.015**	0.005	0.000	**0.041**	**0.036**	0.000	0.008	0.001	0.000	**A**
UTWCNFYPP_2137	**0.016**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.001	0.000	0.003	0.000	0.000	0.000	0.000	0.000	**A**
UTWCNFYPP_2138	**0.029**	0.002	0.005	**0.038**	0.001	**0.031**	**0.012**	**0.019**	0.009	**0.850**	**0.899**	**0.836**	0.002	**0.996**	**0.974**	0.003	**0.878**	0.002	0.001	**A**
UTWCNFYPP_2139	**0.027**	0.000	0.001	0.006	0.000	**0.027**	0.000	0.000	0.011	**0.079**	**0.470**	**0.425**	0.000	**0.264**	**0.392**	0.000	**0.492**	0.010	0.000	**A**
UTWCNFYPP_2140	**0.028**	0.006	0.011	**0.047**	0.001	0.002	**0.012**	**0.023**	**0.026**	**0.723**	**0.266**	**0.163**	0.000	**0.706**	**0.297**	0.001	**0.091**	**0.018**	0.007	**A**
UTWCNFYPP_2141	0.006	0.000	0.001	0.000	0.000	0.001	0.000	0.000	0.000	**0.181**	**0.262**	**0.178**	0.000	**0.320**	**0.023**	0.000	**0.061**	0.000	0.000	**A**
UTWCNFYPP_2142	**0.027**	0.003	0.002	**0.068**	0.001	**0.032**	0.008	**0.026**	0.006	**0.082**	**0.195**	**0.221**	0.000	**0.273**	**0.210**	0.004	**0.171**	0.003	0.000	**A**

Criterion: Rannala & Mountain (1997)
Simulation algorithm: Paetkau et al. (2004)
Number of simulated individuals: 10000

Significant P-values are highlighted by bold, and P-values above 0.5 are highlighted by green.

Table 10. Clusters inferred by Structure

K	Ln	adjL = lnL - minL	exp(adjL)	dK = aep(adjL)/sum(adjL)
2	-13914.1	-611.5	2.68E-266	2.6849E-266
3	-13641.6	-339	5.95E-148	5.9453E-148
4	-13552.5	-249.9	2.95E-109	2.9499E-109
5	-13327.9	-25.3	1.029E-11	1.02884E-11
6	**-13302.6**	**0**	**1**	**1**
7	-13346.1	-43.5	1.283E-19	1.28289E-19
8	-13476.1	-173.5	4.466E-76	4.46588E-76

Table 11. Proportion of membership of each pre-defined population in each of the 6 clusters inferred in the population structure analysis using the Structure v.2.1 software

#	Pops	1	2	3	4	5	6	Inds
20	MT-BiNF-BC-N	**0.909**	0.015	0.037	0.013	0.014	0.013	10
21	MT-BiNF-CC-N	**0.845**	0.020	0.086	0.016	0.015	0.018	10
22	MT-BiNF-PC-N	**0.923**	0.013	0.025	0.012	0.013	0.013	10
23	OR-OcNF-PF-N	**0.746**	0.012	0.193	0.020	0.011	0.018	30
24	OR-UmNF-Um-N	**0.822**	0.033	0.038	0.036	0.037	0.034	30
25	OR-WWNF-LG-N	**0.774**	0.050	0.019	0.050	0.059	0.047	29
28	UT-UNF-BSG-P	**0.808**	0.039	0.040	0.031	0.040	0.042	31
31	UT-WCNF-YP-P	**0.809**	0.053	0.017	0.038	0.050	0.033	47
32	WA-WeNF-We-N	**0.854**	0.035	0.013	0.033	0.038	0.028	30
26	SD-BHNF-BS-N	0.016	**0.303**	0.046	0.149	0.282	0.203	35
29	UT-UNF-PoC-P	0.267	**0.325**	0.089	0.124	0.128	0.065	29
30	UT-WCNF-SC-Q	0.033	**0.439**	0.032	0.219	0.133	0.145	40
1	AZ-ASNF-17-N	0.019	0.036	**0.832**	0.036	0.040	0.037	70
3	AZ-KaNF-Ka-N	0.062	0.097	**0.517**	0.118	0.069	0.138	27
18	CO-SJNF-SN-N	0.022	0.225	**0.318**	0.116	0.167	0.152	30
19	CO-SJNF-SP-P	0.030	0.223	**0.295**	0.126	0.231	0.094	29
7	CO-BLM-VM60P	0.015	0.226	0.053	**0.310**	0.150	0.246	34
8	CO-BLM-VM70P	0.026	0.149	0.050	**0.285**	0.249	0.241	32
15	CO-SJNF-BD-N	0.034	0.197	0.070	**0.252**	0.248	0.199	31
16	CO-SJNF-Na-P	0.020	0.139	0.061	**0.362**	0.124	0.294	31
2	AZ-CoNF-Co-N	0.020	0.196	0.031	0.224	**0.270**	0.259	29
4	CO-BLM-AM60P	0.037	0.140	0.236	0.121	**0.243**	0.224	29
6	CO-BLM-AM90P	0.027	0.210	0.029	0.149	**0.328**	0.258	30
13	CO-SJNF-8m-N	0.093	0.231	0.041	0.148	**0.312**	0.176	30
14	CO-SJNF-8m-P	0.043	0.148	0.204	0.148	**0.269**	0.188	30
17	CO-SJNF-PR-N	0.029	0.255	0.084	0.150	**0.361**	0.121	29
33	WY-MBNF-WC-N	0.071	0.178	0.062	0.216	**0.255**	0.217	32
34	WY-MBNF-WR-N	0.048	0.146	0.061	0.236	**0.274**	0.235	30
5	CO-BLM-AM70P	0.026	0.165	0.153	0.179	0.237	**0.239**	29
9	CO-GMUG-DN-P	0.037	0.184	0.026	0.261	0.160	**0.332**	30
10	CO-GMUG-SM-N	0.026	0.265	0.078	0.215	0.147	**0.269**	30
11	CO-GMUG-Tr-P	0.023	0.116	0.054	0.315	0.069	**0.422**	30
12	CO-RGNF-LW-N	0.018	0.123	0.068	0.196	0.290	**0.305**	33
27	SD-BHNF-MV-P	0.015	0.096	0.025	0.278	0.218	**0.367**	30

Regional Areas of the Forest Service:
red – #1 Northern Region (MT, WY, SD);
blue - #2 Rocky Mountain Region (CO, WY, SD)
pink - #3 Southwestern Region (AZ)
brown - #6 PACIFIC NORTHWEST REGION (WA, OR);

Table 12. Proportion of membership of each individual tree in each of the 6 clusters inferred in the population structure analysis using the Structure v.2.1 software

Individual tree	Pop.#	1	2	3	4	5	6
AZASNF17N_2322	1	0.010	0.019	**0.924**	0.012	0.021	0.014
AZASNF17N_2323	1	0.005	0.010	**0.938**	0.012	0.020	0.015
AZASNF17N_2324	1	0.008	0.013	**0.928**	0.016	0.013	0.023
AZASNF17N_2325	1	0.008	0.023	**0.927**	0.012	0.014	0.016
AZASNF17N_2326	1	0.015	0.034	**0.708**	0.149	0.018	0.076
AZASNF17N_2327	1	0.009	0.018	**0.915**	0.015	0.022	0.021
AZASNF17N_2328	1	0.008	0.049	**0.865**	0.033	0.013	0.031
AZASNF17N_2329	1	0.007	0.043	**0.898**	0.017	0.016	0.019
AZASNF17N_2330	1	0.006	0.061	**0.862**	0.035	0.016	0.021
AZASNF17N_2331	1	0.009	0.035	**0.915**	0.015	0.012	0.015
AZASNF17N_2332	1	0.032	0.193	0.271	0.065	0.250	0.190
AZASNF17N_2333	1	0.017	0.020	**0.901**	0.017	0.024	0.022
AZASNF17N_2334	1	0.116	0.040	**0.806**	0.015	0.010	0.013
AZASNF17N_2335	1	0.007	0.011	**0.686**	0.269	0.012	0.015
AZASNF17N_2336	1	0.025	0.181	**0.732**	0.043	0.012	0.008
AZASNF17N_2337	1	0.011	0.015	**0.905**	0.017	0.037	0.016
AZASNF17N_2338	1	0.015	0.028	**0.903**	0.014	0.016	0.025
AZASNF17N_2339	1	0.011	0.038	**0.694**	0.047	0.129	0.081
AZASNF17N_2340	1	0.008	0.016	**0.916**	0.015	0.027	0.019
AZASNF17N_2341	1	0.012	0.018	**0.913**	0.016	0.023	0.019
AZASNF17N_2342	1	0.017	0.027	**0.841**	0.017	0.065	0.033
AZASNF17N_2343	1	0.013	0.028	**0.898**	0.014	0.017	0.031
AZASNF17N_2344	1	0.010	0.029	**0.880**	0.021	0.032	0.028
AZASNF17N_2345	1	0.010	0.019	**0.889**	0.026	0.029	0.028
AZASNF17N_2346	1	0.012	0.090	0.055	0.219	**0.353**	0.271
AZASNF17N_2347	1	0.015	0.125	**0.421**	0.195	0.154	0.091
AZASNF17N_2348	1	0.010	0.018	**0.924**	0.014	0.019	0.016
AZASNF17N_2349	1	0.034	0.032	**0.856**	0.023	0.038	0.018
AZASNF17N_2350	1	0.021	0.084	**0.601**	0.062	0.110	0.122
AZASNF17N_2351	1	0.011	0.027	**0.904**	0.014	0.016	0.028
AZASNF17N_2352	1	0.013	0.033	**0.892**	0.018	0.016	0.027
AZASNF17N_2353	1	0.009	0.015	**0.921**	0.017	0.018	0.021
AZASNF17N_2354	1	0.025	0.070	**0.665**	0.030	0.124	0.086
AZASNF17N_2355	1	0.041	0.040	**0.865**	0.020	0.011	0.023
AZASNF17N_2356	1	0.015	0.051	**0.617**	0.065	0.075	0.178
AZASNF17N_2357	1	0.014	0.023	**0.822**	0.059	0.012	0.070
AZASNF17N_2358	1	0.019	0.044	**0.871**	0.030	0.025	0.013
AZASNF17N_2359	1	0.010	0.027	**0.891**	0.016	0.019	0.038
AZASNF17N_2360	1	0.089	0.023	**0.838**	0.016	0.022	0.013
AZASNF17N_2361	1	0.012	0.031	**0.900**	0.012	0.017	0.028
AZASNF17N_2362	1	0.156	0.017	**0.777**	0.016	0.020	0.015
AZASNF17N_2363	1	0.010	0.022	**0.886**	0.026	0.016	0.040
AZASNF17N_2364	1	0.005	0.013	**0.838**	0.012	0.115	0.017
AZASNF17N_2365	1	0.012	0.023	**0.912**	0.018	0.019	0.017
AZASNF17N_2366	1	0.012	0.040	**0.868**	0.046	0.020	0.014

Individual tree	Pop.#	1	2	3	4	5	6
AZASNF17N_2367	1	0.008	0.014	**0.922**	0.017	0.017	0.022
AZASNF17N_2368	1	0.009	0.041	**0.892**	0.021	0.019	0.018
AZASNF17N_2369	1	0.013	0.017	**0.912**	0.016	0.024	0.018
AZASNF17N_2370	1	0.010	0.014	**0.889**	0.028	0.034	0.024
AZASNF17N_2371	1	0.010	0.022	**0.914**	0.015	0.013	0.027
AZASNF17N_2372	1	0.008	0.021	**0.914**	0.016	0.020	0.021
AZASNF17N_2373	1	0.008	0.044	**0.901**	0.016	0.016	0.016
AZASNF17N_2374	1	0.009	0.018	**0.916**	0.016	0.020	0.022
AZASNF17N_2375	1	0.013	0.092	**0.533**	0.127	0.103	0.131
AZASNF17N_2376	1	0.007	0.046	**0.801**	0.038	0.024	0.084
AZASNF17N_2377	1	0.007	0.040	**0.911**	0.019	0.010	0.013
AZASNF17N_2378	1	0.009	0.017	**0.925**	0.016	0.017	0.017
AZASNF17N_2379	1	0.013	0.024	**0.894**	0.020	0.013	0.035
AZASNF17N_2380	1	0.010	0.022	**0.908**	0.020	0.021	0.020
AZASNF17N_2381	1	0.021	0.051	**0.731**	0.066	0.114	0.018
AZASNF17N_2382	1	0.008	0.015	**0.922**	0.017	0.017	0.021
AZASNF17N_2383	1	0.109	0.029	**0.779**	0.056	0.015	0.013
AZASNF17N_2384	1	0.011	0.037	**0.900**	0.015	0.020	0.017
AZASNF17N_2385	1	0.007	0.018	**0.924**	0.016	0.015	0.020
AZASNF17N_2386	1	0.008	0.035	**0.868**	0.026	0.038	0.025
AZASNF17N_2387	1	0.007	0.017	**0.907**	0.011	0.047	0.011
AZASNF17N_2388	1	0.098	0.018	**0.829**	0.016	0.014	0.024
AZASNF17N_2389	1	0.009	0.019	**0.915**	0.015	0.022	0.021
AZASNF17N_2390	1	0.010	0.017	**0.903**	0.021	0.029	0.020
AZASNF17N_2391	1	0.009	0.018	**0.914**	0.015	0.021	0.023
AZCoNFCoN_2235	2	0.020	0.167	0.056	0.131	0.196	**0.431**
AZCoNFCoN_2236	2	0.011	0.062	0.027	**0.723**	0.086	0.092
AZCoNFCoN_2237	2	0.007	0.274	0.033	**0.360**	0.045	0.280
AZCoNFCoN_2238	2	0.008	0.132	0.037	0.226	0.092	**0.507**
AZCoNFCoN_2239	2	0.007	0.018	0.012	0.020	**0.921**	0.023
AZCoNFCoN_2240	2	0.012	0.116	0.044	0.246	0.181	**0.401**
AZCoNFCoN_2241	2	0.012	0.285	0.028	0.187	**0.330**	0.158
AZCoNFCoN_2242	2	0.009	0.077	0.017	0.056	**0.805**	0.037
AZCoNFCoN_2243	2	0.013	0.069	0.025	0.043	**0.789**	0.061
AZCoNFCoN_2244	2	0.012	0.120	0.044	0.249	0.176	**0.399**
AZCoNFCoN_2245	2	0.010	0.099	0.014	**0.795**	0.059	0.024
AZCoNFCoN_2246	2	0.013	**0.453**	0.045	0.074	0.033	**0.382**
AZCoNFCoN_2247	2	0.011	0.064	0.014	**0.630**	0.037	0.244
AZCoNFCoN_2248	2	0.011	0.186	0.030	**0.315**	0.277	0.181
AZCoNFCoN_2249	2	0.012	0.211	0.036	0.116	**0.305**	**0.320**
AZCoNFCoN_2250	2	0.010	0.292	0.032	0.187	0.164	**0.315**
AZCoNFCoN_2251	2	0.011	0.030	0.024	0.122	**0.741**	0.072
AZCoNFCoN_2252	2	0.013	0.133	0.034	0.162	**0.350**	**0.308**
AZCoNFCoN_2253	2	0.022	0.097	0.037	0.182	0.056	**0.607**
AZCoNFCoN_2254	2	0.014	0.266	0.042	0.114	0.046	**0.519**
AZCoNFCoN_2255	2	0.009	0.068	0.047	0.086	**0.650**	0.139
AZCoNFCoN_2256	2	0.037	**0.523**	0.023	0.049	0.035	**0.334**
AZCoNFCoN_2258	2	0.009	**0.392**	0.014	**0.402**	0.066	0.117

Individual tree	Pop.#	1	2	3	4	5	6
AZCoNFCoN_2259	2	0.042	**0.517**	0.016	0.215	0.051	0.159
AZCoNFCoN_2260	2	0.186	**0.301**	0.028	0.138	0.131	0.217
AZCoNFCoN_2261	2	0.009	0.040	0.020	**0.435**	0.035	**0.462**
AZCoNFCoN_2262	2	0.007	0.287	0.036	0.070	**0.449**	0.151
AZCoNFCoN_2263	2	0.028	0.103	0.060	0.086	**0.519**	0.203
AZCoNFCoN_2264	2	0.011	**0.303**	0.035	0.074	0.215	**0.362**
AZKaNFKaN_2265	3	0.021	0.037	**0.877**	0.028	0.019	0.018
AZKaNFKaN_2266	3	0.012	0.019	**0.884**	0.026	0.017	0.042
AZKaNFKaN_2267	3	0.018	0.077	**0.503**	0.050	**0.307**	0.045
AZKaNFKaN_2268	3	0.016	**0.614**	0.019	0.041	0.037	0.274
AZKaNFKaN_2269	3	0.012	0.059	0.012	**0.369**	0.024	**0.524**
AZKaNFKaN_2270	3	0.021	**0.429**	0.030	**0.414**	0.016	0.090
AZKaNFKaN_2271	3	0.009	0.020	**0.869**	0.038	0.020	0.045
AZKaNFKaN_2272	3	0.016	0.042	0.020	**0.363**	0.026	**0.533**
AZKaNFKaN_2273	3	0.252	0.109	0.246	0.099	0.058	0.237
AZKaNFKaN_2274	3	0.010	0.012	**0.503**	**0.424**	0.009	0.042
AZKaNFKaN_2275	3	0.091	0.028	**0.825**	0.019	0.014	0.023
AZKaNFKaN_2276	3	**0.448**	0.020	**0.430**	0.029	0.017	0.056
AZKaNFKaN_2277	3	0.016	0.126	0.030	0.107	**0.481**	0.239
AZKaNFKaN_2278	3	0.010	0.017	**0.912**	0.017	0.024	0.020
AZKaNFKaN_2279	3	0.012	0.017	**0.904**	0.026	0.016	0.025
AZKaNFKaN_2280	3	0.008	0.018	**0.906**	0.019	0.026	0.024
AZKaNFKaN_2281	3	0.018	0.018	**0.744**	0.089	0.016	0.115
AZKaNFKaN_2282	3	0.028	0.249	**0.366**	0.167	0.132	0.058
AZKaNFKaN_2283	3	0.019	0.059	**0.449**	0.125	0.052	0.296
AZKaNFKaN_2284	3	0.043	0.178	0.063	**0.311**	0.042	**0.363**
AZKaNFKaN_2285	3	0.017	0.037	**0.445**	0.176	0.040	0.286
AZKaNFKaN_2286	3	0.094	0.019	**0.811**	0.027	0.026	0.024
AZKaNFKaN_2287	3	0.130	0.016	**0.773**	0.026	0.028	0.027
AZKaNFKaN_2288	3	0.012	0.026	**0.900**	0.017	0.019	0.025
AZKaNFKaN_2289	3	0.019	0.265	0.039	0.102	**0.315**	0.260
AZKaNFKaN_2290	3	0.273	0.019	**0.650**	0.017	0.022	0.020
AZKaNFKaN_2291	3	0.041	0.083	**0.751**	0.049	0.059	0.018
COBLMAM60P_2452	4	0.014	0.120	0.040	**0.348**	0.142	**0.336**
COBLMAM60P_2453	4	0.014	**0.464**	0.028	0.239	0.240	0.016
COBLMAM60P_2454	4	0.021	0.200	0.037	0.133	**0.421**	0.189
COBLMAM60P_2455	4	0.011	0.116	0.026	0.085	**0.709**	0.054
COBLMAM60P_2456	4	0.010	0.018	**0.848**	0.070	0.029	0.026
COBLMAM60P_2457	4	0.049	0.075	**0.548**	0.078	0.177	0.074
COBLMAM60P_2458	4	0.022	0.076	**0.488**	0.237	0.039	0.138
COBLMAM60P_2459	4	0.027	0.133	0.030	0.268	0.115	**0.427**
COBLMAM60P_2460	4	0.012	0.067	0.024	0.217	0.117	**0.563**
COBLMAM60P_2462	4	0.016	0.128	0.030	0.105	**0.478**	0.243
COBLMAM60P_2463	4	0.011	**0.353**	0.039	0.036	**0.313**	0.249
COBLMAM60P_2464	4	0.010	**0.354**	0.036	0.092	0.170	**0.337**
COBLMAM60P_2465	4	0.006	0.062	0.014	0.036	**0.854**	0.028
COBLMAM60P_2466	4	0.015	0.076	**0.613**	0.060	0.205	0.031
COBLMAM60P_2467	4	0.011	0.076	**0.375**	0.045	**0.444**	0.050

Individual tree	Pop.#	1	2	3	4	5	6
COBLMAM60P_2468	4	0.014	0.181	0.033	0.081	**0.360**	**0.331**
COBLMAM60P_2469	4	0.009	0.015	**0.864**	0.013	0.082	0.017
COBLMAM60P_2470	4	0.008	0.242	0.031	0.081	0.201	**0.437**
COBLMAM60P_2471	4	0.022	0.115	0.030	0.105	**0.671**	0.056
COBLMAM60P_2472	4	0.010	0.087	0.021	0.207	0.063	**0.612**
COBLMAM60P_2473	4	0.014	0.111	0.029	0.174	**0.485**	0.187
COBLMAM60P_2474	4	0.273	0.127	0.022	0.167	0.052	**0.359**
COBLMAM60P_2475	4	**0.382**	0.061	0.276	0.086	0.068	0.128
COBLMAM60P_2476	4	0.011	0.094	0.022	0.143	0.079	**0.652**
COBLMAM60P_2477	4	0.014	0.018	**0.884**	0.023	0.018	0.044
COBLMAM60P_2478	4	0.010	0.021	**0.916**	0.015	0.020	0.018
COBLMAM60P_2479	4	0.020	0.097	0.027	0.210	0.132	**0.515**
COBLMAM60P_2480	4	0.018	0.101	**0.476**	0.146	0.086	0.173
COBLMAM60P_2481	4	0.007	**0.468**	0.024	0.020	0.277	0.203
COBLMAM70P_2482	5	0.011	0.120	**0.469**	0.191	0.072	0.137
COBLMAM70P_2483	5	0.013	0.056	0.018	**0.330**	0.038	**0.546**
COBLMAM70P_2484	5	0.014	**0.424**	0.040	0.081	0.176	0.266
COBLMAM70P_2485	5	0.020	0.083	**0.317**	0.202	0.299	0.079
COBLMAM70P_2486	5	0.009	0.018	**0.916**	0.015	0.021	0.022
COBLMAM70P_2487	5	0.010	0.138	0.029	0.089	**0.336**	**0.397**
COBLMAM70P_2488	5	0.131	0.139	0.171	0.155	0.031	**0.373**
COBLMAM70P_2489	5	0.009	0.090	0.025	**0.708**	0.068	0.101
COBLMAM70P_2490	5	0.129	**0.385**	0.174	0.210	0.041	0.062
COBLMAM70P_2491	5	0.060	**0.310**	0.032	0.084	0.137	**0.378**
COBLMAM70P_2492	5	0.017	0.084	0.024	**0.357**	0.126	**0.393**
COBLMAM70P_2493	5	0.009	0.159	0.031	0.130	0.279	**0.392**
COBLMAM70P_2494	5	0.022	**0.314**	0.018	0.089	0.022	**0.536**
COBLMAM70P_2495	5	0.099	0.129	0.028	0.184	**0.387**	0.173
COBLMAM70P_2496	5	0.012	0.018	**0.867**	0.026	0.022	0.056
COBLMAM70P_2497	5	0.012	0.017	**0.920**	0.013	0.023	0.015
COBLMAM70P_2498	5	0.019	0.179	0.043	0.069	**0.633**	0.057
COBLMAM70P_2499	5	0.014	0.120	0.026	0.204	0.073	**0.563**
COBLMAM70P_2500	5	0.015	0.299	0.036	0.223	0.238	0.190
COBLMAM70P_2502	5	0.010	0.087	0.025	0.196	**0.446**	0.237
COBLMAM70P_2503	5	0.034	0.167	0.028	0.299	**0.301**	0.171
COBLMAM70P_2504	5	0.011	0.095	0.034	**0.389**	**0.338**	0.133
COBLMAM70P_2505	5	0.010	0.119	0.028	0.167	**0.379**	0.297
COBLMAM70P_2506	5	0.007	0.075	0.029	0.082	**0.644**	0.163
COBLMAM70P_2507	5	0.008	0.020	0.013	0.019	**0.920**	0.020
COBLMAM70P_2508	5	0.012	**0.354**	0.030	0.273	0.224	0.107
COBLMAM70P_2509	5	0.009	**0.358**	0.030	0.118	0.121	**0.363**
COBLMAM70P_2510	5	0.010	**0.330**	0.028	0.084	0.074	**0.474**
COBLMAM70P_2511	5	0.009	0.089	0.022	0.221	**0.420**	0.240
COBLMAM90P_2512	6	0.018	0.257	0.018	0.115	**0.339**	0.253
COBLMAM90P_2513	6	0.016	**0.313**	0.050	0.116	0.284	0.221
COBLMAM90P_2514	6	0.011	0.247	0.032	0.148	0.212	**0.350**
COBLMAM90P_2515	6	0.012	0.167	0.026	0.180	0.209	**0.406**
COBLMAM90P_2516	6	0.016	0.163	0.022	0.244	0.160	**0.396**

Individual tree	Pop.#	1	2	3	4	5	6
COBLMAM90P_2517	6	0.031	0.119	0.035	0.068	**0.678**	0.069
COBLMAM90P_2518	6	0.037	**0.532**	0.023	0.049	0.035	**0.324**
COBLMAM90P_2519	6	0.013	0.112	0.029	0.053	**0.745**	0.047
COBLMAM90P_2520	6	0.042	0.152	0.105	0.134	**0.474**	0.093
COBLMAM90P_2521	6	0.015	**0.401**	0.032	0.077	0.079	**0.397**
COBLMAM90P_2522	6	0.010	0.085	0.025	0.199	**0.446**	0.234
COBLMAM90P_2523	6	0.013	0.116	0.024	0.202	**0.455**	0.190
COBLMAM90P_2524	6	0.049	**0.375**	0.031	0.164	**0.335**	0.046
COBLMAM90P_2525	6	0.019	0.244	0.023	0.177	**0.506**	0.031
COBLMAM90P_2526	6	0.011	0.179	0.021	0.117	0.030	**0.643**
COBLMAM90P_2527	6	0.008	0.207	0.021	**0.325**	0.092	**0.347**
COBLMAM90P_2528	6	0.020	0.160	0.024	0.221	0.248	**0.328**
COBLMAM90P_2529	6	0.020	**0.348**	0.029	0.068	0.095	**0.440**
COBLMAM90P_2530	6	0.013	0.095	0.030	0.188	**0.422**	0.253
COBLMAM90P_2531	6	0.013	0.160	0.033	0.150	**0.397**	0.248
COBLMAM90P_2532	6	0.009	0.159	0.030	0.125	0.284	**0.393**
COBLMAM90P_2533	6	0.012	0.063	0.018	0.242	0.031	**0.635**
COBLMAM90P_2534	6	0.014	0.283	0.019	0.103	0.079	**0.503**
COBLMAM90P_2535	6	0.014	0.084	0.023	0.025	**0.790**	0.064
COBLMAM90P_2536	6	0.059	**0.372**	0.016	**0.433**	0.107	0.014
COBLMAM90P_2537	6	0.061	**0.432**	0.022	0.087	0.083	**0.315**
COBLMAM90P_2538	6	0.131	0.029	0.023	0.039	**0.736**	0.043
COBLMAM90P_2539	6	0.098	**0.305**	0.040	0.128	0.241	0.188
COBLMAM90P_2540	6	0.011	0.089	0.024	0.278	**0.359**	0.239
COBLMAM90P_2541	6	0.009	0.049	0.016	0.018	**0.879**	0.029
COBLMVM60P_0846	7	0.011	**0.423**	0.016	0.262	0.248	0.040
COBLMVM60P_0847	7	0.029	0.161	0.031	**0.463**	0.124	0.192
COBLMVM60P_0848	7	0.014	0.173	0.032	0.083	**0.369**	**0.329**
COBLMVM60P_0849	7	0.006	0.014	0.009	**0.937**	0.011	0.023
COBLMVM60P_0850	7	0.007	0.066	0.024	**0.742**	0.069	0.091
COBLMVM60P_0851	7	0.011	**0.525**	0.021	0.170	0.159	0.115
COBLMVM60P_0852	7	0.014	0.024	0.017	**0.867**	0.032	0.045
COBLMVM60P_0853	7	0.022	0.067	0.022	0.079	**0.760**	0.050
COBLMVM60P_0854	7	0.009	0.054	0.039	0.097	**0.690**	0.112
COBLMVM60P_0855	7	0.011	0.239	0.032	0.252	0.226	0.241
COBLMVM60P_0856	7	0.024	**0.465**	0.033	0.069	0.081	**0.327**
COBLMVM60P_0857	7	0.068	**0.400**	0.047	0.225	0.031	0.230
COBLMVM60P_0858	7	0.013	0.215	0.035	0.115	**0.309**	**0.314**
COBLMVM60P_0859	7	0.010	0.233	0.077	0.285	0.211	0.183
COBLMVM60P_0860	7	0.011	0.283	0.112	0.155	0.176	0.264
COBLMVM60P_0861	7	0.018	**0.578**	0.045	0.211	0.046	0.102
COBLMVM60P_0862	7	0.009	0.047	0.015	0.246	0.026	**0.658**
COBLMVM60P_0863	7	0.009	0.110	0.024	**0.317**	0.086	**0.455**
COBLMVM60P_0864	7	0.009	**0.629**	0.033	0.168	0.103	0.058
COBLMVM60P_0865	7	0.016	0.217	0.038	0.194	0.275	0.261
COBLMVM60P_0866	7	0.013	0.102	0.029	**0.438**	0.037	**0.381**
COBLMVM60P_0867	7	0.007	0.015	0.014	**0.718**	0.015	0.231
COBLMVM60P_0868	7	0.009	0.292	0.031	0.137	0.111	**0.421**

Individual tree	Pop.#	1	2	3	4	5	6
COBLMVM60P_0869	7	0.009	0.103	0.038	0.197	0.125	**0.530**
COBLMVM60P_0870	7	0.011	**0.504**	0.018	0.077	0.025	**0.366**
COBLMVM60P_0871	7	0.006	0.044	**0.756**	0.142	0.020	0.033
COBLMVM60P_0872	7	0.012	**0.500**	0.019	0.082	0.026	**0.362**
COBLMVM60P_0873	7	0.017	0.146	0.035	**0.375**	0.036	**0.391**
COBLMVM60P_0874	7	0.016	**0.302**	0.035	0.135	0.222	0.292
COBLMVM60P_0875	7	0.024	**0.331**	0.033	**0.423**	0.053	0.136
COBLMVM60P_0876	7	0.011	0.044	0.014	**0.885**	0.018	0.028
COBLMVM60P_0877	7	0.020	0.101	0.037	**0.471**	0.079	0.293
COBLMVM60P_0878	7	0.016	0.216	0.037	0.199	0.275	0.258
COBLMVM60P_0911	7	0.009	0.076	0.013	**0.336**	0.023	**0.543**
COBLMVM70P_0879	8	0.008	0.202	0.028	0.165	0.196	**0.401**
COBLMVM70P_0880	8	0.010	0.112	0.020	0.254	0.199	**0.405**
COBLMVM70P_0881	8	0.019	0.151	0.024	**0.706**	0.047	0.054
COBLMVM70P_0882	8	0.013	0.177	0.029	0.227	0.072	**0.482**
COBLMVM70P_0883	8	0.040	0.115	0.029	**0.431**	0.246	0.140
COBLMVM70P_0884	8	0.067	**0.378**	0.021	0.205	0.019	**0.310**
COBLMVM70P_0885	8	0.014	0.046	0.016	**0.447**	0.034	**0.443**
COBLMVM70P_0886	8	0.008	0.030	0.023	**0.818**	0.089	0.033
COBLMVM70P_0887	8	0.008	0.035	0.018	0.028	**0.881**	0.031
COBLMVM70P_0888	8	0.029	0.119	0.031	0.036	**0.762**	0.024
COBLMVM70P_0889	8	0.018	0.238	0.022	0.173	**0.517**	0.032
COBLMVM70P_0890	8	0.012	0.033	0.023	**0.807**	0.094	0.030
COBLMVM70P_0891	8	0.008	0.034	0.015	0.014	**0.909**	0.021
COBLMVM70P_0892	8	0.013	0.097	0.023	0.045	**0.737**	0.085
COBLMVM70P_0893	8	0.016	**0.394**	0.031	0.078	0.079	**0.403**
COBLMVM70P_0894	8	0.015	0.094	0.026	0.283	0.097	**0.485**
COBLMVM70P_0895	8	0.057	**0.579**	0.033	0.163	0.061	0.107
COBLMVM70P_0896	8	0.021	0.202	0.036	0.133	**0.417**	0.191
COBLMVM70P_0897	8	0.017	0.127	0.029	0.258	**0.381**	0.189
COBLMVM70P_0898	8	0.010	0.180	0.029	0.276	0.273	0.233
COBLMVM70P_0899	8	0.208	0.180	0.022	**0.376**	0.075	0.139
COBLMVM70P_0900	8	0.008	0.132	0.030	0.045	**0.701**	0.084
COBLMVM70P_0901	8	0.007	0.015	**0.870**	0.013	0.075	0.020
COBLMVM70P_0902	8	0.011	0.057	0.021	**0.360**	0.112	**0.438**
COBLMVM70P_0903	8	0.008	0.087	0.028	**0.530**	0.162	0.185
COBLMVM70P_0904	8	0.010	0.290	0.015	0.131	0.016	**0.539**
COBLMVM70P_0905	8	0.008	0.252	0.030	0.188	0.167	**0.357**
COBLMVM70P_0906	8	0.129	0.094	0.016	**0.308**	0.051	**0.403**
COBLMVM70P_0907	8	0.013	0.023	0.012	**0.449**	0.021	**0.483**
COBLMVM70P_0908	8	0.008	0.044	0.014	**0.848**	0.023	0.063
COBLMVM70P_0909	8	0.010	0.088	0.024	0.244	**0.318**	**0.317**
COBLMVM70P_0910	8	0.008	0.164	0.022	0.083	0.129	**0.594**
COGMUGDNP_5699	9	0.023	0.101	0.025	**0.304**	0.105	**0.442**
COGMUGDNP_5700	9	0.023	0.172	0.029	0.091	**0.388**	0.297
COGMUGDNP_5701	9	0.129	0.159	0.024	0.197	0.058	**0.434**
COGMUGDNP_5702	9	0.019	0.206	0.033	0.173	0.070	**0.499**
COGMUGDNP_5703	9	0.010	0.149	0.033	**0.379**	**0.344**	0.084

Individual tree	Pop.#	1	2	3	4	5	6
COGMUGDNP_5704	9	0.007	0.044	0.017	**0.496**	0.026	**0.409**
COGMUGDNP_5705	9	0.042	0.284	0.029	0.177	0.060	**0.409**
COGMUGDNP_5706	9	0.012	0.184	0.018	0.143	0.024	**0.619**
COGMUGDNP_5707	9	0.052	0.224	0.020	**0.491**	0.059	0.154
COGMUGDNP_5708	9	0.028	0.198	0.022	**0.486**	0.091	0.174
COGMUGDNP_5709	9	0.010	0.102	0.015	**0.401**	0.033	**0.439**
COGMUGDNP_5710	9	**0.403**	0.191	0.030	0.115	0.061	0.201
COGMUGDNP_5711	9	0.007	0.040	0.010	**0.880**	0.009	0.055
COGMUGDNP_5712	9	0.008	**0.427**	0.018	0.298	0.226	0.024
COGMUGDNP_5713	9	0.014	0.121	0.027	0.204	0.074	**0.560**
COGMUGDNP_5714	9	0.017	0.094	0.021	0.246	0.076	**0.546**
COGMUGDNP_5715	9	0.061	0.083	0.021	0.262	0.027	**0.546**
COGMUGDNP_5716	9	0.012	0.287	0.030	0.127	0.115	**0.429**
COGMUGDNP_5717	9	0.024	0.221	0.039	0.076	**0.374**	0.268
COGMUGDNP_5718	9	0.024	0.222	0.038	0.079	**0.371**	0.267
COGMUGDNP_5719	9	0.008	0.085	0.012	**0.635**	0.069	0.191
COGMUGDNP_5720	9	0.024	0.147	0.032	0.156	**0.494**	0.146
COGMUGDNP_5721	9	0.013	0.100	0.025	0.045	**0.730**	0.087
COGMUGDNP_5722	9	0.009	0.035	0.020	**0.407**	0.048	**0.482**
COGMUGDNP_5723	9	0.012	0.259	0.024	0.102	**0.359**	0.244
COGMUGDNP_5724	9	0.048	0.278	0.045	0.208	0.261	0.160
COGMUGDNP_5725	9	0.020	0.205	0.015	0.247	0.029	**0.485**
COGMUGDNP_5726	9	0.012	0.177	0.029	0.220	0.072	**0.490**
COGMUGDNP_5727	9	0.037	**0.430**	0.036	0.105	0.114	0.279
COGMUGDNP_5728	9	0.008	0.294	0.036	0.087	0.032	**0.542**
COGMUGSMN_5729	10	0.016	0.223	0.052	0.201	0.131	**0.378**
COGMUGSMN_5730	10	0.024	**0.429**	0.054	0.177	0.079	0.237
COGMUGSMN_5731	10	0.009	**0.489**	0.014	**0.333**	0.127	0.027
COGMUGSMN_5732	10	0.039	**0.354**	0.045	0.109	0.138	**0.315**
COGMUGSMN_5733	10	0.011	**0.301**	0.034	0.073	0.214	**0.369**
COGMUGSMN_5734	10	0.007	**0.399**	0.046	0.099	0.078	**0.372**
COGMUGSMN_5735	10	0.036	0.040	**0.628**	0.127	0.077	0.094
COGMUGSMN_5736	10	0.011	0.067	**0.636**	0.080	0.059	0.148
COGMUGSMN_5737	10	0.010	0.275	0.032	**0.494**	0.076	0.114
COGMUGSMN_5738	10	0.013	0.156	0.028	0.175	0.280	**0.349**
COGMUGSMN_5739	10	0.020	**0.467**	0.130	0.274	0.065	0.044
COGMUGSMN_5740	10	0.014	0.243	0.055	0.163	0.100	**0.424**
COGMUGSMN_5741	10	0.006	**0.450**	0.030	0.291	0.198	0.026
COGMUGSMN_5742	10	0.019	0.195	0.033	0.158	**0.303**	0.292
COGMUGSMN_5743	10	0.039	0.018	0.148	**0.761**	0.017	0.018
COGMUGSMN_5744	10	0.013	0.155	0.033	0.146	**0.411**	0.242
COGMUGSMN_5745	10	0.017	0.093	0.024	**0.394**	0.082	**0.389**
COGMUGSMN_5746	10	0.009	0.211	0.019	0.187	0.023	**0.551**
COGMUGSMN_5747	10	0.013	0.158	0.028	0.171	0.278	**0.353**
COGMUGSMN_5748	10	0.010	**0.702**	0.017	0.064	0.024	0.183
COGMUGSMN_5749	10	0.007	0.043	0.020	0.039	**0.829**	0.061
COGMUGSMN_5750	10	0.069	0.083	0.015	0.261	0.024	**0.549**
COGMUGSMN_5751	10	0.014	**0.469**	0.014	0.156	0.049	0.298

Individual tree	Pop.#	1	2	3	4	5	6
COGMUGSMN_5752	10	0.014	0.155	0.032	0.149	**0.404**	0.246
COGMUGSMN_5753	10	0.011	**0.747**	0.019	0.096	0.051	0.076
COGMUGSMN_5754	10	0.285	0.167	0.030	0.192	0.062	0.264
COGMUGSMN_5755	10	0.009	**0.336**	0.024	0.184	0.067	**0.380**
COGMUGSMN_5756	10	0.012	0.158	0.040	**0.354**	0.133	**0.302**
COGMUGSMN_5757	10	0.010	0.253	0.039	**0.400**	0.021	0.278
COGMUGSMN_5758	10	0.009	0.105	0.022	0.143	0.021	**0.700**
COGMUGTrP_5759	11	0.030	**0.377**	0.037	0.144	0.092	**0.320**
COGMUGTrP_5760	11	0.009	0.104	0.038	0.195	0.119	**0.537**
COGMUGTrP_5761	11	0.012	0.055	0.026	**0.330**	0.046	**0.530**
COGMUGTrP_5762	11	0.009	0.110	0.024	**0.320**	0.082	**0.455**
COGMUGTrP_5763	11	0.009	0.134	0.012	**0.617**	0.026	0.202
COGMUGTrP_5764	11	0.009	0.140	0.031	0.184	0.024	**0.613**
COGMUGTrP_5765	11	0.016	0.098	0.026	0.278	0.100	**0.482**
COGMUGTrP_5766	11	0.013	0.131	0.047	0.139	0.178	**0.493**
COGMUGTrP_5767	11	0.012	0.064	0.017	0.243	0.030	**0.633**
COGMUGTrP_5768	11	0.012	0.066	0.018	0.243	0.029	**0.632**
COGMUGTrP_5769	11	0.030	0.157	0.029	0.256	0.187	**0.341**
COGMUGTrP_5770	11	0.063	0.110	0.024	**0.333**	0.061	**0.409**
COGMUGTrP_5771	11	0.012	0.070	0.022	0.212	0.114	**0.570**
COGMUGTrP_5772	11	0.030	0.129	0.026	0.203	0.091	**0.522**
COGMUGTrP_5773	11	0.011	0.031	0.017	**0.362**	0.023	**0.558**
COGMUGTrP_5774	11	0.152	0.074	0.019	**0.461**	0.077	0.216
COGMUGTrP_5775	11	0.007	0.055	0.016	**0.450**	0.035	**0.438**
COGMUGTrP_5776	11	0.085	0.073	0.017	0.188	0.031	**0.607**
COGMUGTrP_5777	11	0.035	0.042	0.053	**0.772**	0.073	0.026
COGMUGTrP_5778	11	0.009	0.098	0.022	**0.316**	0.072	**0.484**
COGMUGTrP_5779	11	0.009	0.159	0.030	0.128	0.281	**0.393**
COGMUGTrP_5780	11	0.013	**0.308**	0.014	**0.581**	0.031	0.054
COGMUGTrP_5781	11	0.018	0.165	0.027	0.298	0.070	**0.422**
COGMUGTrP_5782	11	0.011	0.027	0.019	**0.509**	0.022	**0.414**
COGMUGTrP_5783	11	0.009	0.076	0.025	**0.442**	0.035	**0.414**
COGMUGTrP_5784	11	0.008	0.021	**0.905**	0.023	0.021	0.022
COGMUGTrP_5785	11	0.008	0.023	0.017	**0.564**	0.027	**0.361**
COGMUGTrP_5786	11	0.024	**0.376**	0.040	0.084	0.037	**0.439**
COGMUGTrP_5787	11	0.012	0.123	0.019	0.142	0.030	**0.675**
COGMUGTrP_5788	11	0.020	0.072	0.020	**0.451**	0.024	**0.413**
CORGNFLWN_2202	12	0.031	0.138	0.252	0.098	0.021	**0.461**
CORGNFLWN_2203	12	0.014	0.155	0.032	0.148	**0.408**	0.243
CORGNFLWN_2204	12	0.012	0.093	0.020	**0.565**	0.034	0.277
CORGNFLWN_2205	12	0.021	0.089	0.016	0.042	**0.797**	0.036
CORGNFLWN_2206	12	0.019	0.024	0.286	0.198	**0.457**	0.017
CORGNFLWN_2207	12	0.009	0.068	0.032	**0.312**	0.194	**0.385**
CORGNFLWN_2208	12	0.008	0.068	0.038	0.247	0.060	**0.579**
CORGNFLWN_2209	12	0.126	0.153	0.030	0.190	0.045	**0.457**
CORGNFLWN_2210	12	0.012	0.119	0.045	0.250	0.179	**0.396**
CORGNFLWN_2211	12	0.027	0.139	0.033	0.269	0.116	**0.417**
CORGNFLWN_2212	12	0.054	0.054	**0.349**	0.152	0.016	**0.375**

Individual tree	Pop.#	1	2	3	4	5	6
CORGNFLWN_2213	12	0.007	0.115	0.026	**0.500**	0.091	0.261
CORGNFLWN_2214	12	0.007	0.049	0.038	0.072	**0.675**	0.160
CORGNFLWN_2215	12	0.021	0.198	0.038	0.133	**0.420**	0.190
CORGNFLWN_2216	12	0.017	0.227	0.036	0.104	0.021	**0.596**
CORGNFLWN_2217	12	0.010	0.037	0.018	0.037	**0.859**	0.038
CORGNFLWN_2218	12	0.007	0.136	0.018	**0.433**	0.098	**0.309**
CORGNFLWN_2219	12	0.011	0.083	0.022	**0.344**	0.060	**0.480**
CORGNFLWN_2220	12	0.008	0.141	0.026	0.102	**0.572**	0.152
CORGNFLWN_2221	12	0.014	0.100	0.021	0.154	0.065	**0.647**
CORGNFLWN_2222	12	0.011	0.118	0.019	0.149	0.039	**0.665**
CORGNFLWN_2223	12	0.007	0.146	0.038	0.143	**0.620**	0.046
CORGNFLWN_2224	12	0.010	0.090	0.049	0.242	0.069	**0.540**
CORGNFLWN_2225	12	0.008	0.226	0.029	0.067	**0.415**	0.256
CORGNFLWN_2226	12	0.007	0.137	0.018	**0.430**	0.099	**0.310**
CORGNFLWN_2227	12	0.015	0.048	0.019	**0.351**	0.021	**0.546**
CORGNFLWN_2228	12	0.008	0.130	0.029	0.042	**0.708**	0.081
CORGNFLWN_2229	12	0.007	0.028	0.014	0.019	**0.898**	0.035
CORGNFLWN_2230	12	0.009	0.051	0.022	0.063	**0.784**	0.072
CORGNFLWN_2231	12	0.025	0.092	**0.556**	0.128	0.106	0.093
CORGNFLWN_2232	12	0.019	0.170	0.038	0.139	**0.378**	0.257
CORGNFLWN_2233	12	0.009	0.216	0.019	0.125	0.205	**0.426**
CORGNFLWN_2234	12	0.023	**0.433**	0.024	0.232	0.034	0.253
COSJNF8mN_8274	13	0.010	0.032	0.016	0.023	**0.890**	0.029
COSJNF8mN_8275	13	0.012	**0.603**	0.079	0.062	0.050	0.195
COSJNF8mN_8276	13	**0.602**	0.073	0.034	0.039	0.195	0.058
COSJNF8mN_8277	13	0.084	**0.355**	0.035	0.073	0.132	**0.321**
COSJNF8mN_8278	13	0.011	**0.301**	0.036	0.133	0.249	0.269
COSJNF8mN_8279	13	0.011	**0.346**	0.027	0.187	0.103	**0.327**
COSJNF8mN_8280	13	0.009	0.253	0.024	**0.360**	0.192	0.163
COSJNF8mN_8281	13	0.009	0.179	0.030	0.198	**0.312**	0.274
COSJNF8mN_8282	13	0.007	0.025	0.020	**0.427**	**0.487**	0.034
COSJNF8mN_8283	13	0.022	**0.454**	0.050	0.080	0.093	**0.300**
COSJNF8mN_8284	13	**0.472**	0.165	0.041	0.082	0.051	0.189
COSJNF8mN_8285	13	0.148	**0.354**	0.032	0.061	0.072	**0.334**
COSJNF8mN_8286	13	0.038	0.285	0.258	0.135	0.064	0.219
COSJNF8mN_8287	13	0.013	**0.379**	0.084	0.160	0.267	0.097
COSJNF8mN_8288	13	0.022	0.154	0.040	0.090	**0.627**	0.067
COSJNF8mN_8289	13	**0.404**	0.222	0.018	0.146	0.120	0.090
COSJNF8mN_8290	13	0.014	0.159	0.032	0.150	**0.404**	0.242
COSJNF8mN_8291	13	0.010	0.118	0.029	0.163	**0.377**	**0.304**
COSJNF8mN_8292	13	0.009	0.191	0.023	**0.494**	0.238	0.046
COSJNF8mN_8293	13	0.016	**0.318**	0.021	0.223	**0.363**	0.060
COSJNF8mN_8294	13	0.013	0.214	0.035	0.115	**0.305**	**0.319**
COSJNF8mN_8295	13	0.029	0.282	0.053	0.196	0.083	**0.357**
COSJNF8mN_8296	13	0.007	0.080	0.024	0.054	**0.761**	0.075
COSJNF8mN_8297	13	**0.390**	**0.329**	0.029	0.098	0.066	0.087
COSJNF8mN_8298	13	0.013	0.203	0.025	0.222	**0.414**	0.123
COSJNF8mN_8299	13	0.008	**0.333**	0.022	0.110	0.046	**0.482**

Individual tree	Pop.#	1	2	3	4	5	6
COSJNF8mN_8300	13	0.013	0.102	0.024	0.044	**0.729**	0.089
COSJNF8mN_8301	13	0.007	0.057	0.013	0.028	**0.870**	0.025
COSJNF8mN_8302	13	**0.371**	0.218	0.031	0.233	0.070	0.077
COSJNF8mN_8303	13	0.006	0.143	0.048	0.049	**0.729**	0.024
COSJNF8mP_8244	14	0.052	0.047	**0.780**	0.029	0.047	0.046
COSJNF8mP_8245	14	0.177	0.251	0.042	0.078	0.213	0.239
COSJNF8mP_8246	14	0.023	0.063	0.019	**0.772**	0.088	0.036
COSJNF8mP_8247	14	0.143	0.197	0.034	0.065	0.253	**0.308**
COSJNF8mP_8248	14	0.015	0.080	**0.565**	0.070	0.113	0.157
COSJNF8mP_8249	14	0.012	**0.311**	0.015	**0.417**	0.135	0.111
COSJNF8mP_8250	14	0.010	0.159	0.025	0.292	0.045	**0.468**
COSJNF8mP_8251	14	0.014	0.159	0.033	0.146	**0.401**	0.248
COSJNF8mP_8252	14	0.014	0.120	0.027	0.196	0.072	**0.571**
COSJNF8mP_8253	14	0.024	0.129	0.021	0.052	**0.673**	0.102
COSJNF8mP_8254	14	0.019	0.149	0.019	0.055	**0.727**	0.032
COSJNF8mP_8255	14	0.010	0.038	0.017	0.038	**0.859**	0.038
COSJNF8mP_8256	14	0.018	0.219	0.039	0.173	**0.424**	0.126
COSJNF8mP_8257	14	**0.459**	0.078	0.019	0.030	**0.391**	0.023
COSJNF8mP_8258	14	0.011	0.255	0.039	0.121	0.197	**0.377**
COSJNF8mP_8259	14	0.026	0.081	**0.578**	0.052	0.133	0.130
COSJNF8mP_8260	14	0.010	0.284	0.030	0.081	0.082	**0.512**
COSJNF8mP_8261	14	0.021	0.078	0.049	0.293	**0.354**	0.206
COSJNF8mP_8262	14	0.010	0.047	0.023	**0.466**	0.063	**0.391**
COSJNF8mP_8263	14	0.009	0.266	0.044	0.267	0.054	**0.361**
COSJNF8mP_8264	14	0.019	0.197	0.021	0.133	**0.301**	**0.328**
COSJNF8mP_8265	14	0.010	0.044	0.018	0.028	**0.851**	0.048
COSJNF8mP_8266	14	0.009	**0.308**	0.025	0.084	**0.451**	0.123
COSJNF8mP_8267	14	0.012	0.019	**0.904**	0.014	0.027	0.024
COSJNF8mP_8268	14	0.015	**0.426**	0.022	**0.300**	0.073	0.163
COSJNF8mP_8269	14	0.036	0.140	**0.551**	0.066	0.066	0.141
COSJNF8mP_8270	14	0.039	0.036	**0.832**	0.014	0.065	0.014
COSJNF8mP_8271	14	0.035	0.192	0.033	0.061	**0.408**	0.271
COSJNF8mP_8272	14	0.021	0.036	**0.395**	0.036	**0.476**	0.037
COSJNF8mP_8273	14	0.010	0.017	**0.911**	0.017	0.025	0.020
COSJNFBDN_1927	15	0.027	**0.404**	0.017	0.213	0.152	0.186
COSJNFBDN_1928	15	0.014	0.046	0.020	0.035	**0.853**	0.033
COSJNFBDN_1929	15	0.007	0.035	0.013	**0.593**	0.017	**0.337**
COSJNFBDN_1930	15	0.011	0.019	0.012	**0.824**	0.023	0.112
COSJNFBDN_1931	15	0.016	**0.669**	0.029	0.107	0.032	0.148
COSJNFBDN_1932	15	0.038	0.173	0.078	0.160	0.204	**0.347**
COSJNFBDN_1933	15	0.014	0.220	0.047	**0.542**	0.107	0.071
COSJNFBDN_1934	15	0.008	**0.301**	0.070	0.179	**0.312**	0.130
COSJNFBDN_1935	15	0.009	**0.472**	0.069	0.223	0.063	0.164
COSJNFBDN_1936	15	0.013	0.219	0.048	**0.545**	0.105	0.069
COSJNFBDN_1937	15	0.010	0.084	0.021	0.202	0.061	**0.623**
COSJNFBDN_1938	15	0.014	0.049	0.020	0.036	**0.847**	0.034
COSJNFBDN_1939	15	**0.585**	0.096	0.025	0.066	0.122	0.106
COSJNFBDN_1940	15	0.024	0.143	0.031	0.153	**0.499**	0.149

Individual tree	Pop.#	1	2	3	4	5	6
COSJNFBDN_1941	15	0.043	**0.350**	0.019	0.233	0.269	0.086
COSJNFBDN_1942	15	0.008	0.026	0.014	0.018	**0.911**	0.024
COSJNFBDN_1943	15	0.009	0.020	0.014	**0.893**	0.039	0.025
COSJNFBDN_1944	15	0.025	0.082	**0.582**	0.052	0.131	0.128
COSJNFBDN_1945	15	0.014	0.033	**0.593**	0.026	**0.302**	0.032
COSJNFBDN_1946	15	0.010	0.056	0.129	0.037	**0.721**	0.047
COSJNFBDN_1947	15	0.013	0.044	0.019	0.032	**0.859**	0.033
COSJNFBDN_1948	15	0.010	0.290	0.032	0.187	0.167	**0.313**
COSJNFBDN_1949	15	0.008	0.034	0.012	**0.347**	0.011	**0.589**
COSJNFBDN_1950	15	0.011	**0.808**	0.019	0.097	0.040	0.026
COSJNFBDN_1951	15	0.010	0.039	0.026	**0.366**	0.029	**0.530**
COSJNFBDN_1952	15	0.012	0.143	0.046	0.186	0.134	**0.479**
COSJNFBDN_1953	15	0.013	0.158	0.029	0.172	0.275	**0.354**
COSJNFBDN_1954	15	0.007	**0.357**	0.032	0.121	0.150	**0.333**
COSJNFBDN_1955	15	0.014	0.240	0.021	0.237	0.033	**0.455**
COSJNFBDN_1956	15	0.046	0.045	0.018	**0.842**	0.025	0.025
COSJNFBDN_1957	15	0.014	**0.455**	0.072	0.080	0.188	0.192
COSJNFNaP_5627	16	0.010	0.049	0.022	**0.461**	0.063	**0.396**
COSJNFNaP_5628	16	0.024	0.048	0.022	**0.567**	0.078	0.261
COSJNFNaP_5629	16	0.010	0.084	0.025	0.199	**0.444**	0.239
COSJNFNaP_5630	16	0.067	0.016	**0.513**	**0.382**	0.012	0.010
COSJNFNaP_5631	16	0.017	0.082	0.025	**0.359**	0.127	**0.391**
COSJNFNaP_5632	16	0.037	**0.302**	0.029	0.296	0.040	0.296
COSJNFNaP_5633	16	0.013	0.267	0.021	**0.446**	0.062	0.191
COSJNFNaP_5634	16	0.017	0.181	0.026	0.254	0.076	**0.446**
COSJNFNaP_5635	16	0.020	0.154	0.031	0.159	**0.419**	0.218
COSJNFNaP_5636	16	0.032	0.052	**0.349**	0.166	0.028	**0.374**
COSJNFNaP_5637	16	0.032	0.030	0.012	**0.860**	0.026	0.041
COSJNFNaP_5638	16	0.011	0.127	0.025	**0.388**	0.062	**0.389**
COSJNFNaP_5639	16	0.014	0.154	0.033	0.150	**0.409**	0.242
COSJNFNaP_5640	16	0.015	**0.665**	0.027	0.141	0.025	0.127
COSJNFNaP_5641	16	0.015	0.233	0.031	**0.418**	0.122	0.181
COSJNFNaP_5642	16	0.026	0.158	0.030	0.242	**0.344**	0.202
COSJNFNaP_5643	16	0.034	0.037	0.015	**0.849**	0.024	0.043
COSJNFNaP_5644	16	0.038	0.240	**0.306**	0.053	0.070	0.293
COSJNFNaP_5645	16	0.010	0.189	0.029	0.279	0.262	0.232
COSJNFNaP_5646	16	0.009	0.028	0.013	**0.440**	0.033	**0.477**
COSJNFNaP_5647	16	0.010	**0.395**	0.071	0.185	0.255	0.084
COSJNFNaP_5648	16	0.012	0.056	0.027	**0.332**	0.047	**0.526**
COSJNFNaP_5649	16	0.014	0.178	0.049	0.289	0.071	**0.399**
COSJNFNaP_5650	16	0.009	0.022	0.014	**0.891**	0.032	0.032
COSJNFNaP_5651	16	0.035	0.095	0.037	0.199	0.058	**0.577**
COSJNFNaP_5652	16	0.029	0.118	0.018	0.173	0.104	**0.558**
COSJNFNaP_5653	16	0.009	0.094	0.016	**0.570**	0.063	0.247
COSJNFNaP_5654	16	0.012	0.046	0.025	**0.411**	0.055	**0.451**
COSJNFNaP_5655	16	0.010	0.117	0.029	0.166	**0.375**	**0.304**
COSJNFNaP_5656	16	0.008	0.064	0.019	**0.569**	0.038	**0.302**
COSJNFNaP_5657	16	0.011	0.030	0.015	**0.327**	0.020	**0.597**

Individual tree	Pop.#	1	2	3	4	5	6
COSJNFPRN_8214	17	0.012	0.147	0.018	0.097	**0.713**	0.014
COSJNFPRN_8215	17	0.015	0.136	0.017	0.147	0.018	**0.667**
COSJNFPRN_8216	17	0.009	0.158	0.131	**0.473**	0.167	0.062
COSJNFPRN_8217	17	0.010	0.036	0.018	0.036	**0.863**	0.038
COSJNFPRN_8218	17	0.007	0.026	0.014	**0.903**	0.023	0.027
COSJNFPRN_8219	17	0.018	0.275	0.124	0.181	**0.305**	0.097
COSJNFPRN_8220	17	0.010	0.037	0.018	0.034	**0.862**	0.039
COSJNFPRN_8221	17	0.007	0.057	0.017	0.020	**0.860**	0.039
COSJNFPRN_8223	17	0.012	0.109	0.027	0.032	**0.757**	0.063
COSJNFPRN_8224	17	0.006	**0.681**	0.023	0.207	0.046	0.036
COSJNFPRN_8225	17	0.092	0.096	0.047	0.062	**0.609**	0.095
COSJNFPRN_8226	17	0.238	0.129	0.018	0.181	0.063	**0.372**
COSJNFPRN_8227	17	0.024	0.160	0.020	0.104	**0.364**	**0.329**
COSJNFPRN_8228	17	0.010	0.037	0.018	0.036	**0.860**	0.039
COSJNFPRN_8229	17	0.149	0.067	0.023	0.023	**0.707**	0.031
COSJNFPRN_8230	17	0.014	0.054	**0.730**	0.044	0.109	0.050
COSJNFPRN_8231	17	0.023	**0.430**	0.025	0.177	0.285	0.061
COSJNFPRN_8232	17	0.010	**0.827**	0.018	0.088	0.031	0.026
COSJNFPRN_8233	17	0.013	**0.628**	0.017	0.230	0.041	0.071
COSJNFPRN_8234	17	0.009	**0.614**	0.027	0.212	0.083	0.055
COSJNFPRN_8235	17	0.051	**0.763**	0.014	0.129	0.021	0.022
COSJNFPRN_8236	17	0.010	0.116	0.028	0.163	**0.371**	**0.312**
COSJNFPRN_8237	17	0.009	**0.526**	0.022	0.049	0.075	**0.319**
COSJNFPRN_8238	17	0.010	**0.390**	0.029	0.227	0.106	0.238
COSJNFPRN_8239	17	0.007	**0.531**	0.031	0.258	0.088	0.085
COSJNFPRN_8240	17	0.006	0.030	**0.892**	0.028	0.017	0.027
COSJNFPRN_8241	17	0.014	0.086	0.030	0.028	**0.788**	0.053
COSJNFPRN_8242	17	0.007	0.074	0.014	0.033	**0.845**	0.027
COSJNFPRN_8243	17	0.039	0.189	0.021	0.152	**0.390**	0.209
COSJNFSNN_8184	18	0.012	0.131	**0.645**	0.067	0.059	0.088
COSJNFSNN_8185	18	0.010	0.033	**0.853**	0.050	0.027	0.027
COSJNFSNN_8186	18	0.010	0.145	**0.698**	0.084	0.034	0.030
COSJNFSNN_8187	18	0.080	**0.682**	0.027	0.055	0.026	0.129
COSJNFSNN_8188	18	0.012	0.015	**0.860**	0.014	0.085	0.014
COSJNFSNN_8189	18	0.081	**0.686**	0.027	0.052	0.026	0.128
COSJNFSNN_8190	18	0.035	0.024	**0.893**	0.021	0.015	0.013
COSJNFSNN_8191	18	0.011	0.144	0.021	0.089	**0.678**	0.058
COSJNFSNN_8192	18	0.016	0.125	0.030	0.104	**0.483**	0.241
COSJNFSNN_8193	18	0.020	0.029	**0.853**	0.022	0.014	0.062
COSJNFSNN_8194	18	0.034	0.097	**0.301**	0.143	0.067	**0.359**
COSJNFSNN_8195	18	0.008	0.014	**0.912**	0.018	0.021	0.028
COSJNFSNN_8196	18	0.034	0.084	**0.527**	0.084	0.134	0.138
COSJNFSNN_8197	18	0.005	**0.431**	0.033	**0.416**	0.026	0.089
COSJNFSNN_8198	18	0.013	**0.391**	0.026	0.103	0.059	**0.410**
COSJNFSNN_8199	18	0.087	0.067	**0.733**	0.079	0.016	0.018
COSJNFSNN_8200	18	0.008	0.038	**0.886**	0.029	0.025	0.015
COSJNFSNN_8201	18	0.024	**0.824**	0.015	0.098	0.022	0.017
COSJNFSNN_8202	18	0.006	**0.344**	0.033	0.276	0.088	0.253

Individual tree	Pop.#	1	2	3	4	5	6
COSJNFSNN_8203	18	0.009	0.019	**0.921**	0.018	0.014	0.020
COSJNFSNN_8204	18	0.006	**0.429**	0.015	**0.435**	0.046	0.069
COSJNFSNN_8205	18	0.020	0.096	0.018	0.038	**0.757**	0.072
COSJNFSNN_8206	18	0.019	**0.358**	0.035	0.118	0.116	**0.355**
COSJNFSNN_8207	18	0.032	0.104	0.025	0.067	**0.723**	0.049
COSJNFSNN_8208	18	0.020	**0.661**	0.021	0.117	0.075	0.108
COSJNFSNN_8209	18	0.013	0.210	0.037	0.118	**0.300**	**0.322**
COSJNFSNN_8210	18	0.006	**0.366**	0.018	0.093	0.085	**0.432**
COSJNFSNN_8211	18	0.007	0.104	0.028	0.047	**0.712**	0.102
COSJNFSNN_8212	18	0.014	0.056	0.028	**0.444**	0.271	0.189
COSJNFSNN_8213	18	0.007	0.045	0.012	0.190	0.019	**0.728**
COSJNFSPP_8154	19	0.013	0.091	**0.680**	0.117	0.027	0.072
COSJNFSPP_8155	19	0.007	0.041	**0.890**	0.022	0.022	0.018
COSJNFSPP_8156	19	0.007	0.053	**0.833**	0.052	0.033	0.023
COSJNFSPP_8157	19	0.015	**0.433**	0.059	0.184	0.175	0.134
COSJNFSPP_8158	19	0.199	0.101	0.034	0.154	**0.303**	0.209
COSJNFSPP_8159	19	0.024	**0.338**	0.023	0.143	0.241	0.231
COSJNFSPP_8160	19	0.066	**0.540**	0.036	0.204	0.128	0.027
COSJNFSPP_8161	19	0.123	0.254	**0.409**	0.095	0.040	0.077
COSJNFSPP_8162	19	0.011	0.287	0.042	0.129	**0.511**	0.019
COSJNFSPP_8163	19	0.172	**0.317**	0.031	0.091	0.176	0.213
COSJNFSPP_8164	19	0.011	0.160	**0.782**	0.023	0.015	0.008
COSJNFSPP_8165	19	0.045	**0.687**	0.022	0.121	0.109	0.017
COSJNFSPP_8166	19	0.011	0.149	0.025	0.084	**0.597**	0.134
COSJNFSPP_8167	19	0.014	0.025	**0.905**	0.014	0.027	0.015
COSJNFSPP_8168	19	0.014	0.197	0.024	0.198	**0.505**	0.062
COSJNFSPP_8168	19	0.019	0.017	**0.735**	0.017	0.200	0.013
COSJNFSPP_8170	19	0.011	0.029	**0.903**	0.014	0.015	0.028
COSJNFSPP_8171	19	0.008	0.062	0.042	0.144	**0.574**	0.171
COSJNFSPP_8172	19	0.014	0.129	0.031	0.107	**0.647**	0.072
COSJNFSPP_8173	19	0.008	0.013	**0.928**	0.015	0.013	0.024
COSJNFSPP_8174	19	0.008	0.157	0.020	0.145	**0.588**	0.082
COSJNFSPP_8175	19	0.013	0.030	0.013	0.043	**0.875**	0.025
COSJNFSPP_8176	19	0.014	**0.580**	0.042	0.198	0.064	0.102
COSJNFSPP_8177	19	0.009	0.223	0.025	**0.414**	0.158	0.172
COSJNFSPP_8179	19	0.008	**0.689**	0.032	0.167	0.043	0.062
COSJNFSPP_8180	19	0.008	**0.572**	0.029	0.194	0.066	0.130
COSJNFSPP_8181	19	0.006	0.161	0.028	**0.365**	0.049	**0.391**
COSJNFSPP_8182	19	0.010	0.023	**0.912**	0.018	0.018	0.020
COSJNFSPP_8183	19	0.014	0.111	0.029	0.178	**0.481**	0.187
MTBiNFBCN_1211	20	**0.923**	0.009	0.041	0.009	0.008	0.010
MTBiNFBCN_1212	20	**0.953**	0.012	0.007	0.008	0.008	0.013
MTBiNFBCN_1213	20	**0.960**	0.008	0.010	0.007	0.007	0.008
MTBiNFBCN_1215	20	**0.908**	0.023	0.012	0.018	0.023	0.017
MTBiNFBCN_1217	20	**0.954**	0.009	0.007	0.010	0.009	0.011
MTBiNFBCN_1220	20	**0.808**	0.026	0.120	0.020	0.010	0.016
MTBiNFBCN_1221	20	**0.933**	0.015	0.021	0.009	0.009	0.013
MTBiNFBCN_1223	20	**0.867**	0.025	0.016	0.030	0.039	0.023

Individual tree	Pop.#	1	2	3	4	5	6
MTBiNFBCN_1225	20	**0.834**	0.013	0.124	0.009	0.010	0.011
MTBiNFBCN_1226	20	**0.948**	0.011	0.009	0.011	0.012	0.009
MTBiNFCCN_1250	21	**0.901**	0.023	0.030	0.013	0.013	0.021
MTBiNFCCN_1251	21	**0.910**	0.025	0.010	0.018	0.013	0.025
MTBiNFCCN_1254	21	**0.742**	0.060	0.105	0.040	0.021	0.031
MTBiNFCCN_1255	21	**0.887**	0.010	0.070	0.010	0.013	0.010
MTBiNFCCN_1257	21	**0.801**	0.013	0.150	0.011	0.014	0.012
MTBiNFCCN_1260	21	**0.968**	0.006	0.008	0.006	0.006	0.007
MTBiNFCCN_1261	21	**0.918**	0.021	0.011	0.015	0.017	0.017
MTBiNFCCN_1263	21	**0.448**	0.020	**0.450**	0.028	0.021	0.032
MTBiNFCCN_1266	21	**0.911**	0.018	0.011	0.018	0.021	0.021
MTBiNFCCN_1267	21	**0.960**	0.007	0.011	0.007	0.009	0.006
MTBiNFPCN_1229	22	**0.952**	0.011	0.007	0.009	0.011	0.010
MTBiNFPCN_1230	22	**0.900**	0.010	0.059	0.011	0.010	0.011
MTBiNFPCN_1231	22	**0.901**	0.010	0.056	0.011	0.011	0.011
MTBiNFPCN_1235	22	**0.958**	0.009	0.007	0.009	0.009	0.009
MTBiNFPCN_1236	22	**0.904**	0.016	0.028	0.018	0.014	0.021
MTBiNFPCN_1237	22	**0.937**	0.008	0.032	0.009	0.007	0.008
MTBiNFPCN_1240	22	**0.939**	0.008	0.030	0.008	0.008	0.008
MTBiNFPCN_1243	22	**0.919**	0.018	0.011	0.018	0.017	0.016
MTBiNFPCN_1244	22	**0.895**	0.022	0.014	0.018	0.028	0.022
MTBiNFPCN_1245	22	**0.930**	0.014	0.011	0.012	0.018	0.016
OROcNFPFN_0912	23	**0.820**	0.018	0.113	0.015	0.009	0.025
OROcNFPFN_0913	23	**0.728**	0.011	0.221	0.014	0.012	0.014
OROcNFPFN_0914	23	**0.904**	0.010	0.054	0.011	0.009	0.013
OROcNFPFN_0915	23	**0.875**	0.008	0.086	0.011	0.010	0.010
OROcNFPFN_0916	23	**0.899**	0.010	0.057	0.011	0.009	0.014
OROcNFPFN_0917	23	**0.855**	0.023	0.056	0.021	0.018	0.026
OROcNFPFN_0918	23	**0.942**	0.006	0.032	0.008	0.006	0.007
OROcNFPFN_0919	23	**0.803**	0.011	0.145	0.014	0.013	0.014
OROcNFPFN_0920	23	**0.956**	0.006	0.018	0.007	0.006	0.008
OROcNFPFN_0921	23	**0.897**	0.010	0.059	0.012	0.009	0.013
OROcNFPFN_0922	23	**0.946**	0.007	0.025	0.008	0.007	0.009
OROcNFPFN_0923	23	**0.800**	0.015	0.134	0.018	0.011	0.023
OROcNFPFN_0924	23	**0.939**	0.007	0.027	0.011	0.007	0.009
OROcNFPFN_0925	23	**0.914**	0.007	0.057	0.008	0.006	0.008
OROcNFPFN_0926	23	**0.905**	0.010	0.053	0.011	0.009	0.013
OROcNFPFN_0927	23	**0.899**	0.010	0.054	0.012	0.009	0.016
OROcNFPFN_0928	23	**0.750**	0.013	0.173	0.023	0.016	0.025
OROcNFPFN_0929	23	**0.913**	0.008	0.055	0.008	0.008	0.009
OROcNFPFN_0930	23	**0.685**	0.012	0.241	0.025	0.015	0.023
OROcNFPFN_0931	23	0.064	0.015	**0.760**	0.073	0.019	0.071
OROcNFPFN_0932	23	**0.795**	0.014	0.140	0.019	0.011	0.021
OROcNFPFN_0933	23	0.292	0.014	**0.632**	0.024	0.019	0.020
OROcNFPFN_0934	23	0.026	0.040	**0.787**	0.109	0.020	0.018
OROcNFPFN_0935	23	**0.880**	0.011	0.069	0.015	0.010	0.016
OROcNFPFN_0936	23	**0.806**	0.016	0.126	0.017	0.012	0.023
OROcNFPFN_0937	23	0.034	0.015	**0.880**	0.031	0.017	0.023

Individual tree	Pop.#	1	2	3	4	5	6
OROcNFPFN_0938	23	**0.903**	0.009	0.055	0.011	0.009	0.013
OROcNFPFN_0939	23	**0.404**	0.014	**0.524**	0.021	0.017	0.020
OROcNFPFN_0940	23	**0.837**	0.016	0.102	0.014	0.009	0.022
OROcNFPFN_0941	23	**0.913**	0.007	0.058	0.008	0.006	0.008
ORUmNFUmN_2143	24	**0.884**	0.028	0.015	0.020	0.029	0.024
ORUmNFUmN_2144	24	**0.768**	0.046	0.020	0.073	0.044	0.049
ORUmNFUmN_2145	24	**0.766**	0.121	0.031	0.032	0.030	0.021
ORUmNFUmN_2146	24	**0.787**	0.057	0.021	0.038	0.030	0.067
ORUmNFUmN_2147	24	0.271	0.026	**0.604**	0.028	0.038	0.033
ORUmNFUmN_2148	24	**0.776**	0.061	0.019	0.034	0.064	0.047
ORUmNFUmN_2149	24	**0.945**	0.012	0.010	0.010	0.015	0.009
ORUmNFUmN_2150	24	**0.901**	0.021	0.013	0.021	0.022	0.022
ORUmNFUmN_2151	24	**0.850**	0.023	0.015	0.037	0.032	0.043
ORUmNFUmN_2152	24	**0.954**	0.012	0.007	0.008	0.009	0.009
ORUmNFUmN_2153	24	**0.906**	0.026	0.011	0.017	0.018	0.022
ORUmNFUmN_2154	24	**0.757**	0.096	0.014	0.052	0.061	0.022
ORUmNFUmN_2155	24	**0.827**	0.037	0.019	0.032	0.044	0.042
ORUmNFUmN_2156	24	**0.615**	0.047	0.028	0.100	0.112	0.099
ORUmNFUmN_2157	24	**0.450**	0.031	0.050	0.275	0.032	0.162
ORUmNFUmN_2158	24	**0.952**	0.010	0.008	0.009	0.011	0.010
ORUmNFUmN_2159	24	**0.960**	0.009	0.006	0.008	0.009	0.009
ORUmNFUmN_2160	24	**0.888**	0.019	0.034	0.017	0.021	0.021
ORUmNFUmN_2161	24	**0.897**	0.016	0.031	0.018	0.016	0.022
ORUmNFUmN_2162	24	**0.669**	0.074	0.026	0.056	0.090	0.085
ORUmNFUmN_2163	24	**0.882**	0.024	0.017	0.022	0.030	0.025
ORUmNFUmN_2164	24	**0.899**	0.025	0.013	0.017	0.024	0.022
ORUmNFUmN_2165	24	**0.951**	0.010	0.007	0.010	0.010	0.011
ORUmNFUmN_2166	24	**0.559**	0.068	0.029	0.065	0.225	0.054
ORUmNFUmN_2167	24	**0.969**	0.007	0.005	0.006	0.007	0.006
ORUmNFUmN_2168	24	**0.930**	0.014	0.009	0.016	0.013	0.017
ORUmNFUmN_2169	24	**0.876**	0.024	0.016	0.021	0.032	0.032
ORUmNFUmN_2170	24	**0.933**	0.008	0.036	0.007	0.008	0.008
ORUmNFUmN_2171	24	**0.900**	0.021	0.014	0.015	0.027	0.024
ORUmNFUmN_2172	24	**0.940**	0.014	0.009	0.011	0.013	0.013
ORWWNFLGN_2173	25	**0.796**	0.035	0.019	0.058	0.051	0.041
ORWWNFLGN_2174	25	**0.938**	0.011	0.008	0.013	0.019	0.011
ORWWNFLGN_2175	25	**0.888**	0.022	0.014	0.026	0.026	0.025
ORWWNFLGN_2176	25	**0.792**	0.053	0.022	0.036	0.042	0.054
ORWWNFLGN_2177	25	**0.827**	0.041	0.018	0.029	0.048	0.037
ORWWNFLGN_2178	25	**0.943**	0.012	0.008	0.013	0.011	0.013
ORWWNFLGN_2179	25	**0.501**	0.138	0.025	0.083	0.138	0.115
ORWWNFLGN_2180	25	**0.951**	0.010	0.007	0.012	0.009	0.011
ORWWNFLGN_2181	25	**0.910**	0.017	0.012	0.019	0.026	0.017
ORWWNFLGN_2182	25	**0.807**	0.047	0.025	0.026	0.056	0.039
ORWWNFLGN_2183	25	**0.933**	0.015	0.009	0.013	0.016	0.014
ORWWNFLGN_2184	25	**0.888**	0.038	0.011	0.018	0.018	0.027
ORWWNFLGN_2185	25	0.155	0.184	0.036	0.262	0.095	0.269
ORWWNFLGN_2186	25	**0.867**	0.048	0.020	0.021	0.018	0.026

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ORWWNFLGN_2187	25	**0.853**	0.023	0.017	0.030	0.037	0.041
ORWWNFLGN_2188	25	0.210	0.131	0.032	0.246	**0.337**	0.044
ORWWNFLGN_2189	25	**0.309**	0.059	0.044	0.173	0.290	0.125
ORWWNFLGN_2190	25	**0.955**	0.010	0.007	0.008	0.009	0.010
ORWWNFLGN_2191	25	**0.858**	0.029	0.021	0.027	0.039	0.028
ORWWNFLGN_2192	25	**0.937**	0.014	0.009	0.012	0.015	0.013
ORWWNFLGN_2193	25	**0.802**	0.037	0.020	0.051	0.054	0.036
ORWWNFLGN_2194	25	**0.749**	0.115	0.033	0.046	0.034	0.023
ORWWNFLGN_2195	25	**0.777**	0.079	0.020	0.035	0.036	0.054
ORWWNFLGN_2196	25	**0.826**	0.028	0.014	0.045	0.023	0.064
ORWWNFLGN_2197	25	**0.623**	0.070	0.032	0.055	0.146	0.074
ORWWNFLGN_2198	25	**0.606**	0.145	0.039	0.043	0.050	0.118
ORWWNFLGN_2199	25	**0.923**	0.014	0.011	0.015	0.024	0.013
ORWWNFLGN_2200	25	**0.913**	0.016	0.012	0.020	0.022	0.017
ORWWNFLGN_2201	25	**0.928**	0.015	0.010	0.014	0.016	0.016
SDBHNFBSN_2020	26	0.006	0.033	0.015	0.021	**0.889**	0.037
SDBHNFBSN_2021	26	0.017	0.122	0.028	0.259	**0.389**	0.186
SDBHNFBSN_2022	26	0.007	**0.704**	0.022	0.151	0.063	0.054
SDBHNFBSN_2023	26	0.019	0.143	0.041	0.149	**0.574**	0.074
SDBHNFBSN_2024	26	0.007	**0.396**	0.039	0.272	0.109	0.177
SDBHNFBSN_2025	26	0.020	**0.355**	0.035	0.118	0.116	**0.357**
SDBHNFBSN_2026	26	0.008	0.197	0.024	**0.328**	0.297	0.146
SDBHNFBSN_2027	26	0.013	0.159	0.029	0.174	0.272	**0.354**
SDBHNFBSN_2028	26	0.039	**0.832**	0.009	0.070	0.011	0.040
SDBHNFBSN_2029	26	0.008	0.145	0.026	**0.340**	0.256	0.224
SDBHNFBSN_2030	26	0.014	0.155	0.032	0.151	**0.400**	0.248
SDBHNFBSN_2031	26	0.021	**0.662**	0.021	0.129	0.103	0.065
SDBHNFBSN_2032	26	0.011	**0.630**	0.039	0.090	0.123	0.107
SDBHNFBSN_2033	26	0.027	0.150	0.037	0.110	**0.427**	0.250
SDBHNFBSN_2034	26	0.012	0.151	0.026	0.047	**0.647**	0.117
SDBHNFBSN_2035	26	0.010	0.281	0.026	0.100	0.044	**0.538**
SDBHNFBSN_2036	26	0.014	0.116	0.029	0.178	**0.479**	0.185
SDBHNFBSN_2037	26	0.009	**0.576**	0.038	0.099	0.136	0.142
SDBHNFBSN_2038	26	0.008	0.185	0.028	0.278	0.211	0.290
SDBHNFBSN_2039	26	0.024	0.076	**0.577**	0.075	0.146	0.103
SDBHNFBSN_2040	26	0.008	**0.819**	0.019	0.091	0.033	0.031
SDBHNFBSN_2041	26	0.020	**0.352**	0.029	0.067	0.092	**0.441**
SDBHNFBSN_2042	26	0.008	0.200	0.023	**0.322**	**0.302**	0.145
SDBHNFBSN_2043	26	0.016	0.125	0.030	0.108	**0.481**	0.240
SDBHNFBSN_2044	26	0.008	**0.795**	0.018	0.097	0.027	0.056
SDBHNFBSN_2045	26	0.007	**0.307**	0.028	0.130	0.116	**0.413**
SDBHNFBSN_2046	26	0.010	0.157	0.031	0.138	**0.608**	0.057
SDBHNFBSN_2047	26	0.010	0.139	0.029	0.093	**0.344**	**0.386**
SDBHNFBSN_2048	26	0.024	0.165	0.020	0.101	**0.357**	**0.333**
SDBHNFBSN_2049	26	0.010	0.039	0.017	0.037	**0.862**	0.036
SDBHNFBSN_2050	26	0.009	0.085	0.037	0.261	0.160	**0.449**
SDBHNFBSN_2051	26	0.015	0.223	0.081	0.152	0.289	0.240
SDBHNFBSN_2052	26	0.086	**0.309**	0.027	0.246	0.108	0.225

Individual tree	Pop.#	1	2	3	4	5	6
SDBHNFBSN_2053	26	0.012	0.215	0.035	0.115	**0.303**	**0.319**
SDBHNFBSN_2054	26	0.036	**0.615**	0.066	0.135	0.097	0.050
SDBHNFMVP_5892	27	0.041	0.261	0.025	0.188	0.266	0.218
SDBHNFMVP_5893	27	0.010	0.068	0.022	0.284	0.085	**0.531**
SDBHNFMVP_5894	27	0.050	0.128	0.020	0.283	0.116	**0.404**
SDBHNFMVP_5895	27	0.007	0.013	0.010	**0.911**	0.021	0.037
SDBHNFMVP_5896	27	0.062	0.072	0.041	**0.366**	0.198	0.261
SDBHNFMVP_5897	27	0.009	0.052	0.016	0.248	0.026	**0.651**
SDBHNFMVP_5898	27	0.012	0.113	0.047	**0.320**	0.120	**0.388**
SDBHNFMVP_5899	27	0.013	0.087	0.054	0.256	**0.369**	0.222
SDBHNFMVP_5900	27	0.010	0.089	0.022	0.203	0.065	**0.612**
SDBHNFMVP_5901	27	0.011	0.057	0.021	**0.363**	0.110	**0.439**
SDBHNFMVP_5902	27	0.012	0.071	0.022	0.211	0.117	**0.567**
SDBHNFMVP_5903	27	0.009	0.031	0.019	**0.774**	0.101	0.067
SDBHNFMVP_5904	27	0.013	0.240	0.029	0.241	0.165	**0.311**
SDBHNFMVP_5905	27	0.010	0.029	0.011	**0.479**	0.025	**0.446**
SDBHNFMVP_5906	27	0.024	0.146	0.032	0.151	**0.504**	0.144
SDBHNFMVP_5907	27	0.010	0.088	0.025	0.195	**0.444**	0.238
SDBHNFMVP_5908	27	0.017	0.078	0.025	**0.356**	0.124	**0.401**
SDBHNFMVP_5909	27	0.014	0.050	0.017	**0.332**	0.038	**0.549**
SDBHNFMVP_5910	27	0.011	0.093	0.022	0.143	0.078	**0.653**
SDBHNFMVP_5911	27	0.010	0.087	0.025	0.193	**0.449**	0.236
SDBHNFMVP_5912	27	0.009	0.087	0.022	0.203	0.063	**0.615**
SDBHNFMVP_5913	27	0.009	0.122	0.025	0.185	0.250	**0.409**
SDBHNFMVP_5914	27	0.009	0.235	0.026	0.278	0.177	0.275
SDBHNFMVP_5915	27	0.014	0.114	0.029	0.181	**0.480**	0.181
SDBHNFMVP_5916	27	0.014	0.041	0.017	**0.419**	0.043	**0.466**
SDBHNFMVP_5917	27	0.010	0.100	0.038	0.116	0.197	**0.539**
SDBHNFMVP_5918	27	0.010	0.102	0.023	0.108	0.023	**0.733**
SDBHNFMVP_5919	27	0.010	0.100	0.034	0.112	**0.649**	0.096
SDBHNFMVP_5920	27	0.010	0.088	0.024	0.198	**0.448**	0.232
SDBHNFMVP_5921	27	0.008	0.046	0.019	0.056	**0.793**	0.079
UTUNFBSGP_1556	28	**0.870**	0.011	0.083	0.013	0.012	0.013
UTUNFBSGP_1557	28	**0.960**	0.008	0.006	0.008	0.008	0.009
UTUNFBSGP_1558	28	**0.932**	0.015	0.010	0.011	0.017	0.015
UTUNFBSGP_1559	28	**0.907**	0.019	0.013	0.020	0.025	0.017
UTUNFBSGP_1560	28	**0.861**	0.021	0.044	0.023	0.025	0.027
UTUNFBSGP_1561	28	**0.921**	0.017	0.012	0.014	0.023	0.013
UTUNFBSGP_1562	28	**0.846**	0.061	0.011	0.033	0.035	0.015
UTUNFBSGP_1563	28	0.049	0.073	**0.554**	0.080	0.171	0.074
UTUNFBSGP_1564	28	**0.890**	0.010	0.072	0.009	0.012	0.008
UTUNFBSGP_1565	28	**0.774**	0.092	0.020	0.028	0.031	0.055
UTUNFBSGP_1566	28	**0.627**	0.060	0.030	0.088	0.118	0.076
UTUNFBSGP_1567	28	**0.816**	0.046	0.019	0.032	0.050	0.036
UTUNFBSGP_1568	28	**0.855**	0.032	0.016	0.025	0.047	0.026
UTUNFBSGP_1569	28	**0.917**	0.019	0.012	0.016	0.020	0.016
UTUNFBSGP_1570	28	**0.932**	0.015	0.010	0.013	0.015	0.015
UTUNFBSGP_1571	28	**0.645**	0.044	0.026	0.106	0.090	0.090

Individual tree	Pop.#	1	2	3	4	5	6
UTUNFBSGP_1572	28	**0.728**	0.048	0.025	0.055	0.076	0.067
UTUNFBSGP_1573	28	**0.426**	0.198	0.017	0.047	0.025	0.287
UTUNFBSGP_1574	28	**0.912**	0.021	0.012	0.016	0.022	0.017
UTUNFBSGP_1575	28	**0.918**	0.019	0.011	0.016	0.019	0.017
UTUNFBSGP_1576	28	**0.884**	0.014	0.073	0.009	0.009	0.012
UTUNFBSGP_1577	28	**0.933**	0.013	0.010	0.016	0.016	0.012
UTUNFBSGP_1578	28	**0.807**	0.073	0.018	0.026	0.026	0.051
UTUNFBSGP_1579	28	**0.900**	0.018	0.013	0.023	0.024	0.023
UTUNFBSGP_1580	28	**0.627**	0.084	0.033	0.062	0.097	0.098
UTUNFBSGP_1581	28	**0.745**	0.059	0.018	0.046	0.069	0.063
UTUNFBSGP_1582	28	**0.954**	0.010	0.008	0.010	0.009	0.011
UTUNFBSGP_1583	28	**0.852**	0.027	0.016	0.042	0.034	0.030
UTUNFBSGP_1584	28	**0.961**	0.009	0.007	0.008	0.008	0.008
UTUNFBSGP_1585	28	**0.947**	0.010	0.008	0.011	0.012	0.012
UTUNFBSGP_1586	28	**0.663**	0.060	0.029	0.045	0.107	0.096
UTUNFPoCP_0201	29	0.296	0.018	0.012	0.014	**0.644**	0.016
UTUNFPoCP_0202	29	0.020	0.030	0.013	0.052	**0.857**	0.029
UTUNFPoCP_1524	29	0.008	**0.827**	0.017	0.100	0.022	0.028
UTUNFPoCP_1525	29	0.008	0.124	0.019	**0.433**	0.253	0.163
UTUNFPoCP_1526	29	**0.750**	0.051	0.035	0.034	0.062	0.068
UTUNFPoCP_1527	29	0.010	**0.642**	0.033	0.132	0.112	0.072
UTUNFPoCP_1530	29	0.020	0.058	**0.401**	0.070	**0.411**	0.040
UTUNFPoCP_1531	29	0.007	**0.770**	0.019	0.113	0.049	0.042
UTUNFPoCP_1532	29	**0.514**	0.027	0.016	**0.378**	0.039	0.026
UTUNFPoCP_1533	29	0.013	0.147	**0.589**	0.046	0.053	0.152
UTUNFPoCP_1534	29	**0.651**	0.115	0.035	0.041	0.063	0.095
UTUNFPoCP_1536	29	0.033	**0.406**	0.028	0.112	0.075	**0.347**
UTUNFPoCP_1537	29	0.024	0.143	0.033	0.155	**0.496**	0.149
UTUNFPoCP_1538	29	**0.818**	0.026	0.019	0.056	0.048	0.034
UTUNFPoCP_1539	29	**0.822**	0.045	0.018	0.029	0.046	0.040
UTUNFPoCP_1541	29	**0.876**	0.025	0.014	0.027	0.024	0.034
UTUNFPoCP_1542	29	0.017	**0.318**	**0.498**	0.062	0.042	0.063
UTUNFPoCP_1543	29	**0.637**	0.220	0.057	0.043	0.023	0.020
UTUNFPoCP_1544	29	0.008	**0.728**	0.029	0.142	0.032	0.061
UTUNFPoCP_1546	29	0.010	**0.527**	0.021	0.255	0.050	0.136
UTUNFPoCP_1547	29	0.010	**0.862**	0.015	0.076	0.017	0.021
UTUNFPoCP_1548	29	**0.896**	0.021	0.014	0.014	0.030	0.026
UTUNFPoCP_1549	29	0.162	**0.661**	0.030	0.074	0.047	0.026
UTUNFPoCP_1550	29	0.007	**0.807**	0.018	0.100	0.033	0.035
UTUNFPoCP_1551	29	**0.947**	0.011	0.008	0.012	0.011	0.012
UTUNFPoCP_1552	29	0.020	0.282	**0.544**	0.059	0.061	0.035
UTUNFPoCP_1553	29	0.091	**0.788**	0.013	0.058	0.011	0.039
UTUNFPoCP_1554	29	0.021	**0.656**	0.020	0.135	0.102	0.066
UTUNFPoCP_1555	29	0.054	0.094	0.024	**0.789**	0.016	0.023
UTWCNFSCQ_2055	30	0.057	**0.353**	0.041	0.182	0.075	0.293
UTWCNFSCQ_2056	30	0.041	**0.344**	0.023	**0.439**	0.087	0.067
UTWCNFSCQ_2057	30	0.007	0.154	0.024	**0.767**	0.025	0.024
UTWCNFSCQ_2058	30	0.015	0.251	0.069	**0.302**	0.049	**0.316**

Individual tree	Pop.#	1	2	3	4	5	6
UTWCNFSCQ_2059	30	0.116	0.145	0.037	0.070	**0.457**	0.174
UTWCNFSCQ_2060	30	0.010	0.174	0.047	0.271	0.156	**0.342**
UTWCNFSCQ_2061	30	**0.360**	0.097	0.038	0.128	0.081	0.297
UTWCNFSCQ_2062	30	0.011	**0.622**	0.024	0.036	0.030	0.277
UTWCNFSCQ_2063	30	0.012	**0.645**	0.034	0.142	0.061	0.106
UTWCNFSCQ_2064	30	0.124	**0.343**	0.051	0.175	0.205	0.103
UTWCNFSCQ_2065	30	0.013	**0.497**	0.034	**0.302**	0.103	0.051
UTWCNFSCQ_2066	30	0.142	0.191	0.034	0.065	0.257	**0.311**
UTWCNFSCQ_2067	30	0.020	**0.356**	0.031	0.068	0.092	**0.434**
UTWCNFSCQ_2068	30	0.009	**0.748**	0.025	0.075	0.037	0.106
UTWCNFSCQ_2069	30	0.009	0.095	0.037	0.136	0.154	**0.569**
UTWCNFSCQ_2070	30	0.012	0.108	0.076	**0.473**	0.168	0.164
UTWCNFSCQ_2071	30	0.031	**0.774**	0.013	0.120	0.027	0.036
UTWCNFSCQ_2072	30	0.020	**0.438**	0.014	**0.440**	0.062	0.025
UTWCNFSCQ_2073	30	0.011	0.197	0.032	0.192	0.288	0.280
UTWCNFSCQ_2074	30	0.011	**0.329**	0.027	0.193	0.142	0.297
UTWCNFSCQ_2075	30	0.009	**0.620**	0.030	0.259	0.042	0.041
UTWCNFSCQ_2076	30	0.009	**0.605**	0.011	**0.324**	0.037	0.014
UTWCNFSCQ_2077	30	0.010	**0.399**	0.057	0.164	0.128	0.242
UTWCNFSCQ_2078	30	0.010	**0.812**	0.040	0.062	0.036	0.039
UTWCNFSCQ_2079	30	0.011	**0.691**	0.019	0.175	0.072	0.032
UTWCNFSCQ_2080	30	0.009	0.063	0.026	**0.761**	0.038	0.103
UTWCNFSCQ_2081	30	0.008	0.176	0.031	0.072	**0.596**	0.117
UTWCNFSCQ_2082	30	0.010	**0.816**	0.020	0.085	0.038	0.031
UTWCNFSCQ_2083	30	0.035	**0.825**	0.020	0.088	0.014	0.019
UTWCNFSCQ_2085	30	0.017	**0.826**	0.014	0.091	0.032	0.021
UTWCNFSCQ_2086	30	0.010	0.196	0.021	**0.524**	0.072	0.177
UTWCNFSCQ_2087	30	0.012	**0.576**	0.018	**0.306**	0.064	0.024
UTWCNFSCQ_2088	30	0.042	**0.635**	0.019	0.205	0.026	0.073
UTWCNFSCQ_2089	30	0.011	0.234	0.074	0.034	**0.549**	0.098
UTWCNFSCQ_2090	30	0.011	**0.556**	0.061	0.052	0.292	0.028
UTWCNFSCQ_2091	30	0.010	**0.544**	0.035	0.282	0.064	0.065
UTWCNFSCQ_2092	30	0.017	**0.530**	0.028	0.185	0.096	0.144
UTWCNFSCQ_2093	30	0.007	**0.670**	0.017	0.231	0.043	0.033
UTWCNFSCQ_2094	30	0.010	**0.811**	0.019	0.097	0.038	0.026
UTWCNFSCQ_2095	30	0.014	0.115	0.029	0.175	**0.480**	0.187
UTWCNFYPP_2096	31	**0.918**	0.014	0.010	0.017	0.018	0.024
UTWCNFYPP_2097	31	**0.616**	0.016	0.010	**0.329**	0.012	0.017
UTWCNFYPP_2098	31	**0.894**	0.023	0.015	0.019	0.025	0.024
UTWCNFYPP_2099	31	0.011	**0.863**	0.010	0.092	0.012	0.012
UTWCNFYPP_2100	31	**0.802**	0.035	0.019	0.039	0.048	0.057
UTWCNFYPP_2101	31	**0.688**	0.087	0.027	0.057	0.086	0.055
UTWCNFYPP_2102	31	**0.919**	0.023	0.011	0.015	0.018	0.014
UTWCNFYPP_2103	31	**0.918**	0.025	0.013	0.014	0.015	0.015
UTWCNFYPP_2104	31	**0.963**	0.008	0.006	0.007	0.008	0.008
UTWCNFYPP_2105	31	**0.548**	0.017	0.011	0.012	**0.400**	0.014
UTWCNFYPP_2106	31	**0.910**	0.019	0.012	0.017	0.020	0.022
UTWCNFYPP_2107	31	**0.898**	0.026	0.015	0.019	0.021	0.020

Individual tree	Pop.#	1	2	3	4	5	6
UTWCNFYPP_2108	31	**0.712**	0.067	0.117	0.026	0.026	0.052
UTWCNFYPP_2109	31	**0.932**	0.014	0.009	0.015	0.014	0.017
UTWCNFYPP_2110	31	**0.961**	0.008	0.006	0.007	0.010	0.007
UTWCNFYPP_2111	31	**0.953**	0.010	0.007	0.010	0.009	0.011
UTWCNFYPP_2112	31	**0.666**	0.096	0.018	0.085	0.104	0.032
UTWCNFYPP_2113	31	**0.940**	0.013	0.009	0.013	0.013	0.012
UTWCNFYPP_2114	31	**0.961**	0.008	0.006	0.010	0.008	0.008
UTWCNFYPP_2115	31	**0.890**	0.024	0.014	0.026	0.030	0.017
UTWCNFYPP_2116	31	**0.655**	0.059	0.034	0.126	0.029	0.097
UTWCNFYPP_2117	31	**0.521**	0.099	0.042	0.096	0.143	0.100
UTWCNFYPP_2118	31	**0.957**	0.009	0.007	0.009	0.009	0.010
UTWCNFYPP_2119	31	**0.563**	0.153	0.041	0.044	0.081	0.119
UTWCNFYPP_2120	31	**0.896**	0.019	0.014	0.025	0.026	0.020
UTWCNFYPP_2121	31	**0.744**	0.033	0.018	0.068	0.029	0.108
UTWCNFYPP_2122	31	**0.631**	0.050	0.021	0.029	0.234	0.035
UTWCNFYPP_2123	31	**0.881**	0.032	0.014	0.020	0.014	0.040
UTWCNFYPP_2124	31	**0.810**	0.051	0.021	0.030	0.049	0.039
UTWCNFYPP_2125	31	**0.963**	0.008	0.006	0.008	0.007	0.008
UTWCNFYPP_2126	31	**0.945**	0.011	0.008	0.011	0.011	0.014
UTWCNFYPP_2127	31	**0.930**	0.012	0.010	0.019	0.017	0.013
UTWCNFYPP_2128	31	**0.951**	0.010	0.007	0.011	0.010	0.012
UTWCNFYPP_2129	31	**0.952**	0.010	0.007	0.009	0.010	0.011
UTWCNFYPP_2130	31	**0.947**	0.012	0.008	0.011	0.010	0.013
UTWCNFYPP_2131	31	**0.563**	0.075	0.031	0.083	0.147	0.101
UTWCNFYPP_2132	31	**0.588**	0.073	0.060	0.077	0.059	0.144
UTWCNFYPP_2133	31	**0.941**	0.011	0.008	0.012	0.011	0.016
UTWCNFYPP_2134	31	**0.970**	0.007	0.005	0.006	0.006	0.006
UTWCNFYPP_2135	31	**0.802**	0.043	0.022	0.026	0.059	0.048
UTWCNFYPP_2136	31	**0.897**	0.029	0.013	0.014	0.035	0.013
UTWCNFYPP_2137	31	**0.652**	0.030	0.013	0.009	0.283	0.013
UTWCNFYPP_2138	31	**0.905**	0.022	0.013	0.017	0.023	0.021
UTWCNFYPP_2139	31	**0.867**	0.027	0.016	0.026	0.029	0.036
UTWCNFYPP_2140	31	**0.893**	0.023	0.014	0.020	0.029	0.021
UTWCNFYPP_2141	31	**0.926**	0.024	0.007	0.018	0.016	0.010
UTWCNFYPP_2142	31	**0.601**	0.145	0.019	0.130	0.067	0.038
WAWeNFWeN_2542	32	**0.949**	0.011	0.008	0.011	0.011	0.011
WAWeNFWeN_2543	32	**0.960**	0.008	0.006	0.009	0.008	0.009
WAWeNFWeN_2544	32	**0.869**	0.026	0.015	0.027	0.028	0.035
WAWeNFWeN_2545	32	**0.869**	0.025	0.015	0.021	0.035	0.035
WAWeNFWeN_2546	32	**0.949**	0.011	0.007	0.011	0.010	0.012
WAWeNFWeN_2547	32	**0.939**	0.013	0.009	0.013	0.012	0.015
WAWeNFWeN_2548	32	0.250	0.086	0.038	0.142	**0.342**	0.142
WAWeNFWeN_2549	32	**0.911**	0.018	0.012	0.018	0.020	0.021
WAWeNFWeN_2550	32	**0.926**	0.016	0.011	0.014	0.017	0.016
WAWeNFWeN_2551	32	**0.556**	0.094	0.033	0.088	0.137	0.092
WAWeNFWeN_2552	32	**0.886**	0.030	0.014	0.018	0.035	0.018
WAWeNFWeN_2553	32	**0.940**	0.013	0.020	0.008	0.009	0.011
WAWeNFWeN_2554	32	**0.963**	0.008	0.006	0.007	0.008	0.008

Individual tree	Pop.#	1	2	3	4	5	6
WAWeNFWeN_2555	32	**0.941**	0.012	0.008	0.013	0.012	0.014
WAWeNFWeN_2556	32	**0.924**	0.021	0.009	0.014	0.011	0.021
WAWeNFWeN_2557	32	**0.952**	0.011	0.008	0.009	0.011	0.010
WAWeNFWeN_2558	32	**0.940**	0.014	0.008	0.012	0.014	0.013
WAWeNFWeN_2559	32	**0.899**	0.026	0.013	0.018	0.024	0.020
WAWeNFWeN_2560	32	**0.954**	0.009	0.007	0.010	0.009	0.011
WAWeNFWeN_2561	32	**0.918**	0.014	0.011	0.022	0.017	0.019
WAWeNFWeN_2562	32	**0.858**	0.023	0.016	0.034	0.033	0.036
WAWeNFWeN_2563	32	**0.482**	0.188	0.025	0.157	0.104	0.044
WAWeNFWeN_2564	32	**0.958**	0.010	0.007	0.008	0.009	0.009
WAWeNFWeN_2565	32	**0.966**	0.008	0.006	0.007	0.007	0.007
WAWeNFWeN_2566	32	**0.790**	0.045	0.019	0.041	0.050	0.055
WAWeNFWeN_2567	32	**0.910**	0.020	0.011	0.019	0.018	0.022
WAWeNFWeN_2568	32	**0.930**	0.015	0.009	0.015	0.013	0.018
WAWeNFWeN_2569	32	**0.490**	0.208	0.016	0.179	0.045	0.061
WAWeNFWeN_2570	32	**0.928**	0.016	0.011	0.012	0.018	0.016
WAWeNFWeN_2571	32	**0.811**	0.043	0.021	0.031	0.069	0.025
WYMBNFWCN_2879	33	0.008	0.053	0.021	0.054	**0.812**	0.052
WYMBNFWCN_2880	33	0.048	0.283	0.050	**0.310**	0.095	0.213
WYMBNFWCN_2881	33	0.140	0.155	0.022	0.248	0.117	**0.318**
WYMBNFWCN_2882	33	0.104	0.156	0.024	0.290	0.269	0.157
WYMBNFWCN_2883	33	0.032	0.136	0.031	0.134	**0.627**	0.040
WYMBNFWCN_2884	33	**0.858**	0.031	0.014	0.052	0.027	0.018
WYMBNFWCN_2885	33	0.007	0.040	0.015	0.020	**0.886**	0.032
WYMBNFWCN_2886	33	0.009	0.087	0.022	0.051	**0.804**	0.027
WYMBNFWCN_2887	33	0.040	0.219	0.020	**0.341**	0.281	0.100
WYMBNFWCN_2888	33	0.159	0.084	0.148	**0.359**	0.043	0.207
WYMBNFWCN_2889	33	0.011	**0.446**	0.026	0.111	0.049	**0.357**
WYMBNFWCN_2890	33	0.026	0.065	0.019	**0.428**	0.038	**0.424**
WYMBNFWCN_2891	33	0.160	0.124	**0.523**	0.065	0.072	0.057
WYMBNFWCN_2892	33	0.128	**0.467**	0.044	0.121	0.109	0.132
WYMBNFWCN_2893	33	0.014	0.154	0.033	0.148	**0.410**	0.242
WYMBNFWCN_2894	33	0.024	0.179	0.022	0.178	**0.481**	0.117
WYMBNFWCN_2895	33	0.011	0.041	0.018	0.028	**0.853**	0.049
WYMBNFWCN_2896	33	0.040	0.133	0.019	**0.416**	0.018	**0.375**
WYMBNFWCN_2897	33	0.012	**0.644**	0.048	0.084	0.107	0.105
WYMBNFWCN_2898	33	0.014	0.238	0.027	**0.366**	0.149	0.206
WYMBNFWCN_2899	33	0.047	0.169	0.025	0.243	0.103	**0.412**
WYMBNFWCN_2900	33	0.017	0.072	**0.555**	0.060	0.134	0.161
WYMBNFWCN_2901	33	0.013	0.177	0.039	0.170	**0.458**	0.143
WYMBNFWCN_2902	33	0.018	**0.302**	0.018	0.246	0.038	**0.378**
WYMBNFWCN_2903	33	0.016	0.183	0.024	0.121	**0.344**	**0.312**
WYMBNFWCN_2904	33	0.018	0.210	0.016	**0.314**	0.034	**0.408**
WYMBNFWCN_2905	33	0.010	0.085	0.025	0.196	**0.446**	0.237
WYMBNFWCN_2906	33	0.173	0.221	0.035	0.184	0.070	**0.316**
WYMBNFWCN_2907	33	0.062	0.185	0.029	**0.346**	0.058	**0.321**
WYMBNFWCN_2908	33	0.012	0.116	0.044	0.250	0.182	**0.396**
WYMBNFWCN_2909	33	0.009	0.031	0.014	**0.435**	0.033	**0.478**

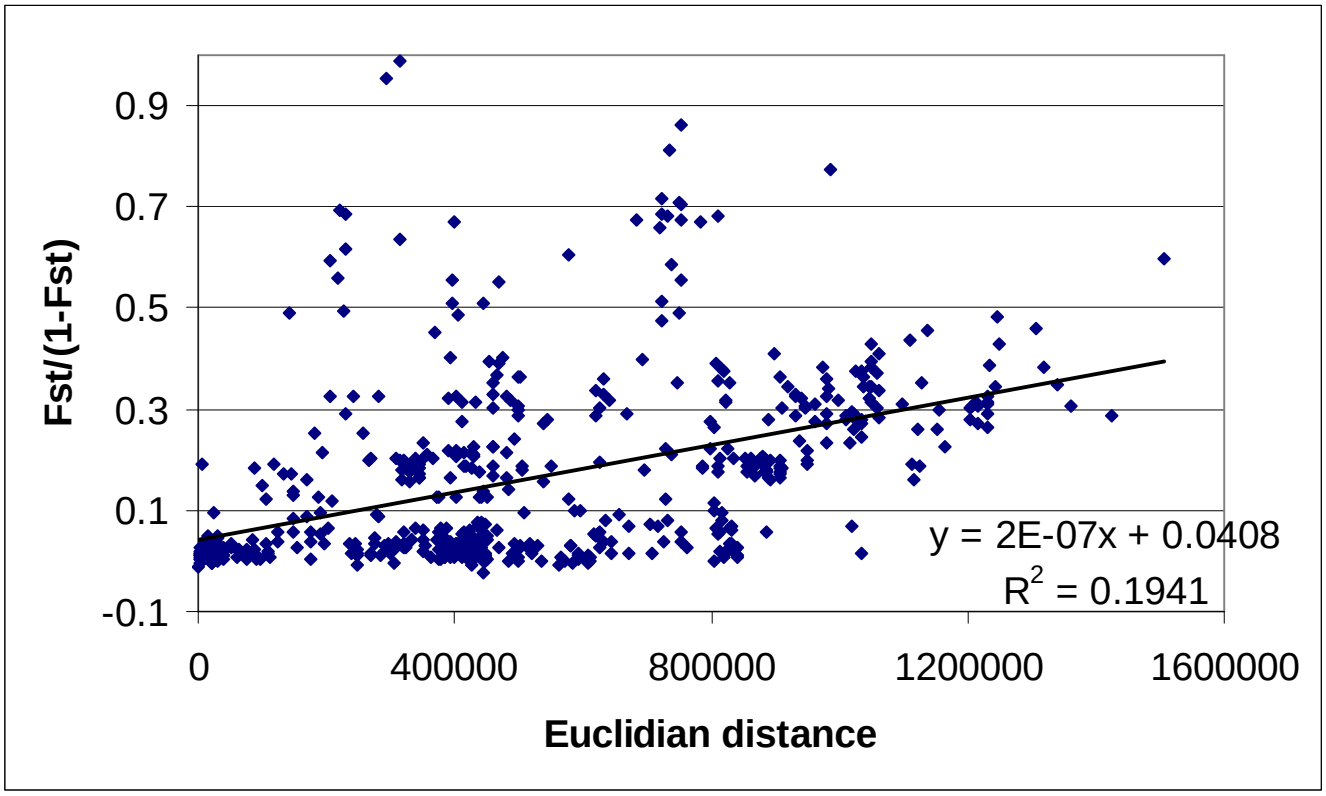
Individual tree	Pop.#	1	2	3	4	5	6
WYMBNFWCN_2910	33	0.044	0.196	0.025	**0.537**	0.028	0.170
WYMBNFWRN_0942	34	0.007	**0.451**	0.019	0.140	0.090	0.292
WYMBNFWRN_0943	34	0.188	0.058	**0.302**	0.127	0.069	0.256
WYMBNFWRN_0944	34	0.012	0.055	0.013	**0.851**	0.049	0.020
WYMBNFWRN_0945	34	0.014	0.067	0.018	0.175	0.037	**0.689**
WYMBNFWRN_0946	34	0.013	0.036	0.017	**0.874**	0.031	0.028
WYMBNFWRN_0947	34	0.015	0.074	0.021	**0.355**	0.086	**0.450**
WYMBNFWRN_0948	34	0.012	0.185	0.013	0.223	**0.468**	0.099
WYMBNFWRN_0949	34	0.006	0.145	0.030	0.082	**0.598**	0.140
WYMBNFWRN_0950	34	0.020	0.100	0.018	0.038	**0.749**	0.075
WYMBNFWRN_0951	34	0.008	0.184	0.029	0.282	0.210	0.286
WYMBNFWRN_0952	34	0.009	0.072	0.024	**0.486**	0.060	**0.349**
WYMBNFWRN_0953	34	0.165	0.107	0.024	**0.451**	0.078	0.175
WYMBNFWRN_0954	34	0.014	0.113	0.027	0.224	**0.355**	0.267
WYMBNFWRN_0955	34	0.015	0.120	0.027	0.201	0.074	**0.564**
WYMBNFWRN_0956	34	0.010	**0.474**	0.026	**0.325**	0.124	0.042
WYMBNFWRN_0957	34	0.026	0.166	0.042	0.062	**0.606**	0.098
WYMBNFWRN_0958	34	0.011	0.187	0.030	**0.317**	0.276	0.180
WYMBNFWRN_0959	34	0.202	0.101	0.025	0.168	0.040	**0.465**
WYMBNFWRN_0960	34	0.011	0.123	0.020	0.067	**0.748**	0.032
WYMBNFWRN_0961	34	0.011	0.065	0.027	0.144	**0.493**	0.260
WYMBNFWRN_0962	34	0.008	0.243	0.017	0.100	0.041	**0.590**
WYMBNFWRN_0963	34	0.008	0.098	0.016	**0.360**	0.035	**0.484**
WYMBNFWRN_0964	34	**0.552**	0.042	0.223	0.039	0.101	0.042
WYMBNFWRN_0965	34	0.010	0.119	0.030	0.162	**0.372**	**0.308**
WYMBNFWRN_0966	34	0.008	0.031	0.017	0.039	**0.858**	0.048
WYMBNFWRN_0967	34	0.031	0.046	**0.654**	0.025	0.210	0.035
WYMBNFWRN_0968	34	0.016	0.158	0.037	0.027	**0.743**	0.020
WYMBNFWRN_0969	34	0.011	0.098	0.028	0.115	**0.448**	**0.301**
WYMBNFWRN_0970	34	0.014	**0.583**	0.021	0.219	0.050	0.112
WYMBNFWRN_0971	34	0.020	0.094	0.022	**0.412**	0.113	**0.339**

Highlighted in pink are memberships of 0.3 and higher.

Table 13. Frequency of four mtDNA haplotypes (***A-D***) found in 34 P. ponderosa populations

Type	#	Population	*A* "West" (A*)	*B* "South" (D*)	*C* "East" (C*)	*D* "Northwest" (B*)	# trees
N	Pop32	WA-WeNF-We-N	0	0	0	1	29
N	Pop23	OR-OcNF-PF-N	1	0	0	0	30
N	Pop24	OR-UmNF-Um-N	1	0	0	0	29
N	Pop25	OR-WWNF-LG-N	1	0	0	0	29
N	Pop20	MT-BiNF-BC-N	1	0	0	0	10
N	Pop21	MT-BiNF-CC-N	1	0	0	0	10
N	Pop22	MT-BiNF-PC-N	1	0	0	0	10
N	Pop1	AZ-ASNF-17-N	0	1	0	0	70
N	Pop2	AZ-CoNF-Co-N	0	1	0	0	29
N	Pop3	AZ-KaNF-Ka-N	0	1	0	0	27
N	Pop15	CO-SJNF-BD-N	0	1	0	0	31
N	Pop17	CO-SJNF-PR-N	0	1	0	0	29
N	Pop18	CO-SJNF-SN-N	0	1	0	0	30
N	Pop13	CO-SJNF-8m-N	0	0.9667	0.0333	0	30
N	Pop10	CO-GMUG-SM-N	0	0.9259	0.0741	0	27
N	Pop34	WY-MBNF-WR-N	0	0.7333	0.2667	0	30
N	Pop12	CO-RGNF-LW-N	0	0.3030	0.6970	0	33
N	Pop26	SD-BHNF-BS-N	0	0	1	0	35
N	Pop33	WY-MBNF-WC-N	0	0	1	0	31
P	Pop28	UT-UNF-BSG-P	1	0	0	0	31
P	Pop31	UT-WCNF-YP-P	1	0	0	0	47
P	Pop29	UT-UNF-PoC-P	0.3793	0.1379	0.1724	0.3103	29
Q	Pop30	UT-WCNF-SC-Q	0	0.8750	0.0000	0.1250	40
P	Pop7	CO-BLM-VM60P	0	0.9412	0.0588	0	34
P	Pop5	CO-BLM-AM70P	0	0.5862	0.4138	0	29
P	Pop6	CO-BLM-AM90P	0.2000	0.5000	0.3000	0	30
P	Pop27	SD-BHNF-MV-P	0	0	1	0	30
P	Pop19	CO-SJNF-SP-P	0	0.0345	0.9655	0	29
P	Pop8	CO-BLM-VM70P	0	0.0938	0.9062	0	32
P	Pop14	CO-SJNF-8m-P	0	0.1000	0.9000	0	30
P	Pop4	CO-BLM-AM60P	0	0.1034	0.8966	0	29
P	Pop9	CO-GMUG-DN-P	0	0.1786	0.8214	0	28
P	Pop16	CO-SJNF-Na-P	0	0.2333	0.7667	0	30
P	Pop11	CO-GMUG-Tr-P	0	0.3000	0.7000	0	30
		Overall	0.2074	0.4245	0.3262	0.0419	1027

* Likely corresponds to haplotype described in Latta and Mitton 1999 and Johansen and Latta 2003.



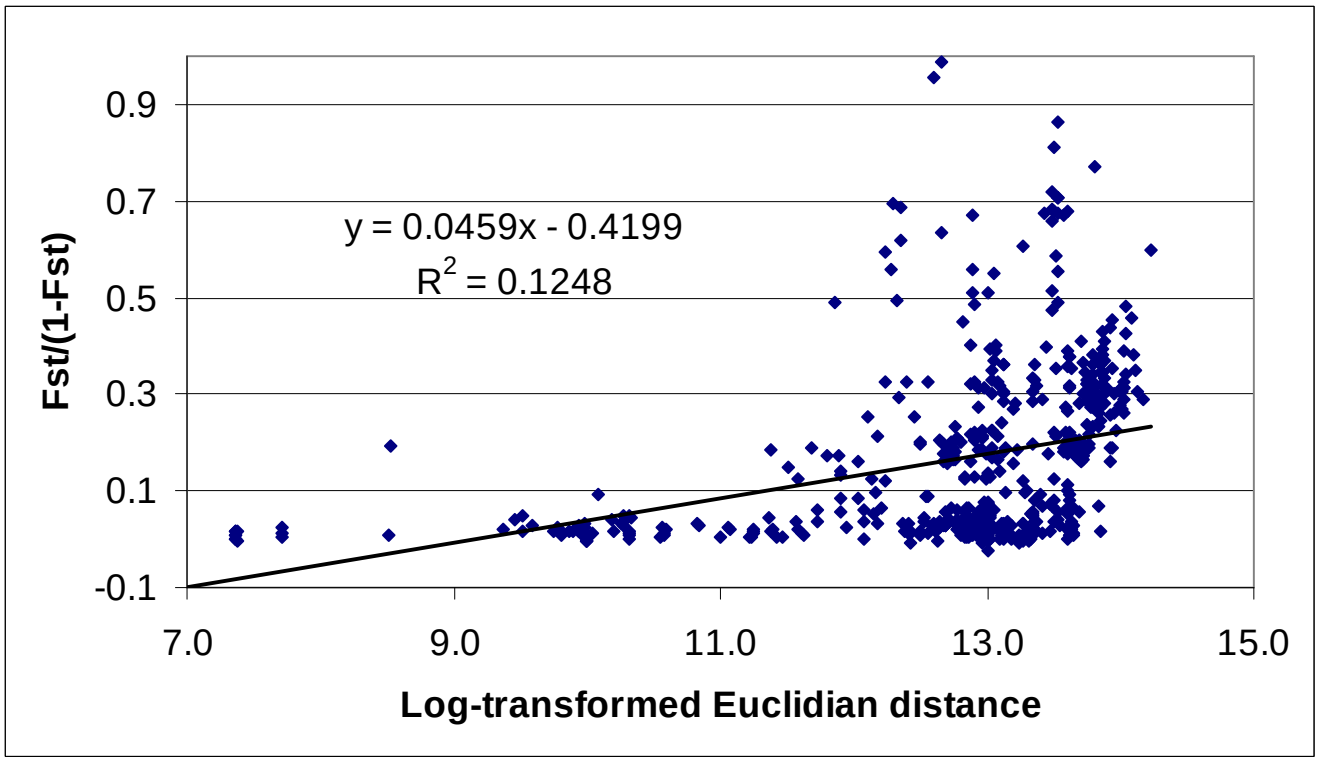


Figure 1 Scatterplots of pairwise genetic differentiation ($F_{ST}/(1-F_{ST})$) between 34 populations of *Pinus ponderosa* vs. pairwise geographic distances between them calculated as Euclidian distances (relative unit) from UTM coordinates X, Y, and Z in Table 2.

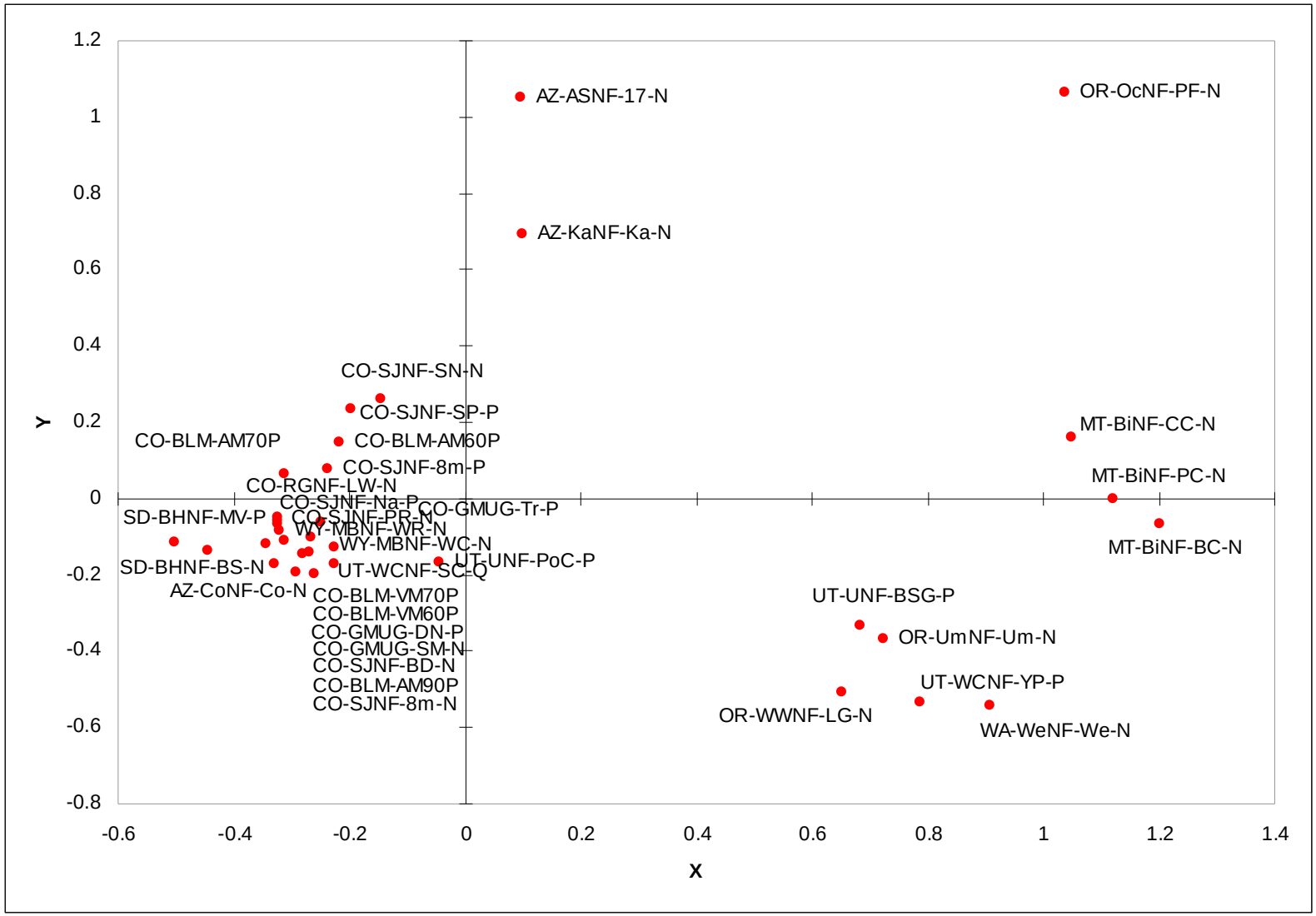


Figure 2 Distribution of 34 populations of *Pinus ponderosa* along Principal Components I (X) and II (Y)

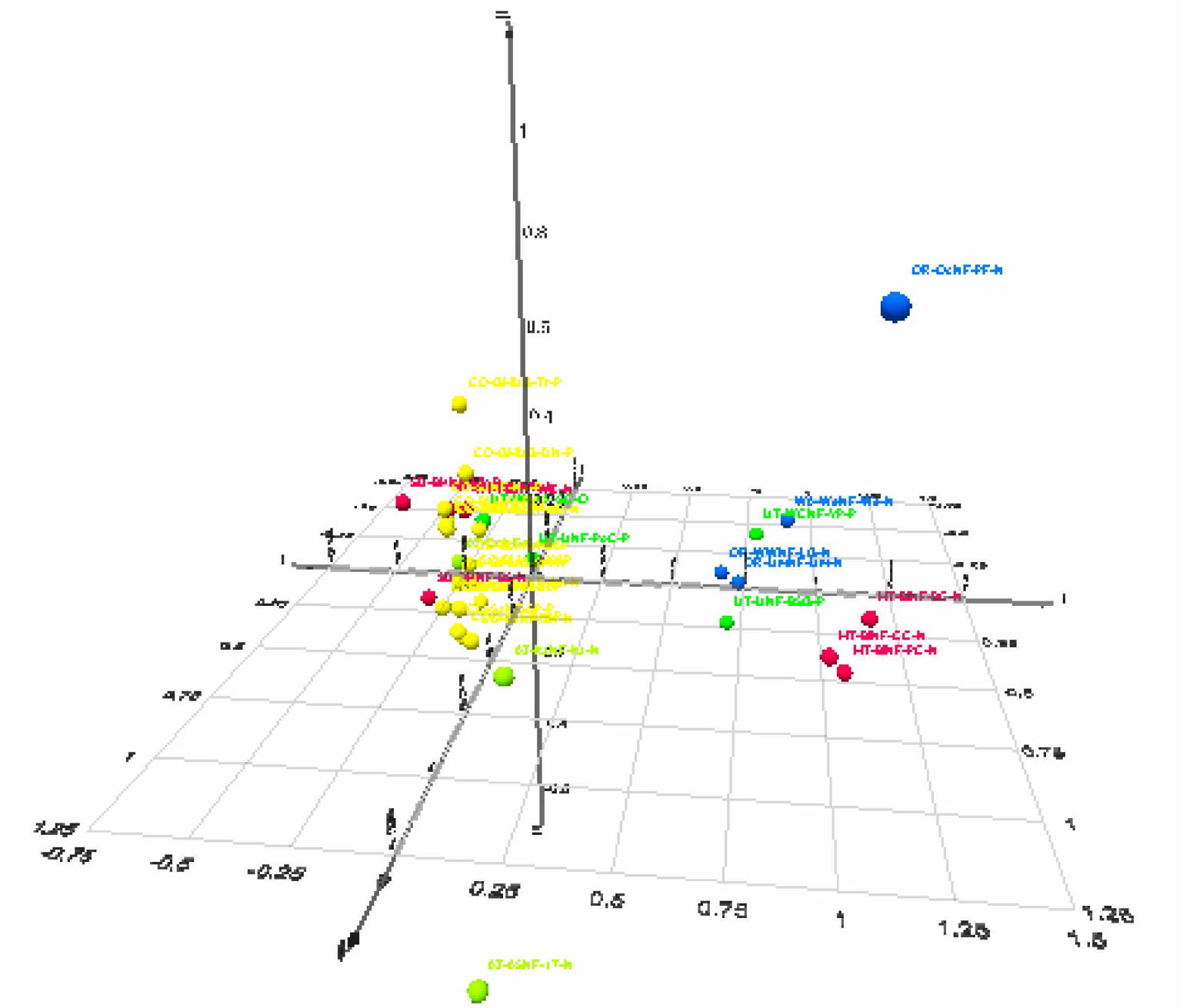


Figure 3 3D distribution of 34 populations of *Pinus ponderosa* along Principal Components I, II, and III.

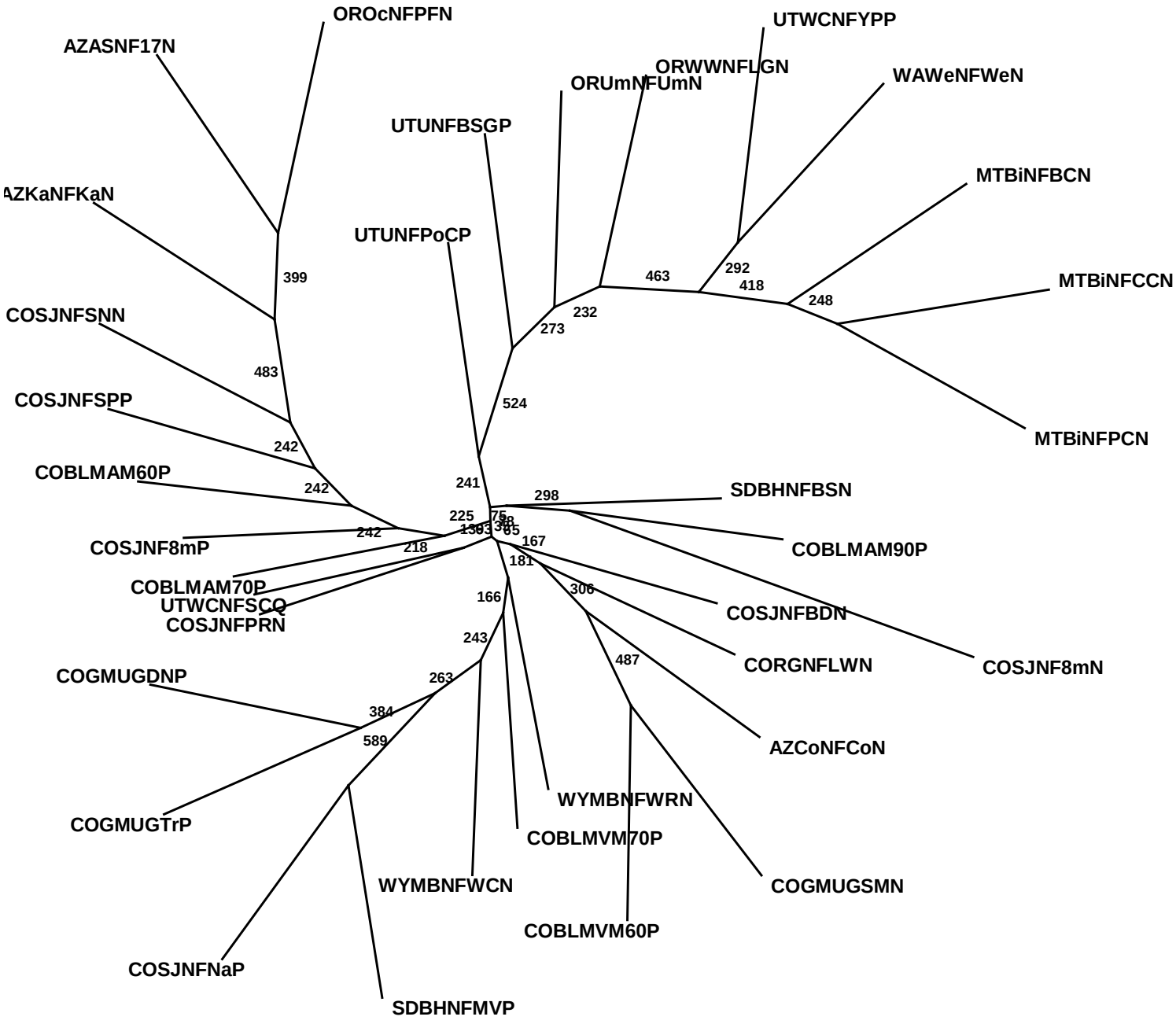


Figure 4. Consensus unrooted Neighbor-Joining Tree of 34 populations of *Pinus ponderosa* based on Nei's (1978) genetic distance calculated using 22 genetic markers. Numbers under nodes are bootstrap values out of total 1000 bootstraps.

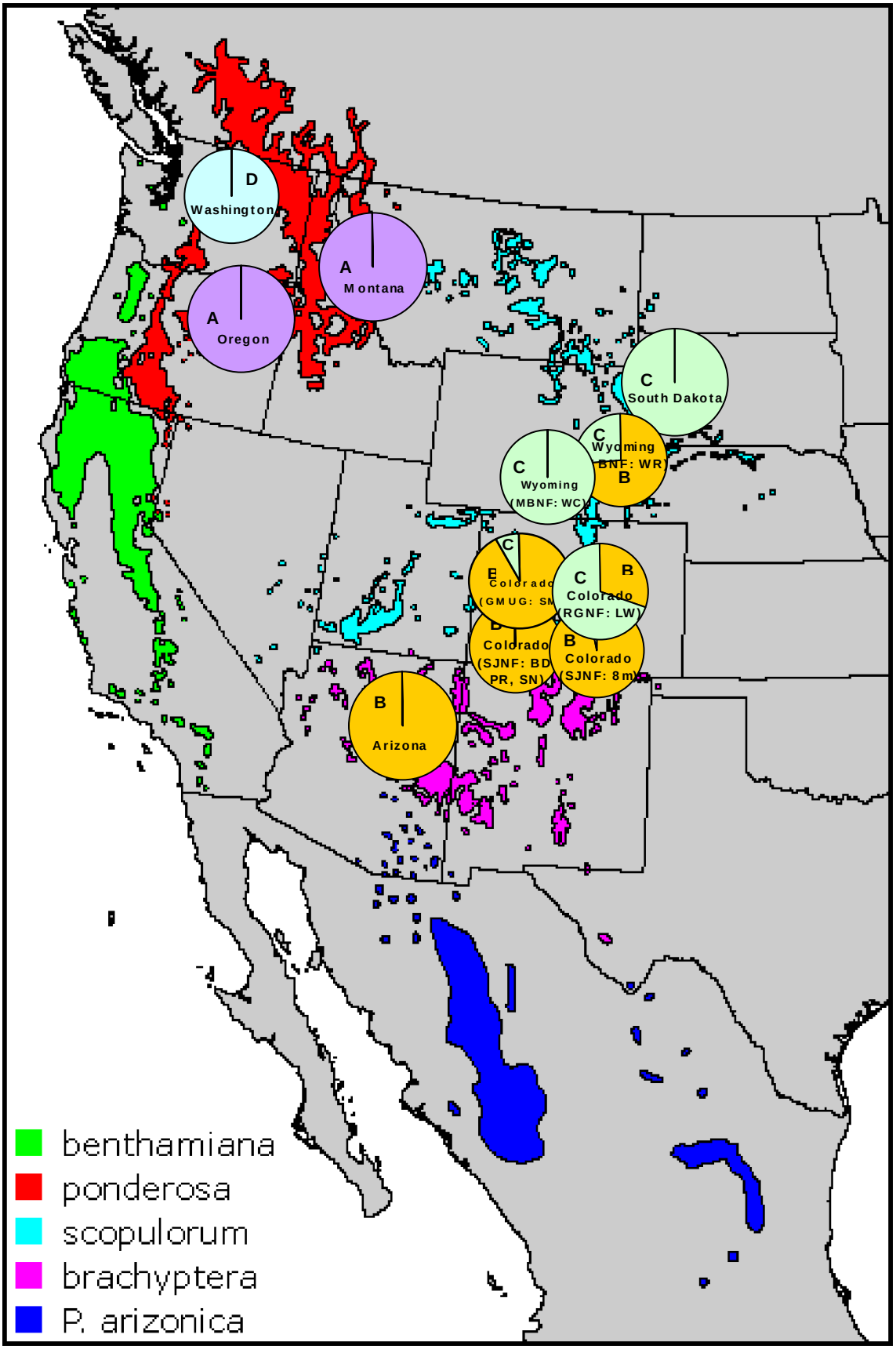


Figure 5 Distribution of *Pinus ponderosa* (USGS 1999) and mtDNA haplotypes in natural populations.

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Final Report

Identification of Ten Unknown Seedlings as *Pinus echinata* (Shortleaf pine) or *P. virginiana* (Virginia pine) through Genetic Testing

Project submitted by: Kathryn Wallace, USDA Forest Service, Bankhead Ranger District, Alabama

Report prepared by: Valerie Hipkins and Konstantin Krutovsky

August 12, 2005

SUMMARY

Genetic testing confirmed that eight of the ten unknown *Pinus* seedlings submitted for analysis are either pure Virginia pine or Virginia pine hybrids. The other two unknown seedlings submitted are either pure Shortleaf pine or Shortleaf pine hybrids.

INTRODUCTION

Ten unknown samples of *Pinus spp.* were submitted for genetic analysis in order to determine whether each sample is *Pinus echinata* (Shortleaf pine), *P. virginiana* (Virginia Pine), or a hybrid of the two species.

DNA testing is able to determine species identity. To begin the species identification, we used the *rbc*L gene, which is highly conserved among plants due to its critical function in photosynthesis. When there are differences in *rbc*L sequences between species, it can serve as an excellent species marker because of this very high degree of conservation. Because the *rbc*L gene is inherited through the father in these species, this sequence lets you know the identity of the taxon that served at the paternal parent.

After determining the identity of the father of the 10 unknown seedlings, we next proceeded to characterize differences among the samples in their mitochondrial DNA (mtDNA). In pines, mtDNA is inherited through the mother. By finding species specific mtDNA variation, we can determine the maternal parent of the unknown samples. Together, the *rbc*L and mtDNA information are used to identify unknown seedlings as being shortleaf pine, Virginia pine, or hybrids.

METHODS

Samples. Ten unknown samples consisting of needle tissue of *Pinus spp.* were submitted for genetic analysis. Sixteen samples of *P. echinata* and 14 samples of *P. virginiana*, all positively identified based on morphological characteristics, were used for comparison and to determine appropriate species-specific markers (Table 1).

DNA Extraction. DNA was extracted from 100 mg of liquid nitrogen ground needle tissue for each sample using Qiagen™ DNEasy Mini kits (Qiagen, Valencia, CA) according to the manufacturer's instructions. DNA concentration was quantified by fluorometry, and quality was assessed by agarose gel electrophoresis. Sufficient quantities of DNA were obtained so that no additional extractions were required. DNA was stored at -80C.

Chloroplast DNA Markers (paternal parent ID). Amplification of the *rbc*L gene (located in the chloroplast genome) was completed using primers designed by Wang *et al.* (1999), following their published amplification reaction and cycling conditions. Amplification was carried out on a MJ Research® PTC-100 thermalcycler. Following amplification, the product was purified using the Qiagen™ Qiaquick PCR Purification Kit (Qiagen, Valencia, CA) following the recommended protocols. Two ul of the cleaned PCR product served as the template in a sequencing reaction, using the ABI Big Dye 3.1 Sequencing Kit (Applied Biosystems, Foster City, CA) following the manufacturer's recommendations for ¼ reactions. Sequencing was performed on an ABI 3100 Genetic Analyzer (Applied Biosystems, Foster City, CA) and edited and aligned with the known sequences from *P. echinata* and *P. virginiana* obtained from Genebank. Comparison of the sequences allows classification of a new sequence into one or the other species.

A second chloroplast DNA gene was partially sequenced to confirm paternal identity. The maturase gene, *mat*K, was amplified using primers designed by Wang *et al.* (1999), following their published amplification reaction and cycling conditions. Amplification and sequencing was carried out as for *rbc*L sequencing.

Mitochondrial DNA Markers (maternal parent ID). Two mtDNA regions, *nad*1 and *nad*7, were characterized to look for species specific sequence variation. The pine sequences available for the *nad*1 region in Genbank (*Pinus cembra* AF160261, *P. densata* AF440388, *P. pinaster* AJ509804-AJ509806, *P. ponderosa* AF231325, *P. pumila* AF227463, *P. sibirica* AF160260, *P. sylvestris* AJ223312, *P. tabuliformis* AF440384, and *P. yunnanensis* AF440385-AF440387) were downloaded and aligned using the GeneDoc software (Nicholas et al. 1997; http://www.psc.edu/biomed/ genedoc). These alignments were used to design forward and reverse PCR primers GGGGCTTATGGGTGAGCAAT (nad1-in2_F2) and CTCTGAATTGACGAATGCCG (nad1-in2_R2), respectively, using the computer program GeneRunner v3.04 (Hastings Software, Hudson, NY; http://www.generunner.com/). *Nad*7 primers were designed similarly. A typical PCR reaction volume was 25 µl and included 10 mm TRIS HCl pH 8.3, 50 mm KCl, 1.5 mm MgCl2, 200 µm of each dNTP, 1 µm of each primer, 1 ng of DNA template, and 0.5 units of HotStar *Taq* DNA Polymerase from QIAGEN (Valencia, CA). Following HotStar *Taq* activation (94º for 15 min), PCR amplification involved denaturation at 94º for 20 sec, annealing for 30 sec, and extension for 2 min. The annealing temperature during the initial 10 cycles was lowered from 65º to 60º by 0.5º every second cycle. An additional 30 cycles of amplification were performed upon reaching the final annealing temperature (60º) followed by a final extension at 72º for 10 min. Amplification product was visualized on ethidium bromide stained, 1.4% TBE agarose gels under UV light. Additionally, *nad*1 fragments were sequenced following the protocol detailed for *rbc*L sequencing.

RESULTS

Identity of the paternal parent. There are 12 nucleotide differences in the *rbc*L gene between Virginia and Shortleaf pines (as determined from *rbc*L sequences obtained from Genebank). Therefore, the sequences from the submitted samples (Table 1) could be easily compared and identified as to matching one species or the other.

- Sequence data from all 14 samples of known Virginia pine submitted for analysis matched the *rbc*L sequence from Virginia pine obtained from Genebank.
- The DNA sequences from the 16 samples of known Shortleaf pine submitted matched the *rbc*L sequence from Shortleaf pine obtained from Genebank.
- Eight of the unknown seedlings had *rbc*L sequences that matched Virginia pine.
- Two of the unknown seedlings had *rbc*L sequences that matched Shortleaf pine.

DNA sequences were submitted to Genbank (http://www.ncbi.nlm.nih.gov) under the authorship of Saich, R, Hipkins, VD, Krutovsky, KV, and Wallace K. Twelve *P. echinata* sequences were submitted with the Accession numbers AY947435, AY947436, AY947438, AY947453 – AY947461. Twenty *P. virginiana* sequences were submitted with the Accession numbers AY947430 – AY947434, AY947437, AY947439 – AY947452.

Sequences from the *mat*K gene confirmed paternal identity as determined by *rbc*L. *Mat*K sequences were also deposited in Genbank: Saich, R, Hipkins, VD, Krutovsky, KV, and Wallace K; AY947428 and AY947429 (*P. echinata*, two samples), AY947423 – AY947427 (*P. virginiana*, five samples).

Because *rbc*L and *mat*K are inherited from the paternal parent, these results indicate the identity of the father for each seedling. Therefore, a seedling that has a Virginia pine type sequence may be a pure Virginia pine seedling if the mother of that seedling was Virginia pine. However, the seedling could also be a hybrid if the mother turned out to be, for example, a Shortleaf pine.

Identity of the maternal parent. Whereas chloroplast DNA is inherited through the father in pines, mitochondrial DNA is inherited through the mother. We used both the *nad*1 and *nad*7 mitochondrial DNA sequences to determine the maternal parent of the unknown seedlings. Both DNA regions have been found to be highly variable among pine species, and the *nad*1sequence has been shown to contain a minisatellite region in the second intron in some pines (Johansen and Latta 2003; Mitton *et al*. 2000).

We characterized two regions in *nad*1, and two regions in *nad*7 (Table 2). We found no differences between the two species in any of these four regions. This was unexpected given how variable these sequences are among other pine species. Because we are unable to distinguish Virginia from shortleaf pine by looking at their mitochondrial DNA, we are not able to determine which species served as the mother to the unknown seedlings.

Without embarking on a large-scale research effort to further characterize mitochondrial DNA variation in these species, we are only able to use the DNA results to identify the father of the unknown seedlings. At this time, the mother of the unknown seedlings remains unknown. However, we can conclusively say that the 10 unknown seedlings tested are not pure Shortleaf pine but some mix with Virginia pine (either pure Virginia pine, some pure Shorteaf pine, and/or hybrid material) (Table 3).

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Wang, XR, Tsumura,Y, Yoshimaru, H, Nagasaka, K. and Szmidt, AE. (1999) Phylogenetic relationships of Eurasian pines (*Pinus*, Pinaceae) based on chloroplast rbcL, MATK, RPL20-RPS18 spacer, and TRNV intron sequences. American Journal of Botany 86(12):1742-1753.

Table 1. *Pinus* samples submitted for genetic analysis.

Species	Orgin of Needle Tissue Submitted	# of Samples
unknown	seedlings	10
Pinus echinata	seedlings submitted by Region 8	10
	adult submitted by Region 8	1
	adults from IFG arboretum	5
Pinus virginiana	seedlings submitted by Region 8	10
	adult submitted by Region 8	1
	adults from IFG arboretum	3

Table 2. Mitochondrial haplotypes observed within and among taxa.

	Primer pair	**nad7-in1_F x nad7-in1_R**	**nad7-in1-in_F x nad7-in1-in_R**	**nad1-in2_F x nad1-in2_R**	**nad1-in2_F2 x nad1-in2_R2**
	Mitochondrial region	**from 3' end of exon1 to 3' end of intron1 in nad7**	**middle of intron1 in nad7**	**middle of intron2 in nad1**	**middle of intron2 in nad1**
Taxon					
P. virginiana		~1.1 kb & ~1.3-1.5 (single or double)	~280-380 bp or 280 bp plus addition (single or multiple)	~520 bp (single)	367 bp (single)
P. echinata		~1.1 kb & ~1.3-1.5 (single or double)	~280-380 bp or 280 bp plus addition (single or multiple)	~520 bp (single)	367 bp (single)
unknown seedlings		~1.1 kb & ~1.3-1.5 (single or double)	~280-380 bp or 280 bp plus addition (single or multiple)	~520 bp (single)	367 bp (single)

Table 3. Species identity of *Pinus* samples submitted for genetic analysis.

Seedling #	Identity of Paternal Parent	Identity of Maternal Parent	Species Identity of Seedling
1	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid
2	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid
3	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid
4	Shortleaf Pine	Unknown	Either pure Shortleaf or a Shortleaf hybrid
5	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid
6	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid
7	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid
8	Shortleaf Pine	Unknown	Either pure Shortleaf or a Shortleaf hybrid
9	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid
10	Virginia Pine	Unknown	Either pure Virginia or a Virginia hybrid

United States Department of Agriculture **Forest Service** **National Forest Genetic Electrophoresis Laboratory (NFGEL)** **2480 Carson Road Placerville, CA 95667 (530) 622-1609 Voice (530) 622-2633 Fax**

(Excerpt from Project #187 Lab Report)

March 14, 2005

We completed the assessment of SMP success for ten Douglas-fir crosses using three SSR markers. SMP success by cross varied between 13.5% to 64.8% (see Table 3).

Three markers developed by the Pacific Northwest Tree Improvement Research Cooperative (PNWTIRC) were used to genotype the parents and progeny: 2C3, 3B2, and 2G12 (the marker names are all preceded by 'OSUPCT_ssrPmOSU_'). We began genotyping the progeny with marker 3B9, but had to drop this marker part-way through the project and re-analyze the samples with marker 3B2. Marker 3B9 was replaced because it yielded inconsistent amplification among the samples. Also, marker 2C3 has limited use for these particular crosses because of the high null allele frequency within the parents. A more intensive prescreening of markers for a given set of parents may be necessary for future projects to optimize markers to parental genotypes.

You provided pedigree information on some of these parents in a prior email. This SSR data addresses some of those relationships. (1) 'K' is not the father of either 'E' or 'F'. (2) 'M' could be the father of 'B'. (3) 'I' could be the mother of 'D'. (4) The data is inconclusive as to whether 'E' and 'F' are full or half-sibs.

Table 1. Genotype data at three SSR loci for 13 Douglas-fir parents. Genotype scores are in base pairs. n=null allele.

				Genotype Data					
Clone#	**Orchard**	**Row**	**Column**	**2C3-1**	**2C3-2**	**3B2-1**	**3B2-2**	**2G12-1**	**2G12-2**
A	R	----	----	177	n	110	163	258	270
B	M	----	----	186	n	125	139	260	270
C	M	----	----	n	n	161	165	270	274
D	M	----	----	186	186	149	171	260	262
E	M	----	----	186	190	99	141	252	n
F	M	----	----	177	190	131	153	258	270
G	S	19	78	170	190	110	143	250	278
H	S	3	21	168	n	110	129	260	262
I	S	15	19	186	n	98	171	260	262
J*	S	20	29	170	181	138	171	264	269
K	S	14	46	181	181	157	161	252	278
L	S	15	10	n	n	136	142	248	272
M	S	7	36	168	186	125	149	260	270

*clone J genotype at 3B2 may be 138/138 or 138/null

Table 2. Number of seed and pollen contaminants per each of ten Douglas-fir crosses using three SSR markers (2C3, 3B2, and 2G12). Six of the ten crosses contained seed that could not have been produced by the expected female parent. This appears to be a significant problem in the "T" cross where 20% of the embryos analyzed could not have come from female parent 'C'.

Cross Identifier (NFGEL #)	Female Parent	Male Parent	# progeny genotyped	seed contaminants		pollen contaminants[1]	
				#	%	#	%
Q	B	I	85	0	0.0	33	38.8
R	B	K	85	0	0.0	54	63.5
S	B	G	82	1	1.2	68	84.0
T	C	G	80	16	20.0	24	37.5
U	M	J	70	1	1.4	33	41.8
V	E	M	79	0	0.0	39	49.4
W	L	D	76	4	5.3	25	34.7
X	H	A	82	6	7.3	50	65.8
Y[2]	G	F	79	0	0.0	27	34.2
Z	I	B	89	1	1.1	71	80.7

[1]calculations made after seed contaminants removed
[2]alleles 131 and 133, marker 3B2, were binned (combined) in the progeny

Table 3. SMP success in ten Douglas-fir crosses using three SSR markers (2C3, 3B2, and 2G12). Calculations were performed as described in "Protocol for estimating SMP success', PNWTIRC.

Cross Identifier (NFGEL #)	Female Parent	Male Parent	# progeny genotyped	% SMP Success (+SE)
Q	B	I	85	60.0 (5.4)
R	B	K	85	34.5 (5.4)
S	B	G	81	13.5 (4.2)
T	C	G	64	61.3 (6.2)
U	M	J	69	50.7 (6.2)
V	E	M	79	49.1 (5.8)
W	L	D	72	64.2 (5.8)
X	H	A	76	32.2 (5.6)
Y	G	F	79	64.8 (5.5)
Z	I	B	88	16.8 (4.3)

United States Department of Agriculture | Forest Service | National Forest Genetic Electrophoresis Laboratory (NFGEL) | 2480 Carson Road Placerville, CA 95667 (530) 622-1609 (530) 622-2633 (fax)

Ramet ID in Douglas-fir

NFGEL Project #190

July 6, 2005

Objective of Work

A Douglas-fir clone bank was established near Port Gamble, Washington in 1979. This facility is now being converted to a second-generation production seed orchard. Two trees in the orchard are listed as elite parental clones, yet they appear to be just escaped rootstock. The objective of the project is to have foliage from these trees compared to foliage from the second ramet of these same clones.

Materials and Methods

Two branch tips, including needles and dormant buds, from each of four individual Douglas-firs trees were submitted for analysis (CLONE-A; CLONE-A1; CLONE-B; CLONE-B1) in April 2005.

Genomic DNA was extracted from bud tissue using the Qiagen DNeasy 96-well format protocol following manufacturers instructions. DNA concentrations were determined by fluorometry using Pico Green, and DNA quality visualized on an 0.8% agarose gel stained with ethidium bromide under UV light.

Samples were genotyped using up to six SSR markers. PCR conditions followed NFGEL Standard Operating Procedures, and amplified fragments were analyzed on an ABI-3100 instrument.

Results and Discussion

Genotypes between 'clonal' pairs mismatched at two or more SSR loci, indicating that the two trees of each pair are not ramets of the same clone.

Table. Genotypes at 4 SSR loci for four Douglas-fir trees (alleles in bp; 0=missing data).

	SSR Locus			
Sample	3B2	3G9	2G12	3F1
A	159/161	140/148	258/270	210/238
A1	120/145	184/186	260/264	0
B	130	160	256/266	184
B1	98/162	158	216/272	182

Contact

Valerie Hipkins, NFGEL Director (vhipkins@fs.fed.us)

Project Submitted by:

Daniel Cress, Olympic Resource Management, regenetics@sprintmail.com

(NFGEL Project #182)

Wheeler N, Payne P, Hipkins V, Saich R, Kenny S, and Tuskan G. 2006. Polymix breeding with paternity analysis in *Populus*: a test for differential reproductive success (DRS) among pollen donors. Tree Genetics & Genomes 2(1):53-60.

Abstract

Polymix breeding with paternity analysis (PMX/WPA) has been proposed as an alternative to traditional full-sib breeding and testing schemes. To fully capture the benefits of PMX/WPA, differential reproductive success (DRS) of pollen parents used in the polymix must be modest. DRS was evaluated in an operational test of PMX/WPA for a hybrid poplar program. A 16 parent pollen polymix (*Populus nigra* L.) was used to pollinate seven clones of *P. deltoides* (Bartr. ex. Marshall) under greenhouse breeding conditions. Progeny were grown out briefly and randomly sampled (357) prior to out-planting in field trials. Twenty-eight SSR loci were evaluated and 15 were selected for genetic characterization in small populations of three *Populus* spp (*P. nigra, P. deltoides,* and *P. trichocarpa* Torr. & Gray). Seven loci were ultimately selected for paternity analysis of progeny. The average exclusion probability of the seven loci in *P. nigra* was 0.604; combined, the theoretical exclusion probability was 0.9999 for the seven loci. However, only 95% of sampled progeny were unambiguously assigned a single paternal parent. Missing data (failure to amplify all primers in all crosses) accounted for most of the ambiguity. DRS was statistically significant though not prohibitive for practical utility of PMX/WPA as a breeding system. Of the 112 potential crosses in this study, 92 were represented. Eight of the 16 pollen parents contributed 83% of the progeny. Good pollen vigor, as measured by germination percent, did not ensure paternal success, but very poor vigor was associated with lack of paternal success. PMX/WPA appears to be logistically and economically attractive for hybrid poplar breeding and testing, though balanced representation of all pollen parents in a mix is desirable.

NFGEL PROJECT SUMMARY
DNA Extraction from Douglas-fir Seed
Project #199

Contact Person

David Neale
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Barnaly Pande
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Species

Douglas-fir (*Pseudotsuga menziesii*)

Project Objectives

Extract DNA from submitted samples.

Dates Submitted

11/4/05
11/10/05

Material Submitted

Four seed per each of 32 trees were received on 11/4/05. Seed has been shipped in 1.5ml tubes and is kept separate by tree (32 total microfuge tubes). On 11/10/05, 100 seed from each of two trees were received.

Sample Name	Date Received	# seed received	# seed extracted
013-A	11/4/05	4	1
013-B	11/4/05	4	1
013-C	11/4/05	4	1
013-D	11/4/05	4	1
412-A	11/4/05	4	1
412-B	11/4/05	4	1
412-C	11/4/05	4	1
412-D	11/4/05	4	1
22-1	11/4/05	4	1
22-2	11/4/05	4	1
22-3	11/4/05	4	1
22-4	11/4/05	4	1
24-1	11/4/05	4	1
24-2	11/4/05	4	1
24-3	11/4/05	4	1
24-4	11/4/05	4	1
26-1	11/4/05	4	1
26-2	11/4/05	4	1
26-3	11/4/05	4	1
26-4	11/4/05	4	1
28-1	11/4/05	4	1

Sample Name	Date Received	# seed received	# seed extracted
28-2	11/4/05	4	1
28-3	11/4/05	4	1
28-4	11/4/05	4	1
30-1	11/4/05	4	1
30-2	11/4/05	4	1
30-3	11/4/05	4	1
30-4	11/4/05	4	1
32-1	11/4/05	4	1
32-2	11/4/05	4	1
32-3	11/4/05	4	1
32-4	11/4/05	4	1
013	11/10/05	100	48
412	11/10/05	100	48
TOTAL			128

Material Preparation

For the 11/4/05 shipment.

Add 1ml 1% H2O2 to each sample tube (on 11/8/05). Let tubes sit at room temp for 48 hrs. Plate one seed out per tube in petrie dishes lined with 1% H2O2 soaked germination paper. Place plates in the germination chamber (11/10/05). Dissect and extract DNA from the one meg per tube. Extract DNA using the 96-well DNease format &/or mini format. Pour off remaining H2O2 from each tube and freeze the three remaining imbibed seed at -80C for possible future extraction. Samples were not given NFGEL #'s (original numbers were maintained).

Extraction date: 11/15/05 (96-well format, plate 178), 11/21/05 (mini format), 12/6/05 (mini format)

For the 11/10/05 shipment.

Soak 60 seed per packet in 1%H2O2 for two days at room temp (11/14/05). Plate seed out in germination boxes and place boxes in the germination chamber (11/16/05). Dissect and extract DNA from 48 single megs per packet (for a total of 96 single meg extractions). Samples were not given NFGEL #'s (original numbers were maintained).

Extraction date: 12/1/05 (plate #181)

Additional Notes

Project letter and packing lists were only sent hardcopy.

Number of DNA extractions:

129 final extractions (see file "PJ199_FinalSamples.xls"). This file contains DNA concentrations as well as a field including number of seeds remaining in the lab. The imbibed seed are stored at -80. Dry seed is stored in the file cabinet in VHs office. DNA samples were hand-delivered, on ice, by VH to Davis on 12/7/05.

NFGEL PROJECT SUMMARY
DNA Extraction from Douglas-fir Needles: Association Studies
Project #189

Contact Person

Glenn Howe, Director
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David Neale
530-754-8431
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Species

Douglas-fir (*Pseudotsuga menziesii*)

Project Objectives

(1) Preserve all submitted samples as liquid nitrogen ground powder at -80C.
(2) Extract DNA from a specified subset of submitted samples.

Dates Submitted

3/18/05 and 3/25/05

Material Submitted

One branch tip, approximately 4 inches in length with needles and dormant terminal bud(s) attached, from each of 208 individuals. One individual was discarded (NFGEL #AM41) because it was a duplicate collection. A second individual was ground and saved before it was learned that it, too, was to be discarded because it was a duplicate sample (NFGEL #AL41). Thirteen samples were ground and saved that are not to be extracted per an email msg from M. Cherry, 5/12/05. A total of 193 samples will be extracted for DNA.

Material Preparation

Sample Preservation.

For each sample, remove needles from stem (discard buds and stem), place needles in a mortar, and grind to a fine powder using a pestle under liquid nitrogen. Transfer powder to a tube pre-labeled with NFGEL number, and freeze at -80C.

Grinding dates: 3/25 – 4/6/05

DNA Extraction.

DNA will be extracted from 193 of the submitted samples (as per email msg on 5/12/05). Extraction method will depend on the required yield. Extraction will be via the Qiagen DNeasy 96-well format using powdered tissue as the starting material.

Extraction dates: 7/28/05, 9/8/05, 9/9/05, 10/28/05, 11/04/05, 11/15/05

Additional Notes

For final extractions: beads were added to all lqN ground powdered samples, and the samples crushed again using the mixer mill under lqN. Approx. 40 mg of ground tissue was used per sample (about '3 scoops' using a small weighing spatula).

Number of DNA extractions:

Final DNA extractions: 193.

DNA was transferred from plates 179, 180, and a partial 178 to individual microfuge tubes.
DNA samples were hand-delivered, on ice, by VH to Davis on 12/7/05.

NFGEL PROJECT SUMMARY
Project #191

Contact Person

Name: Annie Mix
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Address: IFG, Placerville

Species

Douglas-fir (*Pseudotsuga menziesii*), and Bigcone Douglas-fir (*Pseudotsuga macrocarpa*)

Project Objectives

To determine species identity of 27 unknown samples.

Date Submitted

3/31/05

Material Submitted

One branch tip from each of 30 trees. 27 samples are from seedlings of either Douglas-fir or Bigcone Douglas-fir; 3 samples are from known Bigcone Douglas-fir trees.

Material Preparation

Dissect meristems from one to two expanding vegetative buds per tree. Submerge meristems into a microtiter plate well containing 75ul of cold Melody/Neale buffer. Freeze plate at –80C. On the morning of the electrophoretic run, thaw samples, macerate with a dremel tool, and absorb extract onto three 3mm paper wicks. Make one replicate plates per set (two plates in total).

Prep. Date: 4/4/05

Gel Format

three groups of 10; 3 mm wicks

Buffers and Stains for Buds

LB	SB	MC6
Lap-1,2	Ugpp-1	Dia
Pgi-2	Tpi	Mdh-1,2,3
Pgm-1,2	G6pd	6pgd-1
Me7	Got-1,2,3	Skd-1
Fest-1,2	Sod	Idh-1

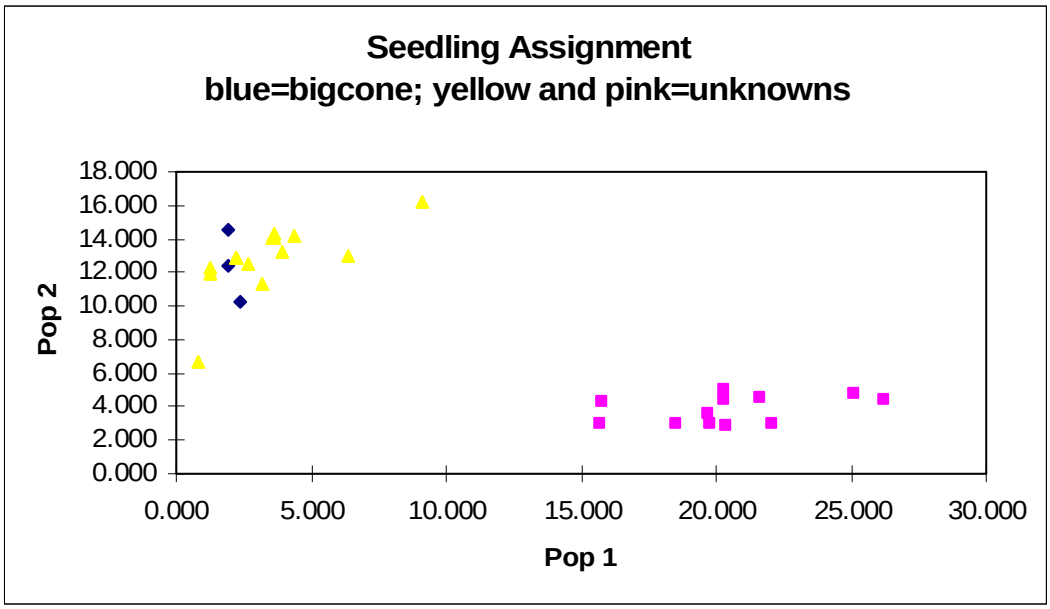
- Use back on Got; cut Fest, Pgm, Tpi, Sod, Ugpp and Lap wide
- Use no albumin in G6pd recipe
- Pour all gels thin

Run Date: 4/22/05

Results

The 30 submitted samples were genotyped at 20 isozyme loci (no activity in Fest) (see Table). Analysis (GenAlEx) shows that seedlings #1 through #12 are Douglas-fir; seedlings #13 through #27 are Bigcone Douglas-fir (see Figure).

seedling id	pgi2	me7	pgm1	lap1	lap2	pgm2	g6pd	ugpp	tpi	sod	got1	got2	got3	6pgd	mdh1	mdh2	mdh3	idh	dia	skd
1	22	11	11	57	11	11	33	12	11	11	11	11	11	11	11	11	13	13	11	11
2	11	11	12	22	12	11	13	22	11	11	11	11	11	11	11	12	13	11	11	11
3	12	11	11	22	11	11	33	22	11	11	11	11	11	11	11	12	11	13	11	11
4	22	11	12	55	12	11	13	22	11	11	11	11	11	11	11	12	11	11	11	11
5	11	11	11	55	12	11	13	12	11	11	11	11	11	11	11	12	11	11	11	11
6	11	11	14	57	11	11	11	22	11	11	11	11	11	12	11	12	13	11	11	11
7	11	11	11	57	22	11	11	12	11	11	11	11	11	11	11	12	11	11	11	11
8	22	11	11	55	11	11	13	22	11	11	11	11	11	11	11	12	13	11	11	11
9	22	11	11	57	11	11	13	22	11	11	11	11	11	11	11	12	13	11	11	11
10	11	11	11	55	12	11	33	22	11	11	11	11	11	11	11	12	11	11	11	11
11	11	11	11	55	11	11	33	12	11	11	11	11	11	11	11	12	11	11	11	11
12	22	11	14	57	11	11	11	12	11	11	11	11	11	11	11	12	13	11	11	11
13	12	11	11	15	22	11	44	11	11	11	11	11	11	22	11	11	12	11	0	11
14	0	11	11	0	0	11	0	11	11	11	11	0	11	22	11	11	12	11	0	11
BC	12	11	11	55	22	11	14	11	11	11	11	12	11	22	11	11	12	11	0	11
BC	22	11	11	55	12	11	14	11	11	11	11	11	11	22	11	11	14	11	0	11
BC	11	11	11	55	22	11	44	11	11	11	11	12	11	22	11	11	14	11	0	11
15	12	11	11	22	12	11	44	11	11	11	11	11	11	22	11	11	12	11	0	11
16	11	11	11	55	22	0	44	11	11	11	11	11	0	22	11	11	12	11	0	11
17	11	11	11	55	22	0	44	11	11	11	11	11	0	22	11	11	12	11	0	11
18	11	11	11	22	22	0	44	11	11	11	11	33	0	22	11	11	0	11	0	11
19	0	11	11	0	22	0	44	11	11	11	0	0	0	22	11	11	12	11	0	11
20	11	11	11	0	22	0	44	11	11	11	11	0	0	22	11	11	12	14	0	11
21	11	11	11	55	22	0	44	11	11	11	11	11	0	22	11	11	12	11	0	11
22	12	11	11	55	22	0	44	11	11	11	14	13	0	22	11	11	0	11	0	11
23	12	11	13	55	22	0	44	11	11	11	11	11	0	22	11	11	12	11	0	11
24	22	11	11	25	22	0	44	11	11	11	11	11	0	22	11	11	12	11	0	11
25	0	11	11	55	22	0	44	11	11	11	11	0	0	22	11	11	12	11	0	11
26	12	11	11	55	22	0	44	11	11	11	11	13	0	22	11	11	0	11	0	11
27	11	11	11	25	22	0	44	11	11	11	11	11	0	22	11	11	0	11	0	11


Seedling Assignment
blue=bigcone; yellow and pink=unknowns
Pop 2
18.000
16.000
14.000
12.000
10.000
8.000
6.000
4.000
2.000
0.000
0.000
5.000
10.000
15.000
20.000
25.000
30.000
Pop 1

NFGEL PROJECT SUMMARY
Project #184

Contact Person

Name: Dr. David Neale
USDA Forest Service
Institute of Forest Genetics
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Species

Douglas-fir (*Pseudotsuga menziesii*)

Project Objectives

Extract DNA and generate genotype data at 6 SSR loci for approximately 1,300 Douglas-fir trees. Data will be used to assess population structure in association mapping (cold-hardiness and phenology related phenotypes) studies.

Dates Submitted

8-26-2004

Material Submitted

10 megagametophytes from each of 1,287 trees, dissected and frozen in 2 mL Fast-Prep tubes (10 megs per tube; one family per tube).

Material Preparation

DNA Extraction: Megagametophytes were disrupted under liquid nitrogen using the MixerMill 300 at two 30hertz, 30 second disruptions. The DNEasy 96-kit protocol was followed for DNA extraction. 800 ul of the lysis solution was added to the disrupted material. 200 ul of lysate was transferred to a new collection tube for extraction; the remaining lysate was transferred to a new microfuge tube and frozen at -80C. DNA concentrations were obtained using picogreen.

Extraction Dates: 8/19/04 – 10/30/04

PCR/ABI: All samples were genotyped at six SSR loci (1C3, 2G12, 3B2, 3F1, 3G9, and 4A7) using multiplexed Qiagen Hotstar Taq and visualizing samples on the ABI-3100. Data was scored at NFGEL and sent to K. Krutovski for analysis and publication.

PCR/ABI Dates: 10/25/04 – 1/5/05

Analysis and Final Product

The following is an abstract presented by K. Krutovsky at the Plant and Animal Genomes XIV Conference, San Diego, CA. January 14 – 18, 2006.

Estimation of Population Structure in the Douglas-Fir Association Mapping Study

Konstantin V. Krutovsky[1], **John Bradley St. Clair**[2], **Robert Saich**[3] , **Valerie D. Hipkins**[3] , **David B. Neale**[4]

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To avoid false associations between phenotypes and genotypes for pooled samples in association mapping due to the demographic or population structure the population differentiation should be carefully estimated using preferably neutral markers. The population structure has been studied in a range-wide sample of ~1300 Douglas-fir trees from Washington and Oregon that are used for association mapping between cold-hardiness and phenology related phenotypes and SNPs in the adaptive trait related candidate genes. All trees have been genotyped for 25 isozyme and 6 SSR markers using individual megagametophytes. Population structure analysis has been done separately for isozyme and SSR markers, as well as for both data sets combined. Results based on isozyme and SSR data sets have been compared and discussed. We also discuss how population structure should be taken into account in the association mapping.

United States Department of Agriculture

Forest Service

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Final Report

Genetic structure of stands of quaking aspen (*Populus tremuloides*) on the Lassen National Forest

http://www.healthyforests.gov/initiative/biomass_conference/harvesting/aspen.html

NFGEL Project 150

Report prepared by: Jennifer DeWoody and Valerie D. Hipkins
Report submitted to: Tom Rickman, Lassen National Forest, Susanville, CA

August 17, 2005

Management Summary

Objective #1: What is the genetic relationship of stands that are spatially separated but in close proximity to one another?

Stands of aspen in the Lassen National Forest tend to consist on multiple clones, or genetic individuals. Sixty of the 125 stands studied (48%) were monoclonal. Between 2 and 89 clones were observed in the polyclonal stands. Clones in close proximity to one another tend to be genetically similar, with 97% of variation contained within groups and 93% of variation contained within stands. The distance between stems sampled from a single clone varied from 5.1 meters to 568.4 meters. Twenty-three of the 432 detected clones occurred in more than one stand. Clones within a stand are significantly but moderately related, with a relatedness coefficient of 0.107. For comparison, full-siblings (which share two parents) have a relatedness coefficient of 0.5, and half-siblings (which share one parent) have a relatedness coefficient of 0.25.

Objective #2: What is the genetic variation of aspen in and among stands (is the genetic diversity organized or patterned with respect to geographic and other known variables)?

High levels of genetic variation were observed within stands and groups of aspen on the Lassen National Forest. High levels of allelic diversity were observed at each of six microsatellite loci (between 7 and 28 alleles per locus). The moderate levels of heterozygosity observed in clones (mean 0.51) is likely due to the presence of null alleles and not ecological factors or inbreeding. Genetic diversity is organized at local and landscape-levels, with low but significant genetic differences observed among stands (7% variation partitioned among stands) and among groups (3% variation partitioned among groups). Although there is no evidence of isolation by distance among stands in this study, the significant genetic differences indicate that the movement of germplasm across large geographic areas should be limited.

Objective #3: What are allele frequencies and stand uniqueness via standard microsatellite analyses?

Allele frequencies vary among groups and among stands. No stand was genetically unique, but stands within groups tend to be more similar than stands in different groups. Allele frequencies for the six groups are provided in Appendix 1. Allele frequencies for stands are available upon request.

A table titled, “aspen_genetics_data.dbf” has been submitted with this report. This table contains four fields: NFGEL_NO (a unique ID for each sample used internally); GENOTYPE (a number which is shared among stems of the same clone); COMMENT (the stand and stem identification for each sample, as provided in “aspen_genetics.dbf”) and DATAFILE (as provided in “aspen_genetics.dbf”). To view this data in ArcView, join this table with the “aspen_genetics.dbf” table, using the COMMENT field in each table to match records.

Introduction

Quaking aspen (*Populus tremuloides*, Michx., Salicaceae) is a dioecious hardwood distributed across North America. Providing critical habitat for many wildlife species, aspen is considered a keystone species in many of the ecosystems where it grows, and is associated with high levels of biodiversity (Kay, 1997). In the arid western United States, aspen establishes in moist riparian areas, and may be the only deciduous tree species in the conifer-dominated forests (Di Orio, Callas, and Schaefer, 2005). Aspen also provides forage for a variety of ungulate (Olmstead, 1979; Kay, 1997) and invertebrate species (Hwang and Lindroth, 1998). Palatability has been found to vary across clones for two insect species (Hemming and Lindroth, 1995; Hwang and Lindroth, 1998), and likely varies for ungulates as well. Variation in palatability is likely due in part to genetic factors (Hemming and Lindroth, 1995). Understanding the size and distribution of aspen clones will not only aid future studies of the ecological importance of aspen stands, but is necessary to effectively manage for the effects of wildlife on this species.

The number and size of aspen clones is currently in decline due to fire suppression (Kay, 1997), conifer succession (Mitton and Grant, 1996) and browsing by ungulates (Kay, 1997; Romme et al., 1997). The USDA Forest Service has undertaken a number of management activities aimed at mitigating this decline. These efforts include prescribed burns, erecting fencing to protect aspen suckers and saplings from browsing by ungulates (Kay, 1997), and growing suckers from rootstock *ex situ* for outplanting efforts (NFGEL, 2002). The Lassen National Forest, located in the northern Sierra Nevada Mountains in California, is currently monitoring the persistence of aspen stands and implementing management activities to prevent their further decline. A successful management strategy will attempt to match patterns of genetic structure observed in natural populations. For example, guidelines for collecting germplasm (rootstock or seed) must consider whether stands tend to consist of a single clone or multiple clones. Similarly, restoration designs should mimic the natural pattern of genetic diversity among stands, with the number of clones planted in new stands similar to that found in surrounding areas. Accurately identifying clones in wild populations of aspen can be difficult, however.

Clones of aspen can be identified using morphological or genetic techniques. Over the past half-century, a variety of morphological traits, including root distribution, bark characteristics, and leaf shape, have been used to distinguish between clones of aspen (Barnes, 1966; Kemperman and Barnes, 1976; Mitton and Grant, 1996). Conclusions based on morphological data indicate that the typical size of aspen clones varies across North America. Barnes (1969) concluded that clone size in eastern North America is small, averaging less than 0.1 acre. In the Midwest, Blake (1964) estimated the average size of clones to be 4.05 acres. Yet in the arid west, morphological studies estimate clone size to be large (10 to 200 acres, Kemperman and Barnes, 1976). The complex root system that promotes growth by suckering over potentially large areas has been suggested as a mechanism for large clones in the west to be ancient (10,000 years old, Barnes, 1966) and potentially immortal (Mitton and Grant, 1996). However, no reliable data exists to verify these claims (Kemperman and Barnes, 1976), and stems of different clones intermix within stands (Steneker, 1973; Mitton and Grant, 1980),

indicating that putative clones based on stand size likely contain more than one genetic individual.

Morphological data can also be subjective in nature, possibly resulting in clonal identifications that vary by observer. In addition, adjacent clones have been shown to be similar morphologically (Bertenshaw, 1965), making distinguishing between clones within a stand using morphological features more difficult. A variety of genetic markers are available that provide objective data and the power to positively identify stems from different clones, regardless of the age of the stem (Cheliak and Pitel, 1984). One such marker system, isozymes, was used to show that putative clones of aspen contain more than one distinct genetic individual in Alberta, Canada (Cheliak and Dancik, 1982) and in Ontario, Canada (Cheliak and Pitel, 1984). These findings are consistent with the theory that clone size in eastern populations tends to be small. To our knowledge no systematic genetic study has been reported supporting the claim that the large stands of the Intermountain West consist of a single genetic individual. The clonal distribution of aspen in the Pacific West of North America shows characteristics of both eastern populations and stands from the Intermountain West, in that stands can be large but tend to be composed of more than one clone. An isozyme study of aspen in northeast Oregon revealed that clonal structure is diverse (NFGEL, 2002). While an important proportion of stands are small and monoclonal (45%), others contain more than one clone, and some genetic individuals are spread across more than one stand, indicating that fragmentation of ancient, large clones has occurred (NFGEL, 2002). Aspen on the Eldorado National Forest, California, show similar structure, with 44% of stand being monoclonal, and several clones extending across more than one stand (Hipkins and Kitzmiller, 2004).

While isozyme data has sufficiently identified clonal structure and described patterns of genetic variation in a number of studies of aspen, novel DNA markers are available that may increase the power of genetic studies to distinguish between clones. Microsatellites (or short-sequence repeats, SSRs) are DNA markers that typically resolve higher levels of genetic diversity than isozymes. In order to provide genetic data to aid management strategies, this study used data from six microsatellite loci to address three objectives: 1) What is the genetic relationship of stands that are spatially separated but in close proximity to one another? 2) What is the genetic variation of aspen in and among stands (is the genetic diversity organized or patterned with respect to geographic and other known variables)? 3) What are allele frequencies and stand uniqueness via standard microsatellite analyses?

Methods

Sample collection: 874 samples were collected from the Eagle Lake Ranger District of the Lassen National Forest during June and July, 2003 (Table 1, Figure 1). The position of each ramet sampled as well as the area of each stand was recorded using GPS. Between 3-5 leaves were collected from each individual, placed in plastic bags on ice, and transported to the NFGEL laboratory.

Isozyme analysis: Samples were prepared for isozyme analysis by submerging two hole-punches of tissue in 100 µL Gottlieb (1981) extraction buffer according to standard protocols (USDA Forest Service, 2003), and frozen at -80C.

DNA analysis: Total genomic DNA was extracted from each sample using Qiagen's DNEasy-96 plant extraction kit, following the provided protocols for liquid nitrogen extraction. DNA quality and quantity were estimated from agarose gel electrophoresis.

Samples were analyzed for six microsatellite loci: ORNL-29, PMGC-420, PMGC-433, PMGC-576, PMGC-649, and PMGC-2571. Primer ORNL-29 is from Tuskan et al. (2004), while all PMGC primers are from the International *Populus* Genome Consortium (http://www.ornl.gov/sci/ipgc/ssr_resource.htm). The forward primer for each locus was fluorescently labeled for automated analysis. All amplifications took place under the following reaction conditions: approx. 1 ng template DNA, 1X reaction buffer (provided with enzyme), 2.5 mM $MgCl_2$, 1.25 mM each dNTP, 10.0 µM each primer, and 0.2 U HotStar-Taq (Qiagen ®), in a 10 µL total reaction volume. All loci except PMGC-2571 were amplified on a program adapted from a protocol provided by S. DiFazio (personal communication): 15 min. at 95˚C followed by four cycles of 94°C for 30 s, 55°C for 30 s, 72°C for 60 s; then four cycles of 94°C for 30 s, 52°C for 30 s, 72°C for 60 s; followed by 25 cycles of 94°C for 30 s, 50°C for 30 s, 72°C for 60 s; and a final extension of 15 min. at 72˚C. Locus PMGC-2571 was amplified using: 15 min. at 95˚C followed by four cycles of 94°C for 30 s, 58°C for 30 s, 72°C for 60 s; then four cycles of 94°C for 30 s, 52°C for 30 s, 72°C for 60 s; followed by 25 cycles of 94°C for 30 s, 50°C for 30 s, 72°C for 60 s; and a final extention of 15 min. at 72˚C. Amplification products were visualized on an ABI-3100 capillary system, and peaks were scored using the peak label function in Genotyper (v3.7, Applied Biosystems, Inc.). Twenty-seven samples (3%) were regenotyped either due to duplicate extractions, or due to failed reactions, and the data were examined for quality assurance.

Ploidy analysis was completed on a subset of 25 samples in order to rule out ploidy variation among clones. For each sample, approximately 25 mg of leaf tissues was macerated and analyzed using Partec® CY-Stain UV Ploidy staining solution following the provided protocol, with a 15 minute incubation step.

Data analysis: Alleles observed at each locus were identified using the binning function employed by Allelogram v1.2 (Manaster, 2002). Clones were identified as matching genotypes using both manual analysis and the allele sharing/distance matrix function employed by the Excel Microsatellite Toolkit (Park, 2001), which identifies redundant genotypes with one allele difference tolerated between each pair. The distribution of clones among stands was determined by plotting the location and genotype of each stem using ArcView GIS v3.2 (Environmental Research Systems Institute, Inc. 2000). Total number of unique genotypes, mean number of clones per stand, and number of monoclonal stands were computed over all stands. The null hypothesis of no correlation between stand size (in acres) and the number of unique genotypes per stand was tested using the Correlation and ANOVA functions in MS-Excel®.

The Euclidian distance between stems of each clone was calculated using the UTM coordinates provided for each sample. Mean distance between stems was estimated over clones occurring within a single stand and over clones occurring in more than one stand.

The genotypic data were analyzed for standard measures of genetic diversity: clone diversity, number of unique genotypes observed, allelic richness, observed heterozygosity, total diversity, and Weir and Cockerham's (1984) fixation index.

Significance of fixation indices was determined by 1000 permutations of genotypes among samples. Estimates were made over all samples, groups, watersheds, and sub-watersheds, as implemented by FSTAT (Goudet, 1995, 2001).

In order to analyze genetic variation and differentiation among stands of Aspen, the data set was reduced to a single sample per genotype per stand. This data set was then tested for genotyping errors using the program MICRO-CHECKER (van Oosterhout et al., 2004). When evidence of a null allele was found at a locus, Brookfield's (1996) adjusted allele frequencies for the case of null-null homozygotes were calculated using the same program. Allele frequencies for loci containing no null alleles, and for stands containing fewer than four unique genotypes were estimated using FSTAT (Goudet, 2001) due to statistical constraints of adjusting alleles based on small sample sizes.

The null hypothesis of no allele frequency differentiation was tested among groups, among watersheds, among subwatersheds, and among stands. Genetic differentiation within groups, watersheds, and subwatersheds were estimated as Wright's (1969) F_{st} using adjusted allele frequencies, with significance calculated from 1000 permutation tests, as implemented by the program Spatial Genetic Software (Degen, 2000). Due to analytical constraints, genetic differentiation among stands was estimated as Weir and Cockerham's (1984) θ, and significance tested over 1000 bootstraps, as implemented by FSTAT (Goudet, 2001).

Relatedness among individuals within stands compared to the whole for each group and over all groups was estimated for genotype data as adapted from (Queller and Goodnight, 1989) and employed in FSTAT (Goudet, 2001). Due to known deviation from Hardy-Weinberg equilibrium (due to null alleles), significance was tested by permuting genotypes among samples.

Finally, the null hypothesis that genetic differentiation does not increase as a function of Euclidian distance between stands was tested for the genotypic data. Correlation between pairwise F_{st}, calculated by FSTAT (Goudet, 2001), and Euclidian distance (from UTM data) for all pairs of populations was tested using the multiple regression and partial Mantel tests implemented by FSTAT (Goudet, 2001).

Results

All six loci were polymorphic, with between 7 and 28 alleles per locus, including nulls. Null alleles were inferred to be present at four of the six loci. See Appendix 1 for allele frequencies observed in the six groups; allele frequencies for stands available upon request. Three samples lack DNA data due to potential contamination or technical errors during analysis, resulting in a dataset containing 871 samples. Thirty-six (36) samples lack geographic data, and are not included in distance analyses.

A total of 432 unique clones were identified across 871 samples, with a mean of 2.02 ramets sampled per clone (range 1 – 14). An average of 3.68 clones were observed per stand (range 1 - 89), with a total of 23 clones being observed in more than one adjacent stand (Table 2). Sixty stands (48%) contained a single clone. The number of clones observed in a stand was significantly correlated with stand area ($r^2 = 0.926$; $F = 1540.5$, $P < 0.01$; Figure 2).

Duplicate samples were compared for quality assurance, and results indicate relatively high error rates over reactions (mean over loci = 0.0309) and over alleles (mean

over loci = 0.0154). These estimates may be inflated by the small number of QA samples, and by the tendency for low-yield or low-quality samples to be repeated.

Of the 432 unique clones, 34 (7.9%) consistently produced three peaks at between one to three loci, indicating potential triploidy. Ploidy analysis of 24 genotypes revealed genome size differences, but variations were not observed as indistinct haploid units, nor were differences consistent among two-peak and three-peak patterns. Based on this information, the most-common allele (allele frequencies estimated using the Excel Microsatellite Toolkit, (Park, 2001)) at each three-peaked locus was dropped from that clone's genotype in order to produce a consistently diploid data set required for thorough genetic analyses.

Relatively high levels of genetic diversity were observed in stands, watersheds, and sub-watersheds (Table 3). The clone diversity over all samples, estimated as G/N where G is the number of clones identified and N is the total number of samples, is 0.497 (meaning about one half of the submitted samples were unique clones). Allelic richness (a measure of variation independent of sample size) decreased with hierarchical level, but values were consistent among observations within each level. Mean observed heterozygosity among all samples (0.510) was lower than the total diversity (0.763), resulting in significant fixation indices. Significant fixation indices were observed at all four hierarchical levels: groups, watersheds, sub-watersheds, and stands.

Significant genetic differentiation was observed among groups (θ = 0.028; 95% CI 0.021 to 0.035), among watersheds (θ = 0.024; 0.015 to 0.033), among sub-watersheds (θ = 0.038; 0.028 to 0.047), and among stands (θ = 0.07; 0.049 to 0.083).

Relatedness among clones within a stand was significant, with a mean relatedness of 0.107 (95% CI 0.07 to 0.132). Relatedness among clones within a group was lower but still significant, with a mean relatedness of 0.042 (95% CI 0.032 to 0.055).

Finally, no evidence was found that genetic differentiation increases as a function of distance. The percent of the variance observed in all pairwise F_{st} values explained by distance was not significant and approached zero (R^2 = 0.01; $P > 0.05$).

Discussion

Genetic variation and stand structure

Aspen stands in the Eagle Lake Ranger District of Lassen National Forest contain high levels of genetic diversity as measured as six microsatellite loci. The mean levels of alleles per locus (9.0) and gene diversity (0.75) are slightly higher than values reported in other microsatellite studies of wild aspen (Table 4). Clone diversity, estimated as the number of clones (G) divided by the total number of samples (N), is affected by the sampling strategy of the study. Thus, the clone diversity of this study is likely lower than those reported in other studies using microsatellites due to the systematic sampling of stems in a stands. Other studies designed collections to minimize the chance of sampling a clone more than once (Dayanandan, Rajora, and Bawa, 1998; Wyman, Bruneau, and Tremblay, 2003). These levels of diversity indicate that, despite the general decline in aspen, high levels of genetic diversity still occur in this species in the northern Sierra Nevada Mountains.

The vast majority of stands sampled in this study contained more than one unique clone. Samples were classified as different clones when they differed at more than one

allele. The number of clones in a stand reported here can be considered the minimum number of clones occurring in that stand. Additional clones may exist in that space but were either not sampled as part of this study, or happened to contain the same genotype at these six loci. How likely is it that two samples would have the same genotype in this study by chance alone? Based on the levels of variation and the allele frequencies at each of the six loci, the probability of a genotype occurring in this data set ranges from 4.37×10^{-4} to 3.88×10^{-17}. These probabilities mean that the chance that two stems with the same genotype are not the same genetic individual, while greater than zero, is small.

Most clones occur within a single stand, although 23 clones were observed in more than one stand (Table 2). Although sixty of the 125 stands (48%) were monoclonal, the size of a stand is positively correlated with the number of genotypes observed within it (Figure 2). This indicates that the greater the size of a stand, the greater amount of genetic variation contained within it. Distance between stems of a single clone is at best a rough measure of the size of the clone since not every stem of a clone is sampled. In this study, the maximum distance between stems of the same clone was 568 m, indicating that although large stands tend to consist of more than one clone, individual clones can cover large areas.

Given the high rate of mutation at microsatellite loci and the long life of aspen clones, is it possible that stems that originated from the same individual may have accumulated more than one difference at the loci used in this study, and were classified as different clones as a result? The rate of mutation varies among microsatellite loci, typically from 0.0001 to 0.01 base pairs per generation (Ellegren, 2004). For a conservative mutation rate of 0.001, and assuming that each new stem of a clone is functionally a new generation, one somatic mutation should occur in every 1000 stems. Thus, we would expect one stem out of 2000 from each clone to be mistakenly identified as having a unique genotype. In other words, if one stand were a single clone, we would expect only stands with greater than 2000 stems to contain more than one unique genotype. The average clone size, however, was much smaller, with an average of 2.02 stems observed per clone in this study. This result provides further evidence that stands of aspen in Lassen National Forest consist of multiple clones (Appendix 2).

The age of a single clone cannot be determined by this data, and currently no test exists to address this question. However, the structure of stands reported here may be used to infer the past structure of these clones. Large stands containing many clones may be younger and provide evidence of relatively recent recruitment by seed. Following the large fires in Yellowstone National Park, large numbers of aspen seedlings were recruited in areas previously lacking aspen (Tuskan et al., 1996). DNA markers revealed that these new stands consisted of many clones, and that over time, the number of clones decreased due to competition and succession (Stevens et al., 1999). This process may be occurring in large stands containing multiple clones. In addition, fragmentation or senescence of large clones may have caused 23 clones to be split between more than one stand (Table 2).

Estimates of relatedness among individuals within stands and within groups were calculated using genotypic data and not the adjusted allele frequency data. Estimates were low but significant, indicating that clones within a stand (0.107) and within a group (0.042) are related. The relatedness observed within stands may be due to localized seed dispersal, although this hypothesis cannot be tested by this data set. For comparison, full-

sibs (samples that share both parents) will have a relatedness coefficient of 0.5, and half-sibs (samples that share one parent) will have a relatedness coefficient of 0.25.

Allele frequencies for each group of samples are provided in Appendix 1. Allele frequencies calculated for the 125 stands in this study are available upon request. Frequencies for loci O-29, P-420-P-576, and P-649 have been adjusted for the presence of null alleles. Null alleles occur when the microsatellite primers do not amplify a visible DNA product, meaning that a sample will have no visible data for that locus. (This differs from a low-quality sample of DNA, which will produce missing data.) The frequency of null alleles in this study was high, likely due to the fact that the primers used were designed for *Populus trichocarpa* (Tuskan et al., 2004). Since nulls are not visible alleles, they cannot be scored in the same manner as true alleles that produce a visible product. Without sequencing all samples in a data set, it is impossible to distinguish between individuals that are heterozygous for a null allele from those that are homozygous for a visible allele. Statistical methods exist to estimate the frequency of null alleles and then adjust the frequency of the observed alleles accordingly. These adjusted values are presented in Appendix 1, and frequencies of visible alleles will appear lower than estimates reported in other studies that do not account for null alleles.

The high frequency of null alleles in this data set is the likely cause of the significant fixation indices (or excess of homozygotes) observed at each level of the analysis. In the absence of null alleles, such a lack of heterozygosity can be due to inbreeding or fine-scale population structure, but knowledge of the breeding system in aspen and the design of this study make these causes unlikely. First, the wind-pollination and dioecious nature of the aspen mating system makes it unlikely that significant self-fertilization occurs during seed production (Stevens et al., 1999). Second, although inbreeding cannot be ruled out, the lack of recruitment from seed in these populations means that the sampled individuals are likely from old clones, and makes it unlikely that the current decline in population size has affected the homozygosity of these samples. Third, the systematic sampling of these groups, and the fact that significant fixation indices were observed at every level, makes it unlikely that fine-scale population structure is the cause of these results.

Genetic differentiation among stands and groups

In addition to the high levels of diversity observed in these aspen samples, significant genetic differences were observed among stands, sub-watersheds, watersheds, and groups. This finding indicates that while levels of variation are even across the landscape (Table 3), no one stand, watershed, or group contains all the variation observed at one locus. The genetic differences reported here are similar to levels reported in microsatellite studies of aspen from eastern North America. Genetic differentiation among groups (0.028) is similar to that reported among populations of aspen in Quebec (0.03 and 0.04), as measured by microsatellites (Wyman, Bruneau, and Tremblay, 2003). Genetic differentiation among stands (0.07) is also similar to one reported by Wyman, Bruneau, and Tremblay (2003), although the values from Quebec varied widely (-0.11 and 0.03). However, all of these values are a fraction of those reported in previous isozyme studies of aspen in the Pacific West. NFGEL (2002) reported differentiation among stands in Oregon to be 0.49, while Hipkins and Kitzmiller (2004) reported differentiation among stands in El Dorado County, CA to be 0.47. The differences in

these values are likely an artifact of the different marker systems, and indicate that caution is warranted when comparing fixation indices from isozyme and microsatellite studies. The high levels of allelic diversity and the lower levels of genetic differentiation may be the result of homoplasy among microsatellite alleles, which can depress estimates of genetic structure (O'Reilly et al., 2004). As a result, microsatellite markers may be more appropriate for clone identification, paternity studies, or fine-scale studies of genetic patterns, while isozymes may be more appropriate for landscape-level studies of genetic structure.

The lack of isolation by distance among stands indicates that stands located kilometers apart have the same probability of being genetically different as neighboring stands. Together, the lack of isolation by distance and the low to moderate genetic differentiation indicate that gene flow occurs across the landscape with some frequency. Gene flow is expected in this species given the dioecious mating system of aspen, and the resulting inability for plants to self-pollinate. Whether the gene flow is occurring as seed movement or pollen dispersal cannot be determined from this data set.

Management implications

These genetic findings may be incorporated into management strategies and can serve as a baseline of genetic structure and variation for future monitoring efforts. The findings that genetic variation is distributed across stands, and that large stands tend to contain multiple clones, indicate that genetic diversity will likely be lost as stand number or stand size decreases across the landscape. In designing gene conservation strategies, collections of germplasm (seed or rootstalks for outplanting) should include samples from across the study area. Genetic variation will be lost if collections are restricted to one stand or even one group.

Although there is no evidence of isolation by distance, the significant genetic differentiation observed among groups indicates that a conservative policy of restricting the movement of germplasm to within geographic areas is warranted. If transfer of germplasm across large geographic areas is absolutely necessary, it may not significantly alter the pattern of genetic differentiation so long as germplasm is not pooled across groups. That is, using germplasm collected from each group in outplantings across all groups will tend to homogenize the genetic structure of aspen, potentially erasing the genetic structure observed in this study.

In order to mimic the natural distribution of clones within and among stands, restoration or stand augmentation should include more than one clone per stand, and may include several clones, depending on the size of the desired area covered by a stand. If available, data describing the use of the stands of Aspen studied here by wildlife (e.g. as forage or shelter) may be analyzed by genotype to determine if use by wildlife varies by clone. The identification of clones that are preferentially browsed, for instance, may be used to design collection and restoration activities for wildlife management. Efforts to manipulate forage availability may move germplasm within groups while maintaining the genetic structure of aspen observed across this landscape.

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Table 1. Aspen samples collected from the Eagle Lake Ranger District of the Lassen National Forest. N is the number of stems sampled in that sub-watershed. G is the number of unique genotypes observed in the complete stand (across all sub-watersheds), as determined by genetic data. *Denotes those stands split between subwatersheds, where G may be greater than N for that subwatershed.

Group	Watershed	Sub-watershed	Stand	N	G
Bogard Buttes (BB)	Eagle	PI2	BUPC01O	2	1
BB total: 232			BUPC01P	2	1
		PI3	BUPC01D	4	2
			BUPC01E*	2	29
			BUPC01F	9	2
			BUPC01G	4	2
			BUPC01H	3	1
			BUPC01I	7	2
			BUPC01J	3	1
			BUPC01K	2	1
			BUPC01L	2	1
			BUPC01M	2	1
			BUPC01N	12	3
			BUPC01Y	7	1
			BUPC01Z	8	2
			BUPC02A	13	4
		PI4	BUPC01A	3	2
			BUPC01B	1	1
			BUPC01C	27	15
			BUPC01E*	28	29
			CCBK01*	2	3
			CCPC01*	49	47
		PI6	CCPC02*	1	3
		PI7	CCBK01*	7	3
			CCPC02*	1	3
			CCPC03	3	2
		PI19	BUPC01	11	6
			CCPC01*	16	47
			CCPC02*	1	3
Fredonyer Pass (FP)	Susan River	SU1	GOWC32	14	4
FP total: 117			GOWC33	2	1
			GOWC34	6	2
			GOWC35	4	4
			GOWC36	12	6
			GOWC37	4	2
			GOWC38	27	11
			GOWC41	2	1
			GOWC42	24	16
			GOWC43	3	2
	Upper North Fork Feather River	MM5	GOCB01	4	1
			GOCB02	7	2
			GOCB03	5	2
			GOCB04	1	1
			GOCB05	2	1

Group	Watershed	Sub-watershed	Stand	N	G
Harvey Mountain (HM)	Eagle	PI18	CCHS01	1	1
HM total: 128			CCLH01	10	9
			CCLH02	4	2
			CCLH03	3	1
			CCLH04	3	1
			CCLH05	3	1
			CCNC01	6	2
		PI19	CCHS01	2	1
			CCHS02	6	2
			CCHS03	3	1
			CCHS04	5	2
			CCHS05	7	1
			CCHS06	7	2
			CCHV01	3	2
			CCHV02	3	1
			CCHV03	8	4
			CCHVA01	12	5
			CCLH06	3	2
			CCLY01	5	3
			CCNC05	25	14
			CCNC09	9	2
Peg Leg Mountain (PL)	Susan River	SU21	APSR02*	1	4
PL total: 89			APSR07	4	2
			APSR08	5	3
			APSR09	2	1
			APSR11	5	2
			APSR16	3	1
			APSR18	2	1
			APSR21	8	2
			APSR22	2	1
			APSR23	8	2
			APSR31	3	1
		SU23	APSR10	16	4
			APSR12	2	1
			APSR14	6	2
			APSR29	3	1
		SU24	APSR01	5	3
			APSR02*	10	4
			APSR05	2	1
			APSR26	2	1
Pine Creek Valley (PC)	Susan River	SU32	APLL04	2	1
PC total: 137			APLL05	8	1
		SU33	APFL01	4	1
			APFL04	3	1
			APFL05	4	1
			APFL06	3	1
			APFL07	3	1

Group	Watershed	Sub-watershed	Stand	N	G
Pine Creek Valley (PC)	Susan River	SU33	APFL08	2	1
			APFL09	2	1
			APFL10	2	1
			APFL11	4	1
			APFL12	1	1
			APFL13	2	1
			APFL14	3	1
			APFL15	3	1
			APFL16	5	1
			APFL17	4	2
			APFL18	4	1
			APLL01	5	4
			APLL02	4	2
			APLL03	3	1
			APLL06	4	2
			APLL07	3	2
			APLL08	3	2
			APLL09	3	1
			APLL14A	3	2
			APLL14B	2	2
			APLL15	5	3
			APLL16	3	1
			APLL17	13	2
			APLL19	12	4
			APLL20	2	2
			APLL21	3	1
			APLL22A	2	1
			APLL22B	1	1
			APLL22C	1	1
			APLL23	3	1
			APLL24	3	1
Prospect Peak (PP)	Hat Creek	HC27	BUBC02	8	3
PP total: 171			BUBS01	16	5
			BUBS02	2	1
			BUBS03	2	1
			BUBS04	2	1
			BUBS05*	7	17
			BUBS06	2	1
		HC34	BUBC03	100	89
			BUBS05*	21	17
			BUBS08	5	2
			BUBS10	6	5

Table 2. Aspen clones occurring in more than one stand. Minimum Distance is measured between sampled stems.

Genotype No.	Stands	Stems	Minimum Distance (m)
036	CCHV01	1	125.40
	CCHV02	1 – 3	
037	CCHS05	1 – 7	48.55
	CCHS06	1 – 2	
038	CCHS06	3 – 7	127.03
	CCLH06	2 – 3	
044	CCHS03	1 – 3	27.07
	CCHS04	1 – 3	
055	APFL01	1 – 4	90.25
	APFL04	1 – 3	
056	APFL05	1 – 4	157.80
	APFL06	1 – 3	
066	APFL16	1 – 5	72.01
	APFL17	1 – 2	
070	APLL01	2	No UTM data available
	APLL16	1 – 3	
101	APLL20	1	56.86
	APLL22B	1	
	APLL22C	1	
102	APLL20	2	370.31
	APLL22A	1 – 2	
104	CCBK01	1 – 2	206.86
	CCPC03	1 – 2	
115	BUPC01A	3	89.27
	CCPC01	38 – 41	
127	BUPC01L	1 – 2	82.10
	BUPC01M	1 – 2	
140	BUBS04	1 – 2	67.23
	BUBS05	18 – 22	
193	BUPC01Y	1 – 7	94.37
	BUPC01Z	1 – 7	
300	BUBS05	26	90.79
	BUBS08	1 – 3	
316	APSR07	4	133.27
	APSR21	5 – 8	
317	APSR08	1 – 3	99.46
	APSR09	1 – 2	
318	APSR08	4	73.93
	APSR16	1 – 3	

Appendix 2 (continued)

Genotype No.	Stands	Stems	Minimum Distance (m)
330	APSR21	1 – 4	209.88
	APSR23	3 – 7	
	APSR31	1 – 3	
331	APSR22	1 – 2	63.51
	APSR23	1 – 2, 8	
387	GOWC32	1 – 2, 14	87.32
	GOWC33	1 – 2	
395	GOWC35	3	159.36
	GOWC36	1 – 2	

Table 3. Variation observed at six SSR loci in 871 samples of *Populus tremuloides* from the northern Sierra Nevada mountains. N = number of genotypes observed; A = allelic richness; H_t = overall gene diversity, F_{IS} = mean fixation index, which equals zero if a population is in Hardy-Weinberg equilibrium. * P <0.05; ** P < 0.01.

Group	N	A	H_t	F_{IS}
BB	125	9.521	0.752	0.272**
FP	53	8.394	0.735	0.270**
HM	49	9.839	0.722	0.285**
PC	51	9.215	0.757	0.375**
PL	32	7.813	0.733	0.358**
PP	118	8.980	0.773	0.332**

Watershed	N	A	H_t	F_{IS}
WS08	105	5.572	0.769	0.320**
WS10	159	5.882	0.742	0.267**
WS14	108	5.646	0.751	0.324**
WS15	7	5.500	0.695	0.280**

Sub-watershed	N	A	H_t	F_{IS}
HC27	13	1.760	0.769	0.313**
HC34	92	1.765	0.766	0.318**
MM5	7	1.679	0.695	0.28**
PI2	2	1.750	0.917	0.545*
PI3	24	1.727	0.732	0.322**
PI4	76	1.744	0.745	0.211**
PI5	11	1.693	0.702	0.287**
PI6	1	1.500	NA	NA
PI7	5	1.551	0.571	0.358**
PI18	15	1.687	0.692	0.223**
PI19	28	1.712	0.715	0.269**
SU1	39	1.725	0.727	0.24**
SU21	15	1.699	0.707	0.326**
SU23	8	1.724	0.744	0.412**
SU24	8	1.704	0.719	0.304**
SU32	1	1.417	0.500	0
SU33	37	1.742	0.745	0.348**

Table 4. Comparison of genetic diversity reported in aspen for isozymes (protein) and microsatellite (DNA) markers. Number of clones or individuals (N), number of loci examined, mean alleles per locus (*A*), expected heterozygosity (or genic diversity, H_e), and clone diversity (G/N), as reported in each study. Table adapted from Wyman et al. (2003).

Reference	Method	N	No. loci	*A*	H_e	G / N
Present study	microsatellite	871	6	9.0	0.75	0.50
Wyman et al. 2003	microsatellite	159	4	7.4	0.725	0.82
Dayanandan et al. 1998	microsatellite	36	4	7.25	0.46	0.94
Hipkins and Kitzmiller 2004	isozyme	663	17	3.1	0.28	0.30
NFGEL 2002	isozyme	789	17	3.9	0.23	0.30
Jelinski and Cheliak 1992	isozyme	156	16	2.4	0.29	0.92
Hyun et al. 1987	isozyme	200	15	2.7	0.24	n.a.
Cheliak and Dancik 1982	isozyme	222	26	2.3	0.42	1.0

Figure 1. Location of study area on the Eagle Lake Ranger District, Lassen National Forest.

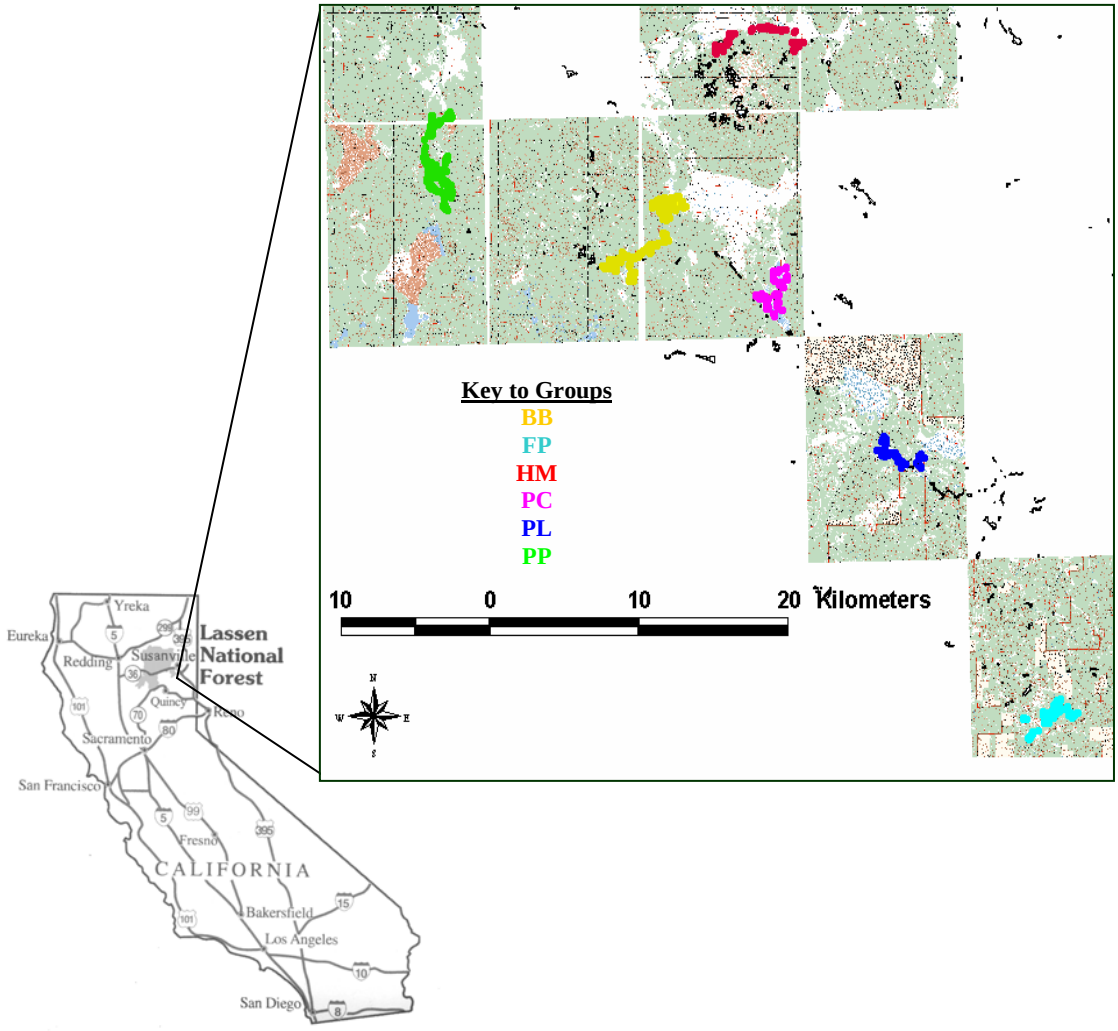
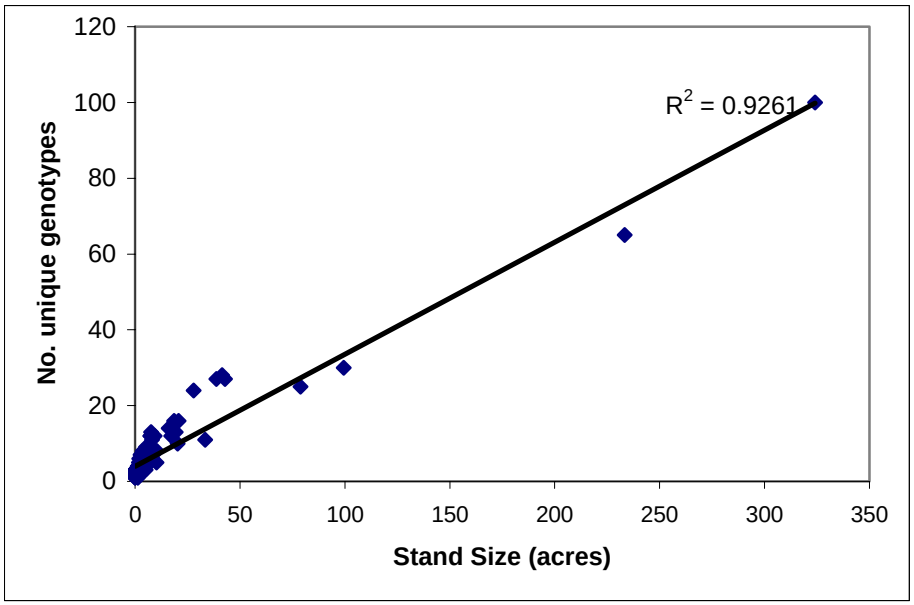


Figure 2. The number of unique genotypes observed in a stand of aspen is strongly correlated with stand size in the Lassen National Forest.



Appendix 1. Allele frequencies observed within six groups of *Populus tremuloides* on the Lassen National Forest. Alleles are in base pairs. Adjusted frequencies are provided for loci where nulls were detected.

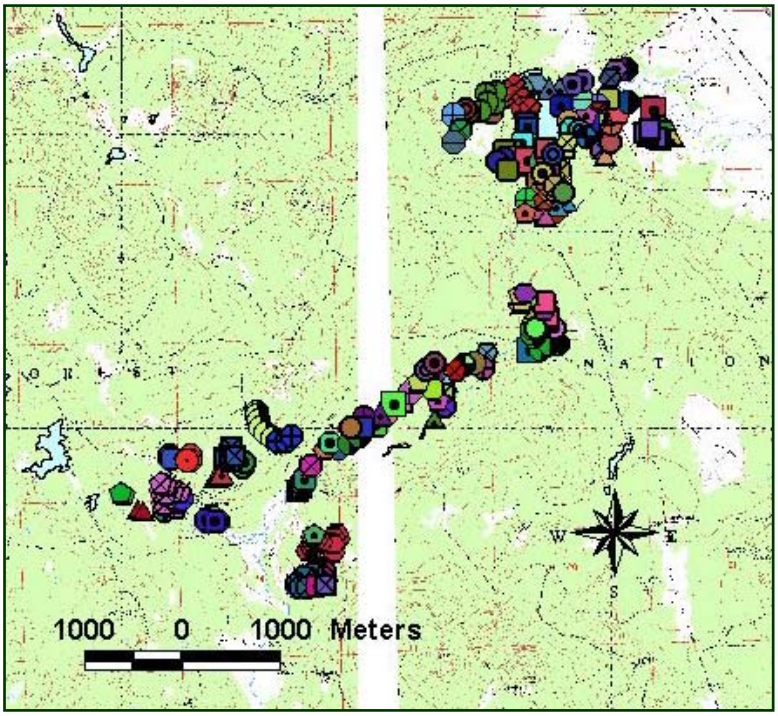
Locus	Allele	BB	FP	HM	PC	PL	PP
ORNL-29	225						0.006
	233	0.252	0.087	0.250	0.214	0.162	0.203
	235	0.022	0.031	0.070	0.032		0.052
	237	0.083	0.124	0.146	0.011	0.076	0.071
	239		0.019	0.029	0.032	0.141	0.003
	241	0.006					
	243	0.050	0.230	0.035	0.016	0.152	0.135
	245	0.102	0.100	0.052	0.123	0.184	0.141
	247	0.014					0.009
	249	0.003					
	251		0.006				
	255	0.064		0.012	0.011		0.012
	257	0.003					
	263	0.019	0.012		0.005		0.018
	265	0.033	0.006	0.012			0.065
	267	0.006	0.006		0.005		0.015
	269						0.015
	271	0.003					
	279						0.003
	Null	0.342	0.378	0.395	0.550	0.286	0.250
PMGC-420	77						0.009
	79	0.062	0.082	0.032	0.058	0.099	0.025
	81	0.111	0.095	0.056	0.124	0.086	0.202
	83	0.677	0.600	0.799	0.610	0.654	0.509
	87	0.007		0.008			0.031
	89				0.007		
	Null	0.143	0.223	0.105	0.201	0.162	0.224
PMGC-433	178	0.004					0.029
	186	0.101	0.046	0.246	0.075	0.094	0.233
	188	0.166	0.083	0.047	0.142	0.125	0.201
	190	0.166	0.083	0.151	0.095	0.094	0.148
	192	0.302	0.185	0.226	0.292	0.375	0.094
	194	0.043	0.297	0.066	0.047	0.047	0.053
	196	0.074	0.093	0.075	0.160	0.203	0.193
	198	0.078	0.083	0.123	0.085	0.031	0.041
	202	0.012	0.130	0.028			
	208	0.054		0.038	0.095	0.031	0.008
	212				0.009		
PMGC-576	100			0.017			0.007
	124		0.008				
	146	0.056		0.008	0.040	0.025	0.007
	148			0.008			
	150						0.007
	152	0.063	0.016	0.008	0.054	0.038	0.107
	160		0.063	0.017		0.013	0.023
	162		0.016	0.025	0.013		
	164	0.063	0.150	0.118	0.060	0.013	0.123
	166	0.260	0.372	0.396	0.221	0.288	0.234
	168	0.056	0.016	0.008	0.054	0.050	
	171	0.035	0.032	0.025	0.027	0.038	0.130
	173	0.035					
	178	0.007			0.013	0.038	
	180	0.042		0.025	0.040	0.013	
	182	0.004				0.013	0.003

Appendix 1 (continued)

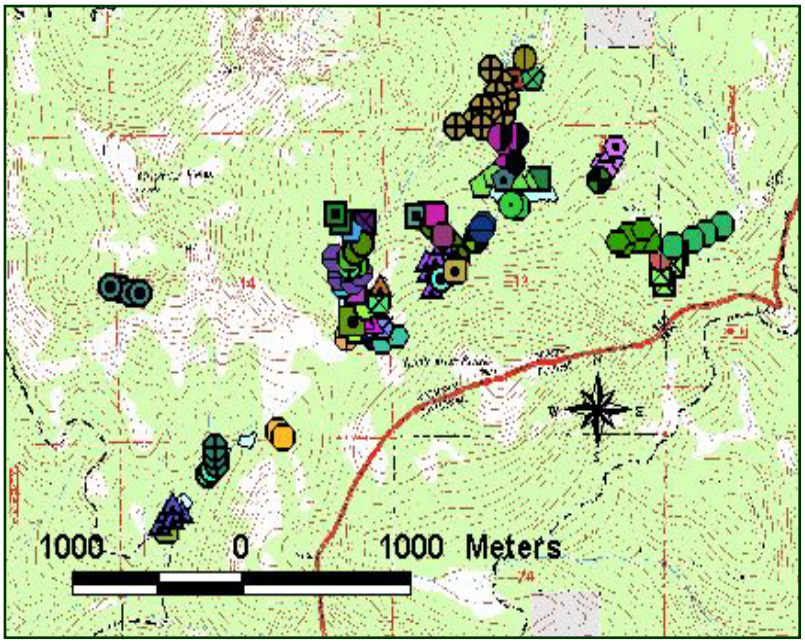
Locus	Allele	BB	FP	HM	PC	PL	PP
PMGC-576	188	0.264	0.230	0.194	0.174	0.325	0.146
	190	0.010		0.034	0.013		0.003
	192	0.004					
	194			0.008			
	200			0.008			
	202			0.034			
	204	0.007		0.008			0.003
	206						0.007
	Null	0.097	0.098	0.057	0.289	0.149	0.202
PMGC-649	75	0.003					
	77	0.006					
	85	0.003					
	89	0.003					
	91	0.047	0.127	0.032	0.021	0.049	0.045
	93	0.006	0.052	0.044	0.014	0.010	0.008
	97			0.013	0.007		0.005
	99	0.076	0.201	0.019	0.085	0.128	0.079
	101						0.021
	103	0.003					
	105	0.015					0.003
	109	0.012	0.007				0.005
	111	0.003					0.003
	113	0.223	0.164	0.177	0.261	0.216	0.029
	115	0.082	0.007	0.114	0.078	0.020	0.037
	117	0.062	0.097	0.057	0.085	0.059	0.118
	118	0.068	0.067	0.032	0.042	0.088	0.155
	120	0.062	0.037	0.089	0.064	0.020	0.032
	122	0.032	0.015		0.042		0.037
	125	0.035	0.030	0.013	0.014	0.029	0.018
	128		0.007	0.006	0.014		
	130	0.006		0.013	0.007		
	131		0.007				
	133		0.015				
	135	0.003					
	145	0.003					
	199					0.010	
	Null	0.248	0.167	0.393	0.267	0.372	0.406
PMGC-2571	82	0.076	0.046	0.138	0.111	0.234	0.069
	84	0.053	0.028	0.056	0.130	0.110	0.016
	86	0.095	0.037	0.074	0.046	0.016	
	88	0.271	0.370	0.268	0.214	0.234	0.379
	92	0.004		0.028	0.009		
	94	0.008		0.028	0.046		
	96	0.008		0.019			
	100	0.084	0.046	0.056	0.009	0.031	0.122
	102	0.027	0.009	0.028	0.065	0.078	0.024
	104	0.015	0.074	0.028	0.046	0.094	
	106	0.260	0.223	0.147	0.250	0.172	0.256
	108			0.019	0.028		0.012
	110		0.019			0.031	0.073
	112	0.099	0.148	0.111	0.046		0.045
	114						0.004

Appendix 2. Distribution of clones in six groups of aspen on the Lassen National Forest. Unique symbols indicate unique genotypes and putative aspen clones.

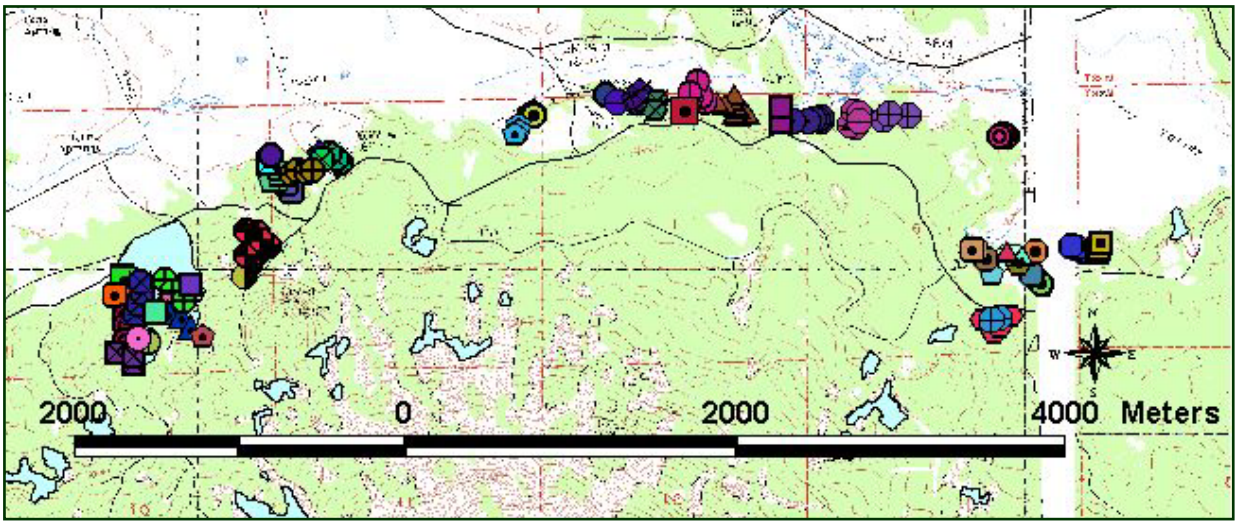
Bogard Buttes (BB) Group



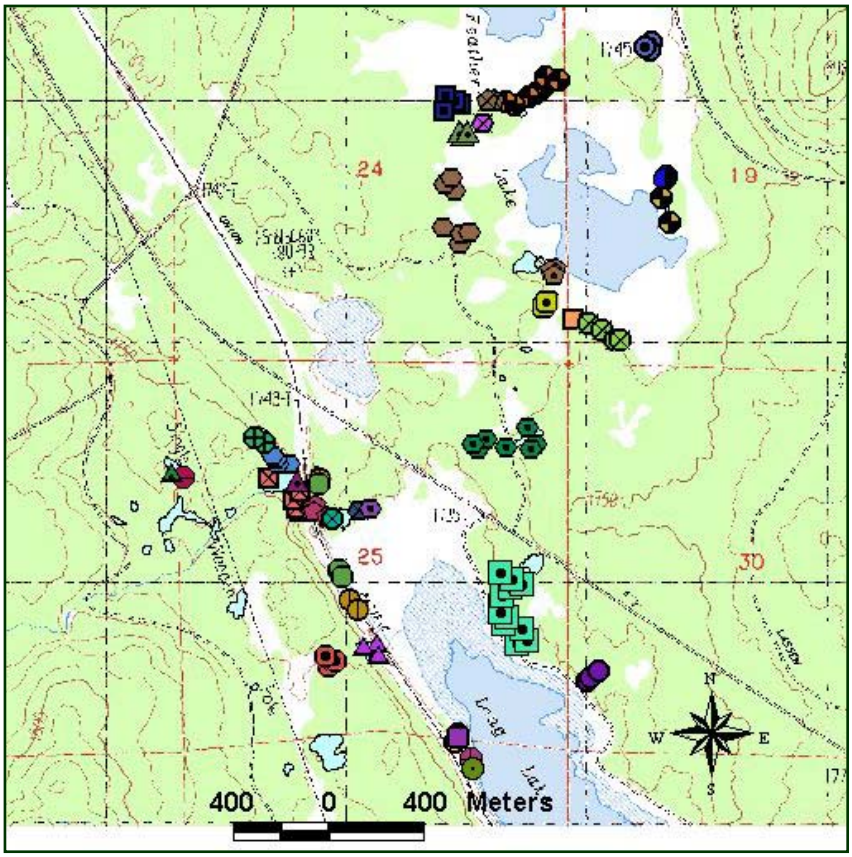
Fredonyer Pass (FP) Group



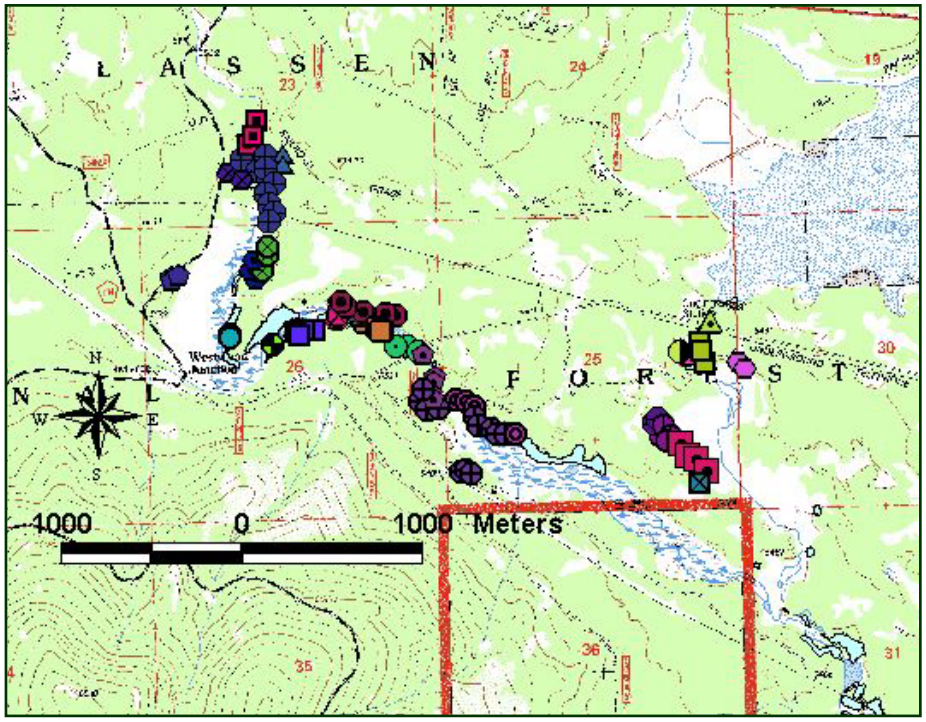
Harvey Mountain (HM) Group



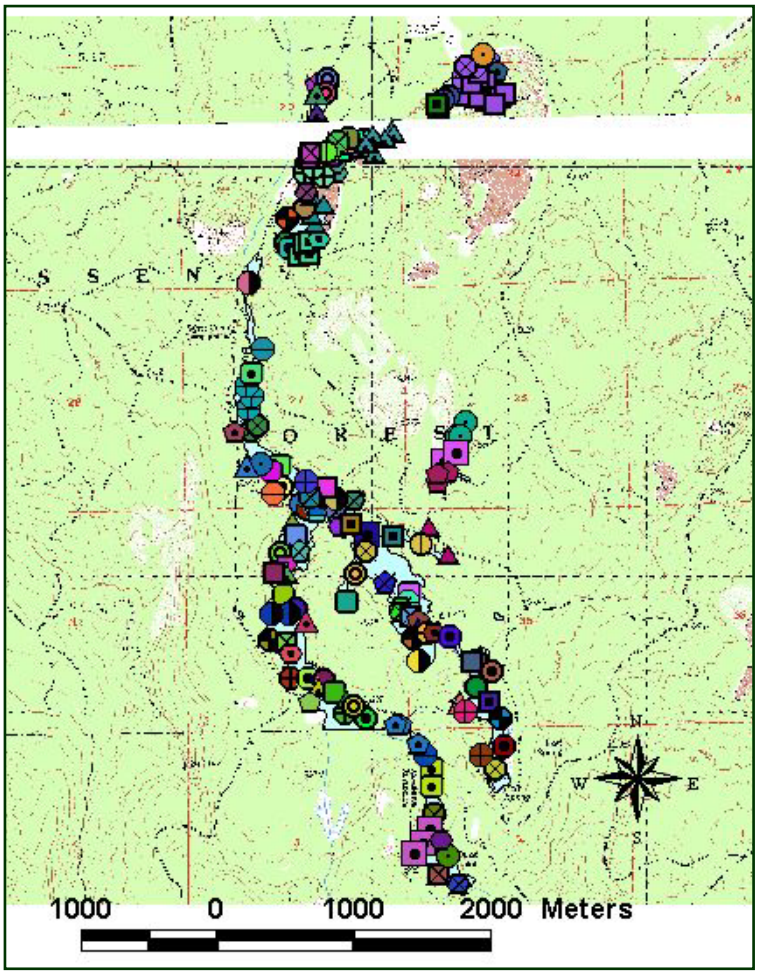
Pine Creek Valley (PC) Group



Peg Leg Mountain (PL) Group



Prospect Peak (PP) Group



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Final Report

Genetic Evidence of Hybridization between *Oenothera wolfii* (Wolf's Evening Primrose) and *O. glazioviana*, a Garden Escape.

Photos provided by D. Imper

NFGEL Project 158

Report prepared by: Jennifer DeWoody and Valerie D. Hipkins, NFGEL
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Date: May 5, 2005

Abstract

Oenothera wolfii (Onagraceae; Wolf's evening primrose), a short-lived perennial threatened by habitat loss throughout its range along the northern California and southern Oregon coasts, is also threatened by hybridization with a common garden escape, *O. glazioviana*. In order to determine if bi-parentally inherited genetic markers could identify and describe hybrid stands, 22 populations, including pure populations of both species, putative hybrid populations, and populations of unknown taxonomy (a total of 288 individuals) were sampled and surveyed for 15 isozyme loci. Low levels of genetic variation were observed in both species ($P \leq 20\%$; $A \leq 1.20$), but high levels of genetic differentiation were observed both among populations within species (mean $F_{SR} = 0.78$) and low to moderate differentiation between the two species ($F_{RT} = 0.049$), including a number of alleles unique to either species. Multivariate analyses identified three clusters of populations (designated *O. wolfii, O. glazioviana*, and unknowns), with two outliers (unknowns). Genealogical class frequency estimates confirmed the taxonomy of one unknown population as *O. wolfii*, and classified the remaining eight unknown populations as hybrids, including four populations considered pure *O. wolfii* based on morphological analysis. This study confirms the occurrence of hybridization between the rare *O. wolfii* and the naturalized *O. glazioviana*, identifies additional putative hybrid populations, and provides a baseline of genetic data for future monitoring efforts.

Introduction

Although habitat loss usually poses the greatest threat to a rare species' survival, there is increasing evidence that hybridization with widespread related taxa poses an immediate threat to some species (Rhymer and Simberloff 1996). Hybridization followed by introgression with the common species may genetically swamp the rare taxa, and may result in the functional extinction of "pure" populations of the rare species (Levin et al. 1996). Thus, conservation strategies for rare or threatened taxa should account for any hybridization potentially resulting from human actions (*e.g.* due to habitat fragmentation or modification, or contact with introduced species; Rhymer and Simberloff 1996; Allendorf et al. 2001). In order to develop monitoring and management plans, robust techniques must be available to identify populations of both the rare and common species, as well as any hybrid individuals that may arise where the two species occur sympatrically. Frequently, hybrid individuals display phenotypes intermediate to either parent species, although hybrids may display morphologies extreme to either parent (Schwarzback et al. 2001). Due to these variations, morphological variation alone may be insufficient to completely describe hybrid swarms of individuals, particularly if second-generation hybrids or back-cross individuals occur with any frequency. Given sufficient variation in neutral, bi-parentally inherited genetic markers (e.g. isozymes), statistical methods exist to identify not only first-generation hybrid individuals, but also second-generation hybrids and introgressed individuals resulting from backcrosses with either parental species (Nason et al. 2002; Reiseberg et al. 1998; Rannala and Mountain 1997).

Oenothera wolfii [Munz] Raven, W. Dietr. Stubbe (Wolf's evening primrose) is a biennial to short-lived perennial native to the coastal areas of northern California and southern Oregon. Populations of this species are rare and patchy in distribution, found on moderately disturbed sites, including the upper margin of beach strand and coastal bluffs (Imper 1997). While disturbance resulting from continued development and recreation along the coast have

created new habitat for *O. wolfii* in some instances, the net effect of human encroachment has been negative for existing populations (Imper 1997). As a result, *O. wolfii* is listed as threatened by the state of Oregon, and is currently a candidate for listing under the U.S. Endangered Species Act (Imper 1997). In addition, both the California Native Plant Society and the Oregon Natural Heritage Program list this species as endangered throughout its range (Imper 1997).

While habitat loss threatens the survival of *O. wolfii*, hybridization with a common garden escape, *O. glazioviana* Micheli, may prove the more immediate threat (Imper 1997). Several factors contribute to this conclusion. First, introgression is common between many members of this genus. Greenhouse experiments have shown that hybridization between *O. wolfii* and other members of the genus readily occurs (Wasmund and Stubbe 1986). Second, individuals of hybrid origin have already been identified at the California-Oregon border area based on morphological traits (Carlson et al. 2001). Hybrids are fertile, vigorous, and display a greater fitness than either parent species (Imper 1997). Although genetic typing of hybrid individuals indicates that hybrids tend to breed true, there is limited evidence of hybrids back-crossing with *O. wolfii* (Imper 1997). Third, *O. wolfii* is expected to be susceptible to genetic swamping by *O. glazioviana* based on the mating systems of each species. Based on pollen exclusion experiments, *O. wolfii* is self-compatible and produces the majority of its seed via self-pollination (Carlson et al. 2001). Cytogenetic studies have shown that *O. wolfii* has a structurally heterozygous genome maintained by balanced lethals that result in approximately half of the mature pollen grains being sterile (Wasmund and Stubbe 1986). In contrast, *O. glazioviana* is an outcrossing species (Imper 1997). Given the asymmetry of available pollen between these parent species, anisotropic, or asymmetric, gene flow might occur as *O. glazioviana* pollen swamps *O. wolfii* stigmas at sympatric sites. Together, these observations provide evidence that hybridization occurs between this rare endemic and the widespread garden escape.

This study reports an investigation into the extent and structure of hybrid zones between the rare endemic *O. wolfii* and the escaped garden variety *O. glazioviana* using putatively neutral, bi-parentally inherited molecular markers (isozymes). Three questions were addressed: Does sufficient genetic variation exist to discriminate between *O. wolfii* and *O. glazioviana* populations? Can hybrid populations be identified using these molecular markers? What is the frequency of hybrid individuals in natural populations of *O. wolfii*? Ultimately, these genetic findings provide greater insight and guidelines for management plans and conservation objectives.

Methods

Samples were collected from a total of 22 sites whose taxonomy was determined by morphological traits (Table 1, Figure 1). Field observations identified thirteen populations as *O. wolfii* (nos. 6-19), four as *O. glazioviana* (nos. 1-4), and three populations as intermediates or putative hybrids (nos. 20-22; unreported data). Field observations could not distinguish between *O. glazioviana* and *O. elata*, a common congener at one site (no. 5), and one population appeared to be *O. wolfii*, but occurred in a novel location (no. 15). A single leaf was collected from between 4 and 25 individuals in each population, placed in plastic bags with moistened paper towels, and shipped on ice to the National Forest Genetics Lab (NFGEL) in Placerville, CA.

Tissue was prepared for isozyme analysis following NFGEL Standard Operating Procedures (USDA Forest Service 2003). Total protein extraction took place by grinding an approximately 4 cm^2 piece of leaf tissue into a fine powder using a mortar and pestle with liquid nitrogen. Approximately 1 mL of Gottleib (1981) extraction buffer was mixed into the powder and allowed to freeze. Once thawed, the resulting slurry was absorbed onto 3mm x 8mm Whatman® paper wicks, which were frozen at –70°C until electrophoresis.

Electrophoresis took place on three buffer systems (adapted from Wendel and Weeden 1989): a tris-citric acid gel buffer (pH 8.3) with a lithium hydroxide-boric acid tray buffer (pH 8.3; LB), a tris-citric acid gel buffer (pH 8.8) with a sodium hydroxide-boric acid tray buffer (pH 8.0; SB), and a citric acid-N-(3-aminopropyl)-morpholine gel and tray buffer (pH 8.0; MC8). A total of fifteen loci were examined: four loci were resolved on the LB system: phosphoglucose isomerase (PGI2), phosphoglucomutase (PGM1), and two loci in leucine aminopeptidase (LAP1 and LAP2). Four loci were also resolved on the SB system: aspartate aminotransferase (AAT1), superoxide dismutase (SOD1), triosephosphate isomerase (TPI1), and uridine diphosphoglucose pyrophosphorylase (UGPP1). Seven loci were resolved on the MC8 system: two loci in esterase (EST1 and EST2), fluorescent esterase (FEST1), isocitrate dehydrogenase (IDH), malate dehydrogenase (MDH), and two in 6-phosphogluconate dehydrogenase (6PGD1 and 6PGD2). All stain recipes were adapted from Conkle et al. (1982). Banding patterns were consistent with known protein structures and diploid Mendelian inheritance, and are consistent with published protein structure (Crawford 1989).

Five standard measures of genetic variation were estimated for each population and over multiple populations for each species: mean alleles per locus, mean alleles per polymorphic locus, percent polymorphic loci, observed heterozygosity, and Wright's fixation index (estimated in the method of Nei 1973). All populations were also tested for linkage disequilibrium using the composite disequilibrium function without assuming Hardy-Weinberg equilibrium, as implemented by the program GDA (Lewis and Zaykin 2001). In order to determine the allele frequencies representative of "pure" *O. wolfii* and *O. glazioviana* populations, a multivariate analysis (canonical discriminate analysis) was completed for all populations over variable loci, as implemented by SAS using PROC CANDISC. The results of this multivariate analysis, which grouped populations according to their genetic similarity, were combined with qualitative morphological information (unreported) in order to identify each population as pure *O. wolfii*, pure *O. glazioviana*, a potential hybrid population, or of unknown taxonomy. Samples from the "pure" populations of each species were pooled and genetic statistics were estimated over all individuals.

Three independent analytical methods were used to characterize hybrid populations and individuals. First, Nei's (1978) unbiased genetic distances and Wright's (1978) fixation indices were estimated for a three-level hierarchical model for the pure populations of each species and the three putative hybrid populations (omitting populations designated unknown): within populations (F_{IS}), among populations within each species (F_{SR}), and among each species (F_{RT}). All estimates were determined using Biosys-1 version 1.7 (Swofford and Selander 1989). Second, maximum likelihood analyses were performed in the method of Nason et al. (2002) in order to estimate the frequency of six genealogical classes [P1 (*O. wolfii*), P2 (*O. glazioviana*), F1 (first generation hybrid), F2 (second generation hybrid), BP1 (first generation backcross to *O. wolfii*), or BP2 (first generation backcross to *O. glazioviana*)] in each hybrid and unknown population. Third, a Bayesian analysis of the admixture of individuals in this study was completed using the MCMC clustering algorithm implemented

in Structure v 2.0 (Falush et al. 2003). Although considered an ad-hoc analysis of population substructure (Pritchard et al. 2000), this program was used to first estimate the number of clusters (or populations) in the entire data set, then to determine the proportion of admixture in each individual genotype. An analysis of 10^6 iterations (following a burn-in of 30,000 steps) for the set of clusters $k = \{1, \ldots, 6\}$ was completed twice: once with no population information included in the data set (all samples considered of unknown taxonomy), and once with prior populations information (the "pure" species described above) incorporated. Once the most likely number of clusters was identified, output for that k was used to determine the relative proportion of admixture from *O. glazioviana*, q(GL), for each genotype. For this analysis, "pure" *O. wolfii* individuals are expected to have a q(GL) = 0, while "pure" *O. glazioviana* individuals are expected to have q(GL) = 1. Hybrid individuals are expected to have an intermediate value of q(GL). Lacking a statistical test for these resulting likelihood values, these analyses were incorporated into the overall analysis of the hybrid structure of these species.

Results

Low levels of genetic variation were observed over all populations surveyed (Table 2). Six of the fifteen loci examined were polymorphic: 6PGD2, AAT1, UGPP1, FEST1, EST1, and EST2. These loci were used in the canonical discriminate analysis that separated these populations into three clusters, with two outliers, based on the first two canonical coefficients (Figure 2). The first canonical coefficient correlates with the presence of the common allele at the locus EST1, separating those populations fixed for the common allele (EST1-1) from those populations containing the alternate allele (EST1-2; Appendix). Interestingly, those populations containing allele EST1-2 are consistently identified as *O. wolfii* based on morphological observation, but appear to be distinct genetically. The second canonical coefficient correlates with the locus 6PGD2, where *O. wolfii* is fixed for allele 1, and *O. glazioviana* is fixed for allele 2 (Appendix).

These results were combined with morphological observations to classify each population for this genetic analysis (Table 1). Genetic and morphological data consistently identify four populations as "pure" *O. glazioviana* (nos. 1 – 4) and nine populations as "pure" *O. wolfii* (nos. 7, 10 – 12, 14, 16 – 19). Intermediate morphology has been observed at three sympatric sites, necessitating the classification of these populations (nos. 20 – 22) as putative hybrids, despite intermediate morphological traits and genetic similarities to *O. glazioviana*. Morphological traits were insufficient to identify the taxonomy of populations 5 (putative *O. glazioviana*) and 15 (putative *O. wolfii*), and as a result, both are classified as unknown. Finally, although morphological observations identified populations 6, 8, 9, and 13 as *O. wolfii*, the intermediate or unique genotypes observed in each population are atypical of other pure stands, and indicate that these populations may contain hybrid or introgressed individuals. As a result, these four populations were classified as unknown.

Fixation indices reveal excess heterozygotes among individuals within species (mean F_{IS} = -0.72), high levels of differentiation among populations within species (mean F_{SR} = 0.78), and moderate levels of differentiation among *O. wolfii* and *O. glazioviana* (F_{RT} = 0.049) (Table 3).

Genealogical class frequency estimates for most unknown and hybrid populations were fixed for a single genealogical class (Table 4). Frequency estimates were 1.0 for the genealogical class noted after each population: no. 5 = BP2; no. 6 = F2; no. 8 = F2; no. 9 =

F2; no. 15 = P1; no. 20 = BP1; no. 21 = P2; no. 22 = P2. Frequency estimates for the two genealogical classes identified in population 13 are P1 = 0.46 and F2 = 0.54.

The results of the Bayesian clustering analyses implemented by Structure v 2.0 (Falush et al. 2003) were consistent between runs with and without prior population information. *Ad hoc* population substructure analysis indicated the most likely number of clusters in this data set to be 5 or 6. Analyses without prior populations indicated $k = 5$ to be most likely (mean relative likelihood of $k = 5$ is 0.9992; of $k = 6$ is 0.0008; for all other k, approximately 0). When prior population information was included, thus defining the "pure" populations of each parent species as described above, the analyses indicated the most likely number of clusters to be 6 (mean relative likelihood of $k = 6$ approaches 1.0; of all other k, approximately 0). As estimated in one cluster analysis using prior population information for $k = 6$, the distribution of q(GL) values (the proportion of each genotype from *O. glazioviana*) indicates the presence of a range of hybrid or admixed individuals (Figure 3, Tables 4 and 5).

Discussion

This survey of fifteen isozyme loci revealed low levels of variation in *O. wolfii* and *O. glazioviana* (Table 2). Greater variation was observed in *O. wolfii* (0 – 20% polymorphic loci) than *O. glazioviana* (6.7% polymorphic loci), and all samples from "pure" *O. glazioviana* populations (nos. 1-4) shared a common genotype: heterozygous at AAT1, but monomorphic at all other loci. *O. wolfii* contained a greater number of alleles per locus (1.20 compared to 1.07 in *O. glazioviana*), but displayed greater levels of fixation (0.007 compared to –0.07 in *O. glazioviana*). While the two species shared most alleles, four loci contained variation unique to one species or the other, given the definition of "pure" populations in this data set, thus providing sufficient genetic variation to distinguish between each pure species and unknown populations (6PGD2, AAT1, EST2, UGPP1, Appendix). Three populations classified as unknown taxonomy, nos. 6, 8, and 9, contained comparable levels of polymorphism and fixation as *O. wolfii* (Table 2), but alternate alleles at these sites were not observed in either "pure" species (Appendix). A single individual collected from a site at Moonstone (not reported in general analysis) contained all *O. wolfii*-like alleles, indicating it to be a pure sample of this species.

Interpretation of this data set, as well as its application in future studies, must be considered in the context of the small sample sizes at some populations and the small number of pure *O. glazioviana* populations sampled (Gitzendanner and Soltis 2000). In addition, classifying population nos. 6, 8, 9, or 13 as "pure" *O. wolfii* would change the observed allele frequencies, and potentially change the classification of hybrid populations.

Those caveats in hand, can hybrid populations be identified using these molecular markers, and at what frequency do they occur? Three of the populations sampled were hypothesized to contain hybrid individuals *a priori* based on morphological traits (nos. 20, 21, and 22). Populations 21 and 22 display the *O. glazioviana*-like genotype, being heterozygous at AAT1 and homozygous for the *O. glazioviana*-type allele at 6PGD2. This genotype indicates either that these populations have been misidentified in field studies and are actually *O. wolfii*-like variants of *O. glazioviana*, or that past hybridization has been followed by sufficient introgression or reproductive isolation that the *O. wolfii* genotype has been lost at these sites. Genealogical class frequency estimates are consistent with these conclusions, having classified both populations as *O. glazioviana*.

The genotype observed at population 20, however, is more complex. While heterozygous at AAT1, indicative of *O. glazioviana*, individuals at population 20 are fixed for three rare alleles. Two loci are fixed for alleles only found in the unique populations 6, 8, and 9 (EST1-2 and EST2-2). The third locus is fixed for an alternate allele unique to this population (FEST1-3). Genealogical class frequency estimates indicate that population 20 is likely a first-generation backcross to *O. wolfii*. This conclusion is more plausible if populations 6, 8, and 9, classified as unknowns based on multivariate analyses, are reclassified as a "pure" population, thereby changing the frequency of the rare alternate alleles in *O. wolfii*, and providing a mechanism for the occurrence of alleles EST1-2 and EST2-2 in population 20. Alternatively, these alleles may be *O. glazioviana* in origin, but unsampled in this collection of "pure" *O. glazioviana* populations. Larger sample sizes (where available) and more comprehensive sampling of *O. glazioviana* populations are necessary to determine the source of these alleles.

Those populations classified as "unknown" in this study actually represent two separate questions. Two populations were designated of unknown taxonomy *a priori*: nos. 15 and 5. Population 15 contains *O. wolfii*-like plants that were included in this study to confirm their taxonomy. All samples from population 15 displayed the common *O. wolfii* genotype, indicating that this population is pure *O. wolfii* since no *O. glazioviana* alleles were observed. Genealogical class frequency tests further support this conclusion, classifying this population as *O. wolfii*. Population 5, however, contains plants that appear to be *O. glazioviana*, but may be a native widespread congener *O. elata* instead of the garden escape. Isozyme analyses reveal alleles unique to both "pure" species, indicating that hybridization has potentially occurred at this site. Genealogical class frequency estimates indicate that these individuals are best described as first-generation backcross to *O. glazioviana*, supporting the possibility of past hybridization. Two factors constrain this conclusion. First, the samples of "pure" populations in this study (especially those of *O. glazioviana*) may not be representative of actual allele frequencies, and further sampling of the garden variety may be necessary. Second, samples from population 5 may be *O. elata*, or a hybrid between *O. elata* and *O. wolfii*. As no known *O. elata* populations were sampled, no information is available for the allele frequencies in this species, and no conclusions can be made about its occurrence here.

The other "unknown" populations were classified as such based on the multivariate analysis. These populations (nos. 6, 8, 9, and 13) are consistently classified as "pure" *O. wolfii* based on morphological information. However, a unique petal shape (curled tips) is observed at sites 6, 8, and 9 (unpublished data). These three populations appear to be unique based on isozyme data (Appendix), and contain a set of alternate alleles not observed in other "pure" populations of *O. wolfii*: EST1-2, EST2-2, and FEST1-2. Interestingly, hybrid population 20 is also fixed for EST1-2 and EST2-2. In addition, populations 6, 8, and 9 are fixed for an allele observed only in pure *O. glazioviana* populations: 6PGD2-2. Four individuals in population 13 were also homozygous for this allele. Given the absence of this 6PGD2-2 allele in other populations of *O. wolfii*, the presence of it in these populations indicates hybridization between *O. wolfii* and *O. glazioviana* may have occurred at these sites.

This hypothesis of past hybridization provides a possible origin of other alternate alleles observed at these sites but not in "pure" populations of *O. wolfii*. The observation of two of the alternate alleles (EST1-2 and EST2-2) in a known hybrid population (no. 20) is consistent with the hypothesis of a hybrid origin of these alleles. However, neither of these alleles was observed in "pure" populations of *O. glazioviana*. Two possible explanations

exist for this fact. First, the number of *O. glazioviana* samples in this study may have been insufficient to capture these alleles. Alternatively, the hybridization leading to the fixation of these alleles in these populations may not have been between *O. wolfii* and *O. glazioviana*, but between *O. wolfii* and another common congener, *O. elata*, which is native to this region but was not included in this analysis. Only further testing of *O. glazioviana* and the addition of *O. elata* to the genetic studies may determine if hybridization between the two native species can explain this pattern.

Genetic analyses identified population 13 as distinct from pure *O. wolfii* populations, although plants at this site are consistently identified as *O. wolfii* based on morphological observations. The multivariate analysis revealed this population to contain genotypes intermediate to the pure species. However, the genealogical class frequency estimates identified half of the samples as second-generation hybrids. Indeed, one allele unique to "pure" populations of *O. glazioviana* occurs in population 13, indicating that hybridization may have occurred at this site in the past.

Despite the uncertainty of the taxonomy of genetically unique populations, this study provides genetic evidence of hybridization among wild populations of *O. wolfii* and the garden escape *O. glazioviana*, and these findings have implications for the conservation of the rare species. First, the pattern of hybridization observed in populations 21 and 22, where the *O. glazioviana*-type genotype was observed in all individuals, indicates that the garden escape has the potential to genetically swamp *O. wolfii* at sympatric sites. This finding is consistent with field observations and previous cytogenetic studies (Imper 1997). In sites where hybridization favors the *O. glazioviana* genotype, efforts to eradicate the garden variety are warranted. The presence of *O. wolfii*-type alleles at population 20 indicates that hybridization at this site has not resulted in the genetic swamping of the threatened genotype. In addition, genealogical class frequency estimates indicate backcrosses with *O. wolfii* occur at this site. However, the alternate alleles observed at this site, as well as populations 6, 8, 9, and 13, indicate that these populations are distinct from the "pure" *O. wolfii* populations, as well as the other hybrid stands. Again, the origin of these alleles cannot be determined from this data set, but if these are determined to be unique to *O. wolfii* and not introduced from *O. glazioviana* or *O. elata*, management activities should take this genetic variation into account. In the meantime, plans to augment small populations should use seed from genetically similar populations. Seed from genetically unique sites should not be introduced into "pure" populations lacking those alternate alleles. Ultimately, this study may be used as baseline information for monitoring efforts, as well as to confirm future hybridization.

A more detailed analysis of the genetic structure of hybrid populations will require genetic markers resolving greater distinction between *O. wolfii* and *O. glazioviana*, as well as greater variation within *O. wolfii*. Pairing maternally inherited markers (e.g. chloroplast DNA) with bi-parentally inherited (nuclear) markers could confirm the genetic swamping of *O. wolfii* by *O. glazioviana*, and provide insight into the direction of hybridization between these species. Finally, the inclusion of *O. elata* in future studies is warranted based on the extensive hybridization observed in this genus, as well as the intermediate genotypes observed at population 5, whose taxonomy was undetermined based on morphological data. Data for all three species is required in order to rule out hybridization between *O. wolfii* and *O. elata* as a source of alternate alleles.

Summary

Isozyme analysis of 22 populations of the rare endemic *Oenothera wolfii* and the garden escape *O. glazioviana* reveal low levels of variation within species, but high levels of genetic differentiation among populations and among species. Multivariate analyses grouped populations into three categories: *O. wolfii*, *O. glazioviana*, and unknown taxonomy, with two outlier populations. Four populations classified as unknown, nos. 6, 8, 9, and 13, had been identified as *O. wolfii* based on morphological traits. Genealogical class frequency estimates classified these populations as hybrid in nature, indicating that hybridization between *O. wolfii* and *O. glazioviana* may be more widespread than morphological evidence indicates. Genetic analyses also confirm the presence of hybridization at three sites classified as hybrid populations (nos. 20, 21, and 22) based on morphological data, and confirm the taxonomy of a pure *O. wolfii* population (no. 15). Finally, the observation of potentially hybrid genotypes at population 5, combined with the lack of pure *O. elata* samples in this data set, make it impossible to determine the taxonomy of plants at this site.

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Table 1. Population number, name, location (latitude, longitude), estimated population size (*N*), and species composition of 22 sites sampled for this study. Species composition was determined by field observations and genetic data, and is indicated by: WO = *O. wolfii*, GL = *O. glazioviana*, HY = intermediate morphology potentially due to hybridization, and UN = unknown taxonomy. See text for details.

Number	Name	Location	*N*	Species
1	Charleston, Coos Co., OR	43.3397N, 124.3308W		GL
2	Crescent City, Del Norte Co., CA	41.7486N, 124.2022W		GL
3	Manila, Humboldt Co., CA	40.8483N, 124.1650W	11	GL
4	Trinidad, Humboldt Co., CA	41.0353N, 124.1058W		GL
5	Junction City, Trinity Co., CA	40.7378N, 123.0575W		UN
6	Port Orford City Park, Curry Co., OR	42.832N, 124.502W	6	UN
7	Houda Point, Humboldt Co., CA	41.0359N, 124.1187W		WO
8	Port Orford Beach, Curry Co., OR	42.7318N, 124.4825W	9	UN
9	Port Orford Bridge, Curry Co., OR	42.7318N, 124.4825W	9	UN
10	Luffenholtz, Humboldt Co., CA	41.0353N, 124.1247W		WO
11	Pistol River, Curry Co., OR	42.2717N, 124.4051W		WO
12	Point Saint George, Del Norte Co., CA	41.7778N, 124.2405W	19	WO
13	Devil's Gate, Humboldt Co., CA	40.4055N, 124.3914W	10	UN
14	Davis Creek, Humboldt Co., CA	40.3765N, 124.3725W	9	WO
15	McKerricher State Park, Mendocino Co., CA	35.5199N, 123.7733W	10	UN
16	Freshwater Spit, Humboldt Co., CA	41.2667N, 124.1058W	200	WO
17	Crescent Beach, Del Norte Co., CA	41.7194N, 124.1447W	30	WO
18	False Klamath Cove, Del Norte Co., CA	41.6027N, 124.1064W	700	WO
19	Crescent Overlook, Del Norte Co., CA	41.7048N, 124.1447W	10	WO
20	Klamath, Del Norte Co., CA	41.5151N, 124.0298W		HY
21	Lucky Bear Casino, Del Norte Co., CA	41.9529N, 124.2022W		HY
22	Fruit Station, Curry Co., OR	41.9984N, 124.2124W		HY

Table 2. Isozyme diversity statistics for 22 populations of *O. wolfii* and *O. glazioviana*. Means over species include only non-hybrid populations. N = number of samples, P = percent polymorphic loci, A = mean alleles per locus, A_p = mean alleles per polymorphic locus, H_o = observed heterozygosity, F = fixation index. Variance reported in parentheses.

Population	N	P	A	A_p	H_o	F
Mean over species:						
O. wolfii	137	13.33	1.200 (0.293)	2.500	0.021 (0.005)	-0.210
O. glazioviana	61	6.67	1.067 (0.062)	2.000	0.067 (0.062)	-1.000
1	25	0.067	1.067	2.000	0.067	-1.000
2	17	0.067	1.067	2.000	0.067	-1.000
3	11	0.067	1.067	2.000	0.067	-1.000
4	8	0.067	1.067	2.000	0.067	-1.000
5	21	0.133	1.133	2.000	0.133	-1.000
6	6	0.133	1.133	2.000	0.078	-0.750
7	12	0.067	1.067	2.000	0.011	-0.048
8	9	0.067	1.067	2.000	0.067	-1.000
9	9	0.067	1.067	2.000	0.067	-1.000
10	13	0.067	1.067	2.000	0.015	-0.091
11	25	0.000	1.000	n/a	0.000	0.000
12	19	0.067	1.067	2.000	0.018	-0.125
13	10	0.200	1.200	2.000	0.073	0.214
14	9	0.133	1.133	2.000	0.067	-0.385
15	10	0.000	1.000	n/a	0.000	0.000
16	25	0.000	1.000	n/a	0.000	0.000
17	5	0.000	1.000	n/a	0.000	0.000
18	25	0.067	1.067	2.000	0.067	-1.000
19	4	0.000	1.000	n/a	0.000	0.000
20	10	0.067	1.067	2.000	0.067	-1.000
21	10	0.067	1.067	2.000	0.067	-1.000
22	5	0.067	1.067	2.000	0.067	-1.000

Table 3. Fixation indices estimated within and among species and putative hybrid populations of *O. wolfii* and *O. glazioviana*. F_{IS}, F_{ST} (fixation among populations) and F_{RT} (fixation among species) from Wright (1978); *D* is Nie's (1978) unbiased genetic distance.

Comparison	F_{IS}	F_{SR}	F_{RT}	*D*
O. wolfii species mean	-0.21	0.29	N/A	0.01
O. glazioviana species mean	-1.00	0.00	N/A	0.00
Hybrid mean	-1.00	0.78	N/A	0.21
O. wolfii – *O. glazioviana*	-0.52	0.61	0.49	0.09
O. wolfii – Hybrids	-0.47	0.70	0.21	0.14
O. glazioviana - Hybrids	-1.00	0.66	-0.06	0.11
Mean over all populations	-0.72	0.78	0.73	0.13

Table 4. Classification of nine populations of unknown or hybrid origin based on 15 isozyme loci. The genealogical class frequency method classifies each population as *O. wolfii*, *O. glazioviana*, hybrid, or backcross to either parent species. The Bayesian clustering method, while able to assign individuals to either parent species, otherwise assigns individuals to anonymous clusters and not genealogical classes; hybrids are inferred when equal portions are assigned to each parental species.

Population	Field Observations	Genealogical class frequency	Bayesian clustering method
5	Unknown	Backcross to *O. glazioviana*	*O. glazioviana*
6	*O. wolfii*	Hybrid	Neither species
8	*O. wolfii*	Hybrid	Neither species
9	*O. wolfii*	Hybrid	Neither species
13	*O. wolfii*	Mix of *O. wolfii* and Hybrid	*O. wolfii*,Hybrid, Neither species
15	Unknown	*O. wolfii*	*O. wolfii*
20	Hybrid	Backcross to *O. wolfii*	Neither species
21	Hybrid	*O. glazioviana*	*O. glazioviana*
22	Hybrid	*O. glazioviana*	*O. glazioviana*

Table 5. Relative proportion of admixture in all genotypes observed in hybrid and unknown populations. q(N) is the proportion of each genotype derived from each cluster, with 1 = *O. glazioviana*, 2 = *O. wolfii*, and 3 – 6 representing anonymous clusters. No variation was observed within populations 5, 8, 9, 15, 20 – 22, resulting in a single genotype for each population. Variation was observed among sites. Multiple genotypes were observed in populations 6 and 13.

Population No.	*q*(1)	*q*(2)	*q*(3)	*q*(4)	*q*(5)	*q*(6)
5	0.523	0.136	0.085	0.085	0.085	0.085
8	0.109	0.066	0.208	0.205	0.207	0.206
9	0.108	0.066	0.208	0.205	0.207	0.206
6, genotype a	0.108	0.065	0.208	0.205	0.207	0.206
6, genotype b	0.131	0.077	0.199	0.196	0.199	0.198
13, genotype a	0.445	0.200	0.089	0.089	0.089	0.089
13, genotype b	0.105	0.548	0.086	0.088	0.087	0.087
13, genotype c	0.242	0.095	0.162	0.169	0.164	0.168
13, genotype d	0.258	0.357	0.096	0.097	0.096	0.096
15	0.126	0.593	0.070	0.071	0.070	0.071
20	0.077	0.097	0.208	0.205	0.207	0.206
21	0.649	0.110	0.060	0.060	0.060	0.060
22	0.650	0.110	0.060	0.060	0.060	0.060

Figure 1. Location of 22 populations sampled for this study. Numbers correspond to populations in Table 1.

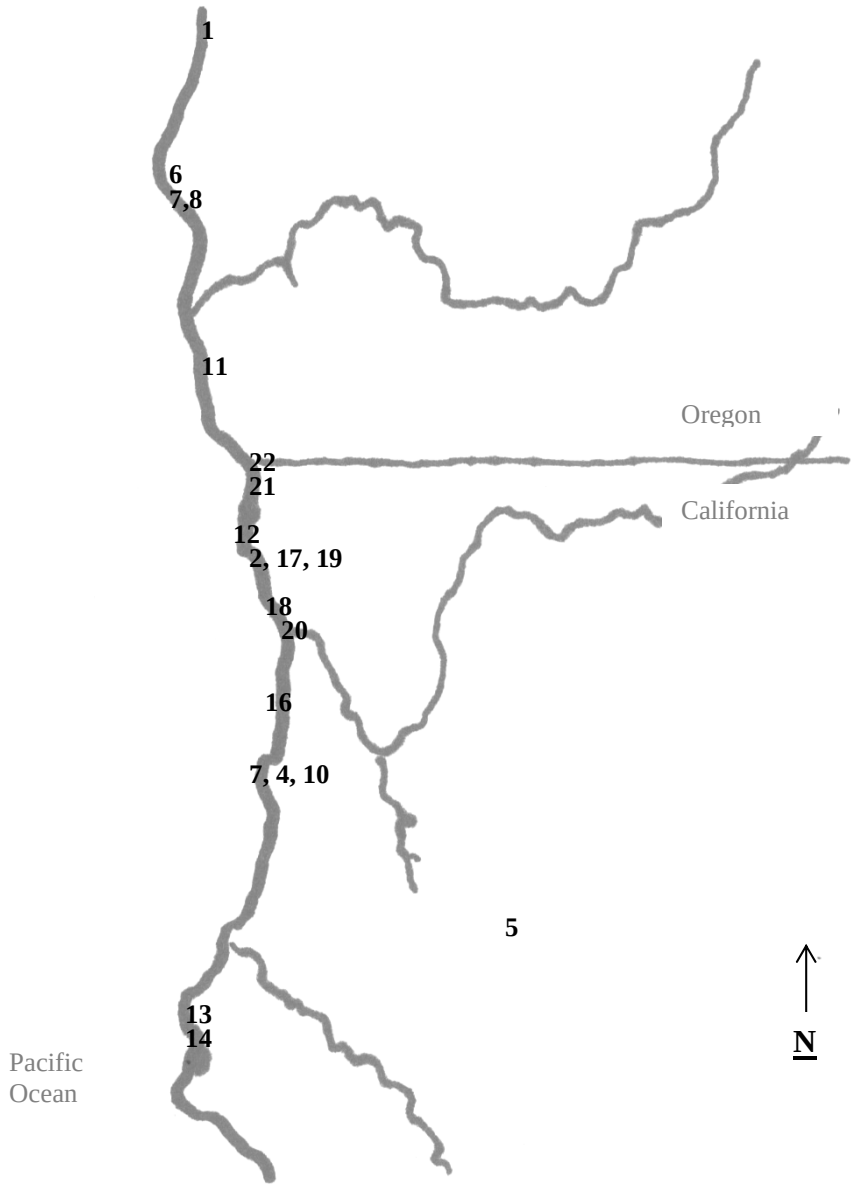


Figure 2. Distribution of 22 sampled populations along the first two canonical variables produced by a discriminate coordinate analysis. Populations are identified by their number. Can1 = first canonical variable, Can2 = second canonical variable.

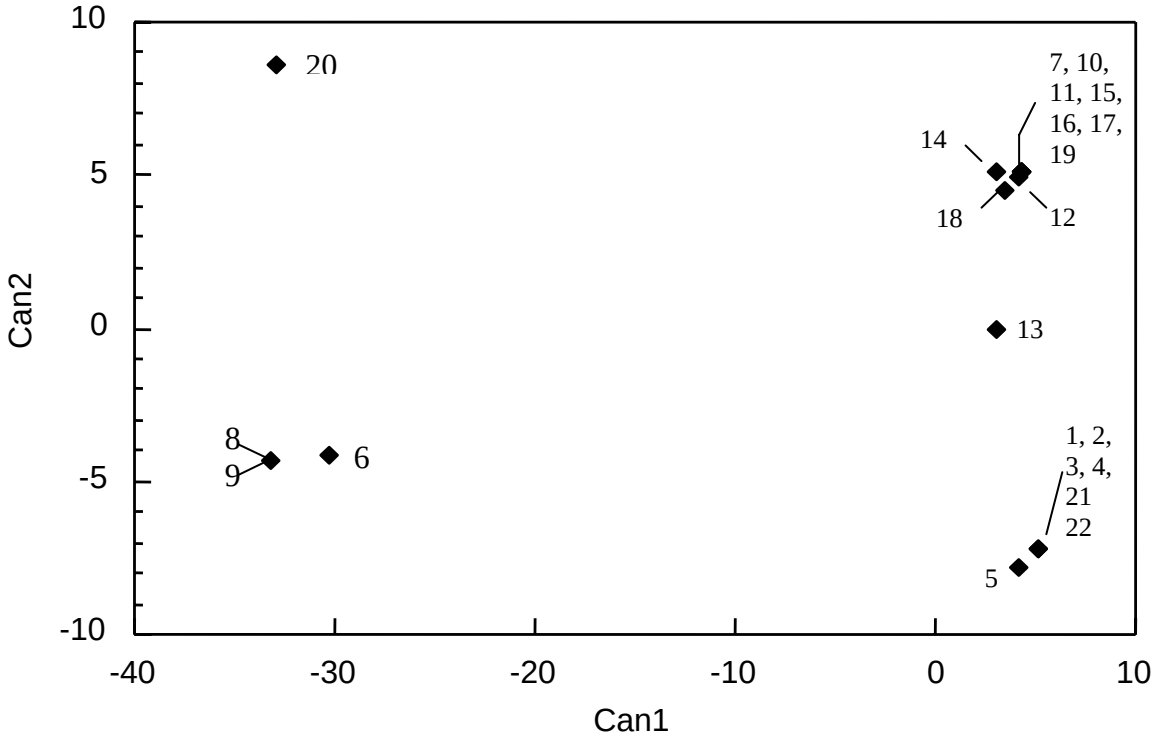
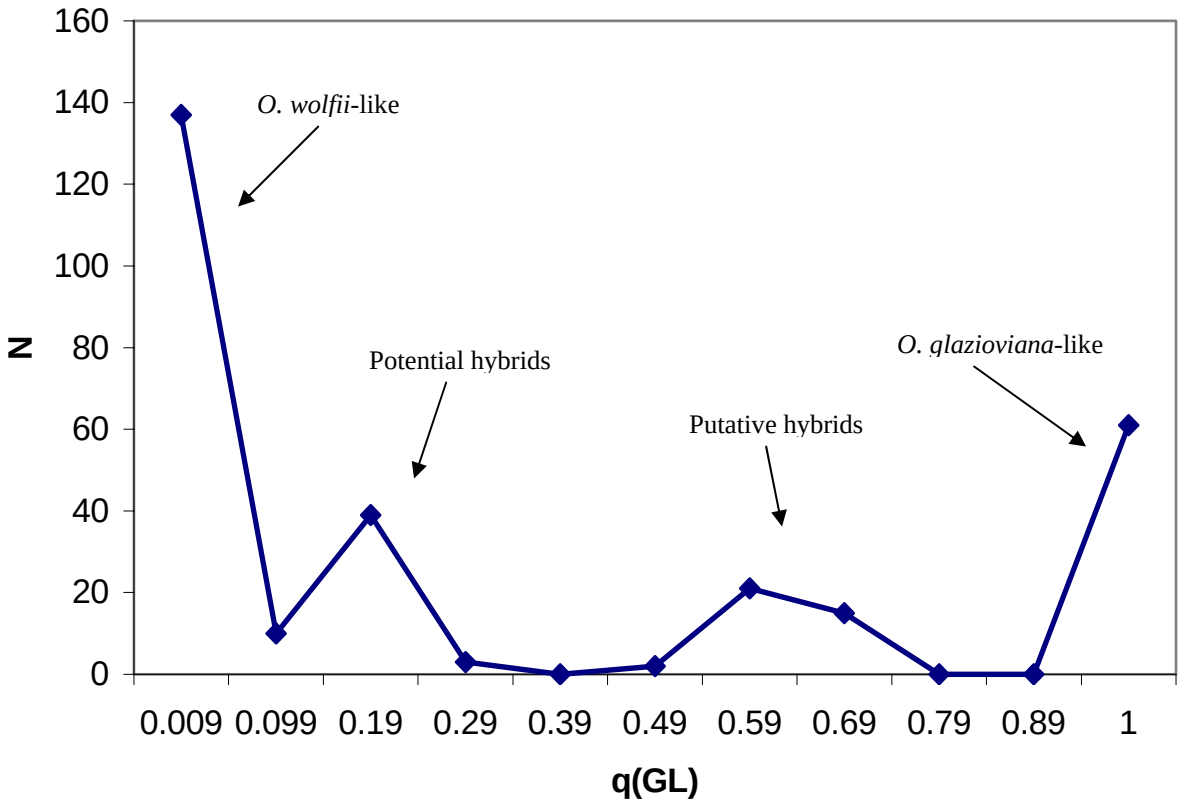


Figure 3. Frequency distribution of *q*(GL), the relative contribution of *O. glazioviana* to each observed genotype for all samples of *O. wolfii*, *O. glazioviana*, hybrid or unknown origin.



Appendix. Allele frequencies for the six variable isozyme loci in 22 populations of *O. wolfii*, *O. glazioviana*, and potential hybrids.

Locus/Allele	6PGD2		AAT1		EST1		EST2				FEST1			UGPP1	
Population	1	2	1	2	1	2	1	2	3	4	1	2	3	1	2
Mean over species:															
O. wolfii	1.000		1.000		1.000		0.975		0.018	0.007	1.000			0.858	0.142
O. glazioviana		1.000	0.500	0.500	1.000		1.000				1.000			1.000	
1		1.000	0.500	0.500	1.000		1.000				1.000			1.000	
2		1.000	0.500	0.500	1.000		1.000				1.000			1.000	
3		1.000	0.500	0.500	1.000		1.000				1.000			1.000	
4		1.000	0.500	0.500	1.000		1.000				1.000			1.000	
5		1.000	0.500	0.500	1.000		1.000				1.000			0.500	0.500
6		1.000	1.000		0.083	0.917		1.000				1.000		0.500	0.500
7	1.000		1.000		1.000		0.9167		0.083		1.000			1.000	
8		1.000	1.000			1.000		1.000				1.000		0.500	0.500
9		1.000	1.000			1.000		1.000				1.000		0.500	0.500
10	1.000		1.000		1.000		0.885		0.115		1.000			1.000	
11	1.000		1.000		1.000		1.000				1.000			1.000	
12	1.000		1.000		1.000		1.000				1.000			0.868	0.132
13	0.550	0.450	1.000		1.000		0.800			0.200	1.000			0.500	0.500
14	1.000		1.000		1.000		0.889			0.111	1.000			0.500	0.500

Appendix continued.

Locus/Allele	6PGD2		AAT1		EST1		EST2				FEST1			UGPP1	
Population	1	2	1	2	1	2	1	2	3	4	1	2	3	1	2
15	1.000		1.000		1.000		1.000				1.000			1.000	
16	1.000		1.000		1.000		1.000				1.000			1.000	
17	1.000		1.000		1.000		1.000				1.000			1.000	
18	1.000		1.000		1.000		1.000				1.000			0.500	0.500
19	1.000		1.000		1.000		1.000				1.000			1.000	
20	1.000		0.500	0.500		1.000		1.000					1.000	1.000	
21		1.000	0.500	0.500	1.000		1.000				1.000			1.000	
22		1.000	0.500	0.500	1.000		1.000				1.000			1.000	

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Final Report

Genetic Diversity in *Bromus carinatus* from Western Oregon: Implications for Seed Collection and Propagation

Unknown@USDA-NRCS PLANTS Database

Final Report NFGEL Project #185
Report prepared by Jennifer DeWoody and Valerie D. Hipkins
Report submitted to David Doede, USDA Forest Service, Mt Adams Ranger Station, Trout Lake, WA

December 14, 2005

Management Summary

Objective 1: Does genetic variation reside mostly among locations, or within locations?

This study of 144 samples of *Bromus carinatus* collected from eleven populations in western Oregon indicates that most genetic variation resides within populations, although a significant portion (19%) is contained among populations. This genetic differentiation indicates that caution should be used in pooling seed from multiple populations or moving seed among populations or regions.

Objective 2: How many locations does seed need to be collected from, and how many different individuals at each location?

Given the variable sample quality observed across locations, the quality of future collections will be greatly improved with proper species identification and knowledge of seed maturity. If the levels of genetic differentiation reported in this study are typical for *B. carinatus* in western Oregon, seed should be collected from several individuals in multiple locations in order to capture the genetic variation observed across the study area.

Objective 3: How much outcrossing occurs within locations?

High rates of outcrossing were observed in six populations of *B. carinatus*. Mean multilocus outcrossing rate was 0.989 over all populations, with observed values ranging from 0.900 to 1.000.

Introduction

The scope of this project was to describe the distribution of genetic variation within and among populations of *Bromus carinatus* from western Oregon, and estimate the rate of outcrossing, in order to inform seed collection and propagation activities. As with any genetic study, the quality of the data depends in part on the quality of the study design and sample collections. The material submitted for this study, seed from each of 490 plants, was less than optimal in that some samples were contaminated with seed that was obviously not *B. carinatus*, some samples contained only seed that was obviously not *B. carinatus*, and much of the submitted material was lacking viable seed. In total, due contamination and lack of germination, genetic data was obtained for 144 (29.4%) of the families submitted (see Appendix 2.) Indeed, without appropriate voucher specimens to confirm the taxonomy of the samples collected at each site, the possibility that this study inadvertently included samples that were not *B. carinatus* must be considered when examining the conclusions based on this data.

Incorporating information on the genetic structure of a species into restoration and seed collection activities is important to maintain the natural pattern of genetic variation across population. In order for seed collections to capture amounts of genetic diversity representative of the species as a whole, knowledge of the distribution of genetic variation within and among individuals, populations, and regions must be incorporated into seed collection guidelines. At the extreme, genetic differentiation among populations may be the consequence of local adaptation. In this case, the movement of individuals between sites may cause a reduction of fitness or survival in the local population.

Several factors affect the amount and distribution of genetic variation in plant species. How genetic diversity is partitioned within and among populations is associated with the reproductive biology of a species as well as the mechanisms of seed dispersal. Variation tends to be contained within populations in species that are highly outcrossing, while genetic diversity tends to be partitioned among populations in selfing species (Godt & Hamrick 1998). Similarly, species that produce seed with mechanisms for long distance dispersal (e.g. by wind or water) tend to contain variation within populations, while gravity-dispersed seed is associated with variation being contained among populations (Hamrick & Godt 1996). However, no one life history trait accounts for a large portion of the genetic diversity observed in a species (Godt & Hamrick 1998).

Bromus carinatus (Hook. & Arn.), or California brome, is an important native species used in restoration throughout its native range along the Pacific Coast of the U.S., as well as in the intermountain and Rocky Mountain states, where it has become naturalized (Howard 1997). Most populations are characterized by a mixed mating system, with self-fertilization being more common than outcrossing (Howard 1997). The degree of selfing may be influence by environmental conditions, as cleistogamous flowers, which remain closed and are self-pollinated, increase in frequency during water stress in greenhouse experiments (Howard 1997). Plants are perennial, surviving three to five years, and seed may persist for some years in the seed bank (Howard 1997). Ploidy states in the genus *Bromus* can vary from diploid to decaploid (Tuna et al. 2001).

This project will aid in seed collection and propagation efforts by addressing three objectives using putatively neutral, bi-parentally inherited markers (isozymes). First, does genetic variation reside mostly among locations, or within locations? Second, how many locations does seed need to be collected from, and how many different individuals at each location? Third, how much outcrossing occurs within locations?

Methods

Sample preparation

Seed from 35 families from each of 14 locations was submitted to NFGEL for study. For germination, seed was placed on four layers of moistened germination paper. Seed was placed in cold stratification for 28 days (4-6°C), then transferred to a germination chamber with a temp/light cycle of 30°C/20°C with 12/12 hr light and dark. During germination, seeds were hydrated as needed with a dilution of Schultz's plant food. Germination occured in 7 to 28 days, and seedlings reached standard preparation size (8-12cm) in 4-8 weeks.

Isozyme analysis

For population genetic analyses, one 8-11cm seedling (measurement excluding root) (approximately 28 days old) from each family from each location were assayed, when available. Individual seedlings (including root) were ground in 12 drops of Melody/Neale buffer (USDA Forest Service 2003). Slurry was frozen in 96 well plates and stored in the ultra-low (-80°C) freezer until electrophoresis.

For the maternity array, a total of 10 seedlings per family were prepped for isozyme analysis (in the method described above) from the following locations/families: Eugene 5/13, Eugene 5/18, Eugene 14/38, Eugene 18/21, MF 4/3, MF 4/5, MF 4/13, MF 4/26, MF 4/34, MF 16/11, MF 16/27, Sal 9/34.

Isozyme diversity was assayed at a total of 14 loci in three buffer systems (USDA Forest Service 2003). Four loci were resolved in a lithium borate electrode buffer-tris citrate gel buffer combination (system LB): malic enzyme (ME), phosphoglucomutase (PGM1 and PGM2), and isocitrate dehydrogenase (IDH). Five loci were resolved in a sodium borate electrode buffer-tris citrate gel buffer combination (system SB): aspartate aminotransferase (AAT1 and AAT2), phosphoglucose isomerase (PGI), phosphogluconate dehydrogenase (6PGD) and uridine diphosphoglucose pyrophosphorylase (UGPP). Five loci were resolved in a morpholine citrate electrode and gel buffer (system MC8): diaphorase (DIA), malate dehydrogenase (MDH1 and MDH3), and shikimic acid dehydrogenase (SKD1 and SKD2). Two people independently scored each gel, and disagreements in scores were resolved.

Data analysis

In order to describe the genetic structure of the locations sampled for this study, one individual per family was randomly chosen and included in the data set (omitting the additional samples analyzed for estimates of outcrossing). For this reduced data set, allele frequencies, Nei's (1978) unbiased estimate of mean heterozygosity, mean alleles per locus, and percentage of polymorphic loci were estimated for each location and over all samples using Biosys-1 version 1.7 (Swofford & Selander 1989). Genetic differentiation, both among individuals within a location, and among locations over the entire collection, was estimated as Wright's *F*-statistics as employed by GDA (Lewis & Zaykin 2001). Genetic distance, a measure of the difference between all pairs of populations, was estimated as Nei's (1978) unbiased genetic distance, as implemented by Biosys-1 version 1.7 (Swofford & Selander 1989). Finally, in order to further detect seed contamination and identify possible structure due to genetic differentiation, ploidy level, or family structure, the number of functional populations in the entire data set was estimated using Markov-chain Monte Carlo simulations, as described by Pritchard et al. (2000) and implemented by Structure version 2 (Pritchard et al. 2000). Probability of k = 1 through k = 10 subpopulations was estimated using 50,000 burn-in iterations followed by 1,000,000 logged iterations. Assignment of each individual sample to one or more subpopulation, without reference to population of origin, was also estimated for each sample.

In order to estimate the rate of outcrossing, ten samples were analyzed from each of thirteen families collected over six populations, and the multilocus outcrossing rate (t_m) was estimated using the Expectation-Maximization (EM) method, with standard errors determined over 1000 bootstraps, with

individuals resampled within populations, due to small sample sizes. All methods were used as employed by the program MLTR (Ritland 2002).

Results

Seed contamination was detected during three steps of the analysis: during seed germination (seed obviously not *Bromus*), during sample preparation (dicot seedlings), and during isozyme analysis (samples fixed at most loci for alternate alleles not observed in *Bromus*) (Appendix 2). Samples that were obviously not *B. carinatus* were removed from the analyses. In total, 281 samples were prepped and assayed for the fourteen isozyme loci. When the data set was reduced to one seedling per family, 144 samples were included in the population genetic analyses. After removing one family that was obviously not *B. carinatus* based on isozyme genotypes (Eugene 18 family 30), 13 families produced ten seedlings that were analyzed for outcrossing rates. Three populations had more than one family represented in outcrossing analyses (Eugene 5, MF 4 and MF16).

All but one locus displayed electrophoretic patterns consistent with diallelic, Mendelian inheritence. One locus in the PGI stain displayed patterns consistent with tetraploidy, but since variation was only observed in two of the four alleles, the locus was interpreted in a diallelic pattern in order to produce a consistent data set for analysis.

Over the entire study, high levels of polymorphism, moderate numbers of alleles per locus, and low levels of expected heterozygosity were observed across loci (Table 2). Fixation indices (a measure of the lack of heterozygosity in a population) varied across populations (Table 2), but over all individuals, levels of fixation were non-significant (F_{IS} = 0.19; 95% CI: -0.10 to 0.59). Genetic variation was partitioned among populations, with significant allele frequency variation detected across the study (F_{ST} = 0.19, 95% CI: 0.11 to 0.29). Nei's (1978) genetic distance indicates most populations are genetically similar, with no value greater than 0.185 (Table 3). Analysis of population structure within the entire data set identified k = 5 as the most likely number of populations [Pr(k=2) ~ 1; Pr(all other k) ~ 0].

Multilocus outcrossing rates for the entire data set was t_m = 0.989 (standard error 0.011). Population-level estimates were consistent with the estimate over the entire study (Table 4).

Discussion

Over this study, high levels of polymorphism (P = 85.7) and moderate levels of heterozygosity (H_e = 0.20) and alleles per locus (A = 2.5) were observed in *Bromus carinatus*. These levels were consistent with mean values observed in all grasses (P = 60; A = 2.38, H_e = 0.191;Godt & Hamrick 1998), and with a phenotypic isozyme study of *B. carinatus* [P = 87.5; mean band patterns per stain (akin to A) = 3.69; (USDA Forest Service 1997)]. The observed levels of variation were slightly higher than the mean observed for grass species that are predominantly self-pollinating (P = 0.33, A = 1.51, H_e = 0.11; Godt & Hamrick 1998), which is consistent with levels of outcrossing measured in this study. Levels of polymorphism and mean alleles per locus were lower in individual populations than the study average (Table 2), likely due to both the genetic differentiation of populations, and the variance in sample size among populations. The percent polymorphic loci observed in each population is correlated, albeit non-significantly, with sample size in this study (r = 0.86, two-sample F-test = 0.39, P = 0.07).

This variance among populations in sample size results from the inconsistent quality of material submitted for analysis, and must be considered when basing conclusions on these data. Seed that were not *Bromus* spp. were observed and removed from the study during seed preparation, during sample preparation, and during data analysis. Despite this careful screening, voucher specimens indicate that at

least two species of *Bromus* are likely included in this data set (Wilson & Brainerd 2005). Indeed, the cluster analysis identified a sufficient number of subpopulations (k = 5) to account for multiple species. Including multiple species is expected to inflate levels of variation and fixation, and may explain the greater levels of polymorphism observed in this study than reported in other grass and *Bromus* species. The variable germination also resulted in variable sample sizes among populations, and in three populations having no samples in this analysis (Tables 1 and 2). As a consequence, levels of variation, outcrossing, and genetic diversity reported for those populations underrepresented in this study ($N < 20$) are likely underestimations, or are accompanied by such variance as to make them imprecise. Low sample sizes may also serve to inflate estimates of population differentiation.

With these caveats in mind, what implications do these results provide for seed collection and propagation? Most importantly, difficulty in identifying *Bromus carinatus* has resulted in seed collection containing non-*B. carinatus* and non-*Bromus* species, as indicated by the voucher specimens and isozyme patterns. In addition to complicating genetic analyses, this contamination may reduce the usefulness of these collections in restoration and propagation activities. Sufficient training of field personnel, detailed field guides, and testing of seed (Apfelbaum et al. 1997) may be necessary to minimize these problems in the future.

Those populations included in the isozyme analysis were genetically differentiated, with 19% of the variation contained within populations. This value is lower than previously observed in *B. carinatus* (38% among populations; USDA Forest Service 1997) and reported for *Bromus* spp. (27% among populations, Godt & Hamrick 1998). Given the significant differentiation among populations, seed will need to be collected from multiple populations in order to capture the genetic variation observed in this region. In general, significant genetic differentiation indicates that caution should be used when pooling seed from multiple populations or moving seed among locations. These findings should be combined with results of the common garden experiment in determining guidelines for the combining or movement of seed.

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Table 1. Names and location information for eleven populations of *Bromus carinatus* assayed for isozyme variation. Three populations (MF 21, Sal 11, and Sal 24) did not produce seedlings for analysis.

Population	Latitude (N)	Longitude (W)	No. Families
Eugene 1	44.1351	122.9739	2
Eugene 5	43.8027	123.2755	32
Eugene 14	43.8315	122.7510	13
Eugene 18	43.6179	123.0163	29
Eugene 23	44.2504	123.4952	4
Sal 1	45.2970	123.3457	2
Sal 9	45.0514	122.4888	7
Sal 15	44.6401	122.537	1
MF 4	43.7310	122.4572	29
MR 8	44.2072	121.9514	11
MF 16	43.7982	122.3017	17

Table 2. Genetic variation observed in each populations. *N* = mean samples per locus; *P* = percent polymorphic loci (no criterion); *A* = mean alleles per locus; H_E = Nei's unbiased expected heterozygosity; *F* = fixation index. Standard errors in parentheses. Study means were estimated over loci.

Population	N	*P*	*A*	H_E	*F*
Study Mean	*137.7*	*85.7*	*2.5 (0.4)*	*0.20 (0.05)*	*0.19*
Eugene 1	2.0	28.6	1.4 (0.2)	0.19 (0.09)	-0.20
Eugene 5	31.0	57.1	1.6 (0.1)	0.11 (0.04)	0.10
Eugene 14	11.8	42.9	1.4 (0.1)	0.09 (0.04)	0.20
Eugene 18	25.8	57.1	1.8 (0.2)	0.16 (0.05)	-0.09
Eugene 23	3.9	35.7	1.4 (0.1)	0.20 (0.07)	-0.12
Sal 1	1.9	28.6	1.3 (0.1)	0.19 (0.08)	-0.20
Sal 9	6.7	35.7	1.4 (0.1)	0.17 (0.07)	-0.16
Sal 15	1.0	16.7	1.7 (0.0)	n/a	n/a
MF 4	28.1	78.6	2.1 (0.3)	0.20 (0.04)	0.30
MR 8	10.1	57.1	1.7 (0.2)	0.26 (0.07)	-0.23
MF 16	16.4	57.1	1.6 (0.2)	0.22 (0.06)	-0.07

Table 3. Genetic distances (Nei 1978) between all pairs of populations.

Population	*Eugene1*	*Eugene5*	*Eugene14*	*Eugene18*	*Eugene23*	*Sal1*	*Sal9*	*MF4*	*MR8*	*MF16*
Eugene1	*****	0.033	0.073	0.018	0.079	0.147	0.185	0.036	0.112	0.085
Eugene5		*****	0.034	0.010	0.023	0.098	0.105	0.012	0.104	0.062
Eugene14			*****	0.048	0.048	0.180	0.130	0.019	0.141	0.065
Eugene18				*****	0.022	0.091	0.119	0.013	0.108	0.052
Eugene23					*****	0.03	0.024	0.010	0.076	0.021
Sal1						*****	0.017	0.081	0.021	0.040
Sal9							*****	0.087	0.039	0.074
MF4								*****	0.079	0.020
MR8									*****	0.061

Table 4. Multilocus outcrossing rates for six populations of *B. carinatus*. Standard deviations are provided in parentheses.

Population	**No. families**	**t_m (σ)**
Study mean	*All thirteen*	*0.989 (0.011)*
Eugene 5	13, 18	1.000 (0.000)
Eugene 14	38	0.900 (0.000)
Eugene 18	22	0.900 (0.000)
Sal 9	34	0.900 (0.000)
MF 4	3, 5, 12, 13, 26, 34	0.982 (0.024)
MF 16	11, 27	0.900 (0.000)

Figure 1. Location of eleven populations of *Bromus carinatus*.

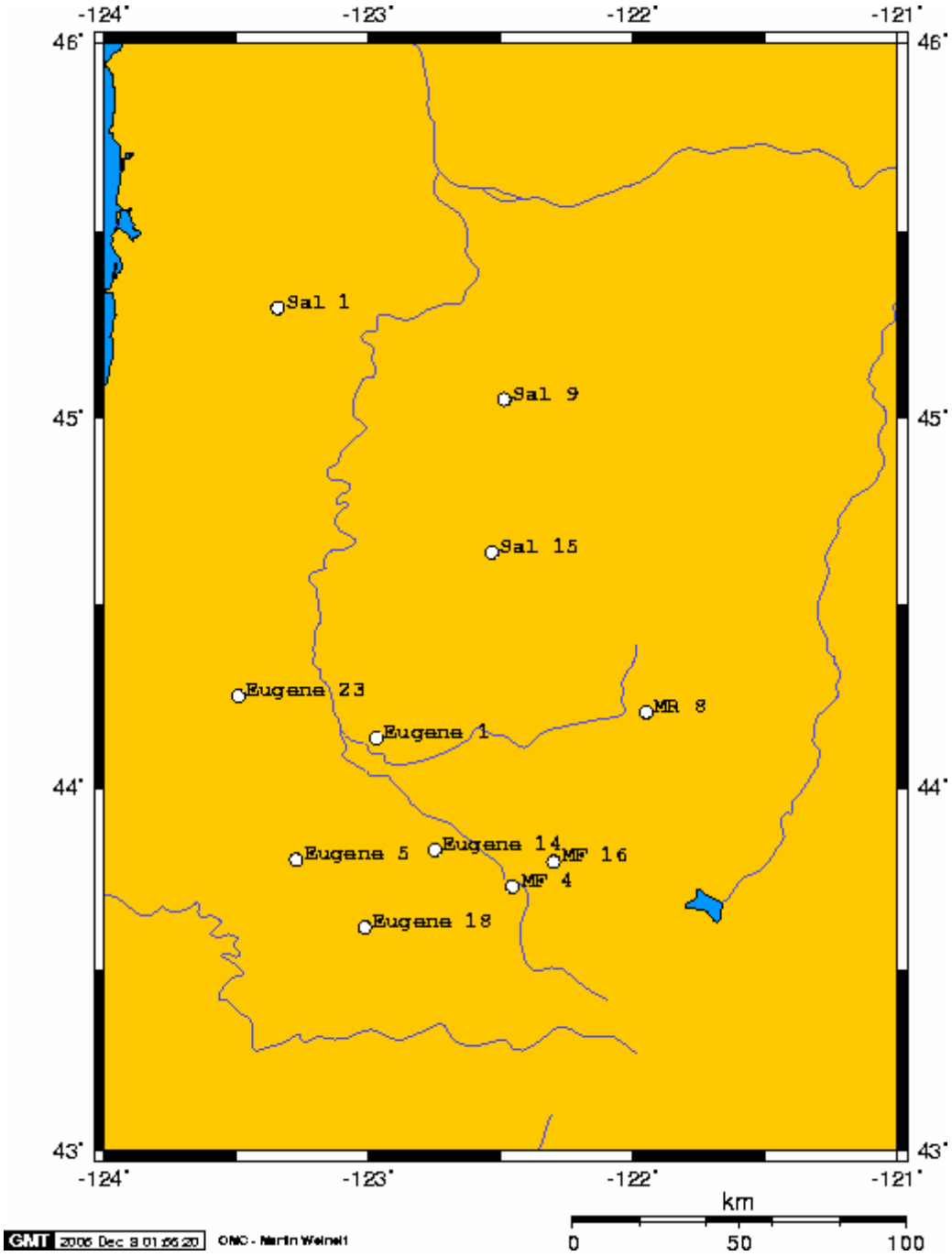
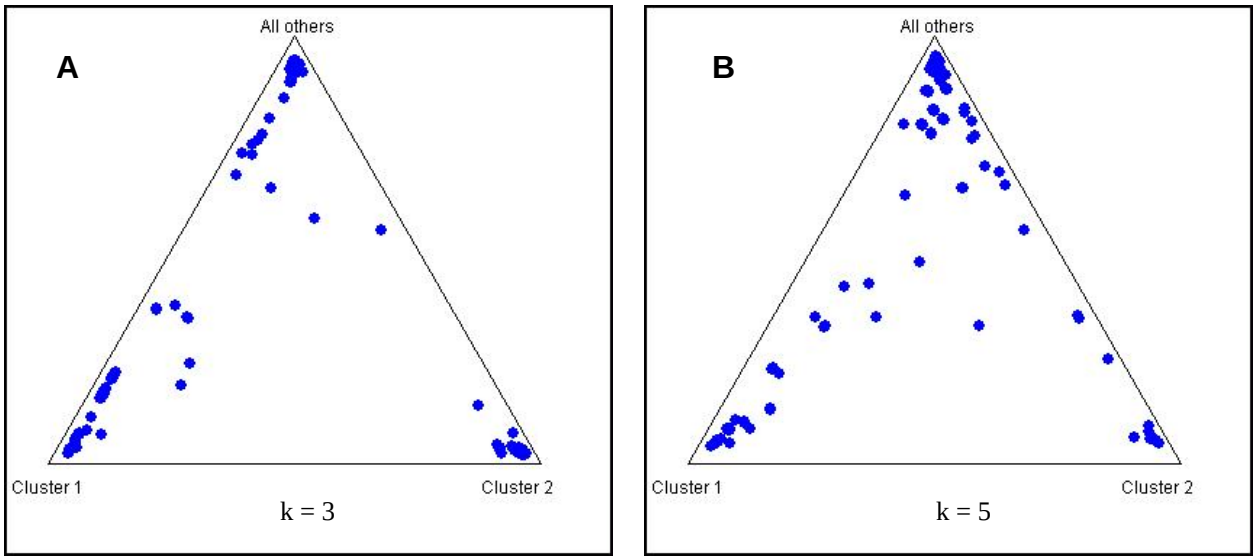


Figure 2. Assignment of individual samples to subpopulations using Markov-chain Monte Carlo simulations. Each point represents an individual sample. Corners of the triangle represent perfect assignment to that subpopulation (or cluster). A) Plot for k = 3 subpopulations, with each corner representing a unique subpopulation. B) Plot for k = 5 subpopulations, the most probable scenario. Subpopulations in bottom corners were chosen to maximize separation of points; top corner represents all remaining subpopulations.



Appendix 1: Allele frequencies observed at fourteen isozyme loci in eleven populations of *Bromus*. Alleles missing were not described in a previous study or were observed in samples determined not to be *Bromus*.

Population	*Mean*	Eugene1	Eugene5	Eugene14	Eugene18	Eugene23	Sal1	Sal9	Sal115	MF4	MR8	MF16
PGM1-1	*0.752*	1	0.859	0.333	0.907	0.625	1	0.429	1	0.724	0.727	0.765
PGM1-2	*0.248*		0.141	0.667	0.093	0.375		0.571		0.276	0.273	0.235
PGM2-1	*0.272*		0.156		0.095	0.333	1	1	1	0.138	0.909	0.353
PGM2-2	*0.728*	1	0.844	1	0.905	0.667				0.862	0.091	0.647
ME-1	*0.003*								0.5	0.017		
ME-3	*0.808*	1	1	1	1	0.625	0.5	0.5		0.759	0.5	0.471
ME-4	*0.189*					0.375	0.5	0.5	0.5	0.224	0.5	0.529
IDH-1	*0.976*	1	0.906	1	1	1	1	1	1	0.983	1	1
IDH-2	*0.021*		0.094									
IDH-3	*0.003*									0.017		
UGPP-1	*0.979*	1	1	1	1	1	1	1	1	0.966	0.818	1
UGPP-3	*0.021*									0.034	0.182	
AAT1-1	*0.957*	1	0.938	0.917	1	1	1	1	1	0.897	1	1
AAT1-2	*0.042*		0.063	0.083						0.103		
AAT2-1	*1*	1	1	1	1	1	1	1	1	1	1	1
PGI-1	*0.647*	0.5	0.563	0.917	0.5	0.5	0.5	0.5	0.5	0.759	0.5	0.882
PGI-2	*0.028*										0.182	0.118
PGI-3	*0.325*	0.5	0.438	0.083	0.5	0.5	0.5	0.5	0.5	0.241	0.318	
6PGD-1	*0.085*	0.25		0.042	0.1			0.143		0.103	0.364	0.029
6PGD-2	*0.915*	0.75	1	0.958	0.9	1	1	0.857	1	0.897	0.636	0.971
MDH1-1	*0.839*	1	0.984	1	0.78	0.5	0.5	0.643	1	0.828	1	0.625
MDH1-2	*0.161*		0.016		0.22	0.5	0.5	0.357		0.172		0.375
MDH3-1	*1*	1	1	1	1	1	1	1	1	1	1	1
SKD1-1	*0.993*	1	1	1	0.963	1	1	1	1	1	1	1
SKD1-2	*0.007*				0.037							
SKD2-1	*0.853*	0.75	0.984	0.958	0.833	1	0.5	1		0.845	0.611	0.676
SKD2-2	*0.140*	0.25	0.016	0.042	0.130		0.5		1	0.155	0.389	0.324
SKD2-3	*0.007*				0.037							
DIA-1	*0.796*	0.25	0.944	0.833	0.708	1	1	1	1	0.794	0.6	0.65
DIA-2	*0.051*			0.167						0.059	0.1	0.2
DIA-3	*0.087*				0.250					0.059		0.15
DIA-4	*0.02*	0.25	0.056		0.021							
DIA-5	*0.01*	0.25			0.021							
DIA-6	*0.031*	0.25								0.059	0.3	
DIA-7	*0.005*									0.029		

Appendix 2: Evidence of seed contamination and poor germination in submitted samples of *B. carinatus*.

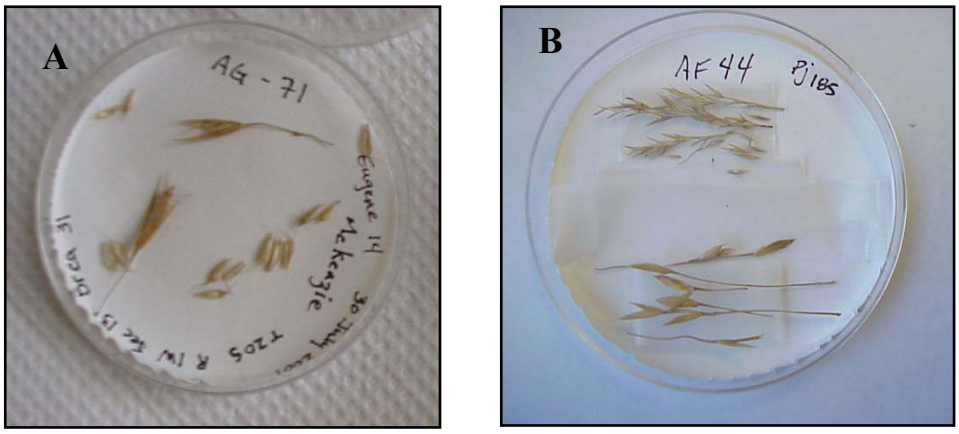


Figure A2-1. Evidence of seed contamination in two families. A) Population Eugene 14, family 37. B) Population Eugene 1, family 16.

Figure A2-2. Typical variation in germination observed in material submitted for isozyme analysis. Folds in germination paper separate families from population Sal 9. From left to right: family 32, family 33, family 34 (good germination), and family 35.

ISOZYME ANALYSIS OF INTERMOUNTAIN PLANTS: PROGRESS REPORT

September 30, 2005

NFGEL Projects 139, 140, 141, 142, 151, 152, 153, 159, 175, 176, 177, 178, and 179

Collaborators: Durant McArthur, USDA Forest Service, Rocky Mountain Research Station
Richard Cronn, USDA Forest Service, Pacific Northwest Research Station

This isozyme study uses two approaches to explore the genetic effects of using non-local native plants in habitat restoration projects. First, gene flow among indigenous populations is assessed. Second, the genetic diversity of certain restored plant populations is compared with variation in local indigenous populations and with the native populations that were sources of the seed for restoration.

This progress report discusses 14 additional species included in the overall study (NFGEL Project #'s 139, 140, 141, 142, 151, 152, 153, 159, 175, 176, 177, 178, and 179). These species are all common perennial plants of the Intermountain West. Therefore, they are frequently used in habitat restoration projects. Included in this series of samples are 14 species, 45 populations, and 901 individuals.

Project#	Species	EDM#	County	State	Date Collected	Category	N	Ploidy
139-140	Artemesia tridentata	2616	Sanpete	UT	8/12/2002	source B	20	
139-140	Artemesia tridentata ssp vaseyana	2796	Tooele	UT	6/3/2003	indigenous B	20	4x
139-140	Artemesia tridentata	2797	Tooele	UT	6/3/2003	seeded B	20	
139-140	Artemesia tridentata ssp vaseyana	3021	Sanpete	UT	8/2/2004	seeded A	20	2x
139-140	Artemesia tridentata ssp vaseyana	3022	Sanpete	UT	8/2/2004	indigenous A	20	4x
141-142	Chrysothamnus nauseosus	2815	Juab	UT	9/1/2003	source A	20	
141-142	Chrysothamnus nauseosus	2817	Utah	UT	8/12/2002	indigenous	21	
141-142	Chrysothamnus nauseosus	2818	Sanpete	UT	8/12/2002	indigenous	20	
141-142	Chrysothamnus nauseosus	2833	Garfield	UT	8/24/2003	seeded A	20	
141-142	Chrysothamnus nauseosus	2834	Garfield	UT	8/24/2003	indigenous A	20	
141-142	Chrysothamnus nauseosus ssp. hololeucus	3015	Sanpete	UT	6/29/2004	seeded B	20	
141-142	Chrysothamnus nauseosus ssp. hololeucus	3016	Sanpete	UT	6/29/2004	native? B	20	
141-142	Chrysothamnus nauseosus ssp. hololeucus	3018	Juab	UT	7/6/2004	source B	20	

151	Balsamorhiza sagittata	2800	Lander	NV	6/17/2003	indigenous	20	
151	Balsamorhiza sagittata	2801	Ada	ID	7/8/2003	indigenous	20	
151	Balsamorhiza sagittata	2806	Sevier	UT	6/4/2003	indigenous	21	
151	Balsamorhiza sagittata	2917	Owyhee	ID	7/28/2004	indigenous	20	
152	Crepis occidentalis	2807	Sevier	UT	6/4/2003	indigenous	20	
153	Purshia tridentata	2798	Wasatch	UT	6/10/2003	seeded A	20	
153	Purshia tridentata	2799	Wasatch	UT	6/10/2003	indigenous A	20	
153	Purshia tridentata	2827	Sanpete	UT	8/19/2003	source A	20	
153	Purshia tridentata	2829	San Juan	UT	8/18/2003	seeded B	20	
153	Purshia tridentata	2830	Franklin	ID	8/26/2003	source B	20	
153	Purshia tridentata	3019	Sanpete	UT	7/6/2004	seeded C	20	
153	Purshia tridentata	3020	Sanpete	UT	7/13/2004	indigenous C	20	
159	Oryzopsis hymenoides	2802	Ada	ID	7/8/2003	indigenous	20	
175	Lomatium dissectum	2907	Ada	ID	6/2/2004	indigenous	20	2x
175	Lomatium dissectum	2953	Utah	UT	6/2/2004	indigenous	20	2x
175	Lomatium dissectum	2956	Lander	NV	6/9/2004	indigenous	20	2x
175	Lomatium grayi	2909	Gem	ID	6/21/2004	indigenous	20	4x
175	Lomatium grayi	2951	Utah	UT	6/2/2004	indigenous	20	4x
176	Phlox longifolia	2954	Utah	UT	6/2/2004	indigenous	20	
176	Phlox longifolia	2955	Lander	NV	6/9/2004	indigenous	20	
176	Phlox longifolia	2957	Whitepine	NV	6/30/2004	indigenous	20	
177	Tragopogon dubius	2952	Utah	UT	6/2/2004	indigenous	20	
177	Tragopogon dubius	2958	Elko	NV	7/1/2004	indigenous	20	
177	Tragopogon dubius	2959	Lander	NV	7/1/2004	indigenous	20	
178	Penstemon acuminatus	2912	Malheur	OR	7/21/2004	indigenous	20	
178	Penstemon deustus	2906	Boise	ID	6/2/2004	indigenous	20	
178	Penstemon deustus	2913	Malheur	OR	7/23/2004	indigenous	20	
178	Penstemon speciosus	2908	Humboldt	NV	6/10/2004	indigenous	19	
178	Penstemon speciosus	2914	Malheur	OR	7/26/2004	indigenous	20	
179	Ceratoides lanata	3009	Sanpete	UT	6/22/2004	indigenous	20	
179	Ceratoides lanata	3010	Sanpete	UT	6/21/2004	seeded A	20	
179	Ceratoides lanata	3013	Sanpete	UT	6/21/2004	native/mixed A	20	

METHODS

DNA extraction was carried out on leaf tissue using either the (1) DNeasy-96 Frozen Leaf Tissue Protocol, or DNeasy Plant Mini Kit following manufacturer's instructions with tissue homogenization achieved via the Mixer Mill 300 (Qiagen), or (2) FastPrep DNA Extraction (Bio-101). DNA quantity was assessed by fluorometry, and quality determined by visualizing all samples against 50ng of Lambda DNA standard on 0.8% agarose gels stained with EtBr under UV light. DNA samples were shipped overnight on dry-ice to Richard Cronn, PNW, USDA Forest Service. Isozyme preparation followed the NFGEL Standard Operating Procedures. Extracts were electrophoresed on 11% starch gels, and stained for a suite of enzyme systems.

RESULTS AND DISCUSSION

All isozyme data has been analyzed and is currently being combined with the DNA data for inclusion in a GTR and several refereed journal publications.

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Salix and *Populus* species diversity on the Hopi Reservation

INTRODUCTION:

The goal of the project is to determine the genetic diversity of willow and cottonwood accessions collected from the Hopi Reservation using publicly available SSR loci developed in poplar species and isozyme data.

The family Salicaceae contains hundreds of common woody shrubs and trees but consists of only 2 genera: the willows (*Salix* spp.) and the poplars, cottonwoods, and aspens (*Populus* spp.). This plant family is unusual for several different reasons: (1) they are dioecious (each plant is either male or female), (2) they commonly reproduce by vegetative processes rather than seed, and (3) members of the Salicaceae dominate woody riparian vegetation in the northern hemisphere.

Restorationists and nursery workers have been collecting cuttings of willow and cottonwood without any consideration to the sex of the parent plant. In nature, these species often reproduce naturally from root sprouts or buried branches and, as a result, adjacent plants on the project site are often from the same clone. Branches often break off parent plants during floods, become buried further downstream, and root into new plants. If there are not many genetically different plants to start with, all the willows or cottonwood plants in a riparian community can be from only a few parents.

The goal of the project is to determine the genetic diversity of willow and cottonwood accessions collected from the Hopi Reservation. In addition to genetic testing, material will be rooted in the greenhouse (by the client) to confirm species and sexual IDs after flushing. It is possible that all collections are from females (and therefore, closely related). Results will be used as part of a recovery plan for these species.

MATERIALS:

Thirty samples of fresh mature leaf tissue (3-5 leaves per bag/individual) of four species of the Salicaceae were received May 20, 2003 from the Hopi Reservation: one individual of *Populus tremuloides* (from Two Dead Bulls Canyon), ten of *P. acuminata* (from Deer Springs), ten of *Salix lutea* (from Blue Bird Springs), and nine of *S. gooddingii* (from Blue Canyon).

METHODS:

Isozyme Analysis: Leaf tissue (2 to 3, 7mm diameter leaf disks per sample) was placed in a microtiter plate wells containing 100ul of Gottlieb extraction buffer. Three replicate plates per set were prepared and frozen at -70C. Isozyme extracts were also prepared in Melody/ Neale extraction buffer. On the morning of the electrophoretic run, samples were thawed, macerated with a glass rod or dremel tool, and absorbed onto five 3mm paper wicks. Three of the wicks were loaded onto gels and the remaining two were frozen as backups. Staining procedures followed NFGEL SOPs. Isozymes were generated on May 28, 2003.

DNA was extracted May 30, 2003 using DNeasy 96 Fresh Leaf Tissue Protocol and the Mixer Mill 300 (QIAGEN). DNA was quantified by use of fluorometry and quality assessed via electrophoresis of 50ng of each sample along with 50ng standards on 0.8% agarose gels stained with EtBr. Samples were re-extracted on June 4, 2003 using DNeasy 96

Fresh Leaf Tissue Protocol as stated above to insure adequate quantity and quality. Individual #SAGO-1 was extracted an additional time due observed low yield (DNeasy Plant Mini Kit QIAGEN).

SSR amplification and electrophoresis. Fifteen SSR markers evaluated in past *Populus* work were applied to a subset of the samples from each species to determine usability. Screening potential SSR markers was done by amplifying approximately 1.5 to 2.5 ng of template DNA in 10 ul of PCR mix including 1 x PCR buffer, 2.0 mM $MgCl_2$, 0.4 uM of each dNTP, 0.4 uM of the forward and reverse primers, and 1 U of HotStarTaq DNA Polymerase (QIAGEN). HotStarTaq requiring a 15 min period at 95°C prior to the touchdown amplification protocol on DNA Engine Dyad Peltier Thermal Cycler: The first three cycles including a denaturing step 94°C for 30 s, an annealing step at 55°C for 30 s, and an extension step at 72°C for 1 min. The next three cycles proceeded with a denaturing step at 94°C for 30s, an annealing step at 52°C for 30 s, and an extension step at 72°C for 1 min. Conditions for the last thirty-five cycles (subsequent programs were reduced to twenty-nine cycles to reduce amplification product) included a denaturing step at 94°C for 30 s, an annealing step at 50°C for 30 s, and an extension step at 72°C for 1 min followed by a final extension at 72°C for 7 min. The amplification product was then diluted to a ratio of 1:50 (amplification:ddH_2O) and 1ul of dilute amplification product was added to 10ul of Hi-Di™ Formamide containing 1.2% GeneScan®-500 [ROX]™ size standard. Samples were then denatured at 95°C for 2 min, and placed immediately on ice for 3 min before sample plate was loaded on an ABI Prism 3100 Genetic Analyzer for detection of amplification product. ABI software packages, GeneScan® Analysis Software and Genotyper® Software v 3.7 were used to visualize and evaluate alleles at each locus. Eleven primers amplified in *Populus tremuloides*, fourteen amplified in *P. acuminata*, and eight showed potential amplification in both *Salix lutea* and *S. gooddingii*.

RESULTS:

Isozymes

Thirty samples were genotyped at 25 isozyme loci. Between 18 and 22 loci resolved per species: 22 loci in *P. tremuloides, P. acuminata*, and *S. gooddingii*; and 18 loci in *S. lutea* (Table 1).

SSRs

Populus acuminata was scored using Genotyper software and data entered into the software CERVUS 2.0 (Marshall 1998.) for analysis of alleles (Table 2). One individual of *Populus tremuloides* (#POTR5-1) was collected for the project. This sample amplified single monomorphic peaks for seven loci, was heterozygous at two loci and did not show amplification at two others (Fig. 1). The ten samples of *P. acuminata* amplified at fourteen of the fifteen loci tested but was only variable at a single locus, PMGC-649, in sample POAC5-6 (106 bp). *Salix gooddingii* sample were monomorphic at loci PMGC-2885, PMGC-2675, and PMGC-433. One allele was amplified in *Salix lutea* samples at locus PMGC-2571. If additional SSR markers are desired in the future, it is recommended that new loci are screened using primers designed more specifically for Salix species (see Barker et al. 2003. Microsatellite markers for diverse Salix species. Molecular Ecology Notes 3:4-6)

Table 1. Genotype scores for 22 isozyme loci.

Customer ID	Species	PGI-1	PGI-2	LAP-1	LAP-2	DIA	SKD-1	MDH-1	MDH-3	CAT	UGPP-1	UGPP-2	6PGD-1 MC8	6PGD-2 MC8	6PGD-3 MC8	IDH	ME7	PGM-1	PGM-2	GOT-1	6PGD SB	FEST-2 LB	FEST-1 MC8	Comments
POTR5-1	P. tremuloides	22	11	33	22	22	33	11	11	11	11	22	12	24	N	11	33	22	11	12	11	22	11	
POAC5-1	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-2	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-3	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-4	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-5	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-6	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-7	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-8	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-9	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
POAC5-10	P. acuminata	22	23	11	22	22	33	11	11	0	11	12	22	12	N	11	22	22	11	11	11	22	11	
SAGO-1	S. gooddingii	11	33	22	11	22	12	22	12	22	33	33	33	33	22	11	11	33	22	22	12	22	22	male
SAGO-2	S. gooddingii	11	33	22	11	22	12	22	12	22	33	33	33	33	22	11	11	33	22	22	12	22	22	male
SAGO-3	S. gooddingii	11	33	22	11	22	12	22	12	22	33	33	33	33	22	11	11	33	22	22	12	22	22	male
SAGO-4	S. gooddingii	22	33	22	11	22	12	22	12	22	33	33	33	35	33	11	11	33	22	23	11	11	22	female
SAGO-5	S. gooddingii	11	33	22	11	22	12	22	12	22	33	33	33	33	22	11	11	33	22	22	12	22	22	male
SAGO-6	S. gooddingii	11	33	22	11	22	12	22	12	22	33	33	33	33	22	11	11	33	22	22	12	22	22	male
SAGO-7	S. gooddingii	22	33	22	11	22	22	22	12	22	33	33	33	33	14	11	11	33	22	22	11	22	22	female
SAGO-8	S. gooddingii	22	33	22	11	22	12	22	12	22	33	33	33	35	33	11	11	33	22	23	11	11	22	female
SAGO-9	S. gooddingii	22	33	22	11	22	22	22	12	22	33	33	33	33	14	11	11	33	22	22	11	22	22	female
SALU2-1	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-2	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-3	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-4	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-5	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-6	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-7	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-8	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-9	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	
SALU2-10	S. lutea	11	33	22	11	11	22	13	N	0	22	33	33	22	11	11	11	11	N	0	11	0	0	

Yellow and green shaded samples indicate matching pairs.

Table 2. *Populus acuminata* SSR results from CERVUS

Locus	k	N	Hets	Homs	H(O)	H(E)	PIC	Excl(1)	Excl(2)	HW	Null freq
127	1	10	0	10	0	0	0	0	0	NA	0
2221	1	10	0	10	0	0	0	0	0	NA	0
649	2	10	0	10	0	0.189	0.164	0.016	0.082	NA	0.907
2804	2	10	4	6	0.4	0.337	0.269	0.051	0.134	NA	-0.1097
433	3	10	7	3	0.7	0.542	0.46	0.133	0.274	NA	-0.1867
29	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
420	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
576	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
2011	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
2235	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
2571	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
2675	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
2885	2	10	10	0	1	0.526	0.375	0.125	0.188	NA	-0.333
14	3	10	10	0	1	0.574	0.441	0.149	0.245	NA	-0.3079

DISCUSSION:

(1) The ten individuals of *P. acuminata* share the same genotype at 22 isozyme loci and 14 SSR loci. One of the ten individuals (POAC5-6) did have an alternate genotype at a 15th SSR locus. It is possible this is just somatic mutation and not indicative of an alternate clone. Given that this variant was not confirmed at a second locus, we believe all ten *P. acuminata* individuals are ramets of the same clone.

(2) The ten individuals of *S. lutea* share the same genotype at 18 isozyme loci and one SSR locus (supporting the theory that they are members of the same clone).

(3) There is not much to say about the single individual of *P. tremuloides* (it was more similar to *P. acuminata* than to either *Salix* species). Genotype data for this individual was obtained from 9 SSR loci and 22 isozyme loci.

(4) The nine individuals of *S. gooddingii* were invariant at three SSR loci. However, isozyme data (from 22 loci scored) indicated clonal differences within this species. The five males (SAGO-1,2,3,5,6) share the same genotype. Females SAGO-4 and SAGO-8 share an alternate genotype. Females SAGO-7 and SAGO-9 share a third genotype. Therefore, a total of three multilocus genotypes were found among the *S. gooddingii* samples (perhaps one male clone, and two different female clones if the gender identification is correct).

Figure 1. Populus tremuloides (POTR5-1) genotype at eleven loci.

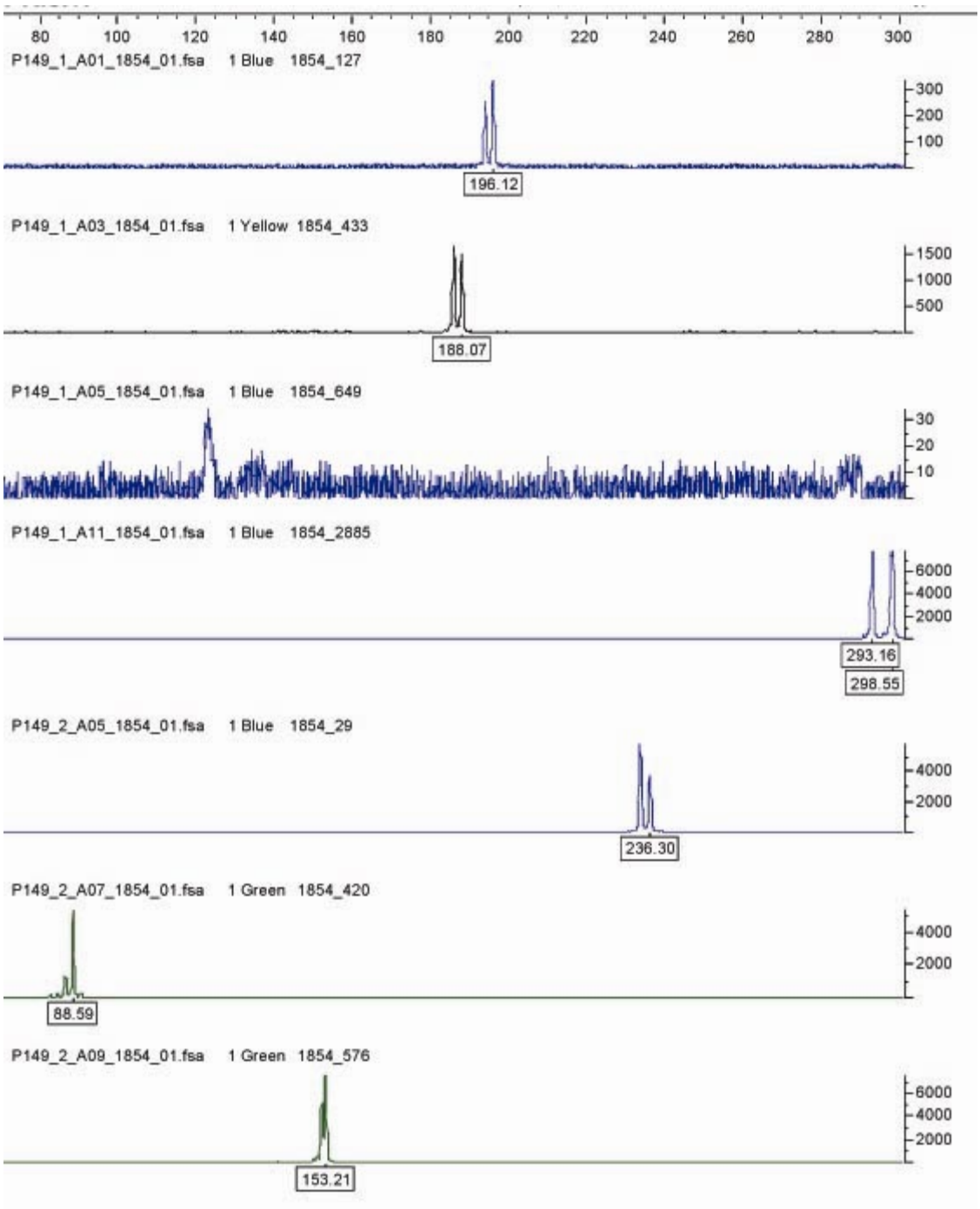
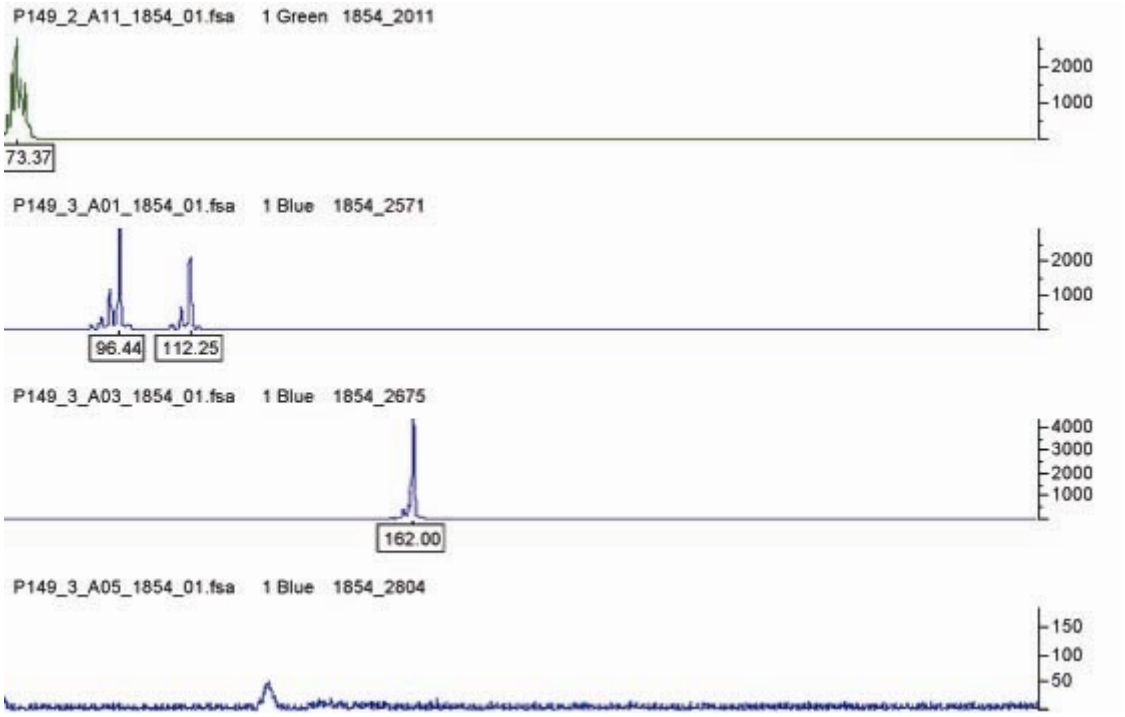


Figure 1. *Continued…*



STAFF ACTIVITIES

Meetings, Shortcourses, and Workshops

Presentations

2004. V. Hipkins and J. Kitzmiller. Genetic diversity and structure of Quaking Aspen in the Central Sierra Nevada, CA. Managing Aspen in Western Landscapes Conference. Cedar City, Utah. September 21 – 23.

2004. V. Hipkins. Tomorrow's applied conservation and management answers in today's basic science. Regional Biologist and Botanist Meeting (Region 8), USDA Forest Service, Jacksonville, FL. October 4 – 8.

2004. V. Hipkins. Plant DNA and Forensic Science. 2004 Women's Conference, USDA Forest Service, Region 5. Sacramento, CA. October 20.

2004. R.C. Schmidtling, J. Myszewski, C.D. Nelson, V. Hipkins, and L.H. Zeng. Growth and Genetic Variability in a Combined Provenance Test of an American Pine Species (*Pinus elliottii*) and a Chinese Pine Species (*P. massoniana*) Planted in the Southeastern USA. IUFRO Forest Genetics Meeting, Charleston, South Carolina. November 1-5

2005. Richard Cronn, E. Durant McArthur, Valerie Hipkins. Patterns of Nuclear and Cytoplasmic Differentiation in Intermountain Restoration Species: Tales from Two Genomes. Great Basin Native Plant Selection and Increase Project Symposium. Society for Range Management Annual Meeting, Fort Worth, Texas. February 10.

2005. V. Hipkins. Western Forest Genetics Association Annual Meeting (moderator). Corvallis, OR. July 19-21.

2005. J. DeWoody. How should ploidy by considered in the management of plant species. Conservation Genetics Symposium. Asilomar, CA. September 25-28.

Attended

2004. V. Hipkins. Attended. Regional Centennial Forum: The Forest Service in the Pacific Southwest Region. Sacramento, CA. November 5 – 6.

2004. V. Hipkins. Cal Poly Forestry and Natural Resources Advisory Board. San Luis Obispo, CA. November 18.

2005. V. Hipkins. PSW Management Team Meeting. Placerville, CA. May 10 – 12.

2005. V. Hipkins. Strategic Planning Budget Process: Genetic Resource Program. Portland OR. May 16 – 20.

2005. V. Hipkins. Forest Service fact-finding processes and procedures. Diamond Springs, CA. May 23-24.

2005. R. Saich. US Forest Service Forest Leadership Focus Group Meeting. Alburquerque, NM. September 14 – 16.

Publications

BL Wilson, VD Hipkins, E Rey-Vizgirdas, and TN Kaye. 2005. Variation in *Lewisia kelloggii* (Portulacaceae) wigh description of a new species endemic to Idaho. Western North American Naturalist 65(3):345-358.

RC Schmidtling and V Hipkins. 2004. The after-effects of reproductive environment in shortleaf pine. Forestry 77(4):287-295.

VD Hipkins and JH Kitzmiller. 2004. Genetic variation and clonal distribution of quaking

aspen in the central Sierra Nevada. Transactions of the Western Section of the Wildlife Society 40:32-44.

Internal Activities

V. Hipkins. Member of Field Leadership Focus Group. Monthly conference calls; survey responses.
R. Meyer. Pacific Southwest Research Station Union President
R. Meyer. Member of USDA Forest Service National Safety Council
R. Meyer. Union President – Pacific Southwest Research Station

Hosted

NFGEL continues to host a variety of visitors. Tours of the facility and operation were provided to Forest Service employees, members of the public and private industry, university faculty and classes, foreign scientists, and employees from other state and federal government agencies.

Collaborations and Cooperations

NFGEL formed collaborations with FS Research Stations, Bureau of Land Management, California Department of Transportation, US Fish and Wildlife Service, University of California at Davis, private companies, and non-profit groups. We hosted local high-school students on a volunteer basis. We also collaborate internally within the Agency to lend expertise in the area of genetics.

STAFFING

During FY05 (10/1/04 to 10/1/05), NFGEL was staffed with three permanent full-time, two TERM, seven temporary employees, and one high-school senior volunteer.

Name	Position	Tour	E-mail Address
Valerie Hipkins	Director	PFT	vhipkins@fs.fed.us
Jennifer DeWoody	Lab Manager/Biologist	TERM	jdewoody@fs.fed.us
Pat Guge	Lab Biotechnician	PFT	pguge@fs.fed.us
Randy Meyer	Lab Biotechnician	PFT	rmeyer@fs.fed.us
Robert Saich	Lab Biotechnician	TERM	rcsaich@fs.fed.us
Robert Westfall	PSW Scientist	Cooperator	rwestfall@fs.fed.us
Ricardo Hernandez	Lab Biotechnician	Temp	ricardohernandez@fs.fed.us
Ashley Lindstrom	Lab Biotechnician	Temp	alindstrom@fs.fed.us
Kenneth Choi	Lab Biotechnician	Temp (6/05 – present)	kchoi@fs.fed.us
Wesley Calidonna	Lab Biotechnician	Temp (6/05 – 9/05)	--
Kostya Krutovski	Scientist	Temp (1/05 – 6/05)	--
Barbara Wilson	Scientist	Contractor	--
John	Volunteer	Volunteer (10/04 – 6/05)	--

BUDGET

Activity	FY04	FY05
Receipts (in thousands)		
Allocation	410.0	410.0
Carryover	0.0	15.6
Soft Money, after indirect removed	268.8	159.1
Fire Transfer dollars returned	27.8	0.0
Total	706.6	584.7
Expenditures (in thousands)		
Salary (permanant)	*273.3	289.5
(temperary)	54.3	94.8
Overhead to Headquarters	42.0	70.4
Overhead to Site	41.9	30.9
Chemicals/Supplies	48.2	65.2
Equipment	189.9	9.4
Travel/Training	12.5	4.9
Awards	1.3	1.6
Books/subscriptions	0.1	0.6
Computers (not including FOR)	1.0	0.0
Repair	2.9	2.9
Photos/Slides/Publications	27.4	12.2
Postage	0.1	0.1
Office Supplies	0.6	0.1
Furniture	3.0	2.0
Total	698.5	584.6
Balance	8.1	0.1

* does not include $24.1 in salary due to alternate salary sources
** does not include $27.5 in salary due to alternate salary sources

FY 05 Soft Money

Source	Amount ($)	Percentage
FS-NFP (WO)	62.5	40.5
FS-R6	12.9	8.3
FSR-R5	6.1	3.9
FSR-PSW	10.0	6.5
USFWS	15.9	10.3
NPS	12.4	8.0
UC Davis	18.3	11.9
Rocky Mtn Elk Found.	10.2	6.6
Private Companies	10.8	3.9
Total	159.1	100.0

Project Workload, FY05

ISOZYMES (starch gel electrophoresis)

By Project

Reagion or Agency	Project#	Species	# gels	# run days	# weeks
R-2/3/4	103	*Pinus ponderosa*	15	3	1.5
RMRS	110	*Astraglus uthensis*	3	1	0.5
RMRS	113	*Eriogonrum umbellatum*	12	2	1
RMRS	119	*Vica americana*	9.25	1.25	0.75
RMRS	132	*Atriplex canescens*	2	1	0.5
RMRS	134	*Stipa comata*	6.25	1.25	0.75
BLM/R-6	138	*Pinus lambertiana*	74	9	4.5
RMRS	139	*Artemisia tridentata*	3.25	1.25	0.75
RMRS	141	*Chrysothamnus nauseous*	18	3	1.5
RMRS	151	*Balsamorhiza sagittata*	9	1	0.5
R-9	155	*Pinus strobus*	6	1	0.5
NPS	156	*Pinus albicauls*	70	11	5.5
R-6	157	*Pinus albicauls*	58	7	3.5
RMRS	159	*Oryzopsis hymenoides*	3	1	0.5
R-6	173	*Chameacyparis lawsoniana*	12	1	0.5
USFWS	174	*Sidalcea* species	34	6	3
RMRS	175	*Lomatium* species	12.25	2.25	1.25
RMRS	176	*Phlox longifolia*	6	1	0.5
RMRS	177	*Tragopogon dubius*	6	1	0.5
RMRS	178	*Pensteman* species	12	2	1
RMRS	179	*Ceratoides lanata*	6	1	0.5
USFWS	181	*Lilium accidentale*	42	10	5
R-6	183	*Chameacyparis lawsoniana*	15	2	1.5
R-6	185	*Bromus carinatus*	36	6	3
PSW	188	*Picea chihuahuana*	36	10	4
PSW	191	*Pseudotsuga* species	3	1	0.5
Private Company	192	*Pseudotsuga menziesii*	12	1	1
R-5	194	*Rorippa subumbellata*	48	8	4
R-2	196	*Pinus aristata*	3	1	0.5
TOTAL			**572.0**	**97.0**	**49.0**

By Forest Service Region or Agency

Region or Agency	#gels	#days	#weeks
Forest Service			
National Forest System			
R-2	18.0	4.0	2.00
R-5	48.0	8.0	4.00
R-6	121.0	16.0	8.50
R-6/BLM	74.0	9.0	4.50
R-9	6.0	1.0	0.50
Research			
RMRS	108.0	20.0	10.50
PSW	39.0	11.0	4.50
USFWS	76.0	16.0	8.00
NPS	70.0	11.0	5.50
Private Company	12.0	1.0	1.00

R = Region
RMRS = Rocky Mountain Research Station
PSW = Pacific Southwest Research Station
USFWS = United Stated Fish and Wildlife Service
BLM = Bureau of Land Management
NPS=National Park Service

NFGEL FY05 Annual Report – Statistics Log for DNA work

BY PROJECT

Region/Agency	Project #	Species	# DNA Extractions	Extraction Method	# PCR Reactions	# ABI Runs (16 capillaries)	Employee hours*
R2	103	Ponderosa Pine			330	132	
R6/BLM	125	Douglas-fir	280	DNEasy-96			35
R8, R9	147	Eastern grasses	41	DNEasy-96			5.125
R5	150	*Populus tremuloides*	27	DNEasy Mini	2544	111	6.75
R9	155	Eastern White Pine	275	DNEasy-96			34.375
NPS	156	Whitebark Pine	80	DNEasy-96	16		10
R6	157	Whitebark Pine	776	DNEasy-96	16		97
UC-Davis	165	Monterey Pine	663	DNEasy-96	8662	48	82.875
R5	171	*Vaccinium*	19 33	DNEasy-96 DNEasy Mini			10.625
R6	173	Port-Orford Cedar	480	DNEasy-96			60
R9	180	Yew spp.	99	DNEasy-96			12.375
Weyerhaeuser	187	Douglas-fir	11	DNEasy-96	2800	66	1.375
PNW, UC, PSW	189	Douglas-fir	130	DNEasy-96			16.25
Private Company	190	Douglas-fir	4	DNEasy-96	54	4	0.5
Private Company	192	Douglas-fir	79	DNEasy-96			9.875
Private Company	193	Loblolly Pine	555	DNEasy-96			69.375
R6	195	*Sisyrinchium*	132	DNEasy-96			16.5
R9	198	*Juglans* spp.	106	DNEasy-96			13.25

PSW	199	Douglas-fir megs	8	DNEasy Mini			
TOTALS			**3798**		**14,422**	**361**	**481.25**

BY REGION/AGENCY

Region/Agency	# DNA Extractions	# PCR Reactions	# ABI Runs (16 capillaries)	Employee hours**
Forest Service, National Forest System				
R2		330	132	548.6
R5	79	2544	111	620.4
R6	1388	16		177.5
R6/BLM	280			35.0
R8, R9	41			5.1
R9	480			60.0
Forest Service, Research				
PSW	138			16.3
Non-Forest Service Groups				
NPS	80	16		14.0
Private Companies	649	2854	70	539.5
UC-Davis	663	8662	48	816.3
TOTALS	**3798**	**14,422**	**361**	**2,832.7**

FS=Forest Service
FSR=Forest Service Research
RMRS=Rocky Mountain Research Station
NFS=National Forest System
R#=Region Number
Private=Private Company
BLM=Bureau of Land Management
USFWS=US Fish and Wildlife Service
NPS=National Park Service
UC-Davis=University of California, Davis

*Calculation of Employee hours (does not include time for PCR and ABI):

For FastPrep: Based on estimate that 12 samples requires 4 hours to complete:
1 person x 4 hours = 4 employee hours / 12 samples
or 0.33 hours per sample

For DNEasy Mini Extraction: Based on estimate that a full "set" of 18 samples requires grinding + extraction:
2 people x 0.75 hour (grinding) + 1 person x 3 hours (extraction) = 4.5 hours / 18 extractions
or 0.25 hours per sample.

For DNEasy 96-well Extraction (Benchtop and BioRobot): a full plate of 96 samples requires dicing/stuffing + extraction:
4 people x 2 hours (dicing) + 1 person x 4 hours (extraction) = 12 hours / 96 extractions
or 0.125 hours per sample.

This estimate may underestimate the employee hours we needed to extract some projects, because there is a minimum amount of time required to do either method. That is, extracting 2 samples using the DNEasy 96 protocol does not take 15 minutes.

**Calculation of Employee hours (includes DNA extraction and time for PCR and ABI):

For PCR: 0.0625hrs/reaction

For ABI: 4hrs/run