

Appendix A

Participants: Monterey pine genetic conservation workshop

Workshop held April 25–26, 2000 in Big Sur, California.

Michael G. Barbour

Department of Environmental Horticulture
University of California
Davis, CA

David T. Bates

Big Sur Land Trust
Carmel, CA

Paul D. Cylinder

Jones & Stokes Associates, Inc.
Sacramento, CA

Ann Dennis

California Native Plant Society
Berkeley, CA

Paul A. Dubsy

Pebble Beach Company
Pebble Beach, CA

Susan J. Frankel

State and Private Forestry
USDA Forest Service
Vallejo, CA

Richard H. Hawley

Greenspace—The Cambria Land Trust
Cambria, CA

Kimberly A. Hayes

California Native Plant Society
Santa Cruz County Chapter
Santa Cruz, CA

Deborah S. Hillyard

California Department of Fish and Game
Morro Bay, CA

Joanne H. Kerbavaz

California Department of Parks and Recreation
San Francisco, CA

Jay H. Kitzmiller

Genetic Resource Center
USDA Forest Service
Chico, CA

Mary Ann Matthews

California Native Plant Society
Monterey Bay Chapter
Monterey, CA

Patrick E. McGuire

Genetic Resources Conservation Program
University of California
Davis, CA

Leonard P. Nunney

Department of Biology
University of California
Riverside, CA

Constance I. Millar

Pacific Southwest Research Station
USDA Forest Service
Albany, CA

Sandra C. Morey

California Department of Fish and Game
Sacramento, CA

Nicole E. Nedeff

Big Sur Land Trust
Carmel, CA

Donald R. Owen

California Department of Forestry
and Fire Protection
Redding, CA

Deborah L. Rogers

Genetic Resources Conservation Program
University of California
Davis, CA

Lisa K. Schicker

Caltrans Environmental Planning Division
San Luis Obispo, CA

Stephen R. Staub

Del Monte Forest Foundation
Monterey, CA

Scott L. Stephens

Department of Environmental Science,
Policy and Management
University of California
Berkeley, CA

J. Jesús Vargas-Hernández

Instituto de Recursos Naturales
Colegio de Postgraduados
Montecillo, Mexico

Detlev R. Vogler

Institute of Forest Genetics
USDA Forest Service
Davis, CA

B. Diane West-Bourke

Rancho Del Oso
Santa Cruz County, CA

Appendix B

Respondents to the survey on *ex situ* reserves and international interests

Sonia Martin Albertos

Jefa de la Sección de Producción e Material Genético
Dirección General de Conservación de la Naturaleza
Ministerio de Medio Ambiente
Madrid, SPAIN

Cecilia Bester

South African Forestry Company Ltd.
Sabie, SOUTH AFRICA

Rowland D. Burdon

Forest Research Institute
Rotorua, NEW ZEALAND

Diane L. Delany

Pacific Southwest Research Station
USDA Forest Service
Albany, CA USA

William S. Dvorak

CAMCORE
Department of Forestry
North Carolina State University
Raleigh, NC USA

Kenneth G. Eldridge

Forestry and Forest Products
CSIRO
Canberra, AUSTRALIA

David R. Johnson

Institute of Forest Genetics
USDA Forest Service
Placerville, CA USA

Laurie A. Lippitt

L.A. Moran Reforestation Center
California Department of Forestry and Fire Protection
Davis, CA USA

Glossary

- Bottleneck:** a sharp reduction in the number of individuals of a species or population in a particular place or time.
- Cline:** a gradient of genetic variation within a population or between populations which often corresponds with an environmental gradient such as elevation.
- Endemic:** native to a given geographic area (i.e., not exotic, introduced, or naturalized).
- Extirpation:** locally extinct (e.g., an extirpated population).
- Fascicle:** a close cluster or bundle of parts, such as flowers, leaves, needles, or stems; in pines, the number of needles per fascicle is often a diagnostic character.
- Gene flow:** the movement of genes over space through seed or pollen movement, for example.
- Genetic bottleneck:** a reduction in the number of individuals of a species or population that is accompanied by a significant loss of genetic diversity.
- Genetic drift:** random changes in genetic composition (i.e., allele frequency) in populations over time; also called random genetic drift. Genetic drift occurs more quickly and dramatically in small populations.
- Genetic integrity:** the natural condition of a gene pool; freedom from genetic contamination (i.e., genes introduced from nonnative or nonlocal populations).
- Genetic load:** the proportion of a population that does not survive or reproduce because of genetic reasons (i.e., lack of adaptation); a measure of the deleterious portion of genetic diversity in a population.
- Genome:** the total DNA of a cell's nucleus or of a cellular organelle, such as a mitochondrion or chloroplast.
- Half-sib:** having one, and only one, parent in common. Thus, half-sibs can usually only be determined for sure when the fertilization has been controlled, so that the parentage of the resulting seedlings is known. In nature, with open pollination, seeds coming from one tree could have both parents in common (i.e., as a result of self fertilization) or one parent in common (if the pollen parent differed between the two).
- Homozygosity:** at a particular genetic locus, the presence of two identical alleles; the degree to which an individual has identical alleles at chromosomal loci.
- Inbreeding:** mating between relatives. Inbreeding increases the homozygosity in a population, and affects all genes.
- Inbreeding depression:** loss of fitness in a population that results from unnaturally high levels of inbreeding; more commonly manifested in typically outbreeding species.
- Landrace:** a group of individuals that have become adapted to a specific area to which they were (artificially) introduced. Therefore, two steps are required for development of a landrace: introduction of some plants to a new area (outside of their natural range) and subsequent reproduction and natural selection. The group of best-adapted individuals that result over time is referred to as the landrace.
- Locus/Loci:** the position on a chromosome occupied by a gene (or set of alternative alleles).
- Microsatellites:** also called *simple sequence repeats* or *SSRs*, lengths of DNA that consist of tandem repeats of short sequences of nucleotides (for example, AAT repeated 15 times in a row). When polymorphism for the number of repeats is found among individuals, the microsatellite can serve as a genetic marker and a measure of genetic diversity.
- Mitigation:** an act that is done to soften or compensate for an act that destroys or compromises habitat or individuals (generally plants and animals). Thus, mitigation may involve protection of habitat in exchange for destruction of other habitat, translocation of individuals, etc.
- Panmictic:** complete randomness in mating. A panmictic population is one in which every individual is equally

likely to mate with any other individual.

Phenotypic: referring to the observed characteristics of an individual, which may be the result of its genes, the environment, or a combination of the two.

Polymorphism: as applied to a gene, it is one that has more than one allelic form. However, technically, the definition also embodies the concept of frequency. Thus, a polymorphic gene, technically speaking, is a gene for which the most common allele has a frequency of less than 0.95 (some prefer a less stringent cutoff of 0.99). Polymorphism is also a term used to describe the proportion of genes that are polymorphic by the above criterion, for an individual, population, or species.

Population: a group of individuals of the same species living within a sufficiently restricted geographical area that any member can potentially mate with any other member. In this report, the term is also used loosely to refer to each of the five geographic occurrences of Monterey pine, regardless of the mating relationships among the trees within each location.

Ramet: a genetically identical copy or propagule taken from a single individual plant. This term is commonly used in forestry, in relation to plants generated by vegetative

reproduction from one plant.

Riparian: pertaining to habitats, or species occupying those habitats, that border or are associated with streams and rivers.

RAPD: acronym for random amplified polymorphic DNA, which can be used as a genetic marker based on its differential PCR amplification from the DNA of individuals. Variation among individuals for a specific RAPD marker can be a measure of genetic diversity.

RFLP: acronym for restriction fragment length polymorphism, detected in the DNA of an individual as variations in DNA fragment sizes that are generated by cutting the individual's DNA with special (i.e., 'restriction') enzymes. These enzymes can cut only at specific DNA sequences, so variation in the pattern of these sequences in the genome results in fragment size variation. Thus, RFLP markers can be used to detect genetic diversity among individuals.

Serotinous: requiring fire or extreme heat to open; commonly used in reference to cones of certain tree species where the cones are assisted in opening (semi-serotinous) by fire or require fire or very high heat to open the scales and release the seeds (serotinous).