



Assessment of Genetic Resources for Managing, Conserving, and Restoring North American Conifers: A Call to Action

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Abstract

Changing climate is impacting the health and sustainability of forests throughout the world. It is important for forest resource managers to have abundant and accurate information about the standing, changing, and adaptive genetic diversity of forest tree populations to successfully manage and restore species impacted by climate change, invasive species, and forest fragmentation. This can only be accomplished if genetic resources are widely available for impacted species. For a small number of commercially important conifer species in North America, such resources have been reasonably well developed. However, for nearly all other conifer species, critical genetic resources are limited or completely absent. The International Union for the Conservation of Nature (IUCN) Red List classification of *Near Threatened* or worse (*Vulnerable*, *Endangered*, *Critically Endangered*) includes many conifer species in North America. We have compiled an inventory of genetic resources available to researchers for these and other at-risk conifer species. With a few important exceptions, such resources barely exist for nearly all of them. We discuss the importance of genetics for managing and restoring forests under climate change and provide a call to action for researchers and managers to develop and implement a coordinated protocol for conserving and restoring the most at-risk conifers.

Keywords Genetic resources · Climate change · Conifer species · Conservation · Restoration

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Threats to North American Conifers

The twenty-first century has seen a marked rise in global temperatures, and with that warming has come a dramatic increase in forest decline and tree mortality in many parts of the world (Hartmann et al. 2022). North America has been particularly hard hit, due in part to multi-year droughts killing trees through hydraulic failure, carbon starvation, or weakening their defenses against insects and diseases (Breshears et al. 2018). Warming has allowed for the expansion of endemic insects, most notably bark beetles in North America, and both globalization and climate change are increasing the rate of spread of invasive pests and pathogens (Hellmann et al. 2008). In addition, wildfires have increased in frequency, intensity, and size (Schoennagel et al. 2017). While most of these agents of mortality are part of natural disturbance regimes, current rates of forest decline are unsustainable. At the same time, we are relying on forests to provide a wide range of goods and services, including carbon sequestration, habitat for biodiversity, and wood and fiber to make sustainable, environmentally friendly products.

Populations of most widespread conifer species are locally adapted to their historic home climates (Alberto et al. 2013; Aitken and Bemmels 2016). Genetic management of tree populations for reforestation and restoration used to be relatively simple: Use local seed and establish local seed zones to maintain the match between genetics and climate (e.g., Schmidting 2001). Similarly, conservation of species was attained through local protection of populations in situ, in parks and protected areas. However, it is no longer that easy, as climate change is disrupting the match between populations and their local environmental conditions. Forest managers now need additional knowledge to understand how to best facilitate the adaptation of tree populations to new climatic and associated biotic and abiotic conditions.

Conifers are found in approximately one third of forests globally, and the majority of forests in North America, where their drought tolerance, cold hardiness, and ability to tolerate nutrient-poor soils have historically allowed them to survive, thrive, and provide raw materials for the forest industry. These relatively ancient taxa have far fewer species than do angiosperm tree taxa, with fewer than 600 species of conifers globally, compared to over 70,000 hardwood species (Cazzolla Gatti et al. 2022). While we have good genetic resources for a few common, widespread, economically important species such as loblolly pine (*Pinus taeda*), Douglas-fir (*Pseudotsuga menziesii*), lodgepole pine (*Pinus contorta*), and white spruce (*Picea glauca*), we have little knowledge of genetic diversity and population adaptation in species with small geographic ranges, fragmented distributions, or limited economic importance. For many species, we lack the knowledge needed to tailor management and restoration activities to increase the probability that they will maintain viable populations in a changing climate.

Globally, 34% of conifer species are threatened with extinction (IUCN 2023). At least 68 North American conifer species or subspecific taxa have a current International Union for Conservation of Nature (IUCN) Red List classification of *Near Threatened* or worse (*Vulnerable*, *Endangered*, *Critically Endangered*)

(IUCN 2023). Many of these taxa are rare and exist in small and isolated populations; some are at risk of extirpation or even extinction. To this roster, we have added four more taxa, some of which were insufficiently known (data deficient) for IUCN to assess and others had different taxonomic status than reflected in the IUCN Red List. For these four taxa, we have made our own risk and resource status assessments. For all 72 taxa, genetic conservation and species restoration will likely be required in the years ahead.

To accomplish conservation and restoration in the most effective and sustainable manner, knowledge of the extent and population structuring of standing genetic variation of these species is needed prior to localized or range-wide extinction. This knowledge can only be obtained if there are sufficient genetic resources for each species to ascertain the relevant genetic parameters. However, for nearly all 72 taxa classified as at risk to some degree, with a few notable exceptions, there are few or no genetic resources readily available to researchers. To address this deficiency, forest genetic and genomic researchers need to develop and communicate the biological and informational resources necessary to generate this knowledge. With knowledge of the amount and distribution of standing genetic variation, conservation managers can develop species-specific management and restoration plans that enable adaptation and resilience under new climates and other challenges.

Our goal is to provide a simplified assessment of the current inventory of various genetic resources for the 72 North American conifer taxa that we have listed in Table 1 and to highlight the large gap in resources that exists for most of these species. Further, we offer a call to action for forest researchers and managers from across North America to develop and implement a coordinated protocol for conserving the genetic resources of these at-risk conifers. We use a color-coding scheme to graphically indicate both the level of species risk and the availability of six categories of genetic resources. The assignment of status colors is based on the collective knowledge and experience of the authors and is admittedly approximate and subjective. Nevertheless, we hope the overall representation gives a first approximation of the large shortfall in genetic resources for many species and provides conservation managers and researchers an indication of where priorities and opportunities lie.

Coding Scheme Used in Table 1

We have combined IUCN categories of *Near Threatened* or more vulnerable into two groups, choosing not to include conifer species with the IUCN classification of *Least Concern*. However, there are only a small number of *Least Concern* species, and they are mostly widespread, common species used for wood production in forestry that have been well studied and have abundant genetic resources. It will be important to continue developing genetic resources for these species, but we submit that the critical urgency is to develop genetic resources for the at-risk species, so we have focused our attention at this time on just the species in these IUCN categories:

Near Threatened or *Vulnerable*, marked with ‘Med’ in Table 1

Endangered or *Critically Endangered*, marked with ‘High’ in Table 1

Table 1 Graphic summary of the status of genetic resources for at-risk North American conifer forest tree taxa

		Genetic resource category ^c					
Family/Genus/Species ^a	Risk status ^b	Field test	Seedling common garden test	Georeferenced population sample	Reference genome sequence	Population genomics using SNP markers	Neutral markers
Cupressaceae							
<i>Chamaecyparis lawsoniana</i>	Med	Good	Good	Some	None	None	Some
Cupressus							
<i>C. abramsiana</i> (goveniana var. <i>abramsiana</i>)	High	None	None	None	None	None	None
<i>C. bakeri</i>	Med	None	None	None	None	None	None
<i>C. forbesii</i> (guadalupensis var. <i>forbesii</i>)	High	None	None	None	None	None	None
<i>C. goveniana</i>	High	None	None	None	None	None	None
<i>C. guadalupensis</i>	High	None	None	None	None	None	None
<i>C. guadalupensis</i> var. <i>guadalupensis</i>	High	Some	None	Some	None	None	None
<i>C. macrocarpa</i>	Med	None	None	None	None	None	None
<i>C. montana</i> (arizonica var. <i>montana</i>)	High	None	None	None	None	None	None
<i>C. nevadensis</i> (arizonica var. <i>nevadensis</i>)	High	None	None	None	None	None	None
<i>C. sargentii</i>	Med	None	None	None	None	None	None
<i>C. stephensonii</i> (arizonica var. <i>stephensonii</i>)	High	None	None	None	None	None	None
Juniperus							
<i>J. angosturana</i>	Med	None	None	None	None	None	None
<i>J. ashei</i> var. <i>ovata</i>	Med	None	None	Some	None	None	None
<i>J. blancoi</i>	Med	None	None	None	None	None	None
<i>J. comitana</i>	High	None	None	None	None	None	None
<i>J. gamboana</i>	High	None	None	None	None	None	None
<i>J. jaliscana</i>	High	None	None	None	None	None	None
<i>J. maritima</i> ^d	Med	None	Some	None	None	None	None
<i>J. martiniezii</i> (flaccida var. <i>martinezii</i>)	Med	None	None	None	None	None	None
<i>J. saltilensis</i>	High	None	None	None	None	None	None
<i>J. standleyi</i>	High	None	None	None	None	None	None
<i>Sequoia sempervirens</i>	High	Good	Good	Good	Good	Good	Good
<i>Sequoiadendron giganteum</i>	High	Good	Good	Good	Good	Good	Good
Pinaceae							
Abies							
<i>A. balsamea</i> var. <i>phanerolepis</i> ^e	Med	None	None	Good	None	None	Good
<i>A. bracteata</i>	Med	None	Good	Some	None	None	Some
<i>A. fraseri</i>	High	Good	Some	Good	None	Good	Good
<i>A. guatemalensis</i>	High	None	None	Some	None	None	None
<i>A. hickelii</i>	High	None	None	None	None	None	None
<i>A. hidalgensis</i>	Med	None	None	None	None	None	None
<i>A. jaliscana</i>	Med	None	None	None	None	None	None
<i>A. vejarii</i>	Med	None	None	None	None	None	None
Picea							
<i>P. breweriana</i>	Med	None	None	Some	None	None	Some
<i>P. chihuahuana</i>	High	None	None	None	None	None	None
<i>P. martiniezii</i>	High	None	Some	Some	None	Some	None
<i>P. mexicana</i> (engelmannii ssp. <i>mexicana</i>)	High	None	Some	Some	None	Some	None
Pinus							
<i>P. albicaulis</i>	High	Good	Good	Good	Good	Some	Some
<i>P. arizonica</i> var. <i>stormiae</i>	Med	None	None	None	None	None	None
<i>P. ayacahuite</i> var. <i>veitchii</i>	Med	None	None	Some	None	None	None
<i>P. balfouriana</i>	Med	None	None	None	Some	Some	None
<i>P. cembroides</i> ssp. <i>lagunae</i>	Med	None	None	None	None	None	None
<i>P. cembroides</i> ssp. <i>orizabensis</i>	High	None	Some	Some	None	None	None
<i>P. chiapensis</i> (strobos var. <i>chiapensis</i>)	High	Some	Some	Some	None	None	None
<i>P. coulteri</i>	Med	None	Good	None	None	None	None
<i>P. culminicola</i>	High	None	None	None	None	None	None
<i>P. durangensis</i>	Med	None	Some	Some	None	None	None
<i>P. elliotii</i> var. <i>densa</i>	Med	Some	None	None	None	Good	Good
<i>P. flexilis</i> var. <i>reflexa</i>	Med	None	None	None	None	None	None
<i>P. greggii</i>	Med	Good	Some	Good	None	None	None
<i>P. jaliscana</i>	Med	None	Some	Some	None	None	None
<i>P. lumholtzii</i>	Med	None	None	None	None	None	None
<i>P. martiniezii</i> ^f	High	None	None	None	None	None	None
<i>P. maximartinezii</i>	High	Some	None	Some	None	None	None
<i>P. monticola</i>	Med	Good	Good	Good	None	None	Good
<i>P. muricata</i>	Med	None	None	Good	None	Good	Good
<i>P. nelsonii</i>	High	None	None	None	None	None	None
<i>P. palustris</i>	High	Good	Good	Some	None	Good	Good
<i>P. praetermissa</i>	Med	None	None	None	None	None	None
<i>P. radiata</i>	High	Good	Good	Good	Some	Some	Good
<i>P. rzedowskii</i>	Med	None	None	Some	None	None	None
<i>P. tecumananii</i>	Med	Good	None	Some	None	Some	None
<i>P. torreyana</i>	High	None	Good	Good	Some	None	Good

Table 1 (continued)

<i>Pseudotsuga</i>							
<i>P. macrocarpa</i>	Med	None	None	None	None	None	None
<i>P. menziesii</i> var. <i>oaxacana</i> ^a	High	None	None	None	None	None	None
<i>Tsuga</i>							
<i>T. canadensis</i>	Med	Good	Good	Good	Some	Good	Good
<i>T. caroliniana</i>	Med	Good	Good	Good	Some	Good	Good
Podocarpaceae							
<i>Podocarpus matudae</i>	Med	None	None	None	None	None	None
Taxaceae							
<i>Taxus</i>							
<i>T. brevifolia</i>	Med	Good	Some	Some	None	None	Some
<i>T. floridana</i>	High	None	Some	None	Some	None	None
<i>T. globosa</i>	High	None	None	None	None	None	None
<i>Torreya</i>							
<i>T. californica</i>	Med	None	None	None	None	None	None
<i>T. taxifolia</i>	High	Some	Some	Good	Some	Good	Good

^aAlternative taxonomic treatments are provided in parentheses

^bFor 68 taxa, we have used the Red List risk status assigned by the International Union for Conservation of Nature (IUCN) of *Near Threatened* or *Vulnerable* (denoted with Med) or *Endangered* or *Critically Endangered* (denoted with High). For four other taxa (flagged with individual footnotes), we have assigned a risk status of Med or High based on our assessment

^cWe have characterized the status of these six categories of genetic resources as None (where none exist), Some (where some exist), and Good (where enough exist that this resource is not a concern)

^dTaxon not listed by IUCN, rather this genetically distinct Puget Sound area taxon (Adams 2007) is subsumed by IUCN under the widespread *J. scopulorum* taxon

^eData are insufficient to estimate risk under IUCN standards

^fTaxon not listed by IUCN, rather this potentially distinct restricted taxon is subsumed by IUCN under the more widespread *P. durangensis* taxon

^gBy *Pseudotsuga menziesii* var. *oaxacana*, we refer to the southernmost populations of Douglas-fir in Mexico, which were described originally as var. *oaxacana*; however, they are now considered as part of *P. m.* var. *glauca*. To date, this variety, by either name, is not listed by IUCN

We have classified the different types of genetic resources into six major categories. The coding scheme for genetic resources is indicated by: ‘None’ where none exist, ‘Some’ where some exist, and ‘Good’ where enough exist that this resource is not a concern. Readers are referred to several publications that provide detailed description of these genetic resources (Neale and Wheeler 2019; Aitken et al. 2024; Feng et al. 2024).

Field test This group includes field tests ranging from long-term provenance trials to shorter-term progeny tests that may have been developed for such purposes as seed zone delineation or breeding zones. Accessions in such tests would be source identified (e.g., provenance, county, or GPS coordinates) and phenotypes evaluated might range from survival and growth to complex physiological, wood-property, or disease-resistance traits. See Supplemental File 1, Part A for examples of this category for species listed in Table 1.

Seedling common garden test This group includes the many types of short-term tests conducted in nursery beds, cold frames, greenhouses, and growth chambers. This group generally does not leave a biological resource for future use unless DNA

is stored, but does generate knowledge. See Supplemental File 1, Part B for examples of this category for species listed in Table 1.

Georeferenced population sample Sample types might include DNA, tissues, seeds, or live plants. Samples may have been collected for conservation collections or specific research studies, including being planted into the above-mentioned tests. See Supplemental File 1, Part C for examples of this category for species listed in Table 1.

Reference genome sequence This is a relatively new type of genetic resource (complete genome sequence of a tree representing the species) that is obtained at a significant expense and has only been completed for a small number of conifer species. It might also include a transcriptome sequence (transcribed or expressed genes only). Transcriptomes, and genomes to some extent, have been developed for many model organisms and agricultural species and are now being developed for many species of conservation and ecological importance. See Supplemental File 1, Part D for examples of this category for species listed in Table 1.

Population genomics using SNP markers Single nucleotide polymorphism (SNP) markers are derived from DNA sequences from population samples. SNPs are found in both non-coding (non-expressed) and coding DNA sequences, the latter of which can potentially reveal adaptive (selective) patterns of genetic variation. See Supplemental File 1, Part E for examples of this category for species listed in Table 1.

Neutral markers Selectively neutral genetic markers, such as isozymes, amplified fragment length polymorphisms (AFLPs), or microsatellite markers (also called simple sequence repeats, SSRs) have been used for several decades for estimating genetic diversity and population structure. These markers generate knowledge about demographic processes such as gene flow, genetic drift, and mating systems but cannot provide reliable information about patterns of local adaptation or the genetic basis of locally adapted traits. See Supplemental File 1, Part F for examples of this category for species listed in Table 1.

Genetic Knowledge Can Guide Management in a Changing Climate

Genetics research that determines how tree populations are adapted can inform several forest management and conservation practices relevant in a changing climate. For example, by understanding variation among populations in adaptation to climate, identifying key phenotypic traits involved in local adaptation, and understanding the climatic drivers of local adaptation to climate and other environmental factors, we can develop strategies to translocate pre-adapted individuals to suitable locations through reforestation and restoration plantings (Ledig and Kitzmiller 1992; Aitken and Whitlock 2013). In many cases, this will involve the assisted migration of individuals to different geographic areas within species ranges through

reforestation or restoration. In some cases, this may inform assisted species migration into geographic areas that are outside of the current species range, but species migration will require more ecological than genetic considerations, and is likely to have lower levels of acceptance by both members of the public and forestry experts (Peterson St-Laurent et al. 2018). In addition, forest geneticists can develop breeding strategies to select trees for drought tolerance, cold tolerance, and insect and disease resistance or tolerance to increase the likelihood that trees will remain healthy and vigorous in a changing climate. Finally, genetic knowledge can be used to identify high-priority populations at risk of extirpation for ex situ conservation, e.g., in seed banks (Hoban and Schlarbaum 2014).

Basic Needs Required to Solve the Problem of Maladaptation Under Changing Climate

Forest geneticists have developed four main approaches for characterizing patterns of genetic diversity among and within natural populations, and for understanding local adaptation to climate and other environmental factors. The traditional approach is to establish long-term **provenance trials**, which are field-based experiments with seed collected from many locations across a species range or portion thereof and with resulting seedlings planted in experiments on several to many sites that span a range of climatic conditions (Leites and Benito Garzón 2023). Trees are assessed periodically over a few decades for relatively few phenotypic traits including survival and growth, and sometimes insect or disease impacts. These experiments are the gold standard for understanding climate adaptation, but they take considerable time, land, and financial resources, and often do not include a wide enough range of provenances or sites to fully evaluate the implications of climate change (Aitken et al. 2008). Provenance trials have been established for the many economically important conifers in North America, but for very few other species (Table 1, Supplemental File 1, Part A). Existing trials have revealed some similarities among species in climate adaptation, e.g., the importance of adaptation to low winter temperatures, but also marked differences among some species in the extent of population differences in climate adaptation.

The second approach is to establish short-term **common garden experiments** under controlled environmental conditions in which complex climate-related traits such as phenology, cold hardiness, or drought hardiness are measured precisely on seedlings (e.g., St. Clair et al. 2005; St. Clair and Howe 2007), and population differences can be determined within a few years. These studies are generally conducted in nurseries, cold frames, greenhouses, or growth chambers. Temperature, moisture and photoperiod treatments can be applied to compare population responses. A disadvantage is that only seedling traits can realistically be assessed, and seedling growth facilities are needed. Nevertheless, correlations between population variation in seedling traits and climatic differences among seed sources suggest natural selection and adaptation of genotypes to the environments in which they evolved (Heslop-Harrison 1964; Endler 1986). The seedling stage may be important for long-term survival and reproduction, and seedling traits may be strongly correlated

to traits at older life-stages. This approach can also provide quantitative genetic estimates of trait heritabilities and the potential for increasing climate tolerance through selection and breeding of individuals within populations. Seedling common garden experiments that include a wide range of populations have been completed for many common species in North America (Aitken and Bemmels 2016; Neale and Wheeler 2019, Chapter 8; Capblancq et al. 2023; Supplemental File 1, Part B).

The third approach is to use a small number of **neutral genetic markers** (i.e., tens of markers) to characterize population differences in genetic composition and diversity that relate to demographic history and population size using population genetic approaches (Neale and Wheeler 2019, Chapter 9; Supplemental File 1, Part F). While this approach was popular late in the 20th and early in the twenty-first centuries and generated considerable knowledge for many conifers in North America, it has now largely been replaced by population genomics, the fourth approach.

Population genomics capitalizes on the technological breakthroughs that have produced high-throughput, low-cost DNA sequencing as well as increased computational capacity and improved bioinformatic methods. By characterizing genetic variation within and among populations at tens of thousands to millions of non-neutral genetic markers (SNPs) throughout the genome, genes can be identified that are associated with population climates (Neale and Wheeler 2019, Chapter 12; Supplemental File 1, Parts C and E), or with climate-related phenotypic traits such as drought or cold tolerance (Neale and Ingvarsson 2008; Neale and Wheeler 2019, Chapter 12). Population genomic data also enable landscape genomic analyses that can parse patterns of variation into those due to local adaptation or genetic connectivity of populations (Capblancq et al. 2023; Aitken et al. 2024). Genomic methods provide data much more rapidly on the extent of local adaptation than do long-term provenance trials, and complement short-term common garden experiments. While DNA sequencing or genotyping can be outsourced to specialized facilities, the bioinformatic analysis and interpretation of results requires highly trained individuals.

Population genomic studies have only been completed for a small number of the North American conifers included in Table 1. **Reference genome** sequences are the starting point for cataloging all coding genes in the genome and beginning to identify non-neutral genetic markers for estimating evolutionary adaptive potential. However, reference genome sequences have only been obtained for three of these North American conifers (Neale and Wheeler 2019, Chapter 3; Supplemental File 1, Part D).

Funding, Prioritizing, and Developing Genetic Resources for North American Conifers

A comprehensive report titled “The Status of Temperate North American Forest Genetic Resources” edited by Deborah L. Rogers and F. Thomas Ledig was published in 1996. The report was prepared in advance of a Food and Agriculture Organization (FAO) meeting in 1996 on global genetic resources. The North American report was focused primarily on **in situ biological genetic resources** in Canada, United States, and Mexico. Less attention was focused on **ex situ genetic resources**

and **prioritizing species** needing attention. The Rogers and Ledig report made 18 recommendations, primarily for the conservation of in situ biological genetic resources, which mostly pertained to policy. More recently, the findings of a 2016 workshop (Gene Conservation of Tree Species—Banking on the Future) also noted the importance of a long-term goal of in situ conservation, but gave much more emphasis on ex situ conservation as a complementary objective and on strategies for targeting species and populations to be conserved (Potter et al. 2017). We focus primarily on **genetic resources** and **biological ex situ genetic resources**, the status of these for **North American conifers**, and how to prioritize and fund the development of genetic resources.

Historically, the types of genetic resources we describe here have been developed in an ad hoc and bottom-up manner. Interested individual researchers at universities and state and federal agencies would initiate a one-off study of some type or in developing genetic marker or genome sequences in one or more conifer species. This work was funded, and therefore prioritized, by competitive grants or appropriated agency funds. Results of this work are generally reported in refereed scientific journals. A significant amount of knowledge has been developed in this manner, but it has not for the most part been strategic. Further, most of this work has been done in Canada and the United States due to the greater availability of funding and expertise in these countries. For example, a smaller proportion of species has been studied in Mexico due to the great number of species and relatively few resources allocated to their study. Given the urgency of changing climate and natural and human-assisted redistribution of species ranges, a multi-national and strategic approach to procuring genetic knowledge and resources is timely. Work has already been done to identify tree species in the United States for which genetic diversity conservation activities are needed (Potter et al. 2019) or for strengthening the utility and value of existing international ex situ tree collections (Cavender et al. 2015). These provide useful strategies to inform our focus on North America conifer species.

A prospectus outlining the need for enhancing the genetic resources that we have identified here would be useful for organizing a continent-wide collaborative to develop conservation priorities for at-risk species and propose a research and development framework to ensure the long-term viability of these species. The prospectus should be vetted with leading forestry agencies and organizations within the USA (e.g., the USDA Forest Service, American Forest Foundation), Canada (e.g., Canadian Forest Service, provincial forestry agencies), and Mexico (e.g., Comisión Nacional Forestal, Unidad de Asuntos Internacionales) for consideration and support. Existing forest genetics organizations that could take on this challenge include the North American Forest Genetics Society, a professional society for the discipline of forest genetics and genomics founded in 2022, and the North American Forestry Commission's Forest Genetic Resources Working Group.

In order to conserve and manage forest genetic diversity in a changing climate in a way that facilitates adaptation and resilience, we need to understand the genetic diversity and local adaptation of the many North American conifer species identified here that to date have been neglected. These species represent ancient lineages with uncertain futures. By directing researchers and resource managers towards these

gaps in genetic resource availability, we can inform conservation strategies for these species that will increase their likelihood of avoiding extinction under new climates and other biotic and abiotic challenges.

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Data availability All data are compiled in Table 1 of the manuscript.

Declarations

Study implications Without understanding the adaptive genetic diversity of at-risk conifer forest tree populations, there can be no successful management and restoration of conifer species impacted by climate change, invasive species, or forest fragmentation. An assessment of the current status of North American conifer genetic resources is a first step. We present this status report along with a call to action for researchers and managers to develop a coordinated protocol for North American at-risk conifer conservation and restoration.

Competing interests The authors have no competing interests.

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