


Article

Genetic Conservation and Use of Genetic Resources of 18 Mexican Pine Species

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Abstract: Genetic conservation is key to maintaining forests for the future; however, these face several threats. Mexico is an example of the degradation of forest genetic resources during the past three decades due to its deforestation rates. This country is considered a center of pine diversity but its genetic conservation efforts are not enough. To define genetic conservation units (GCUs) and propose measures for the conservation and sustainable use of 18 Mexican pine species, we analyzed the distribution of the species at the national level and in germplasm transfer zones, and evaluated the species with a set of minimum requirements for conservation and indicators from the EUFORGEN program. We determined that 13 to 15 genetic zones harbored the target species, in which *Pinus teocote*, *Pinus cembroides*, *Pinus devoniana*, *Pinus maximinoi*, *Pinus douglasiana*, and *Pinus leiophylla* were the most widely distributed. We defined 173 areas for establishing GCUs for the total of the species studied; 50% of them were selected from areas with genetic information, 5% were selected from seed stands, and 45% from natural forests. We detected that most of the forest reproductive material used is collected from seed stands, and the use of seeds from breeding trials is scarce.

Keywords: conservation efforts; dynamic conservation; forest genetic diversity; genetic conservation units; genetic variation; *Pinus*



Citation: Flores, A.; Buendía Rodríguez, E.; Pineda Ojeda, T.; Flores Ayala, E.; Méndez-González, J. Genetic Conservation and Use of Genetic Resources of 18 Mexican Pine Species. *Diversity* **2023**, *15*, 735. <https://doi.org/10.3390/d15060735>

Academic Editor: Adriano Stinca

Received: 12 April 2023

Revised: 23 May 2023

Accepted: 25 May 2023

Published: 2 June 2023



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1. Introduction

Facing continuous environmental changes, genetic conservation is a key to maintaining forest resources for the future. The main objective of genetic conservation is to preserve the genetic integrity and natural levels of genetic diversity [1]. However, conservation activities are limited by the financial, temporal, and technical resources available [2]. For this reason, activities must be selected by keeping in mind the species with ecological, economic, and social potential uses by country based on current conservation status, potential economic use, threat of genetic erosion, genetic distinction, ecogeographic distinction, national or conservation agency priorities, biological importance, cultural importance, relative cost of conservation, conservation sustainability, and ethical and aesthetic considerations [3].

Forest genetic resources have been used for testing of tree species and provenance for different uses and under different environmental conditions [4]. The purpose of a provenance test is to establish the most healthy and fastest growing population among many others of the same tree species, in order to select such a population as a seed source for planting at appropriate sites [5]. This is a tool for improving forest genetics. In common garden experiments, also known as provenance trials, it is possible to test which provenances have adapted to expected climate conditions [6] because tree species possess

numerous local adaptations which represent valuable genetic resources for the long-term survival of the species and for coping with climate change [7].

Forest genetic resources face several threats, such as habitat destruction, fragmentation, pollution, poor silvicultural practices, and the use of low-quality or poorly adapted forest reproductive material [8]. Mexico is an example of the degradation of forest genetic resources for the past three decades due to its deforestation rates which have varied from 260,000 to 1,600,000 ha/year [9]. This country possesses from 43 to 51 pine species (depending on the author) and is considered a center of pine diversity; it also accounts for almost half of the total number of pine species in the world [10]. On the other hand, Mexican pines are very important because they supply 85% of the national timber production and are the main support for the forest industry [11].

For Mexico, some research has been carried out to define the genetic variation of the genus *Pinus*. In the past, provenance and progeny tests have been the most widely used [12–14], but recently, molecular characterization has been the main objective of several studies to define genetic diversity [15]. Although there is genetic information for most *Pinus* species, their conservation efforts are limited, and the proposals to conserve them are few. For *Pinus arizonica* (Engelm.) Shaw, *Pinus ayacahuite* Ehrenb. ex Schltdl., *P. cembroides* Zucc., *Pinus chiapensis* (Martínez) Andresen, *P. douglasiana* Martínez, *Pinus durangensis* Martínez, *Pinus engelmannii* Carrière, *Pinus greggii* Engelm. ex Parl., *Pinus hartwegii* Lindl., *P. leiophylla* Schiede ex Schltdl. et Cham., *Pinus montezumae* Lamb., *Pinus oocarpa* Schiede ex Schltdl., *Pinus patula* Schiede ex Schltdl. & Cham., *Pinus pseudostrobus* Lindl., and *Pinus strobiformis* Engelm., some research analyzes genetic diversity [16–29] and discusses options for in situ or ex situ conservation [24–26,30]; however, these studies did not define any zone for genetic conservation, except for *P. douglasiana*.

In this sense, the authors of [31] prioritized the genetic conservation of four pine species (*P. greggii* Engelm. ex Parl., *P. oocarpa* Schiede ex Schltdl., *P. patula* Schiede ex Schltdl. & Cham., and *P. pseudostrobus* Lindl.) based on establishing a network with genetic conservation units (GCUs), but no other work has been recorded. The gene conservation network is a tool to evaluate the plasticity, adaptation, and migration potential of tree species that face environmental changes [8]. For this reason, it is imperative to define more GCU for other pine species in order to start their genetic conservation. On the other hand, Mexican legislation establishes: “Conserve and protect the country’s forest genetic resources”, but the way to implement it has not yet been defined.

Based on the above and due to the need to establish a genetic conservation network for pine species, the objectives of this work were to define genetic conservation units and propose measures for the conservation and sustainable use of 18 Mexican pines. The distribution of the species was defined at the national level and in the germplasm transfer zones, the gene conservation units were determined based on a set of minimum requirements, and finally, the use and importance of genetic resources were analyzed.

2. Materials and Methods

2.1. Species and Distribution

Eighteen Mexican pine species were chosen for this study: *P. arizonica* (Engelm.) Shaw, *P. ayacahuite* Ehrenb. ex Schltdl., *P. cembroides* Zucc., *P. chiapensis* (Martínez) Andresen, *P. devoniana* Lindl., *P. douglasiana* Martínez, *P. durangensis* Martínez, *P. engelmannii* Carrière, *P. hartwegii* Lindl., *Pinus jeffreyi* Balf., *Pinus lawsonii* Roetz ex Gordon, *P. leiophylla* Schiede ex Schltdl. et Cham., *Pinus maximartinezii* Rzed., *P. maximinoi* H. E. Moore, *P. montezumae* Lamb., *Pinus quadrifolia* Parl. ex Sudw., *P. strobiformis* Engelm., and *Pinus teocote* Schiede ex Schltdl. et Cham. These species are distributed across the country, and some of them are found in more than one of the temperate mountain ranges (Sierra Madre Occidental, Sierra Madre Oriental, Eje Neovolcánico Transversal, Sierra Madre del Sur, and Sierra Madre Centroamericana and Altos de Chiapas) which occupy diverse habitats [32,33] (Supplementary Materials Table S1).

The species distributions were determined based on geographic data (latitude and longitude) using the plots of the National Forest and Land Inventory (NFLI, 2004 to 2007 [34]), which covers Mexico in a systematic stratified random sampling with a grid of 5 km (Supplementary Materials Figure S1). Plots which considered forest plantations were removed. The geographic data were presented using QGIS software 3.28.2. [35].

2.2. Genetic Zones

The germplasm transfer zones (equivalent to seed zones) were used as a proxy because genetic zones are still undefined for the country. Seed zones are homogeneous areas in terms of climate and latitudinal or longitudinal distribution [36] for regulating seeds, fruits, and vegetative material. These seed transfer zones were previously defined by the Mexican National Forest Commission (CONAFOR by its Spanish acronym), and are available at <https://www.gob.mx/conafor> (accessed on 8 August 2022). The genetic zones were obtained for the 18 Mexican pines species by overlapping their distribution with the germplasm transfer zones. All genetic zones with less than 20 trees for each species reported in the NFLI were excluded from subsequent analysis. For the geographic data, QGIS software 3.28.2. was used [35].

2.3. Conservation Units

Genetic conservation units (GCU) were defined as an in situ conservation strategy. It was followed a set of minimum requirements for defining the units based on population size, management, monitoring, and ownership [37] (Supplementary Materials Table S2). We selected at least one GCU per genetic zone and species, but in fragmented distribution, one unit was selected from each patch. During the selection, it was prioritized extensive and centered populations in the genetic zone or patch. For each genetic zone, first, we chose the populations characterized in previous genetic studies or provenance or progeny trials [12,17,18,22–29,38–89] (Table S3), which were selected for possessing representative trees within the zones. The previous studies and trials were obtained from an exhaustive documentary review from printed and digital scientific journals. Secondly, they were chosen populations located in seed stands defined by the Mexican National Forest Commission (CONAFOR, information available for 2021 at <https://www.gob.mx/conafor>, accessed on 5 September 2022). Thirdly, we selected populations from protected areas for biodiversity conservation established by the Mexican Commission for Biodiversity (CONABIO, information for 2016 available at <http://www.gob.mx/conabio>, accessed on 7 September 2022), instead private ownership. Finally, we selected populations situated in private forests. The geographic data were represented using QGIS software 3.28.2 [35].

2.4. Use of Genetic Resources

For each genetic zone, the presence of germplasm production units (seed stands or seed orchards) were used in order to define the use and importance of genetic resources. We assumed that the effort and investment during the establishment and maintenance of those units was an economic indicator of the species in the area. Then, genetic trials established by different institutions, that is, provenance and progeny trials, were used, as they report information about populations identified for choosing forest reproductive material with well-known genetic backgrounds.

2.5. Importance of Genetic Zones for Conservation and Sustainable Use

Based on the previous information, six species indicators were collected in all genetic zones: the number of trees sampled by the NFLI (n_i), the number of populations with molecular data (n_{mk}), the number of populations with seed stands (seed stand plus seed area) (n_{st}), the number of individuals selected for progeny tests (n_{is}), the number of populations present in provenance tests (n_{pt}), and the number of seed orchards (n_{so}). Finally, we estimated the number of GCUs (n_g). For each species, their status was calculated by applying indicators assigned and adapted from the EUFORGEN program [90] (Table 1).

Table 1. Indicators of the genetic zones in conservation and management of genetic resources.

Indicator ¹		Description
I1	Number of genetic zones	Number of genetic zones with the presence of the species
I2	Molecular characterization effort ²	% of genetic zones with at least 1 sample in molecular studies = Number of genetic zones with the presence of molecular studies of the species/Number of genetic zones with the presence of the species
I3	Provenance characterization effort	% of genetic zones with at least 1 population in provenance test = Number of genetic zones with the presence of provenance studies of the species/Number of genetic zones with the presence of the species
I4	Progeny characterization effort	% of genetic zones with plus trees in progeny tests = Number of genetic zones with the presence of progeny studies of the species/Number of genetic zones with the presence of the species
I5	Seed stands index	% of genetic zones with at least 1 forest seed production unit = Number of genetic zones with the presence of seed stands of the species/Number of genetic zones with the presence of the species
I6	Seed orchard index	% of genetic zones with at least 1 seed orchard = Number of genetic zones with the presence of seed orchards of the species/Number of genetic zones with the presence of the species
I7	Genetic conservation index	% of genetic zones with at least 1 conservation unit identified = Number of genetic zones with the presence of genetic conservation units of the species/Number of genetic zones with the presence of the species

¹ I2, I3, I4, and I6 indicators used data from previous studies recorded in scientific journals, and the I5 indicator was estimated from CONAFOR information. ² One sample was defined by stand/population.

The importance of the genetic zones was calculated using the previous information published by studies [91–93], which defined their reforestation and restoration potential, and timber production by genetic zone. In these studies, a proportional assignment to each genetic zone was made using as a basis the distribution of the 18 species and those harbored in genetic zones. We also determined a value for conservation and a value for breeding for the different genetic zones of the species in a subjective scale from 1 to 4 [31], with 4 being the highest priority. For this, the expert knowledge and the recommendations established by the papers or reports previously analyzed were considered.

3. Results

3.1. Species in Genetic Zones

Twenty-three genetic zones were detected and harbored at least one population of the studied species. Particularly, eight zones included 11–13 species, 5 zones included 1–3 species, and 10 zones included 5–9 species (Figure 1). *Pinus teocote*, *P. cembroides*, *P. devoniana*, *P. maximinoi*, *P. douglasiana*, and *P. leiophylla* were the most widely distributed (18, 16, 16, 13, 12, and 12 genetic zones, respectively), *P. arizonica* var. *cooperi*, *P. quadrifolia*, and *P. jeffreyi* had a more restricted distribution (4, 4, and 1 genetic zones, respectively), and *P. durangensis*, *P. engelmannii*, *P. hartwegii*, *P. montezumae*, *P. arizonica*, *P. ayacahuite*, *P. chiapensis*, *P. lawsonii*, *P. maximartinezii*, and *P. strobiformis* had a medium distribution (9, 9, 9, 9, 7, 7, 7, 7, 7, 7, and 7 genetic zones, respectively).

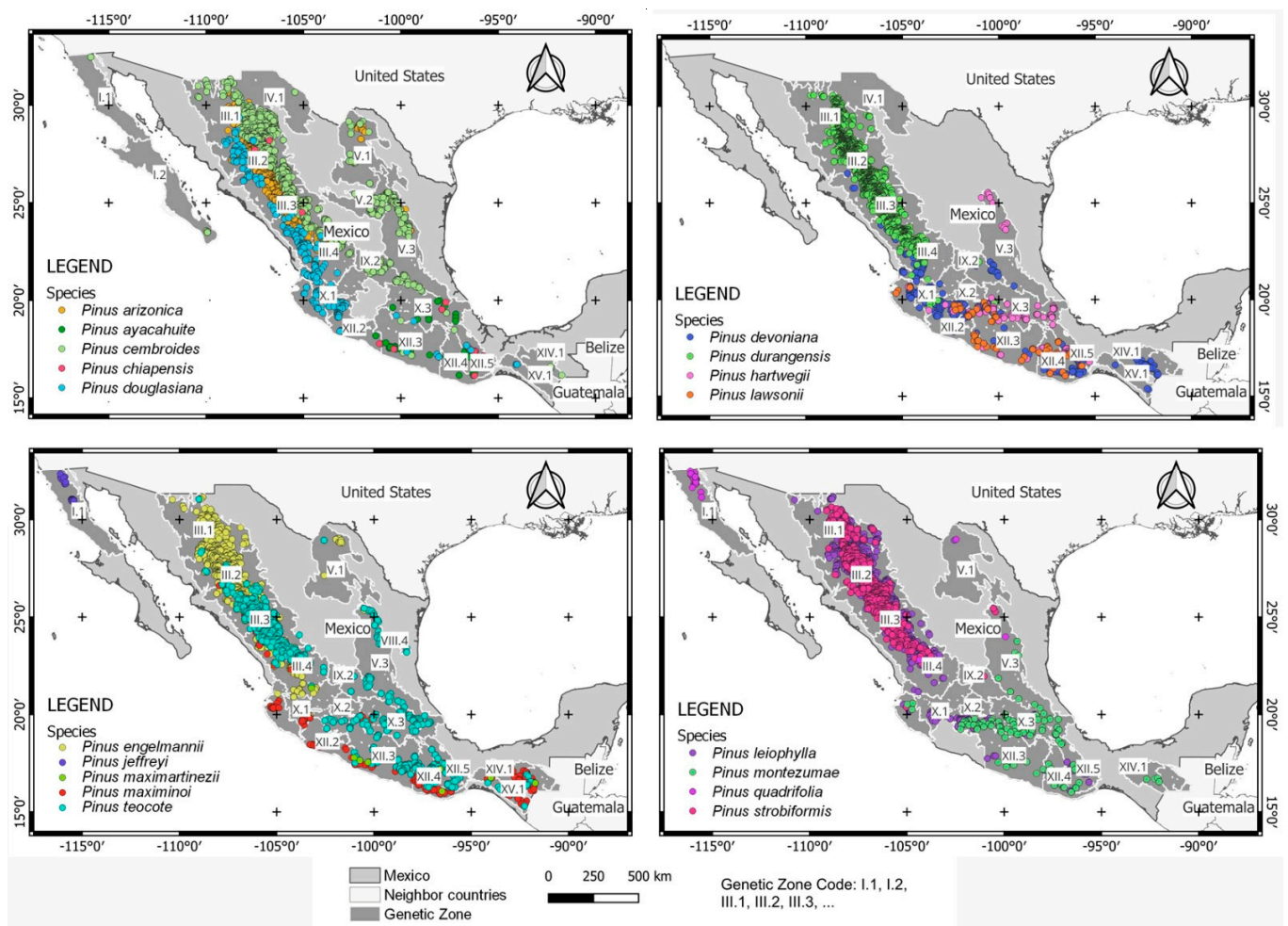


Figure 1. Natural populations of target species distributed in the genetic zones from Mexico.

3.2. Genetic Conservation Units

For the studied species, 173 areas for established GCU were detected (Figure 2 and Supplementary Materials Table S4). Specifically, 13–20 areas for *P. leiophylla*, *Pinus teocote*, *P. cembroides* (with two subspecies: *bicolor* and *cembroides*), *P. devoniana*, and *P. douglasiana*; 7–12 for *P. maximinoi*, *P. engelmannii*, *P. montezumae*, *P. durangensis*, *P. strobiformis*, *P. hartwegii*, *P. arizonica*, and *P. lawsonii*, and 1–2 for *P. arizonica* var. *cooperi*, *P. ayacahuite* var. *ayacahuite*, *P. cembroides* subsp. *cembroides*, *P. ayacahuite* var. *veitchii*, *P. cembroides* subsp. *bicolor*, *P. jeffreyi*, *P. quadrifolia*, *P. cembroides* subsp. *lagunae*, *P. cembroides* subsp. *orizabensis*, *P. chiapensis*, and *P. maximartinezii*. With respect to the selection criteria, 50% of the GCU were selected from areas with genetic information reported in previous research. In the absence of genetic information, 5% of GCU were selected from seed stands defined by CONAFOR and the other 45% in natural forests recorded for NFLI. Additionally, 38% of the GCU were chosen from protected areas.

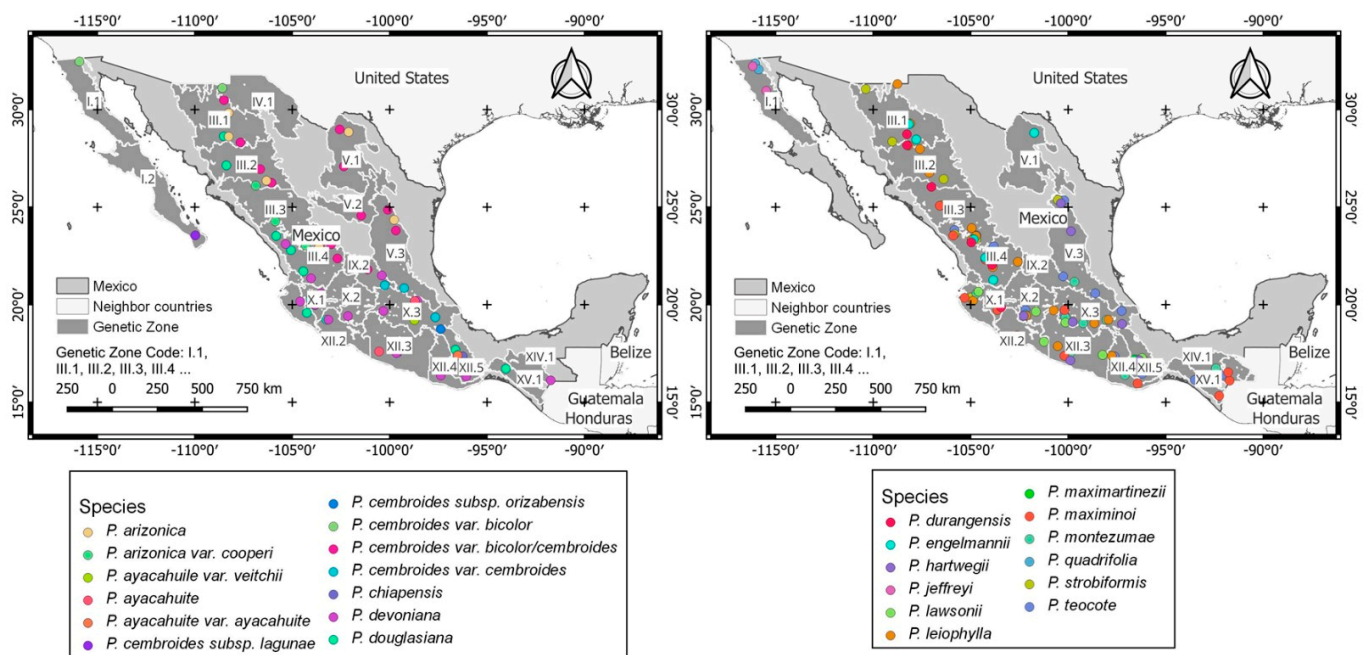


Figure 2. Conservation units proposed by genetic zone for the target species from Mexico.

3.3. Use of Genetic Resources

For the target species, the conservation efforts and use of genetic resources by genetic zone were quite contrasting (Supplementary Materials Tables S5–S9). The genetic characterization was null or narrow for some species and regions, that is, *P. jeffreyi*, *P. lawsonii*, *P. maximartinezii*, *P. quadrifolia*, and *P. cembroides* subsp. *orizabensis*, but broader for others, that is, *P. arizonica*. The efforts to use forest reproductive material were reduced and concentrated on selecting seed stands (Table S7), for example, *P. arizonica* and *P. durangensis* had more seed stands than other species (26 and 20, respectively), but few or no seed orchards (2 and 0, respectively) or provenance/progeny trials (0 for both species). We detected many gaps in different regions for all of the species, but some zones had no efforts to use forest reproductive material; that is, I.2, IV.1, V.2, VIII.1, VIII.3, VIII.4, IX.2, XII.1, XII.2, XII.5, XIII.1, XIV.1, XIV.2, and XIV.3 did not record use of any genetic resources.

3.4. Conservation and Management of Genetic Resources

The conservation efforts, characterization, and use of forest genetic resources for the 18 species were incomplete (Table 2). Most of the genetic zones had gaps for the characterization of forest genetic resources or even seed production. Molecular studies were null for *P. jeffreyi*, *P. lawsonii*, *P. maximartinezii*, *P. quadrifolia*, and low for *P. devoniana*; the rest of the species ranged from 100 to 22.22% where *P. strobiformis* and *P. ayacahuite* possessed the higher values (100 and 85.71%, respectively). *P. arizonica* and *P. leiophylla* were the only species that had seen seed orchards established ($I6 > 0$). Provenance and progeny trials had been established for a few species, in which their efforts were limited ($I3$ and $I4 > 0$). *P. arizonica* and *P. durangensis* had more forest reproductive units, covered several states, and were used for reforestation and restoration of degraded lands and timber production.

3.5. Importance of Genetic Zones for Conservation and Use of Genetic Resources

For reforestation and restoration areas, XII.4, XII.5, X.3, X.2, XII.1, V.3, XII.2, and XV.1 zones were the most important due to having the potential of seedling production, germplasm production units, and seed conservation banks (see [91]); whereas for timber production, X.3, V.3, XII.5, XII.3, X.1, XII.2, III.1, and III.2 were the best zones due to their amount of timber harvested and used for the industry (see Tables 1 and 2 from [93]). Based

on this information, it was defined that V.3, X.2, X.3, XII.1, XII.2, XII.4, XII.5, and XV.1 were the most suitable areas of germplasm for the target species studied (Figure 3), which presented the highest potential for conservation and breeding. Although they were not the genetic zones with the greatest number of trees inventoried, they were the most diverse in the number of species and the ones where the actions dedicated to the conservation and use of genetic resources were more intensive (Table 3).

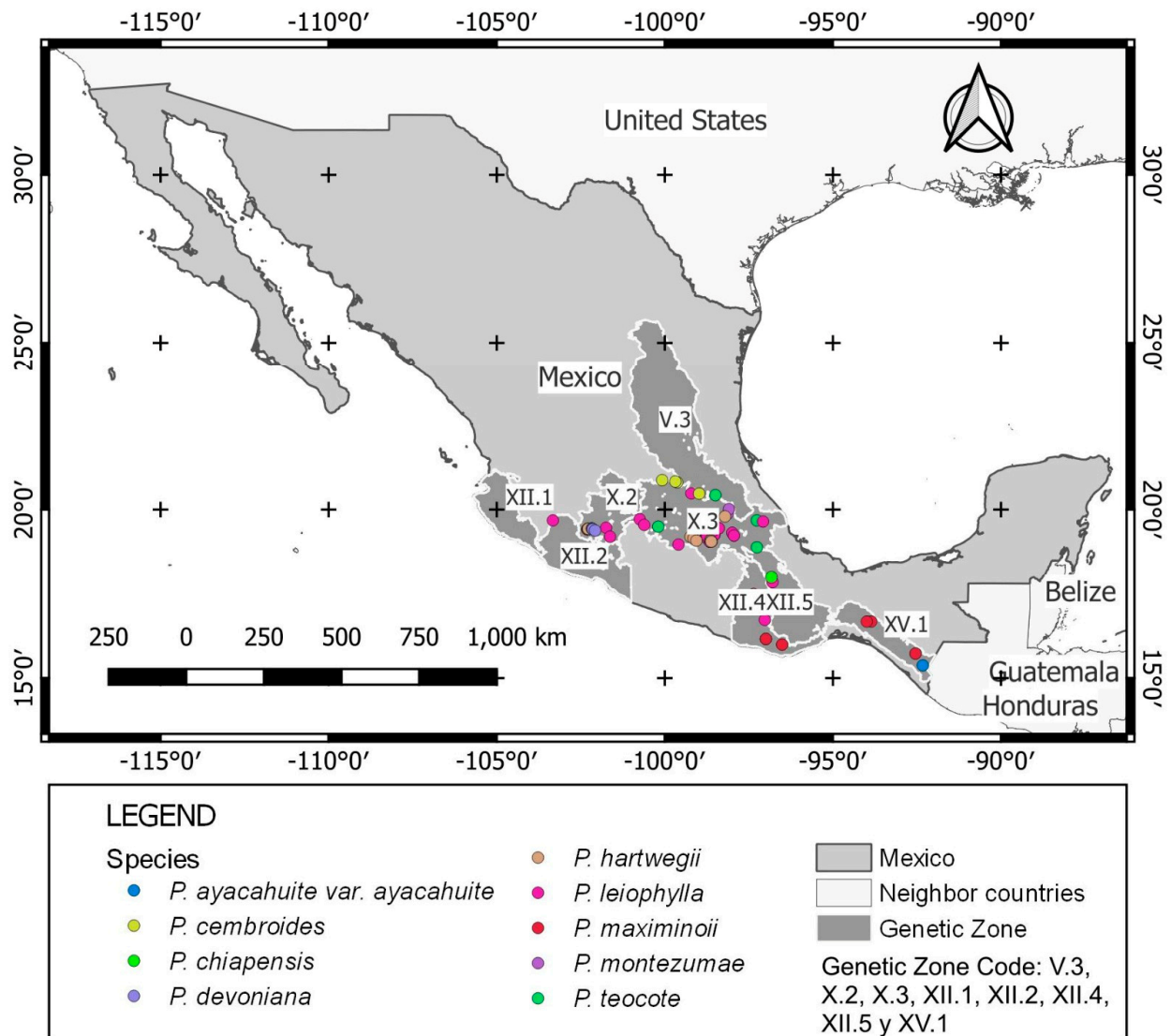


Figure 3. Populations considered as the most suitable source for supplying forest reproductive material for nine species from Mexico.

Table 2. Indicators of the conservation and management of genetic resources.

Code	Indicator ¹	AR ²	AY	CE	CH	DE	DO	DU	EN	HA	JE	LA	LE	MM	MA	MO	QU	ST	TE	Media
I1	Number of genetic zones	8	7	16	7	16	12	9	9	9	1	7	12	7	13	9	4	7	18	10
I2	Molecular characterization effort ³	27.27	85.71	50.00	71.43	6.25	33.33	44.44	44.44	66.67	0.00	0.00	66.67	0.00	53.85	44.44	0.00	100.00	22.22	39.82
I3	Provenance characterization effort	0.00	14.29	12.50	0.00	0.00	0.00	0.00	11.11	11.11	0.00	0.00	8.33	0.00	15.38	11.11	0.00	0.00	5.56	4.97
I4	Progeny characterization effort	0.00	14.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.33	0.00	7.69	0.00	0.00	0.00	5.56	1.99
I5	Seed stands index	27.27	14.29	0.00	14.29	25.00	25.00	33.33	44.44	22.22	100.00	14.29	16.67	0.00	15.38	33.33	25.00	0.00	11.11	23.42
I6	Seed orchard index	18.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.33	0.00	0.00	0.00	0.00	0.00	0.00	1.47
I7	Genetic conservation index	54.55	57.14	75.00	14.29	68.75	83.33	55.56	77.78	66.67	100.00	100.00	91.67	14.29	84.62	88.89	25.00	85.71	66.67	67.22

¹ I2, I3, I4, and I6 indicators used data from previous studies recorded in scientific journals, and the I5 indicator was estimated from CONAFOR information. ² AR—*Pinus arizonica*, AY—*P. ayacahuite*, CE—*P. cembroides*, CH—*P. chiapensis*, DE—*P. devoniana*, DO—*P. douglasiana*, DU—*P. durangensis*, EN—*P. engelmannii*, HA—*P. hartwegii*, JE—*P. jeffreyi*, LA—*P. lawsonii*, LE—*P. leiophylla*, MM—*P. maximartinezii*, MA—*P. maximinoi*, MO—*P. montezumae*, QU—*P. quadrifolia*, ST—*P. strobiformis*, TE—*P. teocote*. ³ Based on 1 sample by stand/population.

Table 3. Importance for conservation and use of forest genetic resources of pines by genetic zone.

Genetic Zone	Trees: National Forest Inventory	Value for Conservation (1 to 4)																	
		AR	AY	CE	CH	DE	DO	DU	EN	HA	JE	LA	LE	MM	MA	MO	QU	ST	TE
I.1	606	-	-	1	-	-	-	-	-	-	4	-	-	-	-	-	4	-	-
I.2	25	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
III.1	20192	2	-	4	-	-	1	1	4	-	-	-	2	-	-	-	-	2	1
III.2	28994	4	-	3	1	1	2	4	4	-	-	-	2	-	1	-	-	4	1
III.3	30663	3	-	3	1	1	1	2	4	-	-	-	3	-	1	-	1	4	4
III.4	5869	1	-	2	-	2	3	1	2	-	-	-	2	1	2	-	-	1	1
IV.1	56	-	-	1	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-
V.1	340	1	-	1	-	-	-	-	1	-	-	-	1	-	-	-	1	-	1
V.2	875	1	-	2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
V.3	4476	1	4	4	1	1	-	-	1	2	-	-	-	-	2	1	1	1	1
VIII.4	8	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1
IX.2	1499	-	-	2	-	1	-	1	-	-	-	-	-	-	-	-	-	1	1
X.1	1812	-	-	1	-	3	4	1	1	1	-	-	1	-	3	-	-	-	1
X.2	1645	-	-	-	-	3	-	-	-	3	-	4	2	-	-	3	-	-	1
X.3	3903	-	3	3	2	4	1	1	-	4	-	1	4	-	4	4	-	-	4
XII.1	538	-	-	-	-	2	1	-	3	1	-	1	1	-	1	1	-	1	-
XII.2	795	-	1	-	1	1	2	-	-	1	-	1	-	1	2	-	-	-	1
XII.3	1480	-	2	1	1	2	1	1	-	1	-	2	1	1	3	1	-	-	1
XII.4	2976	-	1	-	-	2	1	-	1	1	-	4	1	1	4	1	-	-	2
XII.5	1976	1	2	1	4	2	1	-	-	1	-	2	1	4	1	1	-	-	1
XIV.1	596	-	1	1	-	2	-	-	-	-	-	-	-	-	2	1	-	-	1
XIV.2	105	-	-	-	-	1	-	-	-	-	-	-	-	1	1	1	-	-	1
XV.1	111	-	-	-	-	1	1	-	-	-	-	-	-	1	3	-	-	-	1

4. Discussion

The priority zones were defined to help the conservation and the use of forest genetic resources in 18 Mexican pine species. Based on the germplasm transfer zones [36] as a proxy for genetic zones, 173 areas have been identified for establishing conservation units into 22 genetic zones. Additionally, it was considered that eight genetic zones could supply the forest reproductive material in order to be used for the species' afforestation, restoration, and for establishing plantations.

We detected that some species were distributed more than others, and have high levels of genetic variation due to their biological characteristics; for example, *P. cembroides* is one pine that harbors more than one temperate mountain range, and *P. teocote* is the most abundant and widespread in Mexico, both having a high level of genetic diversity [15,51]. It is possible that the species' distributions are influenced by the environment and their ecological factors. This is in line with the authors of [39], who determined that elevation is an important factor that drives the geographical location and genetic diversity of the species. Additionally, they pointed out that *P. cembroides* possesses the ability to adapt to its growth conditions. On the other hand, some species have a more restricted distribution but possess high genetic variation as *P. arizonica* [15,52], which is according to the authors of [22] who studied forests in Chihuahua state. Based on the results of study [38], this is possible due to their populations having enough individuals and sufficient outcrossing to prevent genetic drift.

Most of the species have potential for restoration of land; consequently, they are used during reforestation or conservation programs, for example, seedlings of *P. cembroides* and *P. devoniana* are the most produced in the nurseries for the reforestation of areas across the country [91], while *P. douglasiana*, *P. maximinoi*, and *P. teocote* are species most harvested and used in the forest industry [93]. *P. cembroides* is a tree to tolerate drought and is able to grow in sites in poor soils [94], while *P. devoniana* is a pine to resist drought [95]. These characteristics have been attractive for nurserymen during seedling production and for planters in the restoration of semi-arid regions and dry zones. However, sometimes hard conditions in the sites selected (hydric stress and low mineral nutrition) can strongly reduce their survival [96]. For conservation, *P. cembroides* has been suggested to promote the natural functions of forest dynamics in reforested areas [97].

Although there are efforts to conserve Mexican pine species, the preservation of their genetic resources is limited because the current legislation only points out the use of forest genetic resources [98,99] but does not define conservation strategies. The little conservation actions made for governmental agencies depend on their budget, which is more scarce each year. These conditions demand some activities during forest management proposed by the authors of [100] that help to maintain the populations of target species as (i) limiting livestock grazing, (ii) controlling forest fires, (iii) eliminating competing vegetation, (iv) expanding the present populations by reforestation outside the priority populations' boundaries using local reproductive material, (v) finding new and potentially suitable locations and establishing new populations that are sufficiently large to be genetically viable, (vi) establishing provenance trials and traditional progeny tests as genetic archives, and (vii) storing seeds in gene banks.

The results showed that the information about genetic characterization for most species is not enough; however, the results can help start a national conservation program for the species most used in forest management. Some of the target species have been more characterized than others which could be due to their economic importance, for example, *P. douglasiana* or *P. arizonica*, which produce an average of 56 554 and 13 410 m³ year⁻¹ timber, respectively [93]. The conservation of genetic diversity must be a priority because it is the basis for the eventual adaptation and resilience of tree species studied regarding environmental stress and change [101]. On the other hand, although there is a Mexican network of Natural Protected Areas (NPA) that harbor some of the tree species and could be used as genetic diversity reserves, this is insufficient for future conservation needs. According to the authors of [102], the protection of pine species is inadequate because

they possess a small percentage of the area of the total species, therefore, they suggest directing this strategy (NPA) to species with limited distribution such as *P. cembroides* subsp. *cembroides*.

The purpose of defining genetic conservation units is to generate a network in the country in order to maintain the Mexican pines which are facing current environmental changes in other parts of the world; for example, in Europe, the establishing of genetic conservation units is a tool to assess, monitor, and support the conservation of forest genetic resources [90,103]. This action can allow the future use of pines from Mexico in three programs: breeding, production, and conservation.

The target species have high genetic diversity. According to the authors of [104], the Mexican pines possess high levels of genetic variation and relatively little genetic differentiation among populations. However, there are other species with low levels of diversity such as *P. greggii* Engelm. ex Parl., which is used in national or international breeding programs [12,80]. *P. ayacahuite*, *P. leiophylla*, and *P. teocote* are some pines that have provenance trials to define their potential for commercial plantations, for example, *P. ayacahuite* is one of the species most used for Christmas tree producers [105] while *P. leiophylla* and *P. teocote* are managed in natural forests for timber production [93]. Facing climatic changes, adaptive trials have been tested in the studied species: *P. ayacahuite*, *P. arizonica* (water availability and water stress) [106,107]; *P. arizonica*, *P. leiophylla*, and *P. teocote* (fire damage) [108]; *P. arizonica*, *P. ayacahuite*, *P. cembroides*, *P. chiapensis*, *P. devoniana*, *P. durangensis*, *P. engelmannii*, *P. hartwegii*, *P. jeffreyi*, *P. lawsonii*, *P. maximartinezii*, *P. maximinoi*, *P. montezumae*, *P. strobiformis*, *P. teocote* (frost resistance) [109], and *Pinus cembroides* (salt tolerance) [110].

Some of the areas selected could be affected by illegal extraction of timber [111] or other factors that limit genetic conservation, for example, land use change for agriculture [112]. However, the establishing of GCUs in protected areas can help with maintaining them in the long term because the rate of forest loss is lower [113]. In these areas, the financial resources, human capacity, and appropriate equipment are the main aspects that have the greatest effect on forest land loss [114]. For this reason, administration and finance must be continually evaluated during the management of the protected areas in order to preserve the UCGs selected.

On the other hand, the diversity of pines from Mexico across the mountain regions promotes habitats that harbor local wildlife. This is an element to add more importance to forest conservation. This is in line with the authors of [115], who defined that natural forests dominated by *P. montezumae* and *P. pseudostrobus* conform to the best habitat to comprise the highest bird species richness from Northeast Michoacán, Mexico, for example, *Hylocharis leucotis*, *Archilochus alexandri*, *Selasphorus platycercus*, *Trogon mexicanus*, and *Melanerpes formicivorus*.

Finally, we suggest incorporating these GCUs into a national management program based on three steps. Firstly, the legislation must promote and pay for the conservation of the forest resources to the forest owners as this action will motivate the society to protect the GCUs against fires, illegal extraction, grazing, or changes in land use. Secondly, there must be education provided for the communities regarding banning the extraction of forest resources near and inside of GCUs, for example, wood, land, and resin. Thirdly, government institutions, universities, and research institutes must work together to develop a plan to establish the UCGs defined in this work, install common garden experiments in order to evaluate the future effects of climatic changes and analyze adaptation strategies, and promote the conservation ex situ of germplasm in seed banks, for example, in the National Center for Genetic Resources (CNRG by its Spanish acronym). This plan must be accompanied mainly by silvicultural guidelines, activities for the prevention and control of pests and diseases, use of local seed sources for stand renewal, and control of the germplasm movement.

5. Conclusions

In this study, 173 genetic conservation units were defined for 18 pine species from Mexico in their natural range of distribution and some actions determined for their conservation and sustainable use. *P. leiophylla*, *Pinus teocote*, *P. cembroides* (with two subspecies: *bicolor* and *cembroides*), *P. devoniana*, and *P. douglasiana* were the species with more genetic conservation units due to their broad distribution. These harbored similar or different genetic zones due to their adaptation to different ecological requirements (temperature, rainwater, soil). For the number of areas detected for genetic conservation units, half of them contain genetic information which was reported in journals, and almost 40% of them were proposed in protected areas based on our selection. We found that most of the forest reproductive material used currently is collected from seed stands, and the use of seeds from breeding trials is scarce. The genetic characterization of the target species has gaps in the genetic zones. Therefore, this demands, in the short term, future studies regarding those species most used in the forest industry, breeding programs, and restoration of degraded lands.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/d15060735/s1>, Table S1: climatic and edaphic patterns of target species [32,33] are cited here, Table S2: minimum requirements for genetic conservation units, Table S3: previous genetic studies or provenance or progeny trials reviewed [12,17,18,21–29,32,33,38–89] are cited here, Table S4: proposed conservation units for the target species, Table S5: inventoried trees by genetic zone and species, Table S6: genetic characterization by genetic zone and species, Table S7: germplasm production units by genetic zone and species, Table S8: germplasm orchards by genetic zone and species, Table S9: conservation units by genetic zone and species, Figure S1: Species distribution in Mexico using data from the NFLI.

Author Contributions: A.F. conceived and design the research; T.P.O. contributed materials; A.F. and E.B.R. analyzed the data; A.F., T.P.O., E.F.A. and J.M.-G. wrote the paper. All authors have read and agreed to the published version of the manuscript.

Funding: A.F. is supported by Project No 10283335082 (from National Institute for Forestry, Agriculture and Livestock Research) established in the frame of the research “Definition of areas for the conservation and use of forest genetic resources for species of the genus *Pinus*”. No other external funding was received.

Acknowledgments: The authors are grateful to the National Institute of Forestry, Agriculture, and Livestock Research of Mexico for funding all stages of this study through Project No 10283335082.

Conflicts of Interest: The authors declare no conflict of interest. The funding sponsor had no role in the design of the study; in the collection, analysis, or interpretation of data; in the writing of the manuscript, or in the decision to publish the results.

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