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Priorities for Conservation and Sustainable Use of Forest Genetic Resources in Four Mexican Pines

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Abstract: The strategies for the conservation and sustainable use of forest genetic resources, which are essential for the future adaptation of forest species to changing environments, are also a source of valuable genetic resources for breeding and restoration activities. The first step to define and implement cost-effective strategies is to identify specific priority populations. Mexico, in spite of being characterized by high levels of tree species diversity, mostly lacks a combined strategy for the genetic conservation and use of forest genetic resources. The aims of this work are: (i) to identify areas for gene conservation, and (ii) to propose measures for the conservation and sustainable use of forest genetic resources of four pine species: *Pinus greggii* Engelm. ex Parl., *Pinus oocarpa* Schiede ex Schltdl., *Pinus patula* Schiede ex Schltdl. & Cham. and *Pinus pseudostrobus* Lindl. To do that, we use the existing information on the distribution, genetic variation and conservation and breeding efforts in Mexico. Overall, 51 areas for establishing genetic conservation units were prioritized and 6 genetic zones for the use of forest genetic resources in breeding and selection of forest reproductive material were identified. The current conservation efforts for the four priority Mexican pines should be improved to satisfy the needs of a national breeding and conservation network.

Keywords: genetic diversity; genetic conservation units; forest management; *Pinus greggii*; *Pinus oocarpa*; *Pinus patula*; *Pinus pseudostrobus*

1. Introduction

Forests are essential for the maintenance of biological diversity in terrestrial ecosystems and provide a wide range of goods and services, including genetic resources that are not only indispensable now but also constitute a unique and irreplaceable reserve for the future. However, large perturbation events (e.g., climatic change) or activities from either outside of the forestry sector (e.g., industrial activities, land use changes, etc.) or inside of it (e.g., forest management, seed transfer, etc.) affect, or can affect in the near future, the genetic diversity of species and their distribution over space and

time. Therefore, actions have been requested at the global scale [1] for the conservation and sustainable use of forest genetic resources.

Forest tree species are long lived and widely distributed, with a typically low degree of domestication and remarkable phenotypic and genetic differences in important traits among populations, despite high levels of gene flow [2]. These differences are essential both for breeding, i.e., provenances or seed sources to be used for plantations [3], and for conservation programs whose main objective is intra-specific genetic diversity [4]. However, conservation and a sustainable use of forest genetic resources have not always been considered as part of the same strategy [5].

Genetic conservation priorities are based on the economic and environmental importance of a species, its ecological functions, or other features that contribute to its relevance and/or its level of risk [6]. Although genetic studies of forest tree species have increased enormously throughout this century [7], we still lack information for many of them, and decisions are mostly made in the absence of any genetic knowledge [8].

A “bioregion” approach has been extensively used when planning and implementing the marketing of genetic resources—deployment and procurement zones [9]—and conservation of genetic resources—genetic zones [10]. In the latter, environmental zones have been used as surrogates in different conservation programs [11,12], operating under the assumption that they are areas in which many tree species have a similar genetic background.

From a landscape-level perspective, breeding or planting activities may affect the conservation of genetic resources [13] either positively, by increasing population adaptability [14], or negatively, by favoring introgression with non-adapted materials or substitution with more productive materials [15]. Eventually, these actions can affect the functioning of the ecosystem, and make it unable to provide the environmental services of the original, now replaced ([16,17]). In contrast, an adequate conservation of existing resources can provide additional sources of diversity for future breeding programs.

Practical forestry experience suggests that a sound management of genetic resources must include conservation efforts based on two overlapping strategies: a management of natural forests that pays due respect to their genetic resources, and the establishment of networks of smaller gene-conservation areas [11].

Mexican pines are a good case study for prioritizing areas for both conservation and the sustainable use of genetic resources in the absence of complete genetic information. Mexico is one of the genus *Pinus* diversity centers, presenting 49 out of the 120 species of pines in the world [18], many of which are actively managed. Sixty percent of them are of commercial and industrial importance, providing timber, resin and pulp [19], but they also constitute a valuable source of genetic resources [20]. Despite the importance of Mexican forest trees and their genetic resources, genetic studies are rare, barely covering 1.2% of Mexican species, and 58% of those corresponding to *Pinus* [21]. The level of Mexican pine species’ genetic knowledge is, in most cases, clearly incomplete.

We have selected four species, *Pinus greggii* Engelm. ex Parl. (including var. *greggii* and var. *australis* Donahue & Lopez), *Pinus oocarpa* Schiede ex Schltdl., *Pinus patula* Schiede ex Schltdl. & Cham. (var. *patula* and var. *longipedunculata* Loock ex Martínez) and *P. pseudostrobus* Lindl. They present contrasting distribution ranges and levels of importance [22] for timber production [19], the sawmill industry and resin production [23], and they are also present in commercial plantations [24]. These species have been planted in different continents, e.g., *P. oocarpa* in Europe, Asia, Africa, America and Oceania, or *P. patula* in Africa [25,26]. These species are also considered highly valuable for ex situ gene conservation, i.e., gene conservation banks and genetic tests [20,25].

The aims of this work are: (i) to identify priority areas for gene conservation, and (ii) to propose measures for the conservation and sustainable use of *P. greggii*, *P. oocarpa*, *P. patula* and *P. pseudostrobus* genetic resources. Firstly, we identify the most relevant existing information related to the identification and characterization of their genetic resources. We use information concerning the distribution range of the species and the delimitation of germplasm transfer zones, the conservation of forest tree species

in protected areas and the sustainable use of forest genetic resources (germplasm production units, or populations used at different stages in breeding). We then check for gaps, taking into account the distribution area and the genetic zones of the species, and we prioritize areas to improve the status of conservation and sustainable use of forest genetic resources in the considered species.

2. Materials and Methods

2.1. Data Sources

Four Mexican pine species were selected for the study: *P. greggii* (var. *greggii* and var. *australis*), *P. oocarpa*, *P. patula* (var. *patula* and var. *longipedunculata*) and *P. pseudostrobus*. These species are distributed along different temperate mountain ranges (Figure 1) as pure and mixed coniferous forests and pine-oak forests, in a wide altitudinal range (600–3000 m a.s.l.) (Supplementary Materials Table S1).

We defined the native distribution range of the species using the National Forest and Land Inventory (NFLI, 2004 to 2007 [27]), which covers Mexico in a systematic stratified random sampling with a grid of 5 km (Figure 1). We removed those plots considered plantations [28], or of non-native origin (based on our own knowledge).

Figure 1. (a) Mexican territory with the five “sierras”. (b) Native distribution of *Pinus greggii* Engelm. ex Parl. (black dots), *P. oocarpa* Schiede ex Schltdl. (black crosses), *P. patula* Schiede ex Schltdl. & Cham. (unfilled diamonds) and *P. pseudostrobus* Lindl. (grey squares) in Mexico modified from the NFLI (see Material and Methods), and germplasm transfer zones (contour grey solid lines [29]). Striped germplasm transfer zones are indicative of the presence of at least one of the four pine species.

2.2. Genetic Zones

The existing genetic studies the four species (Supplementary Materials Figure S1, [30]) do not allow for a precise definition of genetic zones, so we have used the germplasm transfer zones (equivalent to seed zones) as a proxy. Seed zones are areas with similar ecological and climatic characteristics that harbor populations with relatively uniform genotypic or phenotypic characteristics [29,31–33]. Mexico has been divided into 41 germplasm transfer zones by the Mexican National Forest Commission (CONAFOR by its Spanish acronym) (Figure 1 and Supplementary Materials Table S2). The genetic zones for each of the four pines were obtained by overlapping their distribution and the germplasm transfer zones. Genetic zones with less than 20 trees for a given species according to the NFLI

were excluded from subsequent analysis, as it would be difficult to identify populations suited for conservation or seed collection.

2.3. Conservation Units

We considered a set of minimum requirements for defining Gene Conservation Units (GCU) (modified from [11] on Supplementary Materials Table S3) by taking into consideration population size, type of management, monitoring and ownership.

The objective was to select at least one genetic conservation unit per genetic zone and species, except in cases of fragmented distribution (e.g., high distance (>50 km) between population cores, or existing barriers to gene flow within the region), in which case one gene conservation unit was selected from each patch (or up to 3, depending on the genetic zone). The main criteria for the selection of GCU were: population size, genetic information availability, dynamic genetic conservation management, and public ownership. In all cases, we prioritized extensive and centered populations in the genetic zone or patch. Then, among all the populations included in a given genetic zone (or patch, in the case of the fragmented ones), we considered first those populations characterized in genetic studies and/or provenance or progeny trials. These populations have been chosen for germplasm collection by genetic experts and, therefore, are good candidates in terms of population size and representation within the area. When we did not manage to cover the required number of GCU, we chose populations among the areas protected for biodiversity conservation, as their type of management (i.e., dynamic genetic conservation) was compatible with the conservation objective for all types of protected areas established by the Mexican Commission for Biodiversity (CONABIO, information for 2016 available at <http://www.gob.mx/conabio>). If the needs for a given region were not yet fulfilled, we chose populations situated in private forests. The georeferenced information was mapped using Arc-GIS 10.5 [34].

2.4. Use of Genetics Resources

We measured the importance of a genetic zone for the use of genetic resources, based on the presence of germplasm production units (seed stands and seed orchards). We assumed that the investment in the establishment and maintenance of such production units is an indication of the species' economic relevance in the area. We also used information from the existing material in genetic trials, i.e., provenance and progeny tests, established by different institutions (Supplementary Materials Figure S1, [30]), as they provide information about populations identified for the selection of forest reproductive material with well-known genetic backgrounds. As these populations have been evaluated, different genetic information is available from papers and reports.

2.5. Importance of Genetic Zones for the Conservation and Sustainable Use of Forest Genetic Resources

Using the previous information, for each genetic zone of the three species studied we collected: 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 calculated the number of GCU (n_g).

The importance of the pine species for timber production was calculated using the official timber production [35] and plantation statistics [36] collected state by state, which did not include disaggregation by pine species. We made a proportional assignment to each genetic zone using as a basis the distribution of the four species and those harbored in genetic zones. A similar approach was followed for the plantation areas. We then estimated productivity and degradation areas based on the land zoning established by the National Forest Commission [37].

Based on this information, expert knowledge and the recommendations established by the papers or reports previously analyzed, we defined 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, with 4 being the highest priority.

As a final step we assessed the status of each species using indicators derived and adapted from the EUFORGEN program [38] (Table 1).

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

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

3. Results

3.1. Genetic Zones

Sixteen genetic zones, in which at least one of the four pine species was effectively present, were identified over the 41 seed zones: four zones included one species, seven included two species, three zones included three species and two included four species (Figure 2). *Pinus oocarpa* had the most widespread representation (15 genetic zones), followed by *P. pseudostrobus* (13 genetic zones). In contrast, *P. patula* (5 genetic zones) and *P. greggii* (2 genetic zones) had a more restricted distribution.

Figure 2. Conservation units proposed by genetic zones (striped polygons) for four Mexican pine species: *Pinus greggii* (black dots), *P. oocarpa* (black crosses), *P. patula* (unfilled diamonds) and *P. pseudostrobus* (grey squares).

3.2. Conservation Units

We identified a total of 51 areas for establishing GCUs for the target species (Figure 2 and Supplementary Materials Table S4): 16 for *P. pseudostrobus*, 23 for *P. oocarpa*, 8 for *P. patula* and 4 for *P. greggii*. In relation to the selection criteria, nearly 60% of the GCUs were chosen in areas with existing genetic information. In the absence of genetic information, the other 35% of the GCUs were located in protected areas situated in public lands, and 5% in private forests.

3.3. Use of Genetic Resources

Breeding and characterization efforts were quite different depending on the species and region (Table 2). Characterization (both molecular and in genetic trials) was limited to some of the areas, and differed among species. The efforts aiming at the use of forest reproductive material had been quite reduced. In all of the cases, the activities were of low intensity and mostly consisted of the selection of seed stands. All the species presented many gaps, with many regions lacking sources of identified forest reproductive material that could be considered local.

3.4. Efforts for Conservation and Use of Genetic Resources

The efforts for the conservation, characterization and use of forest genetic resources in the four Mexican pines, as quantified by 7 indicators (Table 3), were clearly insufficient. Most of the genetic zones still did not have enough data for the characterization of forest genetic resources or even seed production. *P. patula* was the only species that had seen seed orchards established ($I_6 > 0$). In terms of molecular characterization efforts, *P. oocarpa* and *P. greggii* had been the object of more efforts than *P. patula* or *P. pseudostrobus* (I_2). *P. greggii* and *P. patula* had seen more generalized provenance (I_3) and progeny (I_4) characterization efforts than the other species, with indicator values of 0 or near 0. Although *P. greggii* had more forest reproductive material production units than the rest the species, it covered just a few states and was meant to help timber production.

3.5. Prioritization of Regions for Conservation and Use of Genetic Resources in Mexico

It was possible to identify important regions for the use of genetic resources. The Jalisco and Oaxaca regions (X.1, XII.1, XII.2 and XII.4 and XII.5, respectively) were important in terms of forest productivity and pine wood production. Other genetic zones presented high forest productivity (III.2, III.3 and III.4), with a potentiality for land afforestation (III.2 and III.3). Afforestation or forest restoration were necessary also in V.3, X.3, XIV.1 and XV.1, and in more reduced areas of other mentioned genetic zones where soil degradation (III.2, V.3, XII.2 and XII.3) or severe erosion (XII.2, XII.3 and XII.4) could affect forest suitability.

Based on the available information, six genetic zones (V.3, X.2, X.3, XII.3, XII.4 and XII.5) were defined as the most suitable sources of germplasm for use in commercial plantations (Figure 3) for three of the pine species studied (the exception was *P. pseudostrobus*). These areas also presented the highest potential for conservation and breeding. Two of these zones were targeted for conservation and use of the four pines species (V.3 and X.3). 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 (see Table 4).

Table 2. Conservation efforts and use of genetic resources by genetic zone and species (PS: *P. pseudotsobus* Lindl., OC: *P. oocarpa* Schiede ex Schltdl., PA: *P. patula* Schiede ex Schltdl. & Cham., GR: *P. greggii* Engelm. ex Parl.).

Genetic Zone	Trees National Forest Inventory (n _i)				Molecular Characterization (n _{mk})				Seed Stands (n _{st})				Progeny Testing (n _{is})				Provenance Testing (n _{pt})				Seed Orchards (n _{so})			Gene Conservation Units (n _g)				
	PS	OC	PA	GR	PS	OC	PA	GR	PS	OC	PA	GR	PS	OC	PA	GR	PS	OC	PA	GR	PS	OC	PA	GR	PS	OC	PA	GR
III.2	55	587	-	-	0	1	-	-	0	0	-	-	0	0	-	-	0	0	-	-	0	0	-	-	1	1	-	-
III.3	199	593	-	-	0	1	-	-	0	1	-	-	0	0	-	-	0	0	-	-	0	0	-	-	1	2	-	-
III.4	-	1201	-	-	-	3	-	-	-	1	-	-	-	0	-	-	-	0	-	-	-	0	-	-	-	2	-	-
V.3	1136	56	538	308	0	2	3	19	1	0	0	0	0	0	0	0	0	5	22	0	0	0	0	2	1	2	3	
VIII.3	27	-	-	-	0	-	-	-	0	-	-	-	0	-	-	-	0	-	-	-	0	-	-	1	-	-	-	
X.1	61	699	-	-	0	1	-	-	0	0	-	-	0	0	-	-	0	0	-	-	0	0	-	-	1	2	-	-
X.2	777	581	126	-	2	8	0	-	2	1	0	-	13	0	0	-	0	5	0	-	0	5	0	-	1	1	0	-
X.3	1262	177	1028	23	4	2	1	0	8	0	5	0	0	0	36	120	0	0	4	2	0	0	1	0	2	1	2	1
XII.1	240	1222	-	-	0	1	-	-	0	0	-	-	0	0	-	-	0	0	-	-	0	0	-	-	1	2	-	-
XII.2	268	1503	-	-	1	1	-	-	1	2	-	-	0	0	-	-	0	0	-	-	0	0	-	-	1	2	-	-
XII.3	608	2650	81	-	1	2	1	-	0	2	0	-	0	0	0	-	0	0	-	0	0	0	0	-	1	2	1	-
XII.4	1944	1534	66	-	0	1	0	-	0	0	0	-	0	0	0	-	0	0	0	-	0	0	0	-	1	1	1	-
XII.5	1122	924	820	-	0	0	7	-	1	0	0	-	0	0	0	-	0	0	0	-	0	0	0	-	2	1	2	-
XIV.1	88	404	-	-	1	4	-	-	1	0	-	-	0	0	-	-	0	0	-	-	0	0	-	-	1	2	-	-
XIV.2	-	312	-	-	-	0	-	-	-	0	-	-	-	0	-	-	-	0	-	-	-	0	-	-	-	1	-	-
XV.1	-	1123	-	-	-	3	-	-	-	1	-	-	-	0	-	-	-	0	-	-	-	0	-	-	-	2	-	-
Total	7787	13566	2659	331	9	30	12	19	14	8	5	0	13	0	36	120	0	5	9	24	0	0	1	0	16	23	8	4

n_i: number of trees sampled by the NFLI, n_{mk}: number of populations per zone with molecular data, n_{st}: number of populations with seed stands, n_{is}: number of individuals selected for progeny testing, n_{pt}: number of populations present in provenance testing, n_{so}: number of seed orchards and n_g: number of gene conservation units proposed.

Table 3. Indicators for the target species.

	Indicator	<i>P. pseudostrobus</i>	<i>P. oocarpa</i>	<i>P. patula</i>	<i>P. greggii</i>
I1	Number genetic zones	13	15	6	2
I2	Molecular characterization effort	38.46	86.66	66.66	50.00
I3	Provenance characterization effort	0.00	6.66	33.33	100.00
I4	Progeny characterization effort	7.69	0.00	16.66	50.00
I3	Seed stands index	46.15	40.00	16.66	0.00
I6	Seed orchard index	0.00	0.00	16.66	0.00
I7	Genetic conservation index *	100.00	100.00	83.33	100.00

* Based on GCU's proposed for each species (see Table S4).

Figure 3. Populations and their genetic zones (striped polygons) considered as the most suitable source for providing forest reproductive material. *Pinus greggii* (black dots), *P. oocarpa* (black crosses) and *P. patula* (black diamonds).

Table 4. Importance for conservation and use of forest genetic resources by genetic zone and species (PS: *P. pseudostrobus*, OC: *P. oocarpa*, PA: *P. patula*, GR: *P. greggii*).

Genetic Zone	Presence of the Pine Species	Value for Conservation (1 to 4)				Value for Breeding (1 to 4)			
		PS	OC	PA	GR	PS	OC	PA	GR
III.2	50	4	2	-	-	1	2	-	-
III.3	88	3	2	-	-	2	2	-	-
III.4	137	-	2	-	-	-	3	-	-
V.3	143	1	4	4	4	3	1	4	4
VIII.3	2	4	-	-	-	1	-	-	-
X.1	66	3	2	-	-	1	2	-	-
X.2	66	2	4	2	-	3	4	2	-
X.3	144	1	4	4	4	3	1	4	4
XII.1	93	3	2	-	-	2	3	-	-
XII.2	114	3	2	-	-	2	3	-	-
XII.3	300	2	2	4	-	2	3	4	-
XII.4	213	1	2	4	-	3	3	4	-
XII.5	188	1	2	4	-	3	3	4	-
XIV.1	60	4	3	-	-	1	2	-	-
XIV.2	18	-	3	-	-	-	2	-	-
XV.1	109	-	2	-	-	-	3	-	-

4. Discussion

We have identified some priority zones in order to help advance conservation efforts and the use of forest genetic resources in four Mexican pine species. Using forest germplasm transfer zones, defined by [29] as a proxy for genetic zones, we identified 51 areas for delimiting conservation units into 16 genetic zones. Also, based on the existing data, we considered that six of the genetic zones could be the most suitable sources of forest reproductive material to use in these species' afforestation, restoration or replanting actions.

One of our main targets was to integrate conservation and sustainable use of forest resources in Mexican forest management. As of the time of this paper, Mexico's main national conservation program (defined as CONABIO) [39] does not include forest tree species, which is one of the main limitations curtailing the implementation of any long-term activities in the region. The promotion of conservation areas [40,41] is further justified by the prediction, by 2050, of important species area reductions (50.4% for *P. oocarpa*, 23.4% for *P. patula* and 12.8% for *P. pseudostrobus*) [39]. However, neither the governmental authorities nor the nongovernmental agencies have set in situ conservation actions ex professo to face the projected climatic change impacts. Our proposal for the conservation of genetic resources is the establishment in the region of an efficient network in terms of number of units and coverage.

This proposal, as it consists mainly of conservation units located in public lands, could benefit from a cooperation between community groups and the state and federal governments aimed at overcoming one of the main problems of conservation, i.e., its perception, in some cases, by rural societies as an unfair governmental imposition, resulting in frequent changes in land use and forest deterioration [42].

Our definition of genetic zones based on germplasm transfer zones is conservative in the sense that populations in the same region that might differ genetically have not been included. For neutral or nearly neutral markers, most Mexican pine species, as most of the species in the genus, present high levels of genetic diversity and relatively low genetic differentiation among populations [21]. Exceptions such as *P. greggii* [43,44], which present low levels of diversity, are also compatible with our definition of genetic zones. For adaptive traits, e.g., growth potential and frost resistance, *P. oocarpa* shows high genetic diversity [21]. Most of the studied Mexican conifer species have shown high genetic differentiation among populations along altitudinal gradients, such as *Pinus oocarpa* [45–50].

Also, there are significant differences among close populations for *P. greggii* [24,51], *P. oocarpa*, *P. patula* and *P. pseudostrobus* [52]. Therefore, transferring germplasm need to consider the patterning of genetic differentiation among populations for adaptive quantitative traits.

Protected areas alone do not fulfill all specific requirements for the conservation of forest genetic resources [53]. We have also relied on existing information to identify priority areas for the selection of GCUs. These areas can be affected by illegal extraction of various forest products (e.g., logging or conversion of forest timber into charcoal [54]), or other factors that impede genetic conservation in the long term. The management plan of the areas should include [55]: (a) an explicit objective for genetic resource maintenance; (b) an estimation of population size and demography; (c) a protocol for providing information on and access to the genetic resources and, finally, (d) a monitor for the conservation status of the populations [56], as part of a national genetic resources information system.

On the present papery, we have not considered ex situ conservation measures, which are nonetheless important in the context of climate change [57–59]. That would take the form of selecting sites that could in the future potentially become similar to the contemporary climatic habitat of the priority species and, therefore, serve as germplasm sources under the projected future (likely warmer and drier) climate.

Indicators for the use of forest reproductive material show that most of the activities should be based on low-input strategies, disregarding the economic importance of the species [60], and not on intensive (and costly) breeding programs that cover only some species [20]. These strategies could be applied in a small number of regions and would allow for the production of local genetic resources for use in forest management activities. These activities are also compatible with in situ conservation. These low-input activities would benefit the local communities, who are the main stakeholders [61]. Most of the forested land in Mexico (75%) is under collective tenure, and more than 50% of all collective holdings are forest communities [42], which are able to implement low-cost breeding and conservation activities.

The quality of forest reproductive material used in plantations can be improved by setting specific objectives in breeding activities, especially to reduce seedling mortality (at present 14% caused by frost damage and 66% by drought [58,62]), to improve origin identification (33% of the current seeds are from an unknown origin [62]) and intraspecific taxa identification (e.g., *P. pseudostrobus* [63]) and to improve adaptation to local environmental and climatic conditions [64].

5. Conclusions

We have identified genetic zones and areas for delimiting GCUs in four important Mexican pine species, and defined different actions for their conservation and sustainable use in the country. The number of areas proposed was different among species and relied on the minimum requirements that must be followed for conservation. Seed procurement zones were the hub of our conservation proposal in order to ensure known genotypic or phenotypic characteristics for the conservations units. Further genetic studies on the species would be necessary to continue advancing in the conservation and use of genetic resources in the long term. We found that the efforts to use forest reproductive material are limited and mainly focused on forest germplasm production units (seed stands and seed areas). Actions must be initiated to improve the use and conservation of genetic resources, mainly in order to address the challenges imposed by the current climatic changes and the pressure for change in land use for agriculture, grazing and urban development.

Supplementary Materials: The following are available online at <http://www.mdpi.com/1999-4907/10/8/675/s1>, Figure S1: Location of populations selected for genetic diversity (triangles), provenance tests (stars) and progeny tests (circles), and location of tests sites for provenances (big circle with filled star inside) and progenies (big circle with filled star inside) for the four selected pines, Table S1: General climatic and edaphic patterns of target species, Table S2: Physiographic Provinces (PS) and Germplasm Transfer Zones (GTZ), Table S3: Minimum requirements for genetic conservation units, Table S4: Proposed Conservation Units for *P. greggii*, *P. oocarpa*, *P. patula* and *P. pseudostrobus*. References List Online Supplementary Materials.

Author Contributions: A.F., R.A. and J.M.G.d.B.: conceived and design the research; J.L.-U.: contributed materials; A.F., J.M.G.d.B., C.D.R.-S. and A.E.O. analyzed the data; A.F., R.A., J.M.G.d.B. and C.S.-R.: wrote the paper; C.S.-R.: provided meaningful guidance during the development of the study.

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