

Chapter 2

Genetic Diversity and Conservation of Mexican Forest Trees

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Abstract Over the last 200 years, humans have impacted the genetic diversity of forest trees. Because of widespread deforestation and over-exploitation, about 9000 tree species are listed worldwide as threatened with extinction, including more than half of the ~600 known conifer taxa. A comprehensive review of the floristic-taxonomic literature compiled a list of 4331 recorded tree species in Mexico. The highest diversity of pine and oak worldwide is located in the Mexican temperate forests. Because species and genetic diversity are often positively associated, a very high trans-specific genetic diversity in Mexican tree species is thus expected. Contrasting with its high species and genus richness, studies of genetic diversity in Mexican forest trees are rather scarce, and often biased to particular families, like the Pinaceae. Moreover, even within those particular families the available surveys have a penchant for specific genus. The markers used in most of

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these studies include the traditional and “universal” isozymes and chloroplast microsatellites and, to a lesser extent, the anonymous SSRs, AFLPs, and RAPDs. More studies on more varied taxa and using more advanced technologies and markers seem thus necessary. Because of the poor comparability of the genetic diversity estimates among the studied Mexican tree species, it is extremely difficult to discern general trends across species or regions. We thus recommend that genetic diversity should be measured across species with an identical type of genetic marker, by surveying similar numbers of loci, individuals and populations, and using identical indices of genetic diversity, relevant to conservation of trees.

Keywords Tree species diversity • Trans-specific genetic diversity
Species distribution • in situ • ex situ conservation • Genetic erosion
Neotropical species

2.1 Introduction: The Importance of Genetic Diversity

Biodiversity or “biological diversity” can be defined as the variety and variability among living organisms and the ecological complexes in which they occur. It can be subdivided in four hierarchical categories of biological organization: regional landscape, community-ecosystem, population-species, and genetic (Noss 1990). In this context, genetic diversity is the foundation of all diversity levels (Frankham et al. 2010), as it is directly related to the adaptability of biological systems (Gregorius 2001). For instance, in the short term it is vital for increasing population fitness by reducing inbreeding depression in the short term, and, in the longer term, to develop new local adaptations in response to environmental changes (Reed and Frankham 2003; Kremer et al. 2012).

Genetic diversity also affects ecological processes such as primary productivity, population recovery from disturbances, interspecific competition, community structure, and fluxes of energy and nutrients. Thus, genetic diversity is an important factor for the populations, communities, and ecosystems health, whose effects on long-term evolution capability are comparable in magnitude to those of species diversity. Genetic diversity should have the most ecological impact on the four non-exclusive conditions: (1) when one or a few main habitat-providing species dominate a community or ecosystem (like in forests or coral reef ecosystems), (2) when the abundance or distribution of a keystone species is controlled by genetic diversity in other species (like in host parasite interactions), (3) when keystone species show measurable genetic diversity within populations for important traits, and/or (4) when species evolve in highly variable environments or in those subjected to rapid anthropogenic change (Hughes et al. 2008).

The level of genetic diversity in natural populations is influenced by evolutionary forces such as mutation, genetic drift, natural selection, and gene flow/migration (Futuyma 2013), along with other factors including the type of mating system (Schoen and Brown 1991), population size (Frankham 1996),

inbreeding, spatial distribution, social organization, and behavior traits (Amos et al. 1998). For instance in plants, Hamrick et al. (1992) reported in a meta-analysis of 322 woody taxa that genetic diversity within species was higher within populations than among populations, and that genetic diversity was higher in outcrossers and in species with large geographic ranges or that were wind pollinated or dispersed than in inbreeders or in taxa with restricted distributions or that were pollinated/dispersed by animal vectors. They also found that differences in life history and ecological traits among species explained a significant proportion of their genetic diversity (for the genetic parameters measured), the specific evolutionary history of each species has a major role in determining the level and distribution of genetic diversity (i.e., the genetic structure).

Due to the importance of genetic diversity for the successful conservation of long-lived species, like most forest trees (Kahilainen et al. 2014), and for the long-term maintenance of all other forms of diversity (Riggs 1990), Brown et al. (1997) proposed seven indicators to monitor natural genetic diversity in carefully selected indicative taxa: (1) the number of sub-specific taxa; (2) population size, number, and physical location; (3) the environmental amplitude of each population; (4) genetic diversity at marker loci within individuals and populations; (5) quantitative genetic variation; (6) interpopulation genetic structure; and (7) mating system.

2.2 Genetic Diversity and Conservation of Tree Species

Over the last 200 years, humans have impacted the genetic diversity of forest trees by converting their original habitats for agricultural and urban uses, changing the demographic structure of forests (for instance, by forest management practices), fragmenting wildlands, exploiting species (e.g., timber exploitation), introducing exotic competitors and pests, degrading the environment with soil and atmospheric contaminants, and/or domesticating favored species (Ledig 1992).

Because of widespread deforestation and over-exploitation, about 9000 tree species are listed worldwide as threatened with extinction, including more than half of the ~600 known conifer taxa (Newton et al. 1999). Thus, efforts to conserve and manage tree species have been increasing around the world since the late 80s (Farnsworth and Sahotra 2007). Such conservation activities have encouraged studies of within-species genetic variation and distribution to enrich current conservation strategies (Newton et al. 1999). Indeed, such surveys can help designing evolutionarily significant units (ESU) or management units (MU) through the identification of unique and worth-conserving populations and/or hotspots of genetic diversity, while phylogeographic or genomic studies aiming to pinpoint adaptive variation should contribute to the development of new strategies and objectives for conservation (Bowen 1999; Newton et al. 1999). Analyses with molecular markers in tree species have, for example, demonstrated a far higher genetic differentiation between populations than initially shown by isozymes (Newton et al. 1999), while the distribution of cytoplasmic

(both chloroplast and mitochondrial) lineages has allowed the identification of refugial areas and potential postglacial migration paths (e.g., Soltis et al. 2007; Jaramillo-Correa et al. 2009). Refugia are of particular importance for conservation because they often shelter higher genetic diversity than newly colonized areas (Newton et al. 1999). However, despite its importance for the long-term viability and the evolutionary potential of tree species and functioning of ecosystems, the genetic diversity of populations is seldom given explicit consideration in conservation programs (Mace and Purvis 2008; Walpole et al. 2009; GEO BON 2011; Kahilainen et al. 2014).

Because genetic diversity is found at various levels of organization, from the ecosystem, through species, and their provenances and family groups, to individual genotypes and alleles at the molecular level, it is essential that all levels are considered in conservation activities (Namkoong 1990). Moreover, the functioning of the ecosystem and methods for the conservation of genetic variation of individual species are dependent on the organization and structure of genetic diversity at each level (Riggs 1990). In this sense, and whenever it is applicable, *in situ* methods (conservation of genetic resources in natural populations) should be preferred to the *ex situ* strategies, such as conservation in botanical gardens, test plantations, seed orchards, clone banks, or tissue cultures. Indeed, *in situ* programs provide the opportunity for not only preserving individuals or species but also ongoing evolutionary processes, like gene flow or the fixation of new variants through local adaptation (Frankel 1981).

Some of the major problems of *ex situ* activities include the lack of long-term and continuous funding, which can affect the success of the conservation programs, or cause adverse changes in the preserved materials, which can compromise the species survival or regeneration. Some *ex situ* options, such as botanical gardens and arboreta, which are very common, only harbor a few specimens per taxa, which lead to conserve a low percentage of the genetic diversity of each species. Provenance trials, which compare offspring performance from a range of populations of the same species, maintain a broader genetic base than arboreta, but are generally restricted to commercial or potentially commercial taxa, and have a limited lifetime that rarely exceeds 50–100 years. Moreover, these tests are usually not self-perpetuating and occur in alien environments for most of the populations included. Seed orchards are generally established for commercial seed production of important timber species, and often use grafted clones, which can be easily replaced at a short-time period by the next generation of breeding (approx. 20 years). Thus, they usually bear a subset of the total genetic variation of a species, with an important bias for genotypes with desired commercial traits (wood quality, fast growth, pest resistance, etc.). Clone banks, on the other hand, have a broader genetic base and a longer lifespan than seed orchards, but they are commonly established with grafted clones, which also diminish their capacity for preserving an adequate percentage of genetic diversity. Seed banks are an obvious way to preserve genetic diversity, but not all seeds from all species can be stored under current storage conditions (i.e. low light and temperature) and germination rates tend to decline with time. Finally, tissue cultures might be of limited use given that

mutations can accumulate at faster rates in disorganized tissues and because not all genotypes are prone to form somatic embryos or regenerate whole plants from cultured tissues (Ledig 1988).

Despite its limitations, *ex situ* conservation becomes especially important due to climatic change. The progressive decoupling between natural forest tree populations and the site where the climate for which they have evolved and adapted will occur, possess an immense challenge (Tchevakova et al. 2005; Sáenz-Romero et al. 2010). It is necessary to conduct an *ex situ* conservation program that includes the realignment of the natural populations to their suitable climate, by planting individuals in advance to the sites where their corresponding suitable climatic habitat will occur in the future. This has been named assisted migration (Ledig et al. 2010; Ledig 2012; Rehfeldt et al. 2014).

Conservation of genetic diversity in tree species is also essential for the sustainable and productive management of the forest ecosystems in which they occur. Indeed, it can be seen as one of the services of natural forests under multiple-use management. Thus, the reconcilability of economic and genetic conservation objectives may be easier to realize if appropriate levels of sustainable timber production are included as management objectives (<http://www.fao.org/docrep/006/t0743e/T0743E02.htm>).

2.3 Mexican Forests and Their Genetic and Species Richness of Vascular Plants and Tree Species

The total Mexican land area is ~196.7 million ha and about 72% consists of woodland (<http://www.fao.org/docrep/meeting/x4702e.htm>). SEMARNAP-UACH (1999) reported that the Mexican forests (excluding bushlands and grasslands) cover up to 55.3 million ha, including 0.721 million ha of mangroves and 0.163 million ha of gallery (riverine) forest. According to Palacio-Prieto et al. (2000), the main vegetation types in Mexico are temperate forests (which include the montane cloud, pine, and oak forests) that cover about 32 million hectares (ha), the tropical dry forests (encompassing both thorn and tropical deciduous forests) with 16.9 million ha, the tropical humid forests (including tropical rain, sub-evergreen tropical, and semi-deciduous tropical forests) that spread over 14 million ha, and the xeric shrublands with some 55.4 million ha.

Mexico is considered one of the countries with the largest diversity of plants worldwide (WCMC 1992; Mittermeier and Goettsch 1992). Although a complete inventory of its flora is still lacking, estimates range between 18,000 and 30,000 species, with more than 50% of them being restricted to its national territory (Rzedowski 1991a, b; Villaseñor 2003). An updated account of the generic richness of Mexican vascular plants found 2804 native genera, distributed in 304 families (Villaseñor 2004). Subsequently, Villaseñor and Ibarra-Manríquez in Cué-Bär et al. (2006) reported that at least 3639 species of Mexican native flora are angiosperm

trees, which are grouped in 728 genera and 128 families. Families notable for their species richness include Fagaceae (270 species), Mimosaceae (268 species), and Fabaceae (205 species). However, some of them might be even richer. For instance, Sousa et al. (2001, 2003) found 623 tree species of the Fabaceae (Leguminosae) in Mexico. These authors also indicated that endemism at the generic level was marginal (3%), contrasting with at the species level (42.1%). However, a comprehensive review by Villaseñor (2013) of the floristic-taxonomic literature of Mexico compiled a list of 4331 recorded tree species. The highest diversity of pine and oak worldwide with 55 and 161 species, respectively, is located in the Mexican temperate forests (Galicia et al. 2015). This floristic richness is mainly caused by a wide range of climatic conditions, the numerous isolated mountains and mountain ranges, and large arid and semiarid expanses (Rzedowski 1994).

Figures 2.1 and 2.2 show that the tree species and genus richness in Mexico are not equally distributed and are principally functions of climate variables such as minimum temperature of coldest month, precipitation of driest month, and precipitation seasonality. The highest tree species and genus richness occur in the tropical rain forests of the states of Quintana Roo, Veracruz, and Chiapas, and the lowest in the Chihuahuan desert. Because species and genetic diversity are often positively associated (Bergmann et al. 2013; Kahilainen et al. 2014), a distribution of transspecific genetic diversity (Gregorius 2003; Wehenkel et al. 2006) similar to the Mexican tree species diversity shown in Fig. 2.1 is expected.

2.4 Studies About Genetic Diversity in Mexican Forest Trees

Studies of genetic diversity in Mexican forest tree are rare in proportion to the large species diversity in this country. To date (by 2015), the genetic variation has been studied in about only five tree families, ten genera and 52 species (mostly endemic). This represents only 1.2% of all Mexican tree species. Of these species, 58% belong to the genus *Pinus*, 15% to *Quercus*, 10% to *Abies*, and 6% to *Picea*. Thus, most of the information (80%) concerning the genetic diversity of Mexican trees comes from a single family of conifers (Pinaceae) that includes only 2% of all Mexican tree taxa. Moreover, from the studied tree species, approximately 38% are listed as endangered or vulnerable in the Red List of the International Union for Conservation of Nature and Natural Resources (IUCN 2013; Farjon et al. 2017), which indicates that, with the exception of a few species of *Pinus* and *Quercus*, there is virtually no genetic information available to design management plans for most tree taxa native to Mexico. Indeed, genetic diversity has been mostly assessed either in endemic species with narrow or discontinuous distribution, species facing fragmentation, habitat loss or other human-related threats, species with unique habitat or controversial taxonomic status, and only in a few commercially valuable,

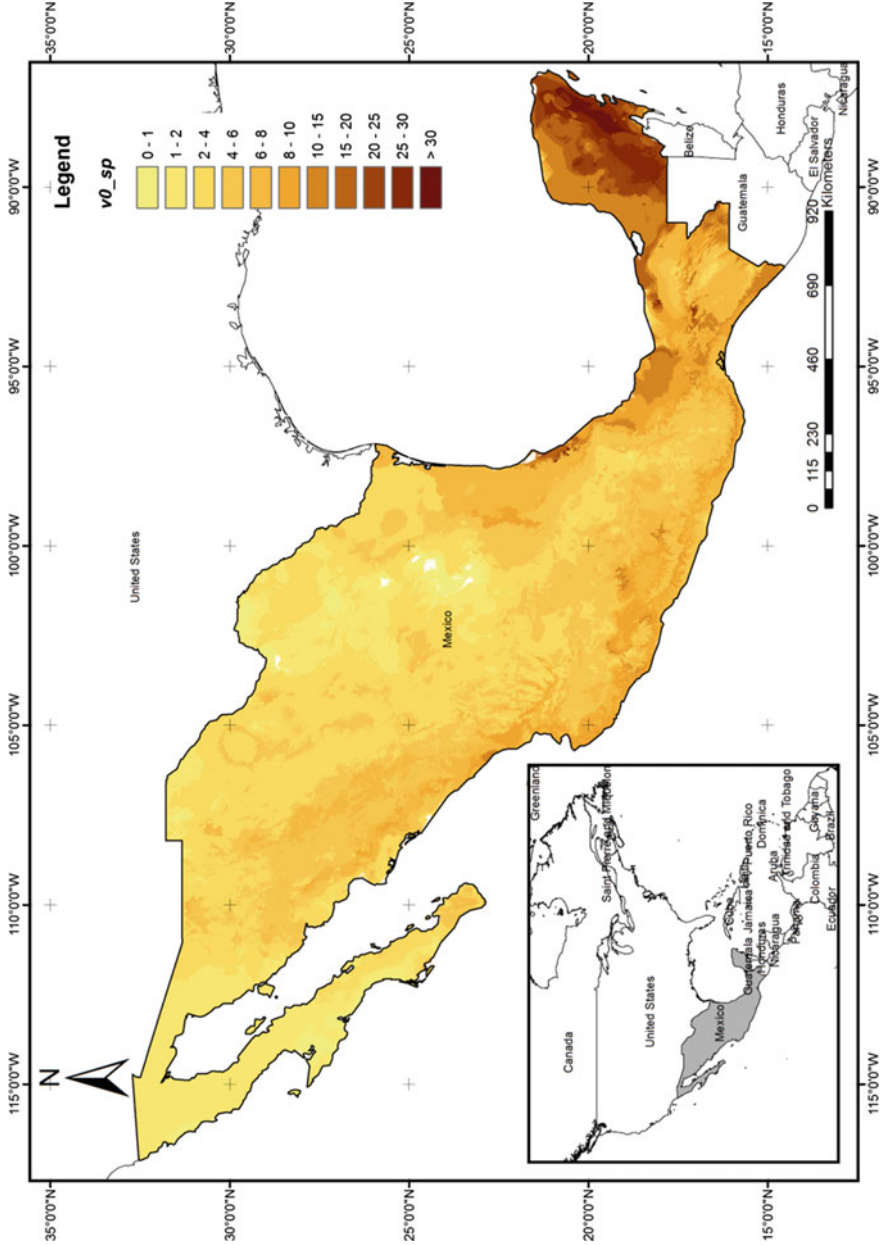


Fig. 2.1 Map of the tree species richness (v_{0_sp}) (in 1600 m²) in Mexico predicted by minimum temperature of coldest month, precipitation of driest month, and precipitation seasonality ($R^2 = 0.59$, standard error = 5.68). Yellow colors indicate lower richness, brown colors highest richness

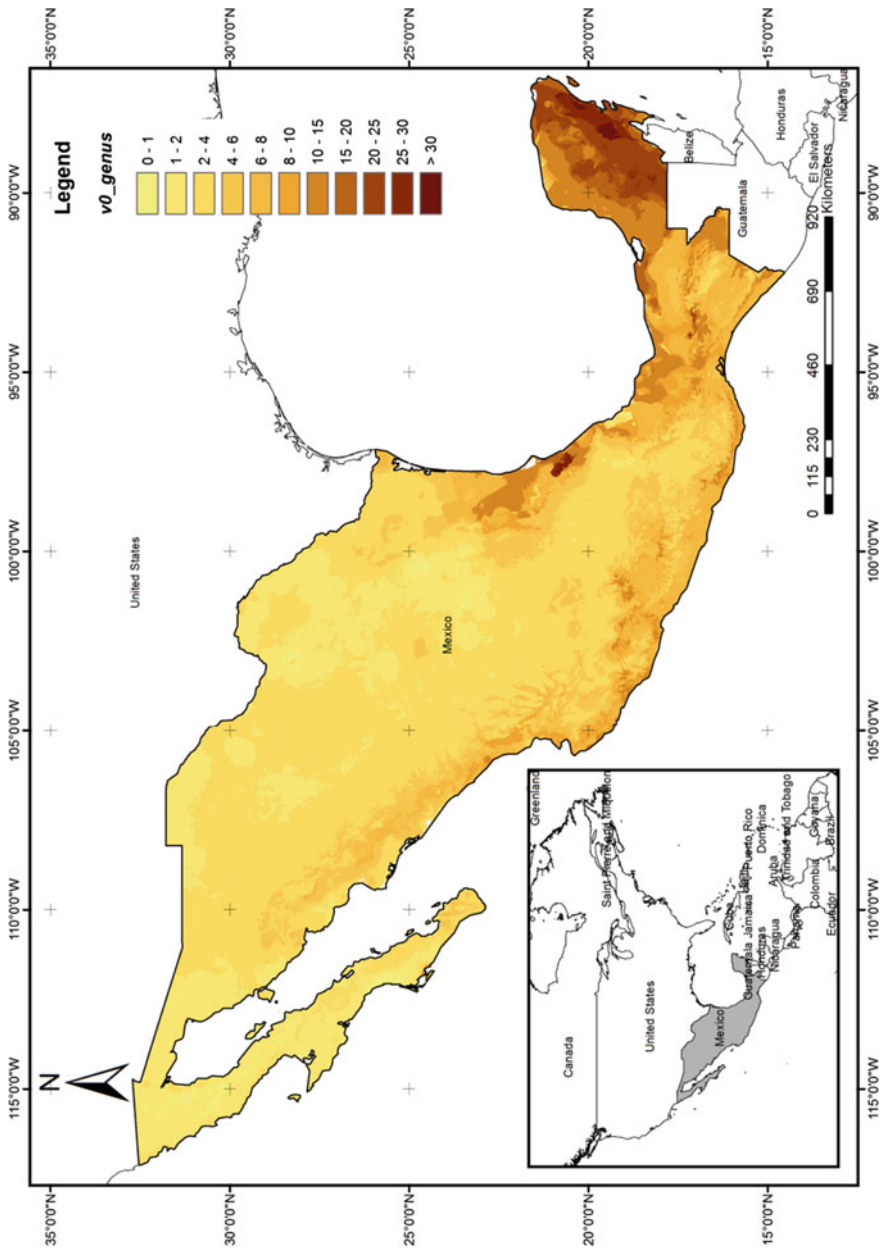


Fig. 2.2 Map of the tree genus richness (v_{0_genus}) (in 1600 m²) in Mexico predicted by minimum temperature of coldest month, precipitation of driest month, and precipitation seasonality ($R^2 = 0.64$, standard error = 4.99). Yellow colors indicate lower richness, brown colors highest richness

wide-ranging timber species, such as those belonging to the genus *Pinus* and *Quercus* (Farjon and Styles 1997; Galicia et al. 2015).

Different molecular marker and isozymes have been traditionally used (Tables 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, and 2.9), including simple sequence repeats or microsatellites (SSR), chloroplast microsatellites (cpSSR), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLP), polymerase chain reaction-restriction fragment length polymorphisms (PCR-RFLP), and sequence variation in both mitochondrial DNA (mtDNA), and chloroplast DNA (cpDNA) regions. Different genetic diversity parameters have been usually calculated, such as the expected heterozygosity (H_e), the percentage of polymorphic loci (% P), the Shannon diversity index (S), the total haplotype diversity (H), the nucleotide diversity (π), the observed degrees of Gregorius' total differentiation (δ_T), and mean genetic diversity ($v_{mean,2}$) among many others (see references in the tables for details). However, given that different genetic markers, laboratories, numbers of loci, individuals, populations, and indices of genetic diversity have been reported, an accurate comparison of the genetic diversity between the studied Mexican tree species is difficult, although most of the general trends are summarized below for particular tree families (Tables 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, 2.7, 2.8, and 2.9).

2.4.1 Family Pinaceae

Genetic diversity studies in the family Pinaceae have centered on the genus *Pinus*, although some individual reports in *Abies*, *Picea*, and *Pseudotsuga* have also been performed (Tables 2.1, 2.2, 2.3, 2.4, 2.5, 2.6, and 2.7).

2.4.1.1 Genus *Pinus*

Pinus is particularly relevant because more than half of the species of this genus occur naturally in Mexico, most of which are endemic, thus making of Mexico one of its main centers of pine diversity (Piñero et al. 2008). Only 14% of pine species studied at genetic level so far is listed as endangered in the Red List of the IUCN. Tables 2.1, 2.2, 2.3, and 2.4 show summary statistics of genetic diversity estimated with molecular markers for different Mexican species of *Pinus*. The majority of the studies were performed using isoenzymes, while the least used type molecular markers to determine the genetic variation in this genus was the RAPD; only two species include this type of marker: *Pinus chiapensis* and *Pinus culminicola* (Newton et al. 2002; Favela-Lara 2010).

On average the expected heterozygosity (H_e) for *Pinus* populations equals 0.21 using isozyme and 0.60 with microsatellite (SSR). While the average genetic diversity assessed by AFLP markers is $d_g = 1.40$. The estimated diversity for the Mexican species of *Pinus* is comparable to that of their European counterparts

Table 2.1 Genetic diversity obtained in Mexican species of *Pinus* using isoenzymes

Genus <i>Pinus</i> Isozymes									
Species	MM	P	I	L	Genetic diversity			Conservation status (IUCN 2013)	References
					He	% P	S		
<i>Pinus cembroides</i> (<i>lagunae</i>)	Iso	4	140	14	0.386	81.6	—	LC	Molina-Freaner et al. (2001)
<i>Pinus coulteri</i>	Iso	1	35	13	0.193	48.5	—	NT	Ledig (2000)
<i>Pinus greggii</i>	Iso	19	366	15	0.123	31.9	—	VU	Parraguire-Lezama et al. (2002)
<i>Pinus hartwegii</i>	Iso	4	107	12	0.120	—	—	LC	Viveros-Viveros et al. (2010)
<i>Pinus johannis</i>	Iso	4	130	16	0.245	88.0	—	LC	García-Gómez et al. (2014)
<i>Pinus maximartinezii</i>	Iso	1	100	26	0.122	30.3	—	EN	Ledig et al. (1999)
<i>Pinus muricata</i>	Iso	3	66	33	0.346	87.7	—	VU	Molina-Freaner et al. 2001; Sáenz-Romero and Tapia-Olivares (2003)
<i>Pinus oocarpa</i>	Iso	5	49	12	0.102	—	—	LC	Sáenz-Romero and Tapia-Olivares (2003)
<i>Pinus pinceana</i>	Iso	8	132	27	0.174	—	—	LC	Ledig et al. (2001)
<i>Pinus pinceana</i>	Iso	5	114	13	0.374	96.9	—	LC	Molina-Freaner et al. (2001)
<i>Pinus pseudostrobus</i>	Iso	8	80	14	0.100	78.6	0.22	LC	Viveros-Viveros et al. (2014)
<i>Pinus rzedowskii</i>	Iso	9	295	14	0.219	46.8	—	VU	Delgado et al. (1999)

MM molecular marker, Iso isozymes, P number of populations, I number of individuals included per populations, L number of loci, H_e expected heterozygosity, % P percent polymorphic loci, S Shannon diversity index, IUCN Union for Conservation of Nature and Natural Resources, LC least concern, EN endangered, VU vulnerable, NT near threatened

Table 2.2 Genetic diversity obtained in Mexican species of *Pinus* using cpSSR

Genus <i>Pinus</i> cpSSR									
Species	MM	PP	P	I	L	Genetic diversity		Conservation status (IUCN 2013)	References
						H	H _e SEQ		
<i>Pinus pseudostrobus</i>	cpSSR	6	3	48	6	0.972	—	LC	Delgado et al. (2007)
<i>Pinus ayacahuite</i>	cpSSR	12	7	75	12	—	0.510	LC	Moreno-Letelier and Piñero (2009)
<i>Pinus leiophylla</i> var. <i>chihuahuana</i>	cpSSR	6	9	101	6	0.511	—	LC	Rodríguez-Banderas et al. (2009)
<i>Pinus leiophylla</i> var. <i>leiophylla</i>	cpSSR	6	15	222	6	0.869	—	LC	Rodríguez-Banderas et al. (2009)
<i>Pinus montezumae</i>	cpSSR	6	4	93	6	0.858	—	LC	Delgado et al. (2007)
<i>Pinus nelsonii</i>	cpSSR	11	9	232	11	0.648	—	EN	Cuenca et al. (2003)
<i>Pinus strobiformis</i>	cpSSR	12	17	312	12	—	0.661	LC	Moreno-Letelier and Piñero (2009)

cpSSR chloroplast microsatellite, MM molecular marker, PP number of primer-pair combinations, P number of populations, I number of individuals included per populations, L number of loci, H_e expected heterozygosity, H_eSEQ genetic diversity of data corrected for molecularly accessible size homoplasy, IUCN Union for Conservation of Nature and Natural Resources, LC least concern, EN endangered

Table 2.3 Genetic diversity obtained in Mexican species of *Pinus* using SSR

Genus <i>Pinus</i> SSR									
Species	MM	PP	P	I	L	H _e	Conservation status (IUCN 2013)	References	
<i>Pinus ayacahuite</i>	SSR	5	—	—	5	0.654	LC	Villalobos-Arámbula et al. (2014)	
<i>Pinus ayacahuite</i> var. <i>veitchii</i>	SSR	4	—	—	4	0.810	LC	Villalobos-Arámbula et al. (2014)	
<i>Pinus chiapensis</i>	SSR	5	—	—	5	0.659	EN	Villalobos-Arámbula et al. (2014)	
<i>Pinus montezumae</i>	SSR	5	1	27	5	0.274	LC	Delgado et al. (2013)	
<i>Pinus oocarpa</i>	SSR	11	27	266	11	0.630	LC	Dvorak et al. (2009)	
<i>Pinus patula</i>	SSR	3	6	108	3	0.802	LC	Alfonso-Corrado et al. (2014a)	
<i>Pinus patula</i>	SSR	11	6	60	11	0.559	LC	Dvorak et al. (2009)	
<i>Pinus pseudostrobus</i>	SSR	5	1	37	5	0.277	LC	Delgado et al. (2013)	
<i>Pinus radiata</i>	SSR	19	2	62	19	0.685	EN	Karhu et al. (2006)	
<i>Pinus strobiformis</i>	SSR	5	—	—	4	0.654	LC	Villalobos-Arámbula et al. (2014)	

SSR simple sequence repeat microsatellite, MM molecular marker, PP number of primer-pair combinations, P number of populations, I number of individuals included per populations, L number of loci, H_e expected heterozygosity, IUCN Union for Conservation of Nature and Natural Resources, LC least concern, EN endangered

Table 2.4 Genetic diversity obtained in Mexican species of *Pinus* using AFLP and RAPD

Genus <i>Pinus</i> AFLP & RAPD											
Species	MM	PP	P	I	L	Genetic diversity			Conservation status (IUCN 2013)	References	
						% P	S	d_g $v_{mean,2}$			
<i>Pinus arizonica</i>	AFLP	1	8	280	319	—	—	1.36	—	LC	Wehenkel et al. (2015)
<i>Pinus cembroides</i>	AFLP	1	3	105	319	—	—	1.50	—	LC	Wehenkel et al. (2015)
<i>Pinus cooperi</i>	AFLP	1	5	35	319	—	—	1.37	—	VU	Wehenkel et al. (2015)
<i>Pinus discolor</i>	AFLP	1	1	175	319	—	—	1.54	—	NA	Wehenkel et al. (2015)
<i>Pinus durangensis</i>	AFLP	1	5	315	319	—	—	1.36	—	NT	Wehenkel et al. (2015)
<i>Pinus engelmannii</i>	AFLP	1	9	105	319	—	—	1.37	—	LC	Wehenkel et al. (2015)
<i>Pinus herrerae</i>	AFLP	1	3	315	319	—	—	1.37	—	LC	Wehenkel et al. (2015)
<i>Pinus leiophylla</i>	AFLP	1	9	175	319	—	—	1.38	—	LC	Wehenkel et al. (2015)
<i>Pinus lumholtzii</i>	AFLP	1	5	70	319	—	—	1.36	—	NT	Wehenkel et al. (2015)
<i>Pinus oocarpa</i>	AFLP	1	2	37	319	—	—	1.47	—	LC	Wehenkel et al. (2015)
<i>Pinus strobiformis</i>	AFLP	1	12	129	243	—	—	—	1.542	LC	Simental-Rodríguez et al. (2014)
<i>Pinus teocote</i>	AFLP	1	9	37	319	—	—	1.36	—	LC	Wehenkel et al. (2015)
<i>Pinus chiapensis</i>	RAPD	8	11	138	49	—	0.546	—	—	EN	Newton et al. (2002)
<i>Pinus culminicola</i>	RAPD	5	2	60	72	57.3	0.569	—	—	EN	Lara (2010)

RAPD random amplified polymorphic DNA, *AFLP* amplified fragment length polymorphism, *Iso* isozymes, *MM* molecular marker, *P* number of populations, *I* number of individuals included per populations, *L* number of loci, % *P* percent polymorphic loci, *S* Shannon diversity index, d_g genetic diversity $V_{mean,2}$ mean genetic diversity, *IUCN* Union for Conservation of Nature and Natural Resources, *LC* least concern, *EN* endangered, *VU* vulnerable, *NT* near threatened

Table 2.5 Genetic diversity obtained in Mexican species of *Abies*

Genus <i>Abies</i>										
Species	MM	PP	P	I	L	Genetic diversity				References
						H _e	% P	H	H _s	
<i>Abies finckii</i>	cpSSR	7	6	105	7	—	—	0.802	—	Jaramillo-Correa et al. (2008)
<i>Abies guatemalensis</i>	cpSSR	7	10	160	7	—	—	0.934	—	Jaramillo-Correa et al. (2008)
<i>Abies hickelii</i>	cpSSR	7	7	112	7	—	—	0.937	—	Jaramillo-Correa et al. (2008)
<i>Abies religiosa</i>	cpSSR	7	11	159	7	—	—	0.908	—	Jaramillo-Correa et al. (2008)
<i>Abies religiosa</i>	cpDNA	2	17	128	2	—	—	0.395	0.187	Heredia-Bobadilla et al. (2013)
<i>Abies religiosa</i>	Iso	—	11	30	16	0.108	31.8	—	—	Aguirre-Planter et al. (2000)
<i>Abies finckii</i>	Iso	—	6	29	16	0.113	30.2	—	—	Aguirre-Planter et al. (2000)
<i>Abies guatemalensis</i>	Iso	—	10	30	16	0.069	20.0	—	—	Aguirre-Planter et al. (2000)
<i>Abies hickelii</i>	Iso	—	6	33	16	0.100	28.2	—	—	Aguirre-Planter et al. (2000)
<i>Abies religiosa</i>	mtDNA	2	17	128	2	—	—	0.319	0.157	Heredia-Bobadilla et al. (2013)
<i>Abies finckii</i>	mtDNA regions sequence	20	6	105	20	—	—	0	—	Jaramillo-Correa et al. (2008)
<i>Abies guatemalensis</i>	mtDNA regions sequence	20	10	160	20	—	—	0.036	—	Jaramillo-Correa et al. (2008)
<i>Abies hickelii</i>	mtDNA regions sequence	20	7	112	20	—	—	0.047	—	Jaramillo-Correa et al. (2008)
<i>Abies religiosa</i>	mtDNA regions sequence	20	11	159	20	—	—	0	—	Jaramillo-Correa et al. (2008)
<i>Abies religiosa</i>	SSR	2	17	128	2	—	—	0.297	0.158	Heredia-Bobadilla et al. (2013)

cpSSR chloroplast microsatellite, cpDNA chloroplast DNA, mtDNA mitochondrial DNA, Iso isozymes, SSR simple sequence repeat microsatellite, MM molecular marker, PP number of primer-pair combinations, P number of populations, I number of individuals included per populations, L number of loci, H_e expected heterozygosity, H total haplotypic diversity, H_s average within-population haplotype diversity, % P percent polymorphic loci, CV conservation status, IUCN Union for Conservation of Nature and Natural Resources, LC least concern, EN endangered, VU vulnerable, NT near threatened

Table 2.6 Genetic diversity obtained in Mexican species of *Picea*

Genus <i>Picea</i>											
Species	MM	PP	P	I	L	Genetic diversity				Conservation status (IUCN 2013)	References
						H _e	% P	H	δT		
<i>Picea chihuahuana</i>	mt DNA	16	16	156	16	—	—	0	—	—	Jaramillo-Correa et al. (2006)
<i>Picea chihuahuana</i>	cpSSR	6	16	156	6	—	—	0.41	—	—	Jaramillo-Correa et al. (2006)
<i>Picea chihuahuana</i>	AFLP	1	14	669	243	—	—	—	—	1.5	Simental-Rodríguez et al. (2014)
<i>Picea chihuahuana</i>	AFLP	1	5	254	319	—	—	—	0.3	—	Wehenkel and Sáenz-Romero (2012)
<i>Picea chihuahuana</i>	Iso	—	10	164	24	0.09	27	—	—	—	Ledig et al. (1997)
<i>Picea martínezii</i>	Iso	—	2	54	22	0.11	32	—	—	—	Ledig et al. (2000b)
<i>Picea mexicana</i>	Iso	—	3	82	18	0.12	35	—	—	—	Ledig et al. (2002)

cpSSR chloroplast microsatellite, mtDNA mitochondrial DNA, Iso isozymes, AFLP amplified fragment length polymorphism, MM molecular marker, PP number of primer-pair combinations, P number of populations, I number of individuals included per populations, L number of loci, H_e expected heterozygosity, H total haplotypic diversity, % P percent polymorphic loci, δT Gregorius' total differentiation, $v_{mean,2}$ mean genetic diversity, IUCN Union for Conservation of Nature and Natural Resources, EN endangered

Table 2.7 Genetic diversity obtained in Mexican species of *Pseudotsuga menziesii*

Species	MM	PP	P	I	L	Genetic diversity				Conservation status (IUCN 2013)	References
						H _e	% P	H	π	$v_{mean,2}$	
<i>Pseudotsuga menziesii</i>	cpDNA segments sequence	2	11	129	2	—	—	0.79	0.0008	—	Gugger et al. (2011)
<i>Pseudotsuga menziesii</i>	cpDNA segments sequence	1	9	107	1	—	—	0.75	0.0008	—	Wei et al. (2011)
<i>Pseudotsuga menziesii</i>	cpSSR	3	11	129	3	—	—	0.91	—	—	Gugger et al. (2011)
<i>Pseudotsuga menziesii</i>	mtDNA segments sequence	2	7	55	2	—	—	0.59	0.0005	—	Gugger et al. (2011)
<i>Pseudotsuga menziesii</i>	AFLP	1	6	63	1	—	—	—	—	1.6	Simental-Rodríguez et al. (2014)
<i>Pseudotsuga menziesii</i>	Iso	—	11	170	18	0.08	28	—	—	—	Cruz-Nicolas et al. (2011)

*cp*SSR chloroplast microsatellite, *cp*DNA chloroplast DNA, *mt*DNA mitochondrial DNA, *AFLP* amplified fragment length polymorphism, *Iso* isozymes, *MM* molecular marker, *PP* number of primer-pair combinations, *P* number of populations, *I* number of individuals included per populations, *L* number of loci, *H_e* expected heterozygosity, *% P* percent polymorphic loci, *H* total haplotypic diversity, *v_{mean,2}* mean genetic diversity, *IUCN* Union for Conservation of Nature and Natural Resources, *LC* least Concern

Table 2.8 Genetic diversity obtained in the family Fagaceae

Species	MM	PP	P	I	L	Genetic diversity				References
						H _e	% P	S	H	
<i>Fagus grandifolia</i> subsp. <i>mexicana</i>	Iso	—	7	164	10	0.20	63	—	—	Montiel-Oscura et al. (2013)
<i>Fagus grandifolia</i> subsp. <i>mexicana</i>	RAPD	18	4	96	62	—	39	0.20	0.135	Rowden et al. (2004)
<i>Quercus laurina</i>	PCR-RFLP	6	6	50	—	—	—	—	—	González-Rodríguez et al. (2004)
<i>Quercus eduardii</i>	RAPD	2	4	120	58	0.33	95	0.50	—	Alfonso-Corrado et al. (2004)
<i>Quercus potosina</i>	RAPD	2	3	90	44	0.35	97	0.53	—	Alfonso-Corrado et al. (2004)
<i>Quercus crassipes</i>	RAPD	18	4	80	121	0.37	—	—	—	Tovar-Sánchez et al. (2015)
<i>Quercus rugosa</i>	RAPD	18	4	80	121	0.28	—	—	—	Tovar-Sánchez et al. (2015)
<i>Quercus rugosa</i>	SSR	3	4	80	3	0.48	—	—	—	Tovar-Sánchez et al. (2015)
<i>Quercus crassipes</i>	SSR	3	4	80	3	0.42	—	—	—	Tovar-Sánchez et al. (2015)
<i>Quercus sideroxyla</i>	SSR	4	9	150	4	0.85	—	—	—	Alfonso-Corrado et al. (2014b)
<i>Quercus sideroxyla</i>	SSR	7	4	44	7	0.82	—	—	—	Peñaloza-Ramírez et al. (2010)
<i>Quercus</i> <i>scytophylla</i>	SSR	7	4	39	7	0.80	—	—	—	Peñaloza-Ramírez et al. (2010)
<i>Quercus</i> <i>Hypoleucoides</i>	SSR	7	2	21	7	0.75	—	—	—	Peñaloza-Ramírez et al. (2010)

Iso isozymes, RAPD random amplified polymorphic DNA, SSR simple sequence repeat microsatellite, PCR-RFLP polymerase chain reaction-restriction fragment length polymorphism, MM molecular marker, PP number of primer-pair combinations, P number of populations, I number of individuals included per populations, L number of loci, H_e expected heterozygosity, % P percent polymorphic loci, S Shannon diversity index, H total haplotypic diversity, H_s average within-population haplotype diversity

Table 2.9 Genetic diversity obtained in the family Meliaceae, family Salicaceae and family Cupressaceae

Family Meliaceae											
Species	MM	PP	P	I	L	Genetic diversity				Conservation status (IUCN 2013)	References
						H_e	h	S	π	$v_{mean,2}$	
<i>Cedrela odorata</i>	RAPD	8	3	34	—	—	—	0.07	—	—	Navarro et al. (2005)
<i>Swietenia macrophylla</i>	RAPD	10	3	31	102	—	—	0.30	—	—	Gillies et al. (1999)
<i>Swietenia macrophylla</i>	SSR	8	4	94	8	0.78	—	—	—	—	Alcalá et al. (2014)
<i>Swietenia macrophylla</i>	SSR	7	1	40	7	0.68	—	—	—	—	Novick et al. (2003)
Family Salicaceae											
<i>Populus tremuloides</i>	AFLP	1	7	76	243	—	—	—	—	1.4	Simental-Rodriguez et al. (2014)
<i>Populus tremuloides</i>	SSR	8	1	13	8	0.610	—	—	—	—	Callahan et al. (2013)
Family Cupressaceae											
<i>Juniperus blancoi</i>	Nuclear loci	6	8	74	8	0.345	—	—	0.0014	—	Moreno-Letelier et al. (2014)
<i>Callitropsis guadalupensis</i>	Plastid DNA	11	1	54	11	—	0.6	—	0.0007	—	Escobar et al. (2011)
<i>Callitropsis forbesii</i>	Plastid DNA	11	6	100	11	—	0.3	—	0.0002	—	Escobar et al. (2011)

RAPD random amplified polymorphic DNA, AFLP amplified fragment length polymorphism, SSR simple sequence repeat, microsatellite, Iso isozymes, MM = molecular marker, PP number of primer-pair combinations, P number of populations, I number of individuals included per populations, L number of loci, H_e expected heterozygosity, h haplotypic diversity, S Shannon diversity index, π nucleotide diversity, v_{mean,2} mean genetic diversity, IUCN Union for Conservation of Nature and Natural Resources, EN endangered, VU vulnerable, NT near threatened, NA none assigned

($H_e = 0.211$, Müller-Starck et al. 1992), and it is slightly higher than that found by Hamrick et al. (1992) in studies published from 1968 to 1990 that reported estimates of allozyme variation for gymnosperms and angiosperms ($H_e = 0.136$ in *Pinus*). Galicia et al. (2015) suggested that most Mexican pine species have high genetic diversity and relatively low genetic differentiation among populations. For example, some species with a high genetic diversity are *Pinus oocarpa*, *P. leiophylla*, *P. johannis*, *P. pinceana*, *P. cembroides*, and *P. muricata* (Dvorak et al. 2009; Rodríguez-Banderas et al. 2009; Molina-Freaner et al. 2001; García-Gómez et al. 2014). Such high levels of genetic diversity have allowed the selection of high-yielding genotypes for reforestation programs and the establishment of commercial plantations in Mexico and other countries (Molina-Freaner et al. 2001). Although, it must also be noted that many exceptions with low genetic diversity figures also exist, such as some endemics and taxa with fragmented distributions, like *P. culminicola* (Favela-Lara 2010), *P. maximartinezii* (Ledig et al. 1999), *P. chiapensis* (Newton et al. 2002), and *P. greggii* (Parraguirre-Lezama et al. 2002).

Wehenkel et al. (2015) found in a study of seed stands of 11 *Pinus* in the Sierra Madre Occidental, that pine species and populations within species that were exposed to prolonged cold periods and low Mg proportion of the cation-exchange capacity in the soil in their distribution range possess lower AFLP diversity. However, Dvorak et al. (2009) reported that *Pinus oocarpa* shows no significant changes in genetic diversity in populations across its geographic range of 3000 km in Mesoamerica.

2.4.1.2 Genus *Abies*

Studies on the genus *Abies* mostly have focused in the southern taxa, namely *Abies flinckii*, *A. guatemalensis*, *A. hickelii*, and *A. religiosa* (Table 2.5). These four species are in the Red List of the IUCN. Although widely distributed, *A. guatemalensis* is considered an endangered species, given that it is distributed in various but isolated populations (Aguirre-Planter et al. 2000). Both *A. flinckii* and *A. hickelii* have restricted distributions and are also considered as endangered (Bello and López-Mata 2001), while *A. religiosa* has a mostly continuous and wide natural range, but its recurrent exploitation for timber has put it at risk (Wallace et al. 2015). In general, the average expected heterozygosity (H_e) in this genus in Mexico, as estimated with isoenzymes, equals 0.10 (Aguirre-Planter et al. 2000), which is far lower than the average for gymnosperms determined by Hamrick et al. (1992; $H_e = 0.151$) or than that found in the European species *Abies alba* ($H_e = 0.41$, Müller-Starck et al. 1992). On the other hand, the average total haplotypic diversity (H) measured with chloroplast microsatellites was 0.80, which is not different from the values found for other temperate firs in Europe or North America (Jaramillo-Correa et al. 2008).

Unlike other conifers, the genus *Abies* in Mexico present low genetic diversity within, but high genetic differentiation among populations; studies of these species have demonstrated that *Abies* populations have likely passed through genetic

bottlenecks that decreased their genetic diversity and steered to interpopulation differentiation (Aguirre-Planter et al. 2000). Furthermore, Jaramillo-Correa et al. (2008) suggested that the four species of *Abies* in Mesoamerica share a recent common ancestor. Given these patterns of genetic structure in the *Abies* populations it has been suggested to implement conservation strategies for these Mexican conifers, proposing in situ conservation of populations along the Transverse Volcanic Belt in central México where most of population differentiation occurs and where they are more threatened by human activities (Jaramillo-Correa et al. 2008).

2.4.1.3 Genus *Picea*

Studies in the genus *Picea* have covered all three Mexican species: *Picea chihuahuana*, *P. martínezii*, and *P. mexicana*. All three taxa are listed as endangered in the Red List of the IUCN (Table 2.6). The average expected heterozygosity (H_e) in this genus estimated by using isoenzymes equals 0.11. This level of genetic diversity is similar to that found in the rare congeners *Picea breweriana*, native of North America ($H_e = 0.129$) and *P. asperata*, native of Southwest China (Western china $H_e = 0.096$) (Luo et al. 2005; Ledig and Johnson 2005). On the other hand, when compared with the values found in the European spruce *P. abies* ($H_e = 0.371$) and in North American black spruce (*P. mariana*, $H_e = 0.300$) these diversity values are much lower (Lundkvist 1979; Isabel et al. 1995).

Picea chihuahuana has been the most genetically studied of all Mexican spruces (Ledig et al. 1997; Jaramillo-Correa et al. 2006; Wehenkel and Sáenz-Romero 2012; Simental-Rodríguez et al. 2014). This species is distributed in the Sierra Madre Occidental in the states of Chihuahua and Durango, forming only 40 populations (Wehenkel and Sáenz-Romero 2012). Its genetic diversity is within the range reported for conifers, although Ledig et al. (1997) found a high fixation index and a 45% of empty seeds, which indicates that inbreeding may be a serious problem for Chihuahua spruce. In addition, Jaramillo-Correa et al. (2006) found only eight chloroplast DNA haplotypes and two mitochondrial DNA haplotypes, which is less than the amount for more boreal spruces. The distribution of mitotypes showed two areas, differentiating the northern populations from the central and southern ones, which suggests that these two areas could represent different ancestral populations. The study also detected recent bottlenecks in some stands and suggested the conservation of southern populations that exhibit high levels of genetic diversity. In a more recent study, Wehenkel and Sáenz-Romero (2012) found significant genetic erosion only in a very small population of 120 individuals and concluded that the loss of genetic diversity per se does not explain the relict status of *P. chihuahuana*. Unexpectedly, Dominguez-Guerrero et al. (2017) found that higher mean temperature in the warmest month are associated to larger mean AFLP diversity.

P. mexicana has three small populations isolated and fragmented on sky islands from the Sierra Madre Oriental and the Sierra Madre Occidental (Sierra el Coahuilón, Cerro Mohinora and Sierra la Marta) and are threatened by global

warming, fire, and grazing (Ledig et al. 2002). The fire affected Mexican spruce in 1975 and most individuals of Sierra la Marta disappeared (Rushforth 1986; Gordon 1991). Ledig et al. (2002) concluded that the populations of *P. mexicana* are genetically viable and their main threat is the environment, while Jaramillo-Correa et al. (2015a) estimated the bottleneck that affects the species to be rather ancient, which suggests that this species has developed some kind of tolerance to stochastic processes. However, Flores-Lopez et al. (2005) found that the reproductive state in the three populations is critical and suggested ex situ conservation, in addition to protecting natural stands along with the establishment of strict measures of management, and protection against grazing and forest fires.

Picea martínezii (Martínez spruce) is a conifer with only four known relict populations of less than 800 trees each (Mendoza-Maya et al. 2015). Ledig et al. (2000b) studied two of those populations, finding levels of genetic diversity comparable to those of *P. chihuahuana* and *P. mexicana*; they further detected that the mating system of Martínez spruce was characterized by a high frequency of selfing, which indicates that this species could be an example of facultative selfing and survival in interglacial refugia. Therefore, for species like *Picea martínezii*, ex situ conservation, including establishment of seed banks and botanical gardens seems required (Ledig et al. 2000b).

Based on the genetic diversity and structure of this three Mexican species of *Picea*, Mendoza-Maya et al. (2015) suggested several in situ conservation activities, including protection, and enlargement of genetic diversity through the expansion of specific populations, by planting individuals originated from seed collected in different locations. The aim of such activities would be getting a genetically viable minimum population size of 1035–3836 individuals. For ex situ conservation, it was recommended the establishment of populations at sites outside the natural range, where the suitable climatic habitat for each species is predicted to occur. For example, such conditions might be encountered in the near future at higher altitudes (which, paradoxically, sometimes occur at southern latitudes in México) at the volcano Cofre de Perote, Veracruz (*P. mexicana*), in the municipality of Guanaceví, Durango (*P. chihuahuana*), and in the region of Tlatlauquitepec, Puebla (*P. martínezii*).

2.4.1.4 Genus *Pseudotsuga*

Douglas-fir (*Pseudotsuga menziesii*, Mirb (Franco)) is an ecologically and economically important coniferous tree species in North America, with a broad natural distribution in western Canada and USA that spreads south into Mexico (Hermann and Lavender 1999). In Mexico, Douglas-fir is distributed along three different mountain ranges, throughout the northwest, northeast, and into the central and southern regions of the country, having an extremely fragmented and discontinuous distribution (Cruz-Nicolas et al. 2011). Even though in the past a controversy was raised about the number of *Pseudotsuga* species growing in this country (Martínez 1963; Little 1979), recent studies using morphological, biochemical, and molecular markers have shown that all Mexican Douglas-fir populations are indeed

Pseudotsuga menziesii (Debreczy and Racz 1995; Reyes-Hernández et al 2006; Wei et al. 2011; Adams et al. 2012, 2013).

The studies of genetic diversity for the Mexican populations of this species showed that its average total haplotypic diversity (H) equals 0.76 (Table 2.7). This genetic diversity is comparable to that of the Canadian ($H = 0.815$) and American stands ($H = 0.745$) (Wei et al. 2011). However, a study using isozymes showed a much lower genetic diversity ($H_e = 0.08$), particularly for the small and isolated populations from the mountains of central Mexico (Cruz-Nicolas et al. 2011). Several studies have shown that *P. menziesii* may be affected by climate change in the future, so it is important to conserve this and other temperate species in Mexico (Gugger et al. 2011). A recent study evaluated the extinction risk of Douglas-fir populations in central Mexico, considering anthropogenic, genetic, and ecological criteria in order to prioritize in situ and ex situ conservation activities, including protection of some natural populations and germplasm collection for assisted gene flow and migration to reduce inbreeding, and increase genetic diversity and population size (López-Upton et al. 2015).

2.4.2 Family Fagaceae

Table 2.8 shows genetic diversity estimates for some species within family Fagaceae, the majority of which focused on the genus *Quercus*. Oaks are one of the most important forest resources of Mexico and represent an important source of firewood and wood for furniture (Galicía et al. 2015). SSR and RAPD molecular markers have been used for the study of this genus. In general, the average heterozygosity (H_e) found for *Quercus* equals 0.33 and 0.69, as estimated with RAPDs and SSRs, respectively. The highest heterozygosity (H_e) was found in *Quercus sideroxyla* (0.86), while the lowest was found in *Quercus rugosa* ($H_e = 0.28$) (Table 2.8). The genetic diversity of the genus *Quercus* in Mexico is comparable with that of *Quercus virginiana* in USA ($H_e = 0.712$) (Cavender-Bares et al. 2010), and it is higher than that of *Quercus petraea* in Europe ($H_e = 0.275$) (Müller-Starck et al. 1992). Some oaks may be susceptible to climate change and forestry exploitation; for example, *Q. sideroxyla* has been exploited for over 500 years to obtain firewood, charcoal for local uses and used for wood production in Mexico's forestry industry, which is thought to have largely depleted its original populations. Therefore, it is important to preserve its genetic diversity, by developing strategies for working with local people in conservation programs and devising conservation policies (Alfonso-Corrado et al. 2014b).

Using RAPD and SSR markers, Tovar-Sánchez et al. (2015) found a positive and significant relationship between genetic diversity and canopy arthropod diversity in *Quercus crassipes* and *Quercus rugosa*. The results of this study represent a potent instrument to predict the effects of the genetic diversity of host-plant species on species diversity, which allows establishing a novel conservation status to foundation species based on their genetic variation.

Another taxa studied within the family Fagaceae is *Fagus grandifolia* (Mexican beech). This species only grows in 11 small and isolated populations in Mexico. The timber harvesting, overgrazing, firewood collection, and seeds for consumption are possible causes that have influenced the reduction in size of its populations (Montiel-Oscura et al. 2013). This species is protected by the Mexican standard NOM-059-SEMARNAT-2010, within the risk category of species in danger of extinction (Semerant 2010), but is not listed in the Red List. The genetic diversity of this species was analyzed with isoenzymes ($H_e = 0.20$) and RAPD markers ($H = 0.14$) (Table 2.8). Rowden et al. (2004) and Montiel-Oscura et al. (2013), respectively, found a moderate to high genetic diversity in *Fagus grandifolia*. The average value of expected heterozygosity (H_e) for this species is comparable with those found in other species of the genus *Fagus* (0.186) (Kitamura and Kawano 2001) and is larger than the average value estimated for angiosperms (0.143) (Hamrick et al. 1992). This variability should be considered in the development of urgent conservation strategies to prevent the extinction of this taxon.

2.4.3 Other Species

The genetic diversity of tropical species has been evaluated only in *Cedrela odorata* and *Swietenia macrophylla* (family Meliaceae), which represent important commercial wood sources in Mexico. These two species are in the Red List of UICN and protected by the Mexican standard NOM-059-SEMARNAT-2010, as a consequence of uncontrolled logging and wood trade. The studies of variation in these species were based on RAPD and SSR markers. Alcalá et al. (2014) found an H_e of 0.78 in four populations of *S. macrophylla* in Mexico, while Novick et al. (2003) found an H_e of 0.68 (Table 2.9). This genetic diversity is comparable to that found in populations of these species in South America ($H_e = 0.65$) (Novick et al. 2003). Conservation suggestions included the preservation of the populations of *S. macrophylla* located in Veracruz or within the Yucatan peninsula, because of their potential adaptation to drier and warmer conditions that could alter the future distribution of Mexican tropical forest (Alcalá et al. 2014).

Finally, other important forest species, *Populus tremuloides* and *Juniperus blancoi*, have been studied to determine their levels of genetic diversity (Table 2.9). *Populus tremuloides* (Quaking aspen) is distributed in North America (Canada, USA, and Mexico) and is a commercially important source of wood fiber. The genetic diversity of Quaking aspen in Mexico ($H_e = 0.61$) is lower than that found in USA and Canada populations ($H_e = 0.79$) (Callahan et al. 2013). Quaking aspen populations from southwestern Mexico have a high risk of mortality with climate change; therefore, it is important to preserve their genetic diversity. *Juniperus blancoi* is an endemic juniper of Mexico with only nine populations located so far. The expected heterozygosity of *J. blancoi* ($H_e = 0.345$) was lower than that observed in junipers from the Tibetan Plateau ($H_e = 0.641$; Li et al. 2012).

2.5 Conclusions

Contrasting with its high species and genus richness, studies of genetic diversity in Mexican forest trees are rather scarce, and often biased to particular families, like the Pinaceae or the Fagaceae. Moreover, even within those particular families the available surveys have a penchant for specific genus, namely *Pinus* and *Quercus*, respectively. The markers used in most of these studies include the traditional and “universal” isozymes and chloroplast microsatellites and, to a lower extent, the anonymous SSRs, AFLPs, and RAPDs. Although some exceptions have been arising in recent years (like Moreno-Letelier et al. 2014, 2015), there is a rampant lack of studies using sequence variation on nuclear genes or more advanced next-generation technologies, which somehow hampers the estimation of genetic variation linked to adaptive processes, such as performed in Europe or northern North America for more than a decade (reviewed in Jaramillo-Correa et al. 2015b). More studies on more varied taxa and using more advanced technologies (e.g., next generation sequencing) and markers seem thus necessary. For instance, because of the poor comparability of the genetic diversity estimates among the studied Mexican tree species, it is extremely difficult to discern general trends across species or regions. Not to mention across taxa with different life-history traits, (such as made in earlier works with allozymes; Hamrick et al. 1992). We thus recommend that genetic diversity should be measured across species with an identical type of genetic marker, and by surveying similar numbers of loci, individuals and populations and using identical indices of genetic diversity.

In spite of such a lack of genetic studies, some trends could be found. For instance, most populations of Mexican forest trees appear to have reduced levels of genetic diversity when compared to their boreal or neotropical counterparts. Given that Mexico represents the southern limit of the distribution of the boreal taxa and the northern bound of the neotropical species, modern populations of forest trees in Mexico are either the rear limit or the advancing colonization front of many genera, which in both cases translates in increased magnitudes of genetic drift over other evolutionary forces. Moreover, most Mexican forest tree species are distributed in fragmented ranges, either because they inhabit fragmented landscapes, like mountain ranges (i.e., most conifers or oaks), or because they have limited dispersal capabilities, which result in scattered stretches of individuals occurring in rather continuous habitats, like most tropical species. This translates in strong population differentiation, which complicates many of the currently established conservation programs.

Based on the available studies it could be recommended that most conservation efforts on Mexican forest trees concentrate in reducing genetic erosion and ensuring the long-term viability of populations and species. Such efforts should focus, among other things, on protecting or encouraging natural regeneration in surrounding areas of current populations, promoting programs of assisted migration, or the establishment of new populations in areas suitable for specific species under future climate change scenarios. In addition, it would be prudent to create real management programs of Mexico’s genetic resources that make good use of current

technologies such as genomic selection of preadapted individuals at the earlier stages of development. A national plan headed by the government in such programs for the conservation of forest trees would be more than necessary.

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