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Assessing spatial patterns of phylogenetic diversity of Mexican mammals for biodiversity conservation

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ABSTRACT

Phylogenetic diversity is a biodiversity measurement that describes the amount of evolutionary history contained by the taxonomic units in a region. It has proven to be an important metric for determining conservation priorities. Mammalian phylogenetic diversity patterns have been suggested as potential surrogates of biodiversity for establishing priority areas for conservation. This study aims to identify areas of high mammalian phylogenetic diversity in Mexico, a megadiverse country with high mammalian richness, and to assess how well protected areas encompass the phylogenetic diversity. IUCN distribution data for 479 Mexican mammals were used to estimate species richness. Data for the molecular markers *cytB*, *12S* and *COI*, was gathered from GenBank and from laboratory extractions for reconstructing a maximum-likelihood phylogenetic tree. Spatial patterns in phylogenetic diversity were estimated by summing the branch lengths of the phylogenetic tree representing species presence across grid cells. The results were compared with the distribution of protected areas in Mexico in order to assess if phylogenetic diversity is effectively conserved. The southeastern part of Mexico was found to be the most diverse. The breadth of the phylogenetic tree was well represented within the protected areas. Beta-diversity analyses showed that the species composition between protected and unprotected areas is very similar. Protected areas group based on the phylogenetic composition of mammal species into three clusters corresponding to the Nearctic, Neotropical, and Mexican Transition Zone biogeographical regions, which suggests that protected areas could be managed based on these clusters.

1. Introduction

Traditionally, conservation strategies for quantifying biodiversity have focused on species richness and patterns of endemism (Noguera-Urbano, 2017; Winter et al., 2013; Voskamp et al., 2017; Rosauer et al., 2017). Regardless, it has become more accepted that species richness alone does not appropriately describe the spatial and temporal dynamics of biodiversity, since it only represents the taxonomic dimension of biodiversity (Safi et al., 2011; Voskamp et al., 2017; Karanth et al., 2019; Grumbs et al., 2019). In response to this challenge, other approaches for measuring biodiversity, such as phylogenetic diversity, are increasingly recognized as important components of conservation planning.

Phylogenetic diversity accounts for the total amount of evolutionary history encompassed by the taxonomic units within a certain region (Safi et al., 2011). Phylogenetic diversity can be estimated by looking at the phylogenetic relations among taxa (McGoogan et al., 2007; Voskamp et al., 2017), and is frequently quantified as the sum of the length of the branches of a phylogenetic tree relating

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all species occurring in a region (Faith, 1992). Phylogenetic diversity has proven relevant for determining conservation priorities as it relates to processes such as extinction, biotic invasion, ecosystem functioning, and even ecosystem services (McGoogan et al., 2007; Winter et al., 2013; Grumbs et al., 2019). Furthermore, it can be used to set conservation priorities at various biogeographical scales in order to maximize future biodiversity and evolutionary distinctiveness (McGoogan et al., 2007). In conservation terms, phylogenetic diversity is useful to highlight areas of high irreplaceability and added value (Voskamp et al., 2017).

One of the main advantages that phylogenetic diversity offers over species richness is that it takes into account the phylogenetic distinctiveness (i.e. evolutionary history) of species (Winter et al., 2013). Phylogenetically unique taxa and the places where they occur must be prioritized in the allocation of conservation resources because their extinction would result in a larger loss of evolutionary history than species with numerous sister taxa (Rodrigues and Gaston, 2002; McGoogan et al., 2007). Thus, increased understanding of the spatial distribution of phylogenetic diversity is an opportunity to support policymakers in the design of conservation strategies.

Biodiversity conservation strategies involve estimating patterns of variation and then trying to conserve as much of that estimated variation as possible (Faith and Baker, 2006). Surrogates can be used to represent certain patterns of biodiversity variation that are to be estimated. For example, using mammal phylogenetic diversity patterns as surrogates of biodiversity can help to establish priority areas of conservation that ensure the protection not only of the mammalian evolutionary diversity, but also other species that have co-evolved with them (Safi et al., 2011).

Spatial turnover in phylogenetic dissimilarity is also of importance in a conservation context. Phylogenetic beta-diversity (phylobeta diversity) measures how phylogenetic relatedness changes across space in the same way beta-diversity measures how species composition changes (Graham and Fine, 2008; Cornejo-Latorre et al., 2020; Mienna et al., 2020). Phylobeta diversity offers a complementary approach to phylogenetic community assembly. The integration of species richness, phylogenetic diversity, and both beta and phylobeta-diversity contribute to a deeper understanding of the biodiversity dynamics of a given area (Thornhill et al., 2016; Gómez-Ortiz et al., 2017; Mienna et al., 2020). Beta diversity is a crucial factor for the high mammal species richness in the country, especially in the southern Mexico due to the environmental and geological heterogeneity (Rodríguez et al., 2003; Cornejo-Latorre et al., 2020).

Mexico is the only continental country that presents the complete intergradation of two biogeographical realms: the Nearctic and Neotropics (Ceballos, 2014). This poses conservation challenges in ensuring that the distribution of protected areas adequately conserves the evolutionary history of both sets of fauna. This study aims to identify areas of high mammalian evolutionary diversity in Mexico. In addition, it aims to compare if the established protected areas in Mexico conserve evolutionary diversity and to identify if these protected areas are complementary in terms of phylogenetic representation. We hypothesize that some regions of Mexico with high levels of phylogenetic diversity are actually unprotected, due to the arbitrary criteria to which protected areas have been designated in the past. We also expect phylogenetic beta-diversity to reveal composition patterns of the protected and non-protected mammal communities.

2. Materials and methods

2.1. Study area

Mexico spans the boundary between the Nearctic and Neotropical biogeographical realms. The area where both the Neotropical and Nearctic biota intersect is known as the Mexican Transition Zone (MTZ), an area with a high degree of endemism (Escalante, 2009; Ceballos, 2014; Morales et al., 2016; Morrone et al., 2017; Morrone, 2018). The great complexity in the distribution ranges and patterns of species in Mexico is related to the great heterogeneity of the physical environment which is product of the country's geological and climatic history (Ceballos, 2014). In accordance, some vegetation classification systems have recognized up to 50 different vegetation types (see González-Medran, 2003). Most mammals' endemism is distributed in the MTZ (Morales et al., 2016). Some endemic mammals of the MTZ have very small ranges (can be as small as few square kilometers) and are rare, therefore catalogued under risk categories (Morales et al., 2016).

Mexico's biological diversity has been widely recognized, and it is considered to be a mega-diverse country, not only for its high number of species but also for its number of endemic species, ecosystem richness, and its great genetic variability shown in many taxonomic groups as a result of natural and cultural diversification in the country (Espinosa et al., 2008; Ceballos, 2014). Mexico supports 496 species of terrestrial mammals (plus 47 marine species) contained in 168 genera, and 34% of these (170 species) are endemic (Ceballos, 2014; Ramírez-Pulido et al., 2014). The order with greatest species richness is Rodentia (rodents), followed by Chiroptera (bats) and Carnivora (carnivores) (see Ceballos, 2014; Ramírez-Pulido et al., 2014).

Despite the great diversity of mammals in the country, their conservation status is not optimal (Sisk et al., 2007; Figueroa and Sánchez-Cordero, 2008; Valdez et al., 2006; Pisanty et al., 2016). In the last decades, economic development has caused significant perturbations, such as soil erosion and deforestation, to Mexican ecosystems (Pisanty et al., 2016). As a response, the government developed environmental policy instruments such the Protected area network (*Sistema Nacional de Áreas Naturales Protegidas*) (Pisanty et al., 2016). Protected areas are representative portions of an ecosystem where the environment has not been highly modified by human activities, and that has ongoing activities related to protection, conservation or restoration (Conanp, 2016). There are 182 protected areas in Mexico managed at three levels—federal, which involves all of the IUCN management categories, regional and private, which have less restrictive management regimes. The total area of Mexico under protection represents 11% of the national territory (Conanp, 2016). Due to the variation in management restrictions across protected area categories, this study focuses on the most restrictive - federal protected areas. Analyses were also carried out across the different IUCN protected area categories represented by the federal protected areas (category II, IV and VI).

2.2. Species selection

The species selection was done based on [Ramírez-Pulido et al. \(2014\)](#), which contains 496 native Mexican terrestrial mammals. Molecular and/or geographical data was not available for 28 of these species (after accounting for synonyms), leaving a total of 468 species for further analysis ([Table A1](#)).

2.3. Molecular data processing and phylogenetic analysis

Molecular sequence data for 434 species was obtained from NCBI's GenBank public repository. Three mitochondrial markers were identified to have broad coverage over the relevant species: cytochrome b (*cytB*), cytochrome oxidase subunit 1 (*COI*), and the 12S ribosomal RNA gene (*12S*). At least one of the relevant markers was obtained for 434 species.

For the rest of the species that did not have available molecular data on open repositories, we attempted to obtain representative samples via institutional loan from various institutions in Mexico and the US. We obtained 30 samples ([Table A2](#)) and generated molecular data via DNA extraction ([Table A3](#)). The successful products were purified, and Sanger sequenced by Eurofins Genomics. The overall sequences were aligned and concatenated using the program Geneious (version 2019.2.3). The phylogenetic tree ([Fig. A1](#)) was generated in CIPRES Science Gateway online platform ([Miller et al., 2010](#)) by conducting a partitioned maximum-likelihood analysis (3 partitions, 500 bootstraps) with RAxML-HPC BlackBox.

The DNA sequences and sequence alignments generated in this study are available on the public repository Dryad (datadryad.org) with DOI <https://doi.org/10.5061/dryad.8kpr4xpd>.

2.4. Biodiversity analyses

The biodiversity analyses were conducted in the R environment ([R Core Team, 2020](#)) using the packages '*raster*' ([Hijmans and van Etten, 2012](#)), '*picante*' ([Kembel et al., 2010](#)) and '*betapart*' ([Baselga et al., 2020](#)). Species distribution data for the study species were taken from the IUCN ([IUCN, 2020](#)) and the Biogeographical Atlas of North American Mammals ([Escalante, 2013](#); [Escalante et al., 2018](#)) and then linked to the phylogenetic trees.

Species richness and phylogenetic diversity were calculated for all 72,594 raster grid cells (equal area 10×10 km). Species richness was calculated the number of species with ranges overlapping a cell. Phylogenetic diversity was calculated with the '*picante*' package ([Kembel et al., 2010](#)) in R. This package calculates the phylogenetic diversity of an area as the sum of the total branch length for the subset of species present within each cell ([Faith, 1992](#)).

Since phylogenetic diversity increases with species richness, the standardized effect size of phylogenetic diversity (SES.PD) was also estimated with the '*picante*' package ([Kembel et al., 2010](#)) as the difference in the observed diversity and the mean expected diversity, divided by the standard deviation of the expected diversity in 1000 randomizations of taxa labels ([Speed et al., 2019](#); [Martín-Regalado et al., 2020](#)). Cells where the observed diversity was ranked in the top or bottom 2.5% of the randomized values were classed as having significantly higher or lower diversity (respectively) than expected (two-tailed $p < 0.05$) ([Speed et al., 2019](#)).

Beta diversity and phylobeta-diversity analyses were conducted to assess the compositional and phylogenetic dissimilarity between the protected areas mammal community and the rest of the country. Beta-diversity (using the Sørensen index) was calculated in R through the '*betapart*' package for each of the cells outside the protected areas, all the cells within protected areas merged as one single community, and for each independent protected area. For assessing the phylogenetic complementarity between protected areas, a hierarchical cluster analysis was carried out based on the phylobeta-diversity of each protected areas ([Mienna et al., 2020](#)). The cluster

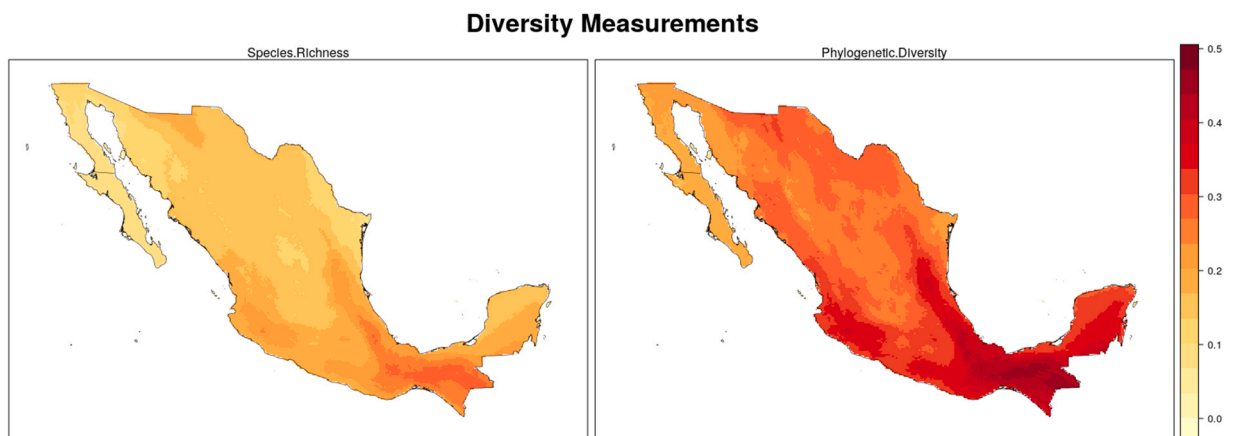


Fig. 1. Maps of species richness and phylogenetic diversity of Mexican mammals. Maps are presented as a proportion of the total diversity pattern. SR is presented as the proportion of the total number of species (468) found in the cell and phylogenetic diversity as the proportion of branch lengths in a cell. The maps are projected in Lambert Conformal Conic projection. A total of 72,594 cells with 10 by 10 km dimensions.

analysis was also carried out based on the compositional beta-diversity of the protected area with the ‘stats’ package (Fig. A4).

The federal protected areas maps were downloaded as polygons from CONABIO database (Conabio, 2018). Only federal protected areas polygons were used. Some federal protected areas were smaller than 100 km², which is the resolution gran of this study, therefore they were excluded. In total, 182 protected areas were used. All maps used for the spatial data analyses were re-projected into a Lambert conformal conic projection.

3. Results

3.1. Biodiversity pattern analysis

The cell with the highest mammalian species richness (Fig. 1) contained 145 species and is in the southeastern part of the country (Chiapas), whereas the cell with the lowest species richness had only two species and is in the Baja California Peninsula. The observed phylogenetic diversity patterns were similar but not identical to the species richness pattern, as expected. Both diversity measures are highly correlated (0.97) (Fig. A2). However, phylogenetic diversity increases slightly more in the MTZ, whereas species richness is highly concentrated towards the southeast of the country (Fig. 1). Like species richness, the highest amount of phylogenetic diversity is located in the southeast of the country, in the states of Chiapas and Oaxaca. The lowest values of phylogenetic diversity remain at the northwest of the country, in the Baja California Peninsula.

The phylogenetic diversity in the Yucatán peninsula was significantly greater than expected given a random distribution of species, with standardized effect sizes between 2 and 3 standard deviations higher than expected (Fig. 2). On the other hand, the area of the western Sierra Madre presented significantly lower phylogenetic diversity than expected by between 2 and 3 standard deviations (Fig. 2).

3.2. Protected areas and phylogenetic diversity conservation

Protected areas contain 90% of Mexican mammal phylogenetic diversity and species richness (Fig. 2). However, there are 48 species whose distribution ranges do not overlap with Mexican protected areas. 68% (33) of these species are considered to be under threat: 3% are vulnerable, 42% are endangered, and 55% are critically endangered (IUCN, 2020). Most of the threatened species are rodents (Table A4). 75% (36) of the species whose ranges do not overlap with protected areas are endemic to Mexico, whereas the remaining 25% (12) are broadly distributed outside the political borders of Mexico, particularly within the US (Table A4).

The protected area with the highest phylogenetic diversity was the Biosphere Reserve *Selva El Ocote* (58% of the total branch length), in the southeastern part of the country (Chiapas), whereas Biosphere Reserve *Lagunar Ojo de Liebre* was the least diverse protected area (41%; Table A5).

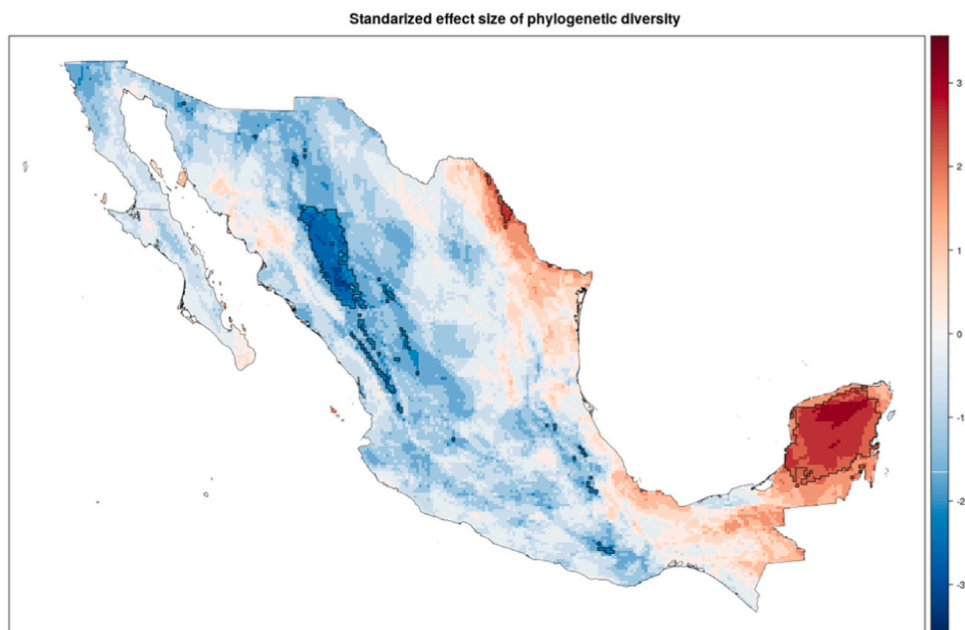


Fig. 2. Standardized effect size of phylogenetic diversity (SES-PD). Effect size was estimated as the difference in the observed diversity with mean expected diversity, divided by the standard deviation expected diversity of 1000 randomizations. Higher diversity than expected is shown in red colors and lower diversity than expected is presented in blue colors. Outlined regions show where the effect size significantly differs from expected, following the methods of Speed et al. (2019).

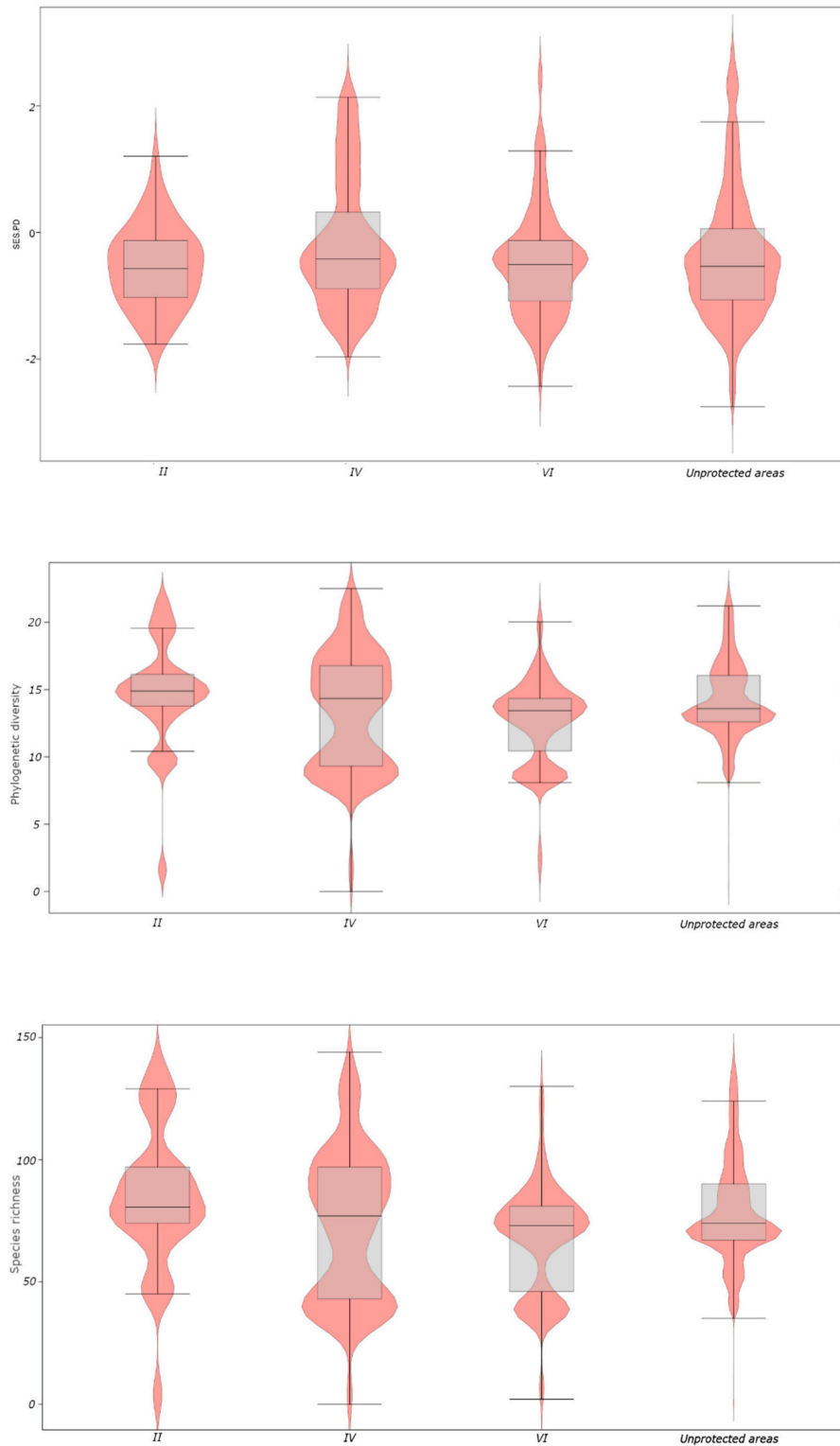


Fig. 3. Diversity measurements' boxplots of the standardized effect sizes of phylogenetic diversity (top), phylogenetic diversity (middle) and species richness (bottom) in protected and non-protected areas. Protected areas are divided in IUCN categories. For this study, only categories II, IV and VI were analyzed. The violin plots represent the distribution of the number of species/branch lengths respectively per cell both inside and outside protected areas. Wider sections of the violin plot represent a higher probability of observations taking a given value, the thinner sections correspond to a lower probability.

The distribution of both phylogenetic diversity and species richness inside protected areas is multimodal (Fig. 3). Most of the cells outside protected areas, and from category II have values closer to the median, whereas the protected areas of category IV and VI have cells with values further away from the median. For these categories (IV and VI), the highest concentration is in the first quartile, between ca. 30 and 50 species, and on the third quartile, closer to the median for both diversity measures. The species richness and phylogenetic diversity of cells inside protected areas were more variable than those outside protected areas. However, the distribution of standardized effect sizes of the phylogenetic diversity did not differ between the protected area categories (Fig. 3).

3.3. Beta-diversity analysis

The beta- and phylobeta-diversity analyses show that the islands in the Baja California Peninsula and Cozumel (in the Caribbean region) are, in terms of species and phylogenetic composition, the most distinct unprotected regions. The areas of highest (phylo)beta-diversity are located towards the northwest part of the country, whereas the areas of lowest phylobeta-diversity are located towards the southeast (Fig. 4).

In order to assess the phylogenetic complementarity of the protected areas, a hierarchical clustering analysis was conducted based on phylo β -diversity. This identified three clusters which largely correspond to the biogeographical regions proposed by Morrone et al. (2017), so they were categorized as Nearctic, Neotropical and the Mexican Transition Zone (Fig. 5). The same pattern was seen in the analysis of compositional similarity (based on species; Fig. A3).

4. Discussion

This study addressed both species richness and phylogenetic diversity of mammal species across Mexico, spanning the transition zone between two biogeographical realms. We found that protected areas overlap with the distribution of the majority of the country's mammalian biodiversity in terms of both species' composition and phylogenetic composition. Compositional and phylogenetic complementarity analyses showed that mammalian phylogenetic similarity groups in clusters that resemble those of the biogeographical regions, dividing them in mainly three clusters: species from the Nearctic region, species from the Neotropical region, and species from the Mexican Transition Zone. We therefore suggest that the management of protected areas takes this phylogenetic divergence across protected areas into account.

4.1. Diversity analyses

The observed geographic distribution of mammalian diversity (Fig. 1) is likely due to the environmental heterogeneity of Mexico, particularly the distinctive vegetation types and great climatic and elevational variability across the country (Rodríguez et al., 2003; Cornejo-Latorre et al., 2020). The most productive ecosystems are found in the southeast, which may explain this region's greater number of species and higher levels of phylogenetic diversity. The least productive ecosystems are located in the northeast, where the least diverse cells were found. A consequence of this heterogeneity is the presence of a high number of endemic species and, in general, species with small distribution ranges. This implies that the species turnover is high and thus explains the high α -diversity of Mexico as a whole (Valdez et al., 2006; Koleff and Soberón, 2008).

Rodríguez et al. (2003) suggested that the high level of species richness in the southern part of Mexico is mainly due to diversity within the chiropterans, which present different geographical patterns than the rest of the terrestrial mammals (Rodríguez et al., 2003; Cornejo-Latorre et al., 2020). Chiropteran diversity tends to increase towards the southern part of Mexico (and other tropical latitudes of America), while the patterns of the other terrestrial mammals are not so pronounced (Rodríguez et al., 2003).

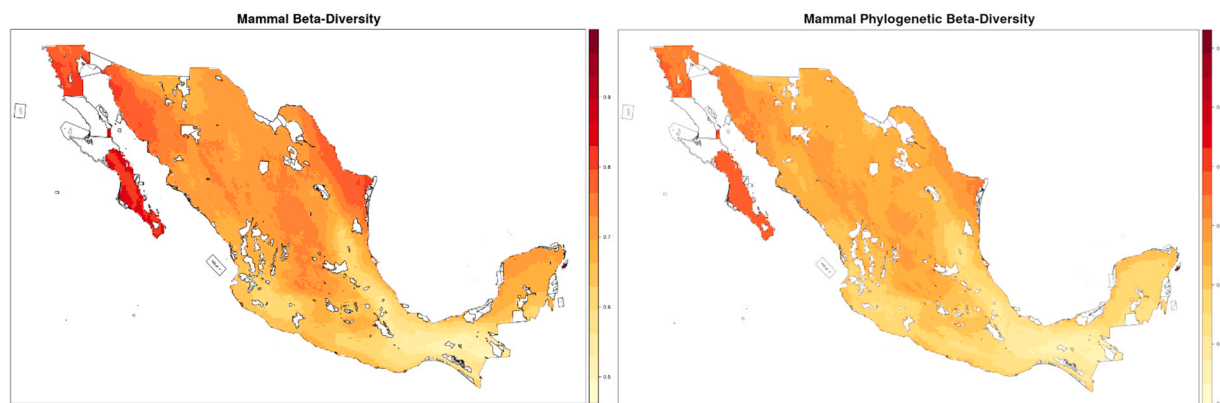


Fig. 4. Beta-diversity (left) and phylogenetic beta-diversity (right) between protected and non-protected areas. Low values of (phylo)beta-diversity represent less dissimilarity between the two communities whereas high levels show greater dissimilarity. The polygons without color represent the protected areas that constitute the federal protected area network.

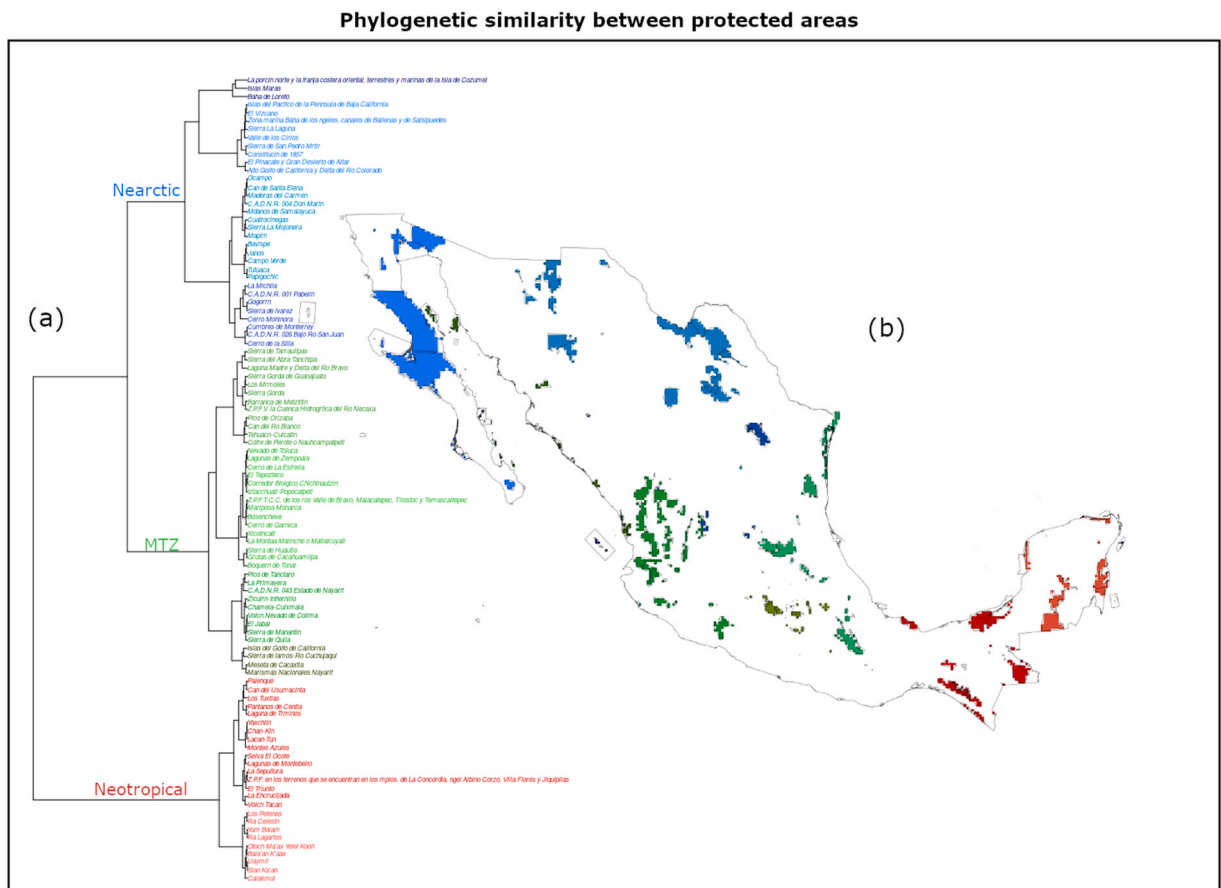


Fig. 5. Hierarchical clustering of the Mexican protected areas based on the phylo-beta similarity index of the Mexican mammals. PA were grouped into 3 clusters. Hierarchical dendrogram (a) and geographical representation of the three clusters of protected areas (b). Colours correspond to the clustering based on the biogeographical regions of Mexico in both figures. Blue protected areas correspond to the Nearctic region, green the Mexican Transition Zone and red the Neotropical region.

In a study conducted by [Gómez-Ortiz et al. \(2017\)](#), where the phylogenetic diversity of Mexican medium- and large-sized mammals was assessed (i.e. excluding Chiropterans and rodents), the area with the highest phylogenetic diversity was the Mexican Transition Zone, in the central part of the country, suggesting that the overall mammalian species richness and phylogenetic diversity patterns are driven mainly by chiropterans ([Rodríguez et al., 2003](#)).

4.2. Phylogenetic diversity in protected areas

The protected areas network overlaps with at least some portion of the ranges of 90% (431 species) of mammal species in Mexico. In an attempt to understand why the remaining 48 species are not conserved by the protected area systems, we can divide them in two types: those that are endemic within certain areas of Mexico and those whose distribution ranges extend beyond the Mexican borders. The latter constitutes 25% of the non-protected species. None are considered as threatened according to the IUCN ([IUCN, 2020](#)) ([Table A4](#)), and for most of them, their distribution within Mexico constitutes only a small part of their total range. This suggests that other countries, where the species holds most of its distribution range, may be more able to take conservation actions to protect those species. Such is the case of *Ondatra zibethicus*, which occurs broadly across the US and only slightly beyond the Mexican border. Some parts of its distribution range are covered by American protected areas ([IUCN, 2020](#)).

For the 36 unprotected endemic species we identified, 96% are assigned to an endangered category from IUCN ([Table A4](#)) 2% are categorized as 'Least Concern' and 2% as 'Data Deficient'. All of these species are small rodents (Rodentia) and moles (Soricomorpha). Small species in general are poorly known. The lack of protection of the small endemic mammals is therefore associated with both of the Linnean and Wallacean shortfalls ([González-Ruíz et al., 2005](#)) – i.e. a lack of both taxonomic and distribution knowledge. Nevertheless, the phylogenetic diversity of Mexican mammals at the genus level is fully contained within the protected area network.

Protected areas contain highly variable levels of phylogenetic diversity and species richness. The bimodal distribution in the protected areas ([Fig. 3](#)) shows that they can be divided mainly into two types: those with higher phylogenetic diversity and species richness, and those with lower. Due to the heterogeneity of the country, it is important that the protected areas comprise a widespread

network across the Mexican territory that protects and represents the highest possible diversity. This is currently the case in Mexico (Fig. 4), where protected areas are complementary in terms of the species and evolutionary lineages that they encompass. Protected areas contain a high range of phylogenetic diversity and species richness (i.e. some have very high diversity and others low). This also explains the more even distribution of the per-cell diversity in non-protected cells.

The most phylogenetically (and compositionally) diverse protected areas are concentrated in Chiapas and the second most diverse set of protected areas in Mexico corresponds to the MTZ area. This is because the MTZ contains biota with the evolutionary history from both the Nearctic and Neotropical biogeographical regions (Morales et al., 2016). 50% of the protected areas in the MTZ are Biosphere Reserves, suggesting that this management category might be the most appropriate for conserving mammal phylogenetic diversity. This has implications for the conservation of Mexican mammals as it proposes a set of areas that can be prioritized for the conservation of the mammalian phylogenetic tree. However, considering that in the Yucatán peninsula, phylogenetic diversity was significantly higher than expected (Fig. 2), protected areas in this part of the country should be prioritized for receiving conservation resources. Nevertheless, because Mexico possesses a high β -diversity (Rodríguez et al., 2003), the phylogenetic dissimilarity analysis (Fig. 5) might be more informative in assessing how to better allocate conservation resources for Mexican mammals.

4.3. Complementarity and priority areas of conservation

The complementarity analysis demonstrated that both species richness and phylogenetic diversity were lowest towards the southeast area and highest in the northwest. Therefore, contrary to our hypothesis, the phylo β -analyses were not informative. The proportion of the total species (and thus the branch lengths) in the protected areas is so high that the differences between protected and non-protected communities are dominated by species missing from the other sites, rather than species missing from the protected areas.

For the particular case of Cozumel, it is important to remember that this study only considers federal protected areas. A small part of the Cozumel island is covered by a federal protected area (*La porción norte y franja costera de la Isla de Cozumel*), which mainly aims to protect the marine zone. However, most of the rest of the island is under regional protection, so the mammal species located in that area are actually under a protection scheme. This is the only case in which a regional area conserves a species not included in the federal protected area network.

The phylogenetic complementarity analysis within the protected area community reveals that none of the protected areas have a particularly distinct phylogenetic composition. Instead, they group into biogeographical regions: the Nearctic region to the north, the MTZ in the center and in the principal mountain systems, and the Neotropical to the south and southeast (Fig. 5). At the same time, the protected areas form subgroups within the biogeographical regions that would correspond to the Mexican biogeographical provinces proposed by Morrone et al. (2017) (Supplementary Fig. B4). The complementarity analysis was also conducted based on species composition, and it presented the same patterns of protected area grouping as phylogenetic complementarity. This shows that protected areas indeed complementary in terms of their phylogenetic and species composition and that it is important to maintain the geographical spread of the current protected areas network. The hierarchical dendrogram suggests that the Nearctic protected areas are the most distinct in terms of phylogenetic composition. One of the clusters within the Nearctic region is composed of protected areas located in islands, which can be explained by the high proportion of mainly paleoendemic species with small ranges (Graham and Fine, 2008), as the compositional complementarity analysis also identified these three protected areas as the most compositionally distinct.

4.4. Conservation implications

Mexico's protected areas network overlaps the phylogenetic diversity of Mexican mammals in a very similar way to species richness, which indicates that this network is similarly effective at preserving both species richness and evolutionary history. However, because the Yucatán peninsula presented greater than expected phylogenetic diversity, this should be considered as a priority area for preserving evolutionary history of Mexican mammals. Even though protected areas overlap with the distribution ranges of most of the Mexican mammals, further work is needed to assess the effectiveness of the protected areas in conserving mammals' populations, as our analyses used only presence/absence data. Protected areas effectiveness analysis can be based on population dynamics, ecosystem integrity and land use change inside protected areas, as well the effects of climate change on species' distributions and how conservation actions should be conducted.

Analysis of population viability within the protected areas allow assessments of long-term preservation of the species. For example, the jaguar (*Panthera onca*) is considered endangered in Mexico mainly due to habitat loss and illegal extraction (Quigley et al., 2017). Although several protected areas overlap its distribution, only two (*Calakmul* and *Sian Ka'an*) are large enough to sustain jaguar viable populations (Valdez et al., 2006). Nevertheless, some species such as the Mexican wolf (*Canis lupus baileyi*) (Lara-Díaz et al., 2015), coyote (*Canis latrans*), gray fox (*Urocyon cinereoargenteus*), and the coati (*Nasua narica*), do not require protected areas to support viable populations as they tend to perform well outside protected areas (Coronel-Arellano et al., 2016).

Although not all mammal species distributed in Mexico fall within the protected area network, at the level of genera, the overall phylogenetic diversity of the group is contained within it. Therefore, phylogenetic diversity provides a framework for resources allocation based on evolutionary history of a group. This prioritization is relevant since the extinction of species with extant close relatives would not represent such a disproportionate loss of evolutionary and genetic diversity as would the extinction of a species that is not closely related to any other living ones (Rodríguez and Gaston, 2002).

In terms of the geographic distribution of the protected area network and the goal of conserving the overall phylogenetic diversity

of the country, it is important to keep a network of diffuse protected areas so that most of the species are covered. This is particularly relevant for countries with high levels of β -diversity, such as Mexico. Clustering of the protected areas in terms of phylogenetic similarity can also be important for future conservation actions, as they could be managed as groups based on their phylogenetically similarity. For example, one sensible strategy might be to promote connectivity between protected areas within a cluster (e.g. the Nearctic protected areas), and to avoid connectivity between protected areas within different clusters, since each biogeographical province has its own evolutionary history, and excessive connectivity between different provinces might promote the fusion of biotas that are naturally disjoint (Morales et al., 2016).

5. Conclusion

This study functions as a basis for a more informed conservation-planning and decision-making process as it advances our understanding on the current conservation status of the mammal phylogenetic diversity based on the Mexican protected area network. It also emphasizes the importance of basing conservation efforts not only on highly species-rich areas, but on areas deemed valuable for the evolutionary history that they contain.

The federal protected areas overlap with the ranges of most of the species of Mexican terrestrial mammals and can be divided in two groups: those containing high levels of phylogenetic diversity/species richness, and those containing low levels of phylogenetic diversity/ species richness. The latter are of conservation relevance due to the presence of endemic species. Phylogenetic diversity was greater than expected in the Yucatán peninsula area, making the protected areas located in this part of the country a conservation priority. Mexican protected areas are complementary in terms of phylogenetic composition: they conserve different parts of the Mexican mammal phylogenetic tree. Based on their phylogenetic composition they can be clustered into three main groups that represent the evolutionary history of the Nearctic mammal biota, the Neotropical, and the intergradation of these two biotas, known as the MTZ. Therefore, protected areas could be managed as groups based on the clusters, promoting connectivity between a cluster but avoiding between them.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at [doi:10.1016/j.gecco.2021.e01834](https://doi.org/10.1016/j.gecco.2021.e01834).

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