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Authors: Galindo-Cruz, Alejandra, Sahagún-Sánchez, Francisco Javier, and Rojas-Soto, Octavio

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Implications on the Use of the Phylogenetic Species Concept in the Risk Categories Assignment: The Case of the Birds of Mexico

Alejandra Galindo-Cruz[1,2], **Francisco Javier Sahagún-Sánchez**[2], and **Octavio Rojas-Soto**[3]

Abstract

Background and Aims: Conservation efforts require a rational basis for taxa prioritization; it is essential to recognize the evolutionary independence of units, typically recognized as species. Because different criteria on species limits lead to different conservation assessment priorities, conceptual problems limit the possibility to accurately assess the conservation status that species are undergoing to protect them effectively.

Methods: We analyze the implications of using the phylogenetic species concept (PSC) in the risk categories determination, based on the analysis of the Mexican endemic avifauna. We modeled the potential distribution areas with the MaxEnt algorithm for those species that have had or could be susceptible to taxonomic updates based on the PSC.

Results: Of the 93 studied species, 68 were highly restricted, and 23 have high scores according to the evaluation of the Partners In Flight conservation status, so they can be considered species with high vulnerability or risk of extinction. Additionally, based on the recognition of several allopatric populations as independent phylogenetic species, 45% are susceptible to reconsideration of their risk categories due to a decrease in the extent of areas where they are potentially distributed.

Implications for Conservation: The use of a taxonomic perspective focused on the phylogenetic relationship of the different populations would directly impact the definition of risk categories, particularly for those endemic or restricted distribution evolutionary units for which there is usually very little information available and which, undoubtedly, are the ones that most need to be studied and, particularly, protected.

Keywords
distribution area, conservation, MER, species distribution models, IUCN

Introduction

Conservation efforts require the delimitation of taxa for their prioritization (Hortal et al., 2015; Moritz, 1994); therefore, it is essential to recognize the evolutionary independence of units, typically recognized as species (Cracraft, 1983; Haig et al., 2006; Moritz, 1994; Ryder, 1986; Zink, 2004), along with their historical relationships (Ryder, 1986). However, when we face species delimitation, the species concept itself has led to decades of controversy concerning the definition of the species category and methods for inferring the boundaries and species numbers (de Queiroz, 2007; Fraser & Bernatchez, 2001; Winker et al., 2007). The lack of agreement on this controversy and the dominance of the biological species concept (BSC) led to the recognition of subspecies as

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[1]Centro Universitario de Ciencias Biológicas y Agropecuarias, Universidad de Guadalajara, Zapopan, México
[2]Departamento de Políticas Públicas, Centro Universitario de Ciencias Económico-Administrativas, Universidad de Guadalajara, Núcleo Universitario Los Belenes, Zapopan, México
[3]Red de Biología Evolutiva, Laboratorio de Bioclimatología, Instituto de Ecología, A. C., Xalapa, México

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Corresponding Author:
Octavio Rojas-Soto, Laboratorio de Bioclimatología, Red de Biología Evolutiva, Instituto de Ecología, A.C. Carretera antigua a Coatepec 351, El Haya, Xalapa 91070, Mexico.
Email: octavio.rojas@inecol.mx

conservation units. Despite different points of view on their usefulness and applicability (e.g., Alström, 2006; Johnson et al., 1999; Remsen, 2010; Wheeler, 1999; Winker, 2010; Zink, 2004), subspecies have been considered as conservation entities by several international conventions and organizations such as CITES (UNEP & WCMC, 2014) and IUCN (IUCN, 2020), as well as in official endangered species lists of mega-diverse countries such as Brazil (MMA, 2014), Australia (EPBCA, 1999), and Mexico (DOF, 2010).

Inconsistent taxonomic criteria for species assignment can impact conservation priorities (Peterson, 2006; Peterson & Navarro-Sigüenza, 1999; Rojas-Soto et al., 2010; Zink, 2014), which limits the possibility of accurately evaluating the conservation state of independent evolutionary units in order to protect them effectively (Nori et al., 2020; Scherz et al., 2019). This issue is particularly exacerbated in Latin America because there is a lack of enough specialists, which generates geographically unbalanced biodiversity inventories (Hughes et al., 2021; Mora et al., 2011), and a shortage of understanding of population distribution and variation within species (Peterson & Navarro-Sigüenza, 1999), increasing the Linnean, Darwinian, and Wallacean shortfalls (Hortal et al., 2015). However, recently re-analyzed groups based on formal phylogenetic methods reveal that the actual diversity patterns are usually underestimated (Cordier et al., 2021). Therefore, splitting/synonymizing the species groups (filling Linnean and Darwinian shortfalls), generates immediate changes in species distributions (filling Wallacean shortfalls; Diniz-Filho et al., 2013; Hortal et al., 2015). These changes also update the species' vulnerability (Scherz et al., 2019) and accurately identify richness and endemism patterns (Peterson & Navarro-Sigüenza, 1999, 2000).

The assignment of risk categories also requires complementary information, such as population sizes, decline rates, threats, land-use change, and vulnerability to climate change (Foden et al., 2018; IUCN, 2019; Mace & Lande, 1990). However, restriction of the species range is one of the most important criteria. The International Union for Conservation of Nature (IUCN) developed the Red List of globally Threatened Species to establish their risk category based on population trends, occupation areas, distribution areas, and the species extinction risk analysis (Cassini, 2011; Harfoot et al., 2021; IUCN, 2020). In Mexico, the Norma Official Mexicana NOM-059-SEMARNAT-2010 (DOF, 2010; NOM hereafter) is the legal instrument that describes species risk categories at the national level. The NOM bases its categorization on the Method for Extinction Risk Assessment of Mexico's Wild Species (MER). This method includes assessing the species' distribution, vulnerability, and the influence of anthropic activities on their survival.

Both lists, IUCN and NOM, base the taxonomic recognition of the conservation units by applying the Biological Species Concept (BSC), defined as "the groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups" (Mayr, 1942, 1957, 1963). Thus, the characteristic of evolutionary units is their reproductive discontinuity from other units (Cracraft, 1983), and whose criterion for identifying species is precisely the ability to produce fertile offspring (Dobzhansky, 1973; Mayr, 1942); although some authors have recently accepted within this concept a relaxation in the strict necessity of reproductive isolation (i.e., Coyne & Orr, 2004; Johnson et al., 1999). Nevertheless, the central issue of differentiation is not reproductive isolation because it has no consistent genotypic or phenotypic correlations to predict allopatric groups' reproductive compatibility. Besides, extensive inbreeding tests are impractical, and one needs to assume that phenetic similarity is directly related to ease of interbreeding (Sokal & Crovello, 1970). The BSC fails to provide unambiguous criteria for grouping organisms (or assigning species rank). Consequently, the resulting species are inappropriate for comparative biology or analyses of evolutionary history, as recognized taxons are frequently conglomerates of several independent, not necessarily monophyletic groups. Also, hybrid zones do not necessarily contribute to clarifying species limits. Alternatively, the Phylogenetic Species Concept (PSC) defines a species as "the smallest diagnosable cluster of individual organisms within which there is a parental pattern of ancestry and descent" (Cracraft, 1983). Various formulations of a PSC (e.g., Cracraft, 1983; de Queiroz & Donoghue, 1988; Donohgue, 1985; Mckitrick & Zink, 1988; Mishler & Brandon, 1987; Nixon & Wheeler, 1990; Zink & Mckitrick, 1995) agree that species concepts and definitions should emphasize criteria of phylogenetic relationship (descent) and not reproductive relationship (interbreeding; Donohgue, 1985; de Queiroz & Donoghue, 1988). Although different versions of the PSC emphasize diagnosability, monophyly, or both (see Mayden, 1997; Mishler & Theriot, 2000), all recognize that the species constitute differentiated basal taxa by the presence of unique characters (autapomorphies) or unique combinations of characters that allow the delimitation of evolutionary units or lineages (Mckitrick & Zink, 1988; Mishler and Theriot, 2000; Nixon & Wheeler, 1990; Zink & Mckitrick, 1995). Thus, the theoretical and practical limitations of the BSC lead us to advocate a PSC, which emphasizes monophyly and where diagnostic characters are considered to flag independent evolutionary histories and are used to delineate species boundaries. Such basal evolutionary units should be used in phylogeny reconstruction, speciation analysis, biogeography, and conservation (de Queiroz & Donoghue, 1988; Donohgue, 1985; Mckitrick & Zink, 1988; Moritz, 1994; Ryder, 1986). Despite many other species concepts, those cited previously are the most commonly accepted in biology and conservation.

By applying the PSC delimitation criteria instead of the BSC in the risk lists, different allopatric and diagnosable populations within some of the current biological species would be recognized as independent evolutionary units (Rojas-Soto et al., 2010). Consequently, several taxa considered as subspecies under the BSC would be considered as species under the PSC

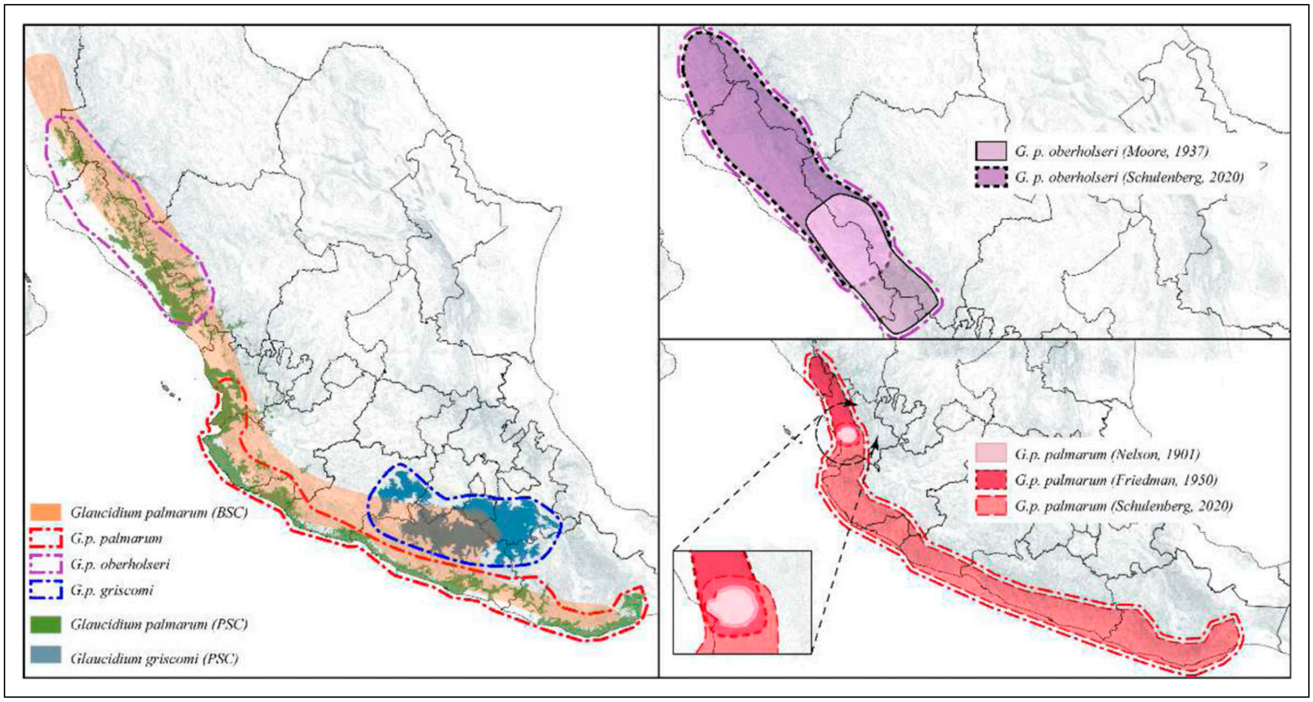


Figure 1. (a) Geographic representation of the actual recognized distribution of *Glaucidium palmarum* considering the BSC (solid light orange) and the three subspecies that conformed the species: *Glaucidium palmarum palmarum* (discontinuous red line), *G. p. oberholseri* (discontinuous purple line) and *G. p. griscomi* (discontinuous blue line) in contrast to the separate distribution of *Glaucidium palmarum* (solid green) and *Glaucidium griscomi* (solid blue) when considering the PSC. (b) Potential distribution area of *G. p. oberholseri* considering two different sources. (c) Potential distribution area of *G. p. palmarum* considering three different sources.

since biological species could be divided into two or more phylogenetic species (Figure 1a), which means recognizing independent distribution areas (i.e., allopatric populations recognized as separate species; Cordier et al., 2021; Zink, 2014). This division implies that, when applying the PSC, a reevaluation for the assignment of the risk categories is needed in some cases, given the presumption that they could be at greater risk due to the intrinsic reduction of the distribution areas and their population sizes (Cordier et al., 2021; Rojas-Soto et al., 2010; Williams et al., 2009). In this sense, one might expect that the consideration of subspecies for protection would not represent a conservation problem if subspecies always agreed with phylogenetic species or evolutionary units (e.g., *Glaucidium griscomi* corresponds with *Glaucidium palmarum griscomi*) but this becomes problematic when subspecies do not correspond with phylogenetic species (e.g., the phylogenetic species *Glaucidium palmarum* include two subspecies: *G. palmarum palmarum*, and *G. p. oberholseri*), which masks the actual conservation target (Figure 1a).

Since changes in the official taxonomic lists (e.g., American Ornithological Society; AOS) are generally made after the publication of systematic studies, omissions inevitably occur in recognition of new lineages (i.e., species) resulting from the application of the PSC. Furthermore, it is common to observe bias in the taxonomic update toward more studied regions (e.g., North America) compared to others (e.g., the Neotropics); and toward certain groups (Hortal et al., 2015), which displaces the study of other taxa of less interest (Ortiz-Pulido, 2018). On the other hand, the official lists (recognized by the AOS, Handbook of the Birds of the World (HBW) & Birdlife International, 2019a) are based on the BSC but tend to omit the 75% rule criterion for subspecies recognition on their classifications, which means that some of them could, or not, qualify as valid taxa (Remsen, 2010) and also, subspecies distributions are not known well enough, there is no explicit geographic information, or there is a disagreement between sources (Friedmann et al., 1950; Moore, 1937; Nelson, 1901; Schulenberg, 2020; Figures 1b and c). As expected, these committees frequently dismiss the studies that demonstrate and support the phylogenetic species status (AOU, 1998 and its supplements, last: Chesser et al., 2021), which can generate vulnerability for populations of species that are not included in the risk lists. Therefore, the assignment of risk categories using the PSC constitutes an alternative to the BSC to protect the uniqueness of avian diversity throughout the re-analyses and new interpretation of the variation of characters that ponders an evolutionary recognition of the units to be protected (Haig et al., 2006; Isaac et al., 2004; Moritz, 1994; Rojas-Soto et al., 2010; Ryder, 1986; Zink, 2004).

The main goal of this study was to analyze the implications of the application of the PSC in the risk status' assignment in NOM-059-SEMARNAT-2010 and the IUCN Red List of Threatened Species, based on the ranges of the phylogenetic species recognized from the new taxonomic reassessments, using the Mexican endemic avifauna as an example. We compared the species recognized under the PSC and the traditional taxonomy based on the BSC as an input for their possible updating or inclusion in the current risk lists.

Materials and Methods

Species selection

We made a list of species following a taxonomic proposal by Navarro-Sigüenza and Peterson (2004) since they included and compiled all the taxonomical modifications in a complete and detailed list for Mexico, as well as other subsequent studies (Supplementary Appendix 1), although other previous efforts are also relevant in phylogenetic and evolutionary terms (e.g., Peterson & Navarro-Sigüenza, 2000). They developed an alternative taxonomy for the Mexican birds based on the specific recognition of genetically and morphologically differentiated allopatric populations, that is, based on the PSC. Several studies have recognized these populations as independent species; however, they are still considered subspecies according to the traditional BSC taxonomy. We removed species from the resulting list according to the following criteria: (1) when subsequent studies did not justify their recognition as differentiated phylogenetic species; (2) when they were insular phylogenetic species, or (3) when they had less than six occurrences for modeling techniques (Proosdij et al., 2016). The resulting list comprises 93 phylogenetic species that correspond to endemic lineages to continental Mexico.

Because the risk lists compared in this study follow different taxonomic authorities, we used the species name recognized by the AOS (which follows the NOM), the species names recognized by the HBW (Followed by the IUCN), and the species names defined by Navarro-Sigüenza and Peterson (2004) for the lineages used in the study (See Supplementary Appendix 1).

International organizations such as the IUCN use different criteria assessment for the designation of risk categories, being population size reduction (A1, reversible population reduction; A2, population reduction that has not ceased or is irreversible; A3, projected population reduction in the future; A4, population reduction in the past and with projection into the future), geographic range (B1, extent of occurrence; B2, area of occupancy), small population size and decline (C1, projected reduction of mature individuals; C2, the observed decrease of mature individuals; D, small or restricted population; D1, number of mature individuals; D2, reduced area of occupancy with restricted populations), quantitative analyses of extinction risk (E), or combinations and adjustments among them. Integrating this result can lead to assign one of the following risk categories: extinct (EX), extinct in the wild (EW), critically endangered (CR), endangered (EN), vulnerable (VU), near threatened (NT) and least concern (LC) (IUCN, 2019). In Mexico, the assignment of risk categories for species and subspecies listed in the NOM is carried out following the Risk Evaluation Method (MER). This method considers factors such as (A) the extent of the taxon's distribution in Mexico, which refers to the relative size of the current natural distribution range as a percentage of the representativeness at the national level, (B) the conservation status of the habitat in which the taxon under analysis naturally occurs, (C) the intrinsic biological vulnerability of the species which is related to the taxon's natural history, and (D) the impact of human activity on the taxon (Tambutti et al., 2001). NOM uses four risk categories: probably extinct in the wild (E), endangered (P), threatened (A), and subject to special protection (Pr).

We compared the list of selected phylogenetic species with the species and subspecies listed in the NOM (BSC) and assigned them the risk category that could be equivalent for each phylogenetic species, that is, if the lineage is derived from the division of a species, we assigned the risk category of the species. If the lineage corresponds to a subspecies, we assigned the subspecies' risk category (Supplementary Appendix 1).

In the NOM's case, not all the evolutionary units included in the lists of species and subspecies in the risk category have been evaluated by the MER. Some species were included based on expert knowledge of the status of the populations. Therefore, we stated in Supplementary Appendix 1 if the species or subspecies were evaluated following the MER. Likewise, we identified the risk categories of the IUCN Red List and got the corresponding risk category according to the biological species category when the phylogenetic species was not recognized.

Also, we placed the population trend determined for each taxon as published in the IUCN Red List of Threatened Species, considering it a factor that could affect the species' susceptibility to extinction risk. Because some lineages evaluated in this study have been recognized by the HBW/Birdlife as independent species and the IUCN recognizes the changes, we place population trends corresponding with the taxon. If they have not accepted the taxon split, we consider the population trend equivalent to the taxon it derived. Similarly, we placed the population trend and the total score resulting from the Partners In Flight species conservation status assessment (PIF, 2020). It includes factors such as distribution in the reproductive and non-reproductive season, population size, population trend, threats in the reproductive and non-reproductive season, and the species' vulnerability.

For the reconstruction of the distribution areas of each of the species defined under the PSC, we got all records from various sources, such as the Global Biodiversity Information Facility (GBIF), the Atlas of the Birds of Mexico (Navarro-Sigüenza et al., 2003), "Naturalista" curatorial validated data (CONABIO, 2018) and those of the eBird digital database (2018). We eliminated those duplicated in the same pixel of the climatic coverages (<1 km^2) to decrease spatial autocorrelation between nearby presence points from the total number of records. To reduce geo-referencing errors, we eliminated all the records that were over 200 km from each species' known geographic distribution. The number of records per species ranged from 6 to 1,336 (Supplementary Appendix 2).

Species Distribution Modeling

We use the MaxEnt algorithm to construct the species distribution models (SDMs; Phillips et al., 2006) since it produces consistent results with small sample sizes (Cassini, 2011; Hernandez et al., 2006; Pearson et al., 2007). To delimit the calibration area for each species (i.e., the area of accessibility or M *sensu* Soberón & Peterson, 2005; see also Barve et al., 2011), we used as a limit the intersection between the biogeographic provinces (Morrone et al., 2017), the ecoregions of the world (Olson et al., 2001), and other biogeographically and topographic elements such as the Isthmus of Tehuantepec, and extended hillsides (Supplementary Appendix 3), that could represent a dispersal barrier for the species (Peterson et al., 1999). We selected and edited all the coverages, and other geographic information layers with ArcMap 10.3 (ESRI, 2011).

We ran a MaxEnt preliminary model for each species that included all 19 bioclimatic coverages with a spatial resolution of 30 seconds (~1 km^2) derived from the precipitation and temperature variables (Cuervo-Robayo et al., 2013). With a Jackknife test run within the same algorithm, we selected those variables with at least a 2% contribution to each species' model based on each variable's relative contribution percentages. In those species where the variables with a contribution more significant than 2% were less than five, to provide more information to the model, we added the ones that contributed up to 1% if they were not correlated ($R<0.80$; Pearson, 1955). We use the selected variables to develop the final model for each species. For the models of those species with 20 or fewer records, we carried out the models using the Jackknife test proposed by Pearson et al. (2007), in which we use all the records for their construction; this method comprises testing the algorithm performance by creating replicates but eliminating one point at a time (n - 1). To do this, we run a significance test through the Pvaluecompute.exe program that defines a predicted performance based on each model's ability to predict the record that was previously left out and measure the remaining points' predictive ability.

For species of which we had over 20 records, we used 80% of the data to calibrate the model, while the remaining 20% was used for validation. We performed five replicates with a limit of 1,000 iterations based on the Bootstrap resampling method. For the selection of the best model among the five replicates, we used the following criteria and in that order: (1) the lowest values of omission rate of the validation points, (2) the highest values of AUC, and (3) the smallest predicted surface area (Anderson et al., 2002). Subsequently, we validated each final selected model by implementing a Partial ROC (Barve, 2008).

Once we determine the potential distribution areas (based on SDMs), we calculate the approximate area in km^2 for each species. Then we contrast the resulting areas with the MER criterion "A" for which (1) assigned a score of four when the species is distributed in less than 5% of the national territory, considering them as highly restricted; (2) a score of three when species have a restricted distribution, which means that its area of distribution in Mexico ranges between 5% and 15% of the national territory; (3) a score of two when its distribution is greater than 15% but less than 40% of the national territory (widely distributed), and finally; (4) a score of one when its distribution in the national territory is extensive with an area equal to or greater than 40% of the national territory (Tambutti et al., 2001).

In contrast with IUCN, we considered the parameters established in the guide for the use of IUCN categories and criteria (IUCN, 2019) for the criterion "B1" to determine the risk category to the species based on their distribution area, for which: (a) species could be considered as critically endangered (CR) when species have a distribution area of fewer than 100 km^2; (b) species are susceptible to be considered threatened (EN), if their distribution area is less than 5,000 km^2; (c) species are considered vulnerable if their distribution area is less than 20,000 km^2; (d) for the near-threatened category (NT), must follow a set of assumptions, among which we can consider that the population trend is decreasing and their distribution area is 30,000 km^2 or minor.

Results

From the 93 phylogenetic species evaluated, we found that 31 are currently under some conservation concern. Eleven are listed as species and 20 as subspecies according to the NOM (Supplementary Appendix 1). There are 20 species found to belong to an at-risk category and that are also recognized as independent units based on IUCN: 18 as LC and two as NT. Of these 20 species, five have a decreasing population trend, nine are stable, and one is increasing, and trend is unknown for the other five. For the 73 remaining phylogenetic species, we considered the established population trend for their related species recognized under the BSC. That results in 34 phylogenetic species with a decreasing trend, 29 as stable, six increasing, and four with an unknown trend (Supplementary Appendix 1).

The potential distribution models reveal that 68 species were highly restricted (73%), 16 species (17%) were restricted; eight are considered widely distributed, and only one resulted in the extensive distribution classification. 73.2% of the potential distribution models for the species meet high scores for criterion "A" of the MER. In terms of the IUCN classification and according to the "B1" criterion, for 62 species (66%), the distribution areas determined from the SDMs would remain in the LC category, nine species could be susceptible to having the NT category, 15 as vulnerable and seven as threatened in the EN category (see examples in Table 1).

Of the 68 highly restricted species, 23 have a score between 15 and 18, according to the evaluation of the PIF conservation status, and most of them have decreasing population trends (Table 2) so they can be considered species with high vulnerability or risk of extinction (Supplementary Appendix 1). Of these, only five have a risk category assigned by the NOM as subspecies equivalent to the phylogenetic species recognized by PSC.

Finally, 31 species are susceptible to a reconsideration of the risk category assigned by the IUCN, of which 22 could be re-categorized based on the potential distribution models obtained, nine could change to NT due to the combination of factors, and 62 species would maintain their category under criterion "B1" when considering the PSC.

Discussion

Red lists have used the BSC as a unit to determine species risk categories; however, the use of traditional taxonomy has ramifications in cases of specific phylogenetic species (e.g., Cortés-Rodríguez et al., 2008; Domínguez-Domínguez & Vázquez-Domínguez, 2009; González et al., 2011; Puebla-Olivares et al., 2008; Zink et al., 1997), where delimitations are not accurate for conservation purposes since they fail to recognize species evolutionary history, masking the fragility of taxa, leading to biases in conservation efforts (Moritz, 1994; Peterson & Navarro-Sigüenza, 1999; Rojas-Soto et al., 2010). In the case of NOM and partially in IUCN, the application of the BSC recognizes two taxonomic categories (i.e., species and subspecies) that correspond to one evolutionary unit (i.e., lineages) under the PSC. For example, some of the phylogenetic species considered correspond to biological species, others to subspecies, and even some correspond to two subspecies, such as *Cyrtonyx sallei,* which includes the subspecies *C. montezumae sallei* and *C. m. rowleyi* (Navarro-Sigüenza & Peterson, 2004), of which the NOM protects only the first. In these cases, the NOM segregates some populations of *C. sallei* as it fails to recognize the entire lineage as a single evolutionary unit.

There are complexes of species such as *Lampornis amethystinus* (Cortés-Rodríguez et al., 2008), *Pampa curvipennis* (González et al., 2011), and *Aulacorhynchus prasinus* (Puebla-Olivares et al., 2008) that have restricted distributions and under the PSC are divided into independent species. In these cases, importance should first be given to the extent of distribution for the assignment of risk categories and then to analyze other aspects, such as habitat modification pressures generated by anthropic activities and land-use change (MER, Tambutti et al., 2001; IUCN, 2019). For this reason, it is essential to focus studies and efforts on including the consideration of specific phylogenetic species in the environmental policy agenda, increasing their visibility to policymakers and the general public. Furthermore, the application of the PSC as a taxonomic criterion also reduces the ambiguity of the patterns that lead to subspecies delimitation, for example, when the interpretation of the different characters is not distributed geographically in a concordant manner (Remsen, 2010).

We highlighted some cases to exemplify the implications of the results found following. In the IUCN list, there are five subspecies endemic to Mexico from the separation of *Colinus virginianus* (*C. ridgwayi, C. coyolcos, C. pectoralis, C. graysoni,* and *C. godmani;* Figure 2). If they were recognized as independent species (as suggested by the PSC), they would have an

Table 1. Examples of Some Phylogenetic Species Whose Categories Could Be Modified by the Implementation of the PSC. Columns from Left to Right are Included: (1) The Phylogenetic Species, (2) The Population Trend According to IUCN, * The Category is Assigned to the Species from Which the Phylogenetic Species is Derived (PT); (3) Vulnerability Value According to PIF (Where Values Close to One are Low Vulnerability and Maximum Vulnerability Corresponds to 20); (4) The Potential Distribution Area of the Phylogenetic Species in Square Kilometers; (5) The Current Risk Category by IUCN Corresponding to the Species: LC= Least Concern, NT= Near Threatened, *= the Category Comes from the Taxon from Which it is Split (RC IUCN); 6) The Category When Considering the B1 Criterion: LC= Least Concern, NT= Near Threatened, VU= Vulnerable, EN= Endangered (PC IUCN). NOM Category: P= Endangered, A= Threatened, ** The Category is Assigned to the Subspecies, *** The Category is Assigned to the Species from Which the Phylogenetic Species is Derived (RC NOM); Value to Criterion A of the MER.

Species	PT	PIF	Potential distribution area km^2	RC IUCN	PC IUCN	RC NOM	MER Value
Colinus ridgwayi	Decreasing*	12*	168,006.25	NT*	LC	P**	3
Colinus coyolcos	Decreasing*	12*	12,990.40	NT*	VU		4
Colinus pectoralis	Decreasing*	12*	14,139.02	NT*	VU		4
Colinus graysoni	Decreasing*	12*	65,168.21	NT*	LC		4
Colinus godmani	Decreasing*	12*	52,672.82	NT*	LC		4
Glaucidium palmarum	Decreasing*	16*	68,117.39	LC*	LC	A	4
Glaucidium griscomi	Decreasing*	16*	23,801.27	LC*	NT	A***	4
Coturnicops godmani	Stable*	15*	1,313.90	LC*	EN	P**	4
Campylorhynchus rufinucha	Decreasing	12*	6,363.31	LC	VU	A**	4
Campylorhynchus humilis	Decreasing	12*	47,116.71	LC	LC		4
Phaethornis mexicanus	Unknown	16	22,255.31	LC	NT		4

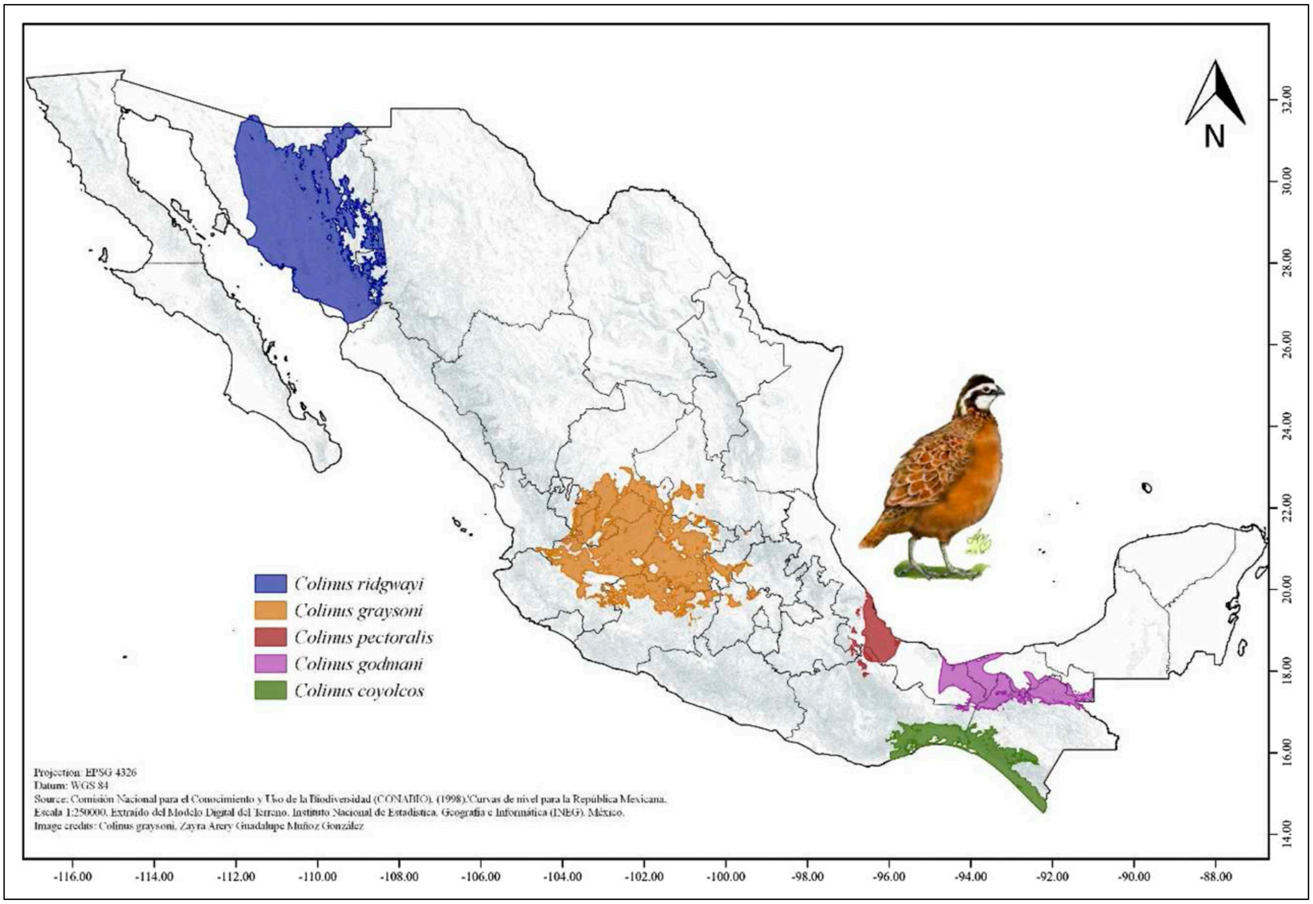
Table 2. List of Species With High Vulnerability or Risk of Extinction Columns from Left to Right are Included: (1) The Phylogenetic Species, (2) The Population Trend According to PIF, * The Category is Assigned to the Species From Which the Phylogenetic Species is Derived (PT) 1= Large Significant Increase, 2= Small Significant Increase, 3= Uncertain Population Change, 4= Possible Moderate Decrease or Moderate Significant Decrease, 5= Large Significant Decrease, * if from the Taxon from Which the Phylogenetic Species is Derived; (3) Vulnerability Value According to PIF (Where Values Close to One are Low Vulnerability and Maximum Vulnerability Corresponds to 20); (4) NOM Category: P= Endangered, A= Threatened, *The Category is Assigned to the Subspecies; (5) The Potential Distribution Area in Square Kilometers; (6) Percentage Relative to Distribution in México (%).

Species	PT	PIF	NOM	Potential distribution area km^2	%
Phaethornis mexicanus	4	16		22,255.31	1.14
Campylopterus curvipennis	4*	15		46,515.19	2.37
Campylopterus excellens	4	17	Pr*	69,511.15	3.55
Coturnicops goldmani	3*	15	P*	1,313.90	0.06
Megascops lambi	4*	16	Pr	9,814.17	0.5
Glaucidium palmarum	4*	16	A	68,117.39	3.47
Glaucidium griscomi	4*	16	A	23,801.27	1.21
Aulacorhynchus wagleri	4*	15	Pr/A*	11,823.42	0.6
Psittacara brewsteri	4*	16	A/P*	34,224.81	1.74
Forpus cyanopygius	4*	17	Pr	84,001.04	4.28
Grallaria binfordi	5*	15	P	27,661.16	1.41
Grallaria ochraceiventris	5*	15	P	68,355.29	3.48
Dendrocolaptes sheffleri	4*	15	Pr	31,517.71	1.6
Aphelocoma guerrerensis	4*	16		11,862.65	0.6
Campylorhynchus megalopterus	4*	16		71,134.18	3.62
Campylorhynchus nelsoni	4*	16		41,993.84	2.14
Polioptila albiventris	4	18		30,810.68	1.57
Toxostoma arenicola	5*	17		29,926.67	1.52
Rhodinocichla schistacea	4*	17		57,535.24	2.93
Junco bairdi	3	16	Pr*	7,054.48	0.35
Atlapetes albinucha	4*	16		42,085.66	2.14
Cardellina melanauris	4*	15		71,215.15	3.63
Amaurospiza relicta	4*	17	P	41,255.92	2.1

NT classification because they would be assigned the taxon category to which they are associated. However, *C. coyolcos* and *C. pectoralis* could be included in the vulnerable category as phylogenetic species with more restricted distribution. Regarding the NOM, only *C. ridgwayi* has an assigned category (Table 1). However, because the *C. virginianus* complex is susceptible to extractive use for human consumption which would further decrease their populations, the revision of the risk category for all phylogenetic species could be pertinent to ensure the maintenance and establishment of sustainable management programs for its populations.

Other examples include the *Glaucidium palmarum, Coturnicops noveboracensis* and *Campylorhynchus rufinucha* complexes (Table 1). The IUCN considers the extensive distribution of these biological species as a continuous area without distinguishing between phylogenetic species with allopatric distribution. Furthermore, the area includes ecosystems that are unsuitable for the species. In the *G. palmarum* complex, the distribution considered areas of high mountain forests; however, this species shows a direct and strict association with arid and tropical ecosystems (Howell & Robbins, 1995; Stotz et al., 1996). Specifically, with the tropical dry forest and the cloud forest's lowlands, the use of the distribution area proposed by the IUCN when using the BSC can lead to inefficiency in defining conservation strategies and actions. This complex splits in *G. palmarum* y *G. griscomi* under the PSC, and *G. griscomi* could be considered in the NT category due to the extension of its range, PIF score, and the cloud forest vulnerability to which it is associated (Ponce-Reyes et al., 2012; Sierra-Morales et al., 2021; Stotz et al., 1996).

There are cases, such as *Coturnicops goldmani* (separate phylogenetic species from *C. noveboracensis*), that turned out to be "very restricted" because the estimated potential distribution area for this species is 0.06% of the national territory. Moreover, it turned out to be the most restricted lineage of all those evaluated, indicating that *C. goldmani* could be considered CR (critically endangered). *C. noveboracensis* is considered an LC biological species due to its stable population trend and wide distribution; however, it is presumed that *C. goldmani* is a separate phylogenetic species extinct in the wild (Howell & Webb, 1995). Although there are elements to consider *C. golmani* as a different species due to its limited dispersal capacity, neither the NOM nor the



Projection: EPSG 4326
Datum: WGS 84
Source: Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO). (1998).'Curvas de nivel para la República Mexicana. Escala 1:250000. Extraído del Modelo Digital del Terreno. Instituto Nacional de Estadística, Geografía e Informática (INEG). México.
Image credits: Colinus graysoni, Zayra Arery Guadalupe Muñoz González

Figure 2. Potential distribution of five phylogenetic species separated from the biological species *Colinus virginianus*.

IUCN has considered that designation, not even as a subspecies, which suggests omissions in the risk assessment when considering a minor taxon.

Another example is *Campylorhynchus rufinucha*, a resident species of the tropical dry forest; this complex has a continuous distribution that ranges from western Mexico to northwestern Costa Rica with an isolated population in the central Veracruz plains near the Gulf of Mexico (under the BSC). However, Vázquez-Miranda et al. (2009) confirmed the genetic differentiation between the three subspecies that comprise it, resulting in *C. rufinucha* and *C. humilis* as Mexican endemic new phylogenetic species and a third species: *C. capistratus*, with distribution in southern Mexico and Central America. The AOS has not considered the taxonomic implications of the evidence showed by Vázquez-Miranda et al. (2009), ten years after its publication; however, the IOC (Gill et al., 2020) and HBW (2019b) have already accepted the separation and currently consider them as independent species. The suggested changes could mean that *C. humilis* as a recognized species would merit a new category and be assigned special protection based on MER criterion “A,” as it is a species with a very restricted distribution (*C. rufinucha* has the category of threatened as a subspecies thus the category could be maintained). On the other hand, for IUCN criterion B1, *C. rufinucha* could be considered VU.

Likewise, *Phaethornis mexicanus* has not been considered for inclusion in either of the two lists of species at risk, despite being recognized as a separate species from *P. longirostris* (Arbeláez-Cortés & Navarro-Sigüenza, 2013). This species distribution area is equivalent to 1.82% of the national territory, suggesting it could be assigned to a risk category considering the precautionary principle, which states that where there are threats of irreversible damage, and lack of scientific certainty shall not be used as a reason for postponing conservation actions (United Nations, 1992). Therefore, based on its restricted distribution, population decline, and vulnerability to climate and land-use change (Prieto-Torres et al., 2021; Sierra-Morales et al., 2016), *P. mexicanus* could be categorized as NT and Pr (Subject to Special Protection) according to the IUCN and the NOM, respectively.

Because the species analyzed in this study are Mexican endemic, it is crucial to consider them when categorizing risk at the national level by applying the risk evaluation method. Of all the 392 bird species and subspecies, only 91 (23%) were evaluated by the MER (DOF, 2010), which means that the rest of the species in risk categories were assigned with a sense of urgency based on "expert" knowledge. This situation highlights the relevance of enhancing studies that provide inputs for the re-categorization of the species. Of the species considered in this study, only 11 were evaluated by the MER, four as subspecies consistent with phylogenetic species under the PSC (*Arremon apertus, Chlorospingus wetmorei, Glaucidium hoskinstii, and Campylopterus excellens*) and the remaining in the species category under the BSC (*Amaurospiza relicta, Amazilia viridifrons, Crypturellus occidentalis, Grallaria binfordi, G. ochraceiventris, Glaucidium palmarum,* and *G. griscomi*). The correspondence of the category after the splitting considering the range reduction and population size reduction could be discordant.

It is currently difficult to determine how many Mexican species are or should be included under a risk category (Ortiz-Pulido, 2018) due, among other causes, to the lack of taxonomic coincidence among sources (Rojas-Soto et al., 2010; Zink, 2004), which produces uncertainty in taxa's recognition. In this sense, given that the BSC considers reproduction for the delimitation of species, it generates uncertainty in recognizing their risk status, which can be clarified by considering finer aspects of species limits, such as the ancestry-descent patterns that the PSC addresses (Isaac et al., 2004; Moritz, 1994; Ryder, 1986; Zink, 2004).

In the absence of information and lack of resources to conduct extensive studies on species status, risk categorization systems inevitably tend to arbitrariness, exemplifying the importance of using a species concept that favors the recognition of evolutionary units as a conservation target (Alström, 2006; Frankham et al., 2012; Mayden, 1997). Since the PSC recognizes the individuality of taxa based on the uniqueness of the ancestral descent pattern, it increases the stability granted by being defined as a base unit (Domínguez-Domínguez & Vázquez-Domínguez, 2009; Leslie, 2015; Wheeler, 1999; Zink, 2004), with more assertive impact on the definition of public policies on biodiversity. Besides, one major problem is the fact that several of the current officially recognized subspecies (under the BSC) are not diagnosable by any mean (morphologically, genetically, geographically, and environmentally), and thus, they do not are considered, neither correspond to any phylogenetic species (Rojas-Soto et al., 2010; Zink, 2004).

Implications for Conservation

The current biodiversity crisis demands urgent actions to conserve all species realistically. However, decision-making will not be effective without a proper taxonomic basis. In the case of environmental legislation in Mexico, protection is established for some subspecies, although none of the laws or regulations define subspecies [e.g., Ley General del Equilibrio Ecológico y Protección al Ambiente (DOF, 2021), Ley General de Vida Silvestre (DOF, 2018), NOM (DOF, 2010)], making impossible to law enforcers the understanding of the taxonomic units they are protecting.

In the last decades, more studies have found a lack of correspondence between subspecies boundaries and historical groups obtained by phylogenetic analyses, particularly in species showing continuous distributions and clinal variation based on morphology, molecular, and vocal data sets (e.g., García-Moreno et al., 2004; Vazquez-Miranda et al., 2017; Zink et al., 1997). Within this framework, conservation policies compose endangered taxa lists based on the agreements of the scientific community. Thus, scientists using diverse taxonomic criteria to recognize forms encompassing in the catalogs should devote their efforts to conserving biodiversity by compiling, advising, and commenting on such lists. However, diverse taxa remain unstudied, creating a notably unbalanced alpha taxonomy for the global avifauna (Navarro-Siguenza & Peterson, 2004; Peterson, 2006).

Also, current conservation actions are biased because the recognized taxonomic status undermines understanding the actual threats to species. The approach of this study suggests the need to consider species from a phylogenetic perspective and update the official list to focus conservation actions on those lineages whose risk category assignment is a priority. The recognition of independent phylogenetic species generates new reduced ranges, which underlines lineages' geographic marginality in several cases and might increase their vulnerability to climate change and landscape fragmentation (Nori et al., 2015; Vásquez-Aguilar et al., 2021). Our results show that at least 18 species could be candidates for a reassessment of risk category assignment under the PSC after recognizing a new distribution summed with the current vulnerability status.

Although we focus on the assignment of risk categories in this work, it is necessary to consider other essential aspects to conserve biodiversity effectively. Some of the key activities include: (1) a call for attention to research approaches, (2) generating information that reflects the conservation status of the species, (3) results used as inputs for priority species listing, (4) the possibility of including marginalized taxa in federal programs for urgent actions (e.g., Species Conservation Action Programs (PACE) in the case of Mexico), (5) elaborating focused conservation plans, and 6) implementing medium and long-term conservation actions.

In diverse cases, subspecies might not represent evolutionary units and processes at any scale, failing in the detection of several significant conservation units. Since conservation priorities depend critically on the particular authority employed, we suggest that taking into account the PSC will significantly improve progress in the delimitation of conservation units in species and subspecies concept debate (Winker et al., 2007; Zink, 2004). We need an agreement on the taxonomic basis for taxa, which would improve bird conservation policies.

Author Contributions

The authors' contribution was equal for the study's concept and design; data collection, data analysis and interpretation, manuscript preparation, and critical revision, adding intellectual content.

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ORCID iD

Alejandra Galindo-Cruz https://orcid.org/0000-0001-7470-1449

Supplemental Material

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