Conservation hotspots of insular endemic mammalian diversity at risk of extinction across a multidimensional approach

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Abstract

Aim: Islands are one of the most threatened worldwide biotas. Based on their taxonomic diversity, some insular regions have been identified as key areas of conservation. Recently, systematic conservation planning has advocated for the use of multiple biodiversity facets to protect unique evolutionary and functional processes. Here, we identified priority areas for threatened insular endemic mammals across three key dimensions of biodiversity (taxonomic, phylogenetic, and functional), as well as their protection level and threats affecting them.

Location: Worldwide.

Methods: We applied diversity–area relationships to identify insular regions that harbored a disproportionately high rate of threatened endemic mammal diversity (whether taxonomic, phylogenetic, or functional) given their area for 1,799 islands across 19 insular regions. We also assessed the level of protection and the threats affecting biodiversity within each insular region.

Results: We showed a fairly good congruence between top-ranked insular regions based on taxonomic, phylogenetic, and functional diversity. Specifically, we identified four hotspots for endemic mammalian conservation through the three diversity facets: Indo-Burma, Madagascar and the Indian Ocean Islands, Mesoamerica and Galápagos Islands, and Wallacea. Except for Mesoamerica and Galápagos Islands, the protected areas coverage is low (<8%) within the hotspots. We also showed that most of the mammal species occurring in the hotspots was prone to either direct threats that affect their mortality or indirect threats that only alter their habitat, while mixed threats such as biological invasions or climate change were less represented in those regions.

Main conclusions: Our findings reinforce the importance of investigating the multiple diversity facets in a conservation concern and to link with the associated threats to ensure an effective conservation strategy.

Keywords: endemic species, functional diversity, hotspots, islands, phylogenetic diversity, protected areas, taxonomic diversity, threats
INTRODUCTION

Biodiversity is declining globally at rates accelerated and unprecedented in human history (Barnosky et al., 2011). Current records showed that more than 8,850 vertebrate species are decreasing in population size and range (Ceballos et al., 2017) and that 390 vertebrates have already disappeared in the last 500 years (Ceballos et al., 2010). The main drivers of biodiversity loss are multiple, including agricultural expansion, overexploitation and introduction of invasive alien species (Maxwell et al., 2016). One way to provide species protection against global changes is the development of effective protected areas. Protected areas are the mainstay of the conservation strategies and intend to provide biodiversity refuges to human pressure (Rodrigues et al., 2004).

To date, systematic conservation planning is usually conducted on a site basis to protect areas containing an exceptional concentration of biodiversity, measured by total species richness, species endemism, or threatened species richness (Margules & Pressey, 2000). This approach puts taxonomic diversity at the first front to decide conservation priorities. However, by focusing only on taxonomic diversity we assume that all species are equivalent entities, while they are a product of complex ecological and evolutionary processes that make each of them particularly unique (Faith, 1992; Iknayan et al., 2014; May, 1990; Vane-Wright et al., 1991). This is particularly problematic as it could lead to prioritizing areas with similar assemblage composition at the cost of areas hosting unique assemblages (Brown et al., 2015; Kukcala & Moilanen, 2013). Therefore, selecting regions based only on species richness may not be the best conservation strategy as it does not capture other facets of diversity such as phylogenetic or functional diversities (Díaz et al., 2007; Faith, 1992; Mazel et al., 2014). Phylogenetic diversity represents the diversity in species genetic composition and evolutionary history (Faith, 1992; Vane-Wright et al., 1991) essential to maintain evolutionary potential of communities (Purvis et al., 2005), while functional diversity is the variation of ecological traits of species (Tilman, 2001; Viole et al., 2007) needed to preserve community productivity, ecosystem stability and ecosystem services (Oliver et al., 2015). If such diversities are not considered, the possibility to have the right feature at hand as well as the resilient capacity in a future changed environment is overlooked (Biggs et al., 2020; Forest et al., 2007), which could have large consequences for biodiversity and ecosystems (Díaz et al., 2007). Therefore, each diversity facet offers valuable information that are all important to consider in order to maximize diversity in the context of complementary reserve selection (Brum et al., 2017; Pollock et al., 2017; Rodríguez & Gaston, 2002; Rodríguez et al., 2011), especially that the different diversity facets are not necessarily good surrogates for each other. While several studies have evidenced spatial congruence between each diversity facet (Rapacciuolo et al., 2018; Rodrigues & Gaston, 2002; Sechrest et al., 2002), some others have not (Brum et al., 2017; Devictor et al., 2010; Pollock et al., 2017). Taxonomic, phylogenetic, and functional diversities could not be easily inferred from each other and yet may bring important properties to protect biological communities. Consequently, conservation strategies need to rely on the three facets to fully represent biodiversity.

A remarkable biota for conservation biology is islands as they contribute to global biodiversity disproportionately to their land area. Even if they only represent 5% of the Earth surface, insular ecosystems represent more than 20% of all known plant and vertebrate species (Kier et al., 2009). Also, island ecosystems harbor a high level of uniqueness due to the presence of many endemic species (Whittaker & Fernandez-Palacios, 2007). Most of them are particularly vulnerable to extinction as they have a narrow geographical range, few populations remaining, small population size and little genetic variability (İşik, 2011). In fact, 60% of species extinctions led by human activities took place on islands (Whittaker & Fernandez-Palacios, 2007). As many island species are extremely restricted in space and highly threatened by global changes, more than continental ones (Kueffer et al., 2010), urgent protection is required (Calado et al., 2014).

Here, we aimed to identify (i) hotspots and coldspots of insular mammal diversity that are at risk of extinctions through the taxonomic, phylogenetic, and functional diversities, (ii) their level of protection, and (iii) their threats. We used diversity–area relationships for 19 insular regions (i.e. 1,799 islands) to account for expected area effects on the different diversity facets, which is of particular importance to ensure a good cost–benefit ratio for conservation. We focused our study on insular endemic mammal biodiversity ($n = 1000$) because among all clades, mammals are particularly jeopardized by global changes (Ceballos et al., 2015; Leclerc et al., 2020) and are characterized by limited dispersal abilities. Also, a consequent amount of data (phylogeny and species traits) is available on this taxon. By taking into account the different facets of diversity as well as protection level and threats information, this study puts into perspective relevant conservation priorities of insular regions.

METHODS

2.1 Species data

The IUCN expert range maps were used to estimate species’ geographic range of mammal species (IUCN, 2020). By overlapping geographic range of species with mainland boundaries and a global vector database of islands (larger than 1 km² and smaller than Greenland; Weigelt et al., 2013), we assigned an insularity-mainland status to each species (i.e. if the species occurs on mainland and/or island(s)), and then we only keep species endemic to one (i.e. single-island endemics) or many islands (i.e. multi-island endemics) because of their key interest for conservation (Fattorini, 2017). A total of 1,000 mammal species distributed among 1,799 islands worldwide from 19 insular regions (based on hotspots biodiversity delimitation; CEPF, 2019) were considered (Figure S1; Table 1). More particularly, 459 mammal species are single-island endemics while the rest of the species ($n = 541$) are multi-island endemics (mean ± s.d.: $20 ± 33$ islands). Among them, 410 mammals were identified as threatened (i.e. vulnerable, endangered, and...
critically endangered) by the IUCN Red List (Table 1). The IUCN Red List assessed the conservation status of species worldwide through a series of criteria such as population sizes and trends, geographic distribution, species’ ecology and habitat preferences (Rodrigues et al., 2006). Evaluation of species extinction risks has been done exhaustively for mammals (Meiri & Chapple, 2016).

| Insular regions                        | Abbreviation | Area (km²) | Number of islands | Number of endemic mammals | Number of threatened endemic mammals |
|----------------------------------------|--------------|------------|-------------------|--------------------------|-------------------------------------|
| Bering and East Siberian Sea Islands   | BESSI        | 17,735     | 13                | 6                        | 1                                   |
| California Islands                     | ClI          | 2,315      | 20                | 11                       | 10                                  |
| Caribbean Islands                      | CrI          | 227,796    | 211               | 47                       | 20                                  |
| East Melanesian Islands                | EMI          | 97,485     | 215               | 70                       | 24                                  |
| Gulf of Guinea Islands                 | GGI          | 2,805      | 2                 | 6                        | 5                                   |
| Indo-Burma                             | IB           | 39,846     | 25                | 11                       | 10                                  |
| Japan                                  | Ja           | 448,483    | 133               | 46                       | 15                                  |
| Madagascar and the Indian Ocean Islands| MIOI         | 599,736    | 82                | 146                      | 84                                  |
| Mediterranean Basin                    | MB           | 66,907     | 33                | 8                        | 6                                   |
| Mesoamerica and Galapagos Islands      | MGI          | 3,165      | 12                | 11                       | 10                                  |
| New Caledonia                          | NC           | 18,502     | 8                 | 7                        | 5                                   |
| Papua New Guinea                       | PNG          | 819,801    | 255               | 205                      | 48                                  |
| Philippines                            | Ph           | 293,368    | 302               | 120                      | 28                                  |
| Polynesia-Micronesia                   | PM           | 23,843     | 77                | 10                       | 8                                   |
| Sri Lanka                              | SL           | 65,627     | 6                 | 16                       | 14                                  |
| Sundaland                              | Su           | 1,338,195  | 216               | 169                      | 65                                  |
| Taiwan                                 | Ta           | 36,007     | 5                 | 14                       | 1                                   |
| Tasmania and New Zealand Islands       | TNZI         | 334,742    | 26                | 9                        | 6                                   |
| Wallacea                               | Wa           | 331,347    | 158               | 182                      | 63                                  |

2.2 | Biodiversity indices

**Taxonomic diversity (TD).** We used the number of threatened species occurring in each region as the taxonomic diversity metric.

**Phylogenetic diversity (PD).** We relied on the Faith index that is the sum of phylogenetic branch length of the studied species pool (Faith, 1992) to assess phylogenetic diversity represented by threatened species from each insular region. We used a time-calibrated molecular phylogeny of extant mammals (Upham et al., 2019) to compute phylogenetic diversity. From this phylogeny, 1,000 trees were generated to capture root-to-tip uncertainty in topology and divergence times. Phylogenetic trees were pruned to the 1,000 species of the global pool. The pdf function of the picante package (Kembel et al., 2010) was used to compute, through Faith index, the phylogenetic diversity represented by threatened species of each insular region. Then, the multiple values of Faith index are averaged for each species pool of insular regions.

**Functional diversity (FD).** Functional diversity can be seen as the value and range of organism traits that influence their performance and thus ecosystem functioning (Hooper et al., 2005; Violle et al., 2007). It can be estimated through a multidimensional niche space that encompasses all trait values of a species pool (Villéger et al., 2008). Here, the measure of functional diversity of threatened species from each insular region relied on the measure of functional richness (FRic). This index reflects the proportion of occupied space by the studied pool of threatened species compared to the volume occupied by the global species pool (n = 1000) (Villéger et al., 2008). Based on scripts developed by Villeger (2017), we computed the FRic index using a matrix of species’ presence and absence information within insular regions and a matrix of species’ traits information. We used five traits: body mass, habitat niche breadth, foraging niche, foraging period, and dominant diet (for more details about the variables, see Table S1 and Leclerc et al., 2020). Because all traits were coded using few categories, species were then gathered into 270 functional entities (FE: group of species that share the same trait values) that hosted between 1 and 48 species. Once FEs were determined, we computed the pairwise functional distances between each FE of species using the Gower dissimilarity index (Gower, 1971), which gives the same weight to each variable. Then, based on the distance matrix, a functional space of four dimensions was built thanks to the PCoA method. This functional space has a good representation of the initial distance for all pairs of FEs (The error rate between initial and final functional distances is about 10% here; Maire et al., 2015) while being able to calculate FRic values for a large number of insular regions (n = 16). Due to mathematical constraints in computing convex hulls in the four-dimensional space,
FRic was not computed for insular regions harboring threatened species that are represented by less than five FEs (i.e. Bering and East Siberian Sea Islands, New Caledonia, and Taiwan).

2.3 | Diversity Area Relationships

In order to identify insular regions with high endemic mammalian diversity at risk of extinction, we used the Diversity–Area Relationship approach (DAR; Mazel et al., 2014). The DAR is one of the most valuable biogeographical tools available to conservationists in order to identify key areas of conservation concern and provides a basis for setting priorities for allocating limited resources (Guilhaumon et al., 2008). Using DAR is mandatory in a wide range of conservation applications that require the comparison of diversity patterns (whether taxonomic, phylogenetic, or functional) when regions differ in area (Smith, 2010). Larger regions are more likely to represent more diversity because they are more likely to hold more diverse habitats (Kallimanis et al., 2008). Thus, biodiversity comparisons among insular regions need to take into account the effect of area. By applying the DAR approach, we attempt to identify regions that have a higher threatened diversity than expected given area to identify insular conservation priorities. The DAR approach requires standardized diversity value and information about area. Here, threatened diversity data for each of the three facets has been standardized (between 0 and 1) by the maximum value of diversity found within insular regions. We also calculated the area of each insular region as the sum of the area of the islands based on data from Weigelt et al. (2013).

Most of the DAR studies are using a power model to fit data of diversity and area. However, the power model is not always the best model, and other models have been reported by studies to provide better fit (Matthews et al., 2019). Therefore, 20 DAR models, described in the literature and using linear and non-linear regressions, were tested on our data using the sars package (Matthews et al., 2019). DAR models are selected based on residual normality and heterogeneity tests, and any model that fails the tests is not considered. Based on those criteria, all of the 20 models were selected for taxonomic, phylogenetic, and functional diversity. Then, a multimodel-averaged DAR curve that is a linear combination of the individual models weighted by the Akaike information criterion (AIC) was computed for each diversity facet. Finally, from the multimodel-averaged DAR for taxonomic, phylogenetic, and functional diversity, residuals were calculated between observed and predicted diversity values of each insular region. A positive residual for a given insular region means that observed threatened diversity is higher than expected given its area. On the contrary, a negative residual for a given insular region means that observed threatened diversity is lower than expected given its area. Then, insular regions were ranked according to their residual values to identify hotspots (regions with the highest residual values) and coldspots (regions with the lowest residual values) (Mazel et al., 2014). A consensus ranking was obtained by summing up the ranking for each region based on the different facets. To test congruency between diversity facets, we examined relationships between residual values of taxonomic, phylogenetic, and functional diversity, using Spearman’s rank correlation test. We also compared rank of insular regions based on DAR approach with rank of insular regions based on raw diversity indices to discuss the advantages of using the DAR approach.

2.4 | Threats and protection level

To take into account the different threats that are affecting the insular endemic mammals studied, we used the list of direct threats provided by the IUCN, which are proximate human activities or processes impacting the status of the taxa being assessed (Salafsky et al., 2008). This framework classified threats into 11 broad types (Table S2). We reclassified the IUCN threats into three general categories: (1) direct – threats that directly affect species’ survival or fecundity; (2) habitat – threats that only modify or destroy the habitat; and (3) mixed – threats that affect species survival or fecundity and that modify or destroy the habitat. Reclassifying threats into broader categories allows us to provide conservation recommendations according to the general threatening mechanisms by disentangling threats that impact extrinsic (i.e. habitat) and/or intrinsic (i.e. survival, fecundity) characteristics of species. We calculated, for each region, the diversity of threatened species affected by each threat category through the three biodiversity indices previously described. Afterward, we computed a representativeness index (RI) for each threat category within insular regions ($RI_{THR} = DivThr_i / \sum_{3} DivThr_i$). This index is based on the threatened diversity impacted by a threat category (DivThr) compared to the threatened diversity impacted by the three threat categories. The representativeness index is calculated separately for each diversity metric (taxonomic, phylogenetic, and functional) and is then averaged. Representativeness of direct, habitat and mixed threats informs on the importance of a threat compared to others within a region. Concerning the level of protection, the percentage of protected areas coverage among insular regions was assessed. Information on protected areas come from the WDPA (World Database on Protected Areas, available at http://protectedplanet.net/; see Supporting Information for more details).

All analyses were performed with R software (version 3.3.1, R Development Core Team, 2008).

3 | RESULTS

3.1 | Hotspots and coldspots of insular endemic mammals at risk of extinctions through the three diversity facets

All endemic threatened diversity–area relationships had a convex up shape (Figure 1a–c). Our analysis revealed that ten, eight, and five out of 19 insular regions are characterized by positive residuals based on taxonomic, phylogenetic and functional facets,
respectively. Among insular regions showing positive residuals, only four could be considered as hotspots across the three diversity facets: Wallacea, Madagascar and the Indian Ocean Islands, Mesoamerica and Galápagos Islands, and Indo-Burma (Figure 1a-d). At the other end, the insular coldspots were Japan, Tasmania and New Zealand Islands as they showed lowest negative residuals across the three diversity facets. In addition, we found that Gulf of Guinea Islands is characterized by positive residuals based on both taxonomic and phylogenetic facets, and Philippines is the sole insular region to present positive residuals for both phylogenetic and functional facets. Although for some insular regions, residual values can be negative or positive according to the diversity facet, the residual values of diversity facets are correlated to each other (Spearman’s rho > 0.7; Figure S2). We can also notice that the two largest regions in terms of area (i.e. Sundaland and Papua New Guinea) are not necessarily the regions with the highest value of threatened diversity (Figure 1; Table 1 but see Sundaland for phylogenetic diversity). However, such insular regions are important in terms of raw diversity harbored (Table 1). Thus, the rank of insular regions differs depending on whether the raw diversity values or the diversity values corrected by area are used, and especially for taxonomic diversity index (Spearman’s rho < 0.7; Figure S3).

3.2 | Level of protection and threatened diversity of endemic mammals within insular regions

Wallacea and Madagascar and the Indian Ocean Islands represented insular regions harboring both high value of residual (> 0) and standardized (> 0.5) threatened diversity of endemic mammals (Figure 2). However, these regions have low protected area coverage (<8%). In addition, although Sundaland and Papua New Guinea are characterized by negative residual values, these regions also harbor important values of absolute threatened diversity compared to other regions (standardized threatened diversity > 0.5) and yet the protected areas coverage is low, respectively 9% and 6% within these two regions. The other 15 insular regions are characterized by both low values of residual and/or standardized threatened diversity of endemic mammals. However, among these regions, five of them had a protected area cover higher than 25%: California Islands, Mesoamerica...
and Galápagos Islands, Gulf of Guinea Islands, Sri Lanka, and Tasmania and New Zealand Islands.

3.3 | Threats pressure within insular regions

The relative importance of direct, habitat and mixed threats varies according to insular regions (Figure 3). We can disentangle a first group composed of six insular regions including Mesoamerica and Galápagos Islands, which is mostly associated with mixed threats (representativeness >0.5; Figure 3) such as biological invasions, climate change, or human intrusions and disturbance (Figure S4). A second group of insular regions identified includes the rest of the hotspots of diversity (i.e. Wallacea, Madagascar and the Indian Ocean Islands, Indo-Burma, but also Sundaland and Papua New Guinea) and is mainly associated with both direct (biological resource use) and habitat threats (agriculture, urbanization) (representativeness >0.4; Figure 3; Figure S4). Overall, the representativeness of each threat category (mixed, habitat, and direct) is linked to the threatened diversity hosted by insular regions. The higher the threatened diversity harbored by the insular region, the lower the representativeness of mixed threats. An inverse pattern is observed for direct threats and habitat threat even if it is less marked (Figure S5).

4 | DISCUSSION

Our investigation of priority insular regions for endemic mammals at risk of extinction revealed four hotspots that are similar for the three diversity facets. Indeed, Indo-Burma, Madagascar and the Indian Ocean Islands, Mesoamerica and Galápagos Islands and Wallacea harbored a threatened diversity higher than expected given their area. Our results reaffirm the importance of those regions for conservation programs that should pay particular attention to them to ensure protecting their highest endemic mammal diversity. Such regions have already been depicted as priority areas based on taxonomic, phylogenetic and functional diversity of worldwide mammals (Brum et al., 2017; Pollock et al., 2017). We also showed that two insular regions are considered as coldspots across the three diversity facets: Japan, Tasmania, and New Zealand Islands. It was not surprising because none of these regions harbor an important species richness of mammals, either global or threatened (Ceballos & Ehrlich, 2006;
Jenkins et al., 2013), and recently it has also been showed for phylogenetic and functional diversity facets (Brum et al., 2017; Pollock et al., 2017). However, coldspots can also play an important ecological role by contributing to many ecosystem services (Jung et al., 2021) or hosting species with a special interest for the global mammal phylogenetic diversity (Robuchon et al., 2021). Thus, by focusing exclusively on biodiversity hotspots, the risk is to neglect areas with other types of conservation value. Although conservation strategy will always need a measure to determine priorities to be effective, future perspectives to set out an optimal conservation network is a complex task that requires to include both areas with high levels of diversity as well as coldspots that might be ecologically important (Marchese, 2015).

We also found that **Sundaland** and **Papua New Guinea** are relatively less important compared to other regions based on threatened endemic mammal diversity standardized by area, though they are among the largest regions in terms of area that harbor the highest number of threatened species. Our results differed from previous studies that identified these regions as priority areas based on multiple diversity of terrestrial mammals (Brum et al., 2017; Rosauer et al., 2017) but did not focus exclusively on endemic species. Moreover, while the other studies identified conservation priorities based on the biological value of sites having the similar area surface (Brum et al., 2017; Pollock et al., 2017), in our case, we focused on insular regions of different area surfaces and highlighted that **Sundaland** and **Papua New Guinea** harbored lower threatened diversity than expected given their area. Thus, the choice of metrics and spatial scale to define hotspots is an important and sensitive issue that may lead to different conclusions regarding the identification of biodiversity-rich areas (Marchese, 2015). However, to compare diversity between sites of varying size, removing the effect of area is mandatory as diversity is known to increase with area at a decelerating rate (i.e. a nonlinearity relationship between area and diversity). Even if the diversity-area ratio seems to be the most intuitive way to identify areas containing an exceptional concentration of biodiversity, this method is only based on an assumption of a simple linear relationship between area and diversity (Brummitt & Lughadha, 2003; Ovadia, 2003). Thus, the DAR approach is valuable to determine priority areas for biological conservation (Guilhaumon et al., 2008) even if no area-based approach alone can prevent mass extinction (Boyd et al., 2008). Nevertheless, as insular regions with the biggest areas and harboring the highest diversity values were not necessarily identified as hotspots, area did not seem to be a good predictor for a high endemic mammal diversity in some insular regions. Diversity can be related to environmental and latitudinal conditions but also to geological histories, biogeographical processes and spatial structure of islands (Ficetola et al., 2021; Whittaker & Fernandez-Palacios, 2007; Willig & Presley, 2018). For instance, Kalmar and Currie (2006) found that 87% of the global variation in non-marine bird species richness among worldwide islands was related not only to island size but also to climate and island isolation. Moreover, the spatial configuration of islands and archipelagos may also explain why the sole total area of islands is insufficient to predict diversity. Therefore, further studies accounting for environmental variables are needed to determine diversity conservation priorities, even if in a conservation concern, maximizing biodiversity on a given surface to protect seems the best strategy.

The identification of priority insular regions for endemic mammals at risk of extinction is based on residual values from the DAR. We found a strong congruency between residual values of the three diversity facets revealing that TD can be used effectively as a proxy for PD and FD in the conservation framework of insular endemic mammals at risk of extinction. This confirms previous studies that showed species diversity can be a good surrogate for conserving both the phylogenetic and functional diversity facets (Rapacciuolo et al., 2018; Rodrigues & Gaston, 2002; Sechrest et al., 2002). However, for some insular regions, residual values can be either negative or positive according to the diversity facet, which can have repercussions on the ranking priority among insular regions if only one diversity facet is considered. For instance, **East Melanesian Islands** is the third priority region based on TDAR but is the tenth priority region based on PDAR and FDAR due to negative residuals. It means that despite high species richness values found in this region, it is of lower importance concerning the other dimensions. This result might be partially explained by more phylogenetically and functionally clustered mammal assemblage owing to particular environmental conditions or biogeographical processes for example (Jacquet et al., 2017; Qian et al., 2019). In addition, the magnitude of match and mismatch along the three diversity facets may depend on the metric of diversity considered (Daru et al., 2019; Mazel et al., 2014). Thus, it is important to consider multiple diversity facets and metrics to determine comprehensive rankings of areas containing an exceptional concentration of biodiversity.

Regarding the protection on diversity within insular regions, the coverage rate of protected areas was overall low (~19%) and distributed unevenly. Only five insular regions out of the 19 had a protected area cover higher than 25%, and these regions have not been identified as hotspots. Thus, expanding protected areas may be required to protect threatened endemic mammal diversity particularly when protected areas are one of the cornerstones of conservation actions (Godet & Devictor, 2018). Such a conservation measure is much needed for the identified hotspot areas of multifaceted diversity such as **Madagascar and the Indian Ocean Islands** or **Wallacea** in order to reduce or halt habitat loss and fragmentation (Supriatna et al., 2020; Vieilledent et al., 2018). However, further investigations must be undertaken to better evaluate spatial overlap at a local scale between protected areas and multifaceted diversity of endemic mammals at risk of extinction. As historically reserves were not selected to protect multiple forms of diversity, it has been shown that currently worldwide protected areas network poorly represents the three facets of mammalian biodiversity (Brum et al., 2017; Daru et al., 2019; Pollock et al., 2017). For instance, of the 4.6% of the area identified as priority for conservation of mammal biodiversity across all facets only 1% is currently covered by protected areas (Brum et al., 2017). A slight expansion of protected areas could remedy the existing gaps in the coverage for each facet of diversity and can thus...
potentially protect a more important range of species or phylogenetic or functional units (Pollock et al., 2017). Even if protected areas are a solution to conserve biodiversity, they are not optimal and vary in the extent to which they can contribute to preventing extinctions face global changes, and other conservation actions should be taken to avert species’ declines (e.g. habitat restoration, control of invasive species or pathogens, limitation of human activities, Godet & Devictor, 2018; Le Saout et al., 2013; Maxwell et al., 2020).

To implement pertinent conservation actions, it is essential to identify the mechanisms responsible for the changed state of a population, community, or ecosystem (Williams et al., 2020). By disentangling threats that impact extrinsic and/or intrinsic characteristics of species, we showed that the importance of threats varies among insular regions. Thus, the conservation responses to set up in order to protect diversity (taxonomic, phylogenetic, and functional) can differ from one region to another. The insular regions harboring high threatened diversity of endemic mammals, such as Madagascar and the Indian Ocean Islands or Wallacea, showed a lower representativeness of mixed threats compared to other regions. Given that those regions are mainly associated with direct (biological resource use) and habitat threats (agriculture, urbanization), as already shown (Leclerc et al., 2018), enforcing protected areas and/or improving law enforcement to combat illegal wildlife trade would help to protect threatened diversity. In contrast, insular regions like Caribbean Islands and Polynesia-Micronesia are mainly associated with mixed threats like biological invasions or climate change. For those regions although protected areas can help species to follow/track their favorable climate, as part of the islands, this action could be limited because of physical barriers. Thus, to preserve species in the face of climate change, other actions should be considered such as potential translocations (Thomas, 2011). Further investigations to determine effective management strategies are needed at the individual threats scale (e.g. pollution, invasive alien species, etc.), as their effects and impacts differ in time and space. For instance, in the years to come, climate change and its impact on endemic mammal diversity should increase in all insular regions (Bellard et al., 2014; Leclerc, Courchamp, et al., 2020).

Regarding the present study, some limitations need to be acknowledged. We identified priority insular regions for conservation taking into account only insular endemic mammal diversity information. However, optimal identifying sites for conservation must take into account numerous potentially competing priorities ranging from biological to sociological and economical (Bennett et al., 2014; Faith & Walker, 2002; Herrera, 2017). Such an approach, which integrates multiple sources of information is particularly valuable, especially if it identifies high-priority sites that were undervalued when using species diversity-centric approaches. Also, data-deficient species represent 14.3% of our dataset. We did not consider data-deficient species as threatened, which can lead to an underestimation of the species considered at risk of extinction, especially that it has been shown that 63.5% of the data-deficient species can be threatened with extinction (Bland et al., 2015).

Despite these limitations, our study allows to identify priorities of insular endemic mammalian diversity across several facets and their level of protection and the threats that affect them. Because most conservation planning are undertaken at a local scale (though biodiversity hotspots attract billions over the years; Mittermeier et al., 2011; Myers, 2003; Myers et al., 2000), we call for further study of local spatial distribution of three diversity facets within insular regions to target areas of high diversity and see how it overlaps with protected areas network and with each anthropogenic threat.

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CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

The IUCN Red List data are available from the IUCN website (https://www.iucnredlist.org), which includes information about IUCN Red List status, identity of the threats, list of occupied habitats and species range. Body mass, foraging niche, foraging period and dominant diet traits used in this study are freely available from EltonTraits 1.0 (https://esapubs.org/archive/ecol/E095/178/). We also used mammal phylogeny in open access from www.virtlife.org. The R scripts and data are available at https://doi.org/10.5281/zenodo.5616745

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