



Prioritizing protected areas in Madagascar for lemur diversity using a multidimensional perspective



James P. Herrera

Department of Mammalogy, Division of Vertebrate Zoology, American Museum of Natural History, New York, NY 10024, USA

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ABSTRACT

Biodiversity is affected by anthropogenic activities, with a trend of decreasing species richness with habitat degradation. Decreasing species richness erodes evolutionary history and ecosystem function, but taxonomic, phylogenetic and functional diversity can have contrasting patterns. It is essential to measure these dimensions of biodiversity explicitly and assess how they are valued in prioritizing protected areas (PAs) to conserve diversity. Madagascar is a biodiversity hotspot, with high diversity and endemism coupled with heavy anthropogenic pressure. The endemic primates – lemurs – are the most endangered mammal taxon. A recent action plan prioritized PAs based on lemur species richness, weighted by endangerment. This scheme does not capture the evolutionary, functional, or biogeographic components of biodiversity, nor does it directly assess the level of human threat to those PAs. I compiled the largest dataset on lemur community composition in 100 PAs, including almost all lemur species (98 species). I combined data on lemur occurrence, their phylogeny, functional traits, IUCN Red List status, and environmental variables including deforestation between the years 2000 and 2014. I ranked PAs based on 14 metrics as well as the sum of metrics to determine how PA priorities compare under different valuation schemes. Based on the sum of seven metrics, I identified the top 25 PAs for lemur conservation. With these priority rankings, I propose areas of high lemur diversity, habitat heterogeneity and productivity, and deforestation be the focus of future conservation activities to maximize community resilience and prevent the erosion of evolutionary diversity and ecosystem function.

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1. Introduction

Variation in the distribution of endangered, geographically restricted, functionally and evolutionarily distinct species has made the prioritization of conservation areas difficult (Karp et al., 2015). By what measure should conservation biologists and policy makers quantify and rank areas to compare them and choose which deserve protection and funding? Are there habitat features that promote exceptional biodiversity, such as heterogeneous or highly productive habitats, and if so can these habitat variables be used as proxies for biodiversity to rank areas? The sum of multiple dimensions of biodiversity and habitat productivity, weighted by the threat of species extinction and rate of local habitat loss, provides a multidisciplinary measure of biodiversity and endangerment to rank conservation areas.

Species richness has been quantified for many areas around the globe, and there is a general trend for decreasing species richness with human disturbance (e.g., Newbold et al., 2015). Species richness has long been used as a measure of biodiversity and proxy for ecosystem function, but it does not capture the evolutionary history represented

by species, nor does it always reflect the influence of evolutionary history and trait diversity on community function, stability and resilience. The functional and evolutionary distinctiveness of species and communities provides unique, historical depth to measures of biodiversity, as well as direct ties to ecosystem function and services provided for people (Naem et al., 2016; Purvis and Hector, 2000). For example, conservation practitioners may opt to weigh species' presence by their phylogenetic diversity and distinctiveness, which directly measure the evolutionary history represented by a community or individual species (Faith, 1992; Faith et al., 2004; Graham and Fine, 2008; Isaac et al., 2007). In two communities with the same species richness, one community may encompass more of the phylogeny than another (Fig. 1). Preserving evolutionary history may warrant higher priority than species richness alone when some species represent the irreplaceable heritage of a lineage (Faith, 1992). Similarly, phylogenetic endemism reflects the geographic isolation of evolutionary history, identifying areas that may be relicts of deep-time biodiversity found nowhere else (Rosauer et al., 2009) (Fig. 1). Such areas may be higher priority for conservation because of the ancient geographically restricted biodiversity they harbor. Species and phylogenetic complementarity capture variation in the uniqueness of species and the phylogenetic history represented if certain species are preserved (Jensen et al., 2016), and

E-mail address: jherrera@amnh.org.

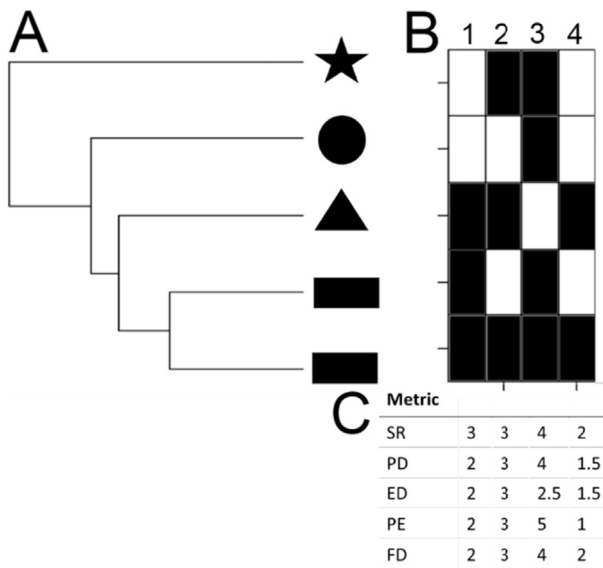


Fig. 1. Schematic illustrating how community diversity varies depending on the metric used to quantify diversity. A) Phylogeny of species with shapes representing functional traits of species. B) Diagram illustrating the presence (black) and absence (white) of each species (rows) in each of four sites (columns, labelled 1–4). C) Diversity metrics for each site, illustrating how sites with the same species richness (sites 1 and 2) can have different phylogenetic and functional diversities. SR: species richness, PD: phylogenetic diversity, ED: evolutionary distinctiveness, PE: phylogenetic endemism, FD: functional diversity.

complementarity of communities quantifies the degree to which protected areas represent unique biomes (Faith et al., 2004). Functional diversity directly measures the traits of species that make up communities (Fig. 1), especially ecologically relevant traits related to how species partition niches (Zuppinge-Dingley et al., 2014), how productive communities are (Gamfeldt et al., 2013), and how resilient they are to changes in the environment (Oliver et al., 2015). Taxonomic, phylogenetic and functional diversity are frequently assumed and/or found to be positively related, but they are not always, making it imperative to have functional trait data to complement taxonomic and phylogenetic information (Devictor et al., 2010).

The diversity of communities on its own does not reflect the level of anthropogenic threat to those communities. One scheme for assessing the value of an area that integrates anthropogenic threats is to weight the presence of species by their endangerment status; e.g., by their IUCN Red List status (Schwitzer et al., 2014). Similarly, the evolutionary distinctiveness of species, as measured by the amount of unique evolutionary history represented by a species, can be weighted by the Red List status, yielding the evolutionarily distinct and globally endangered index, EDGE (Isaac et al., 2007). Incorporating the phylogenetic complementarity of species with their probability of extinction yields the I-HEDGE index (Jensen et al., 2016). These schemes allow the community composition to be weighted by the threat level to individual species, but the level of threat to particular areas should also be a factor in conservation priority zonation. For example, data on land cover over time in areas may be used to assess the rate of habitat loss and quantify anthropogenic threat, and these data are available at global scales (e.g., Hansen et al., 2013). While the IUCN Red List status takes habitat loss (measured or estimated) into account, it is also weighted heavily by the projected population change (measured or estimated), hunting pressure, and harvesting for trade. Where new habitat loss data have not been incorporated into the IUCN status, including the latest estimates of deforestation is important to re-evaluate the threat status of species and communities. Therefore, I argue that in prioritizing conservation efforts, the diversity of the area as well as the anthropogenic threats should be taken into account.

Madagascar is a biodiversity hotspot (Myers et al., 2000), with rapid loss of hundreds of threatened, endemic species (Allnutt et al., 2008;

Goodman and Jungers, 2014) and a high rate of habitat loss due to slash-and-burn agriculture, clearing land for pasture and commercial mining (Harper et al., 2007; Scales, 2014), as well as heavy hunting pressure in some regions (Borgerson, 2015; Borgerson et al., 2016; Golden, 2009). The primates of Madagascar – the endemic lemurs – are the most endangered mammal taxon, with ~95% considered threatened with extinction (Schwitzer et al., 2014). Recent efforts to prioritize protected areas (PAs) for lemur conservation have weighted the species richness of PAs by the IUCN Red List categories of those species, and set conservation initiatives for the top-ranking PAs (Schwitzer et al., 2014). The Lemur Action Plan specified activities to be conducted in the top-ranking PAs between the years 2013 and 2016 to stave off further lemur extirpations (Schwitzer et al., 2013). The PAs were not evaluated for their ranks in other measures of diversity, however, potentially prioritizing sites that would not have high rank based on other dimensions of biodiversity.

Measuring diversity at the species level does not capture the evolutionary histories of species and contrasts with others who have advocated assessing conservation priorities based on the phylogenetic distinctiveness of species as a measure of the evolutionary history represented by each species (Isaac et al., 2007; Lehman, 2006; Purvis and Hector, 2000). Hotspots of evolutionarily distinct lemur species, phylogenetic diversity and endemism, and taxonomic richness do not align perfectly, each suggesting different priority areas (Gudde and Venditti, 2016; Gudde et al., 2013; Lehman, 2006). Previous studies on phylogenetic diversity of lemurs have used incomplete and poorly resolved phylogenies, and no previous study has quantified functional trait diversity. Importantly for this study, previous evaluations of phylogenetic diversity have not quantified diversity at the level of PAs, but rather at coarse resolutions of regions or grid-cells, the latter without ground-truthed verification of species occurrences. PAs should be the unit of analysis given that these are the designated localities of conservation action, and rather than seek out new areas, this paper aims to evaluate the conservation priorities of existing PAs. Finally, previous priority rankings have not taken into account environmental factors such as habitat heterogeneity, plant productivity, or the amount of habitat loss. I argue that priority rankings based solely on species richness weighted by species' threat statuses fail to capture diversity in multiple dimensions and should be reconsidered. This paper evaluates PAs in a new light with comprehensive data that have not been combined until now, including almost all lemurs, their phylogenetic relationships, functional traits, extinction risk, and the quality of the environment.

Here, I examined 100 PAs, quantifying lemur diversity in terms of species richness and complementarity, phylogenetic diversity and endemism, evolutionary distinctiveness and complementarity of species, and functional trait diversity, with and without weighting by species endangerment. I measured elevational heterogeneity and plant productivity from remotely-sensed data, which have been shown to be significant predictors of diversity (Jetz and Fine, 2012), and the amount of recent forest loss. I compared the ranks of PAs from each of my metrics as well as a combined metric to previous priority rankings (Schwitzer et al., 2013), and found differences that suggest previous rankings under-represented threatened biodiversity. I rank the top 25 PAs and find that PAs in the northeastern rainforests and northwestern mosaic dry forests are the highest priorities, while PAs in the southwest ranked lower based on lemur diversity, but highest based on deforestation. This new ranking system provides a more comprehensive assessment of the lemur and habitat diversity as well as threat status of Madagascar PAs than previous efforts, although I suggest socio-cultural and economic data are also needed to measure the value of PAs for people.

2. Methods

I first assembled a database of Madagascar bioregions and protected areas (PAs), lemur geographic ranges, and environmental variables. I then quantified taxonomic, phylogenetic and functional alpha diversity

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