Phylogenetic and Functional Structure of Indomalayan Raptor Communities

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Introduction

The loss of global biodiversity is one of the most significant environmental challenges[1]. However, it is important to evaluate many aspects of a species, community or area that requires protection when applying conservation strategies with limited funding[2]. The classical approach of prioritizing species richness in conservation planning[1] has been challenged by phylogenetic and functional diversity, which have increasingly become variables for measuring diversity[3,4,5]. The Indomalayan region boasts the world's highest raptor diversity[6], but also contains the most globally threatened raptor species[7]. While the conservation status and some ecological traits of several Indomalayan raptors have been studied [8, 9, 10], there remains a gap in understanding how functional and phylogenetic structure of communities might contribute to conservation strategies. My research begins to explore this gap by calculating the functional and phylogenetic dispersion of 6 select Indomalayan raptor communities, and how that dispersion compares to dispersion under a neutral model of assembly.

Methods and Materials

Data collection

We selected raptor communities in 6 national parks within the Indomalayan realm to represent the raptor diversity of the region (Figure 1), and constructed a presence-absence matrix containing all species within those communities and species in the regional pool. Functional ecology data such as hunting mode, habitat preference, prey mass and prey locomotory category for each raptor was collected from primary literature and relevant books. Morphological trait data (beak, wing, tarsus, and foot measurements) were collected from each species (2 male, 2 female) from the Field Museum (Chicago), the American Museum (New York), and the Bell Museum (St. Paul) by a collaborator. Our phylogenetic tree was based on a distribution of trees from Jetz et. al.[11] (Figure 2).

Analysis

We defined the regional species pool as species occurring in the "Oriental Region" by the International Ornithological Congress[12]. We first calculated the mean trait distance (MTD) among species in all 6 communities using the linear morphological data. We then calculated functional distance in a community using a Bray-Curtis dissimilarity matrix via R package *vegan*[13]. We averaged the trait distance and functional distance matrices to obtain the trait distance matrix. To determine phylogenetic and functional dispersion, we calculated the mean phylogenetic pairwise distance (MPD)[14] among the community members using R package *picante*[15]. We then calculated the standardized effect size (SES) of both the MPD and MTD. The SES allows us to assess the statistical significance of differences between phylogenetic distances in the observed communities versus randomly generated null communities (in this case, n=999).

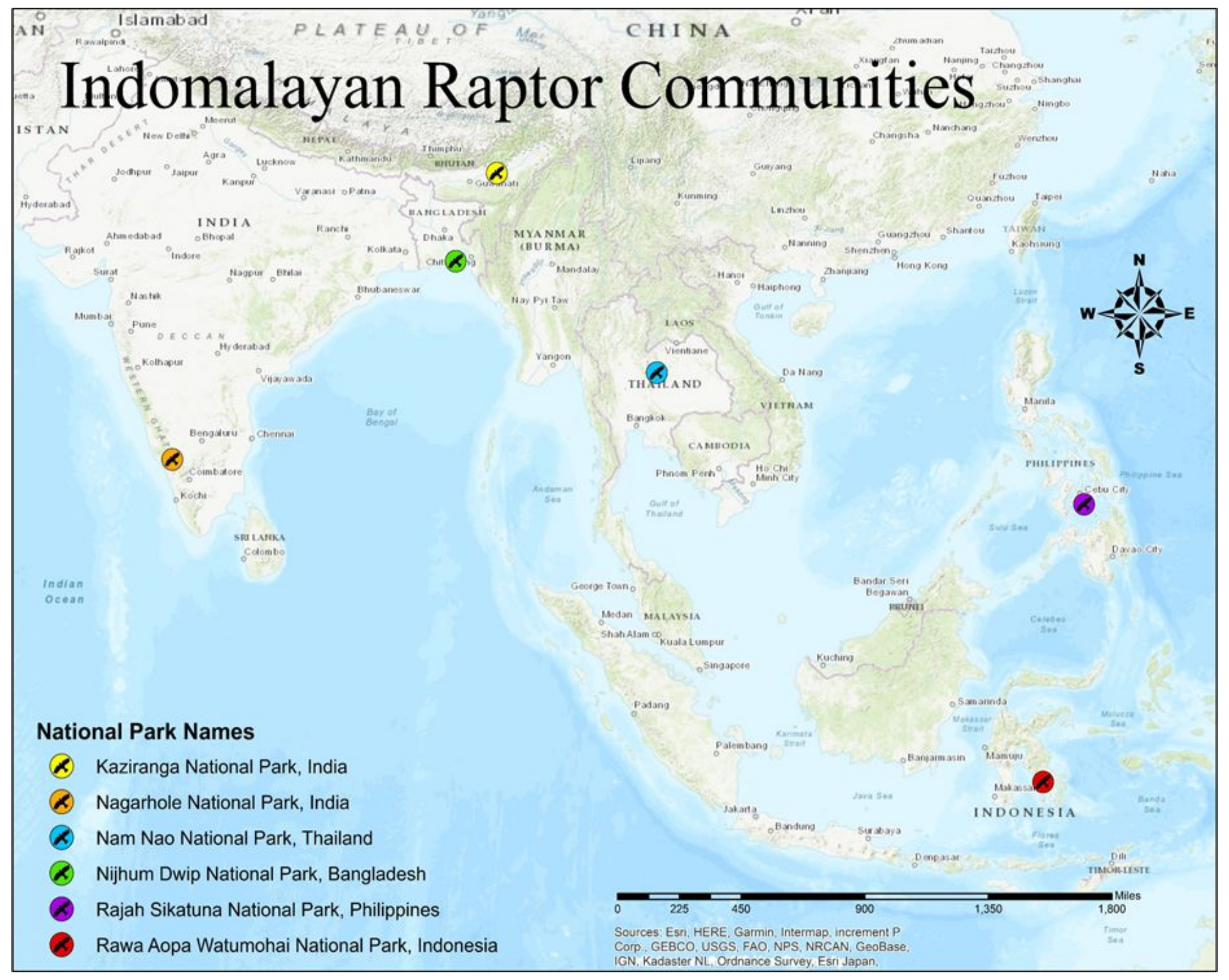


Figure 1: Map depicting the 6 selected Indomalayan raptor communities used in the analysis.

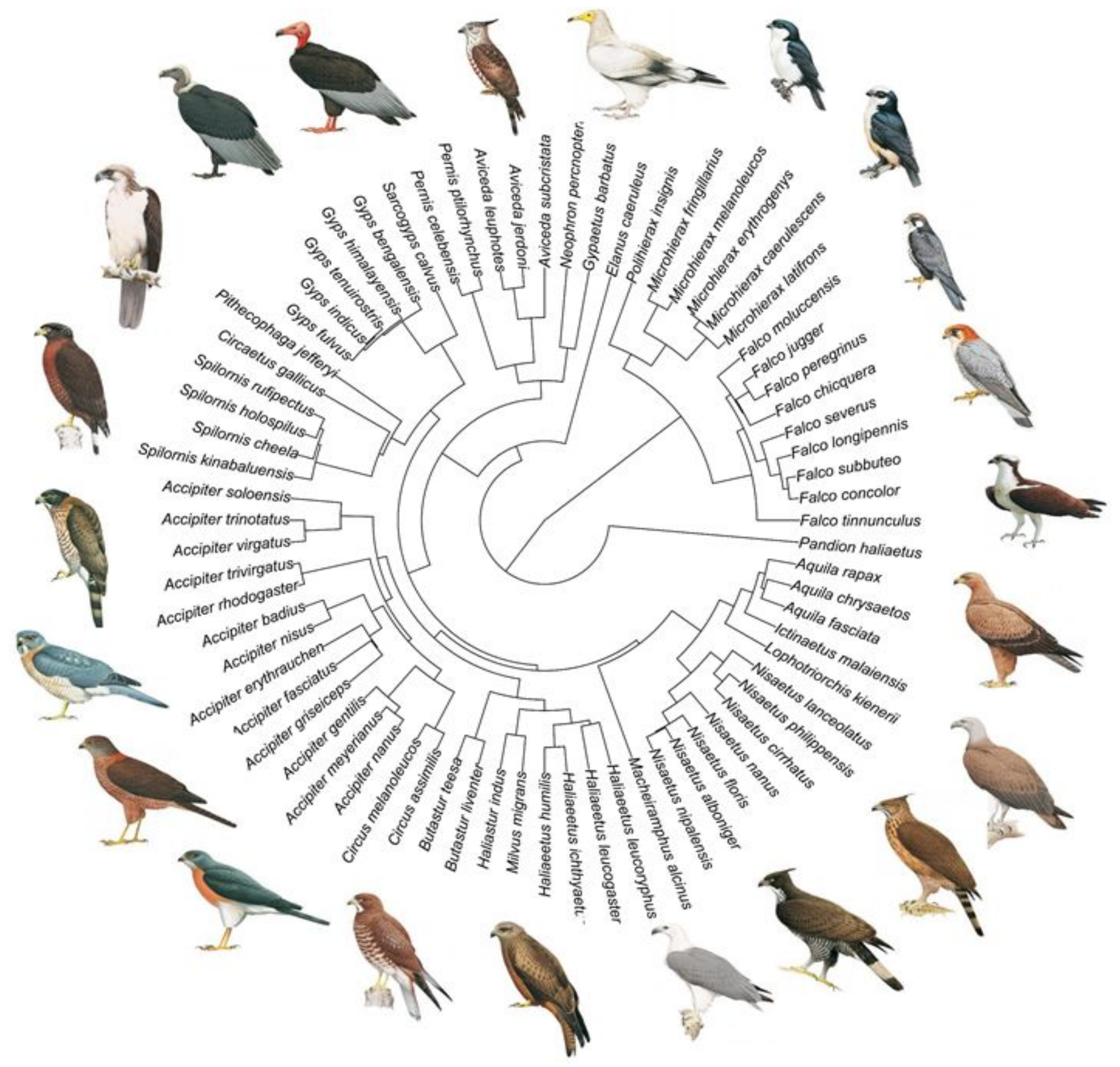
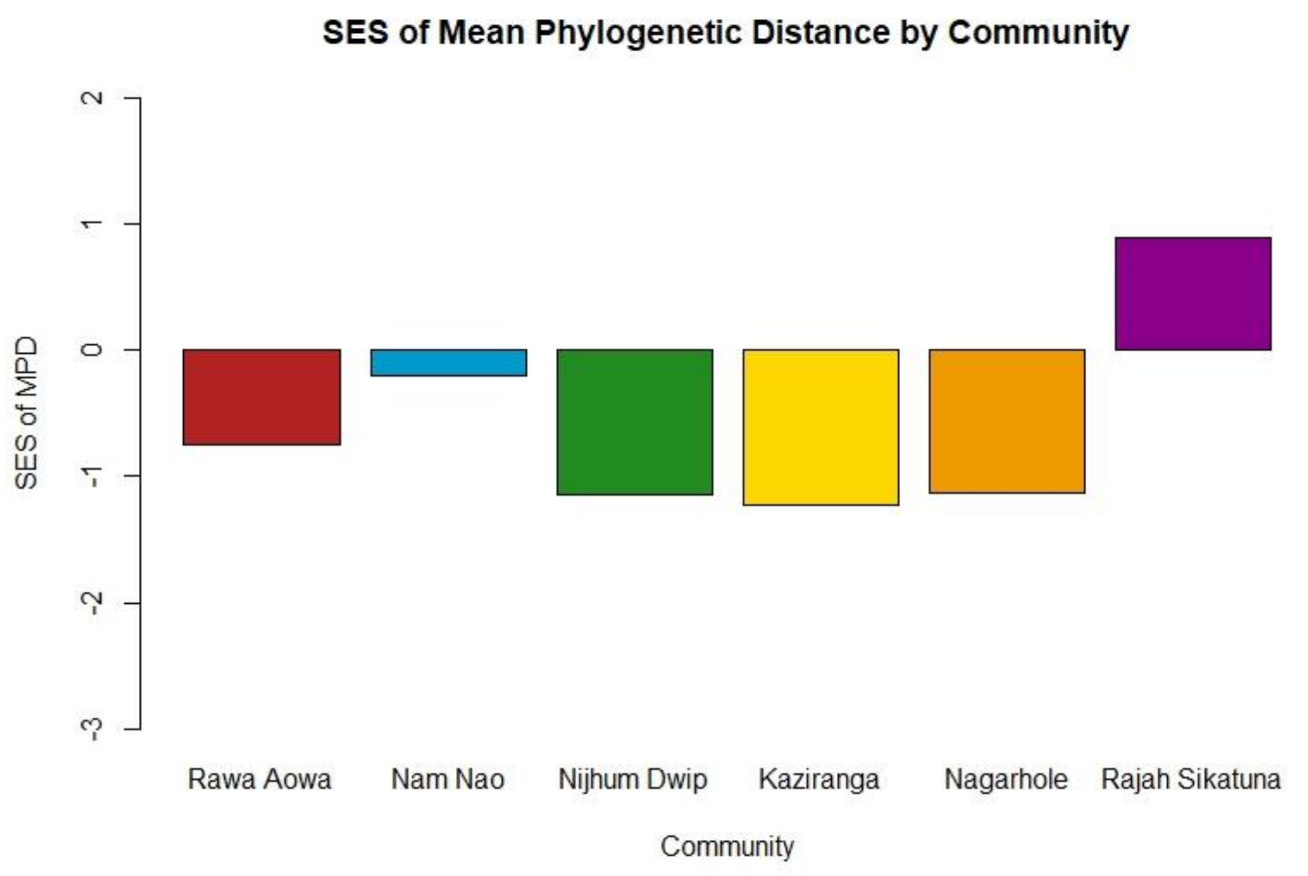


Figure 2: Phylogenetic tree of raptors in the 6 selected Indomalayan communities. Pictures from Handbook of the Birds of the World Alive (HBW)

Results

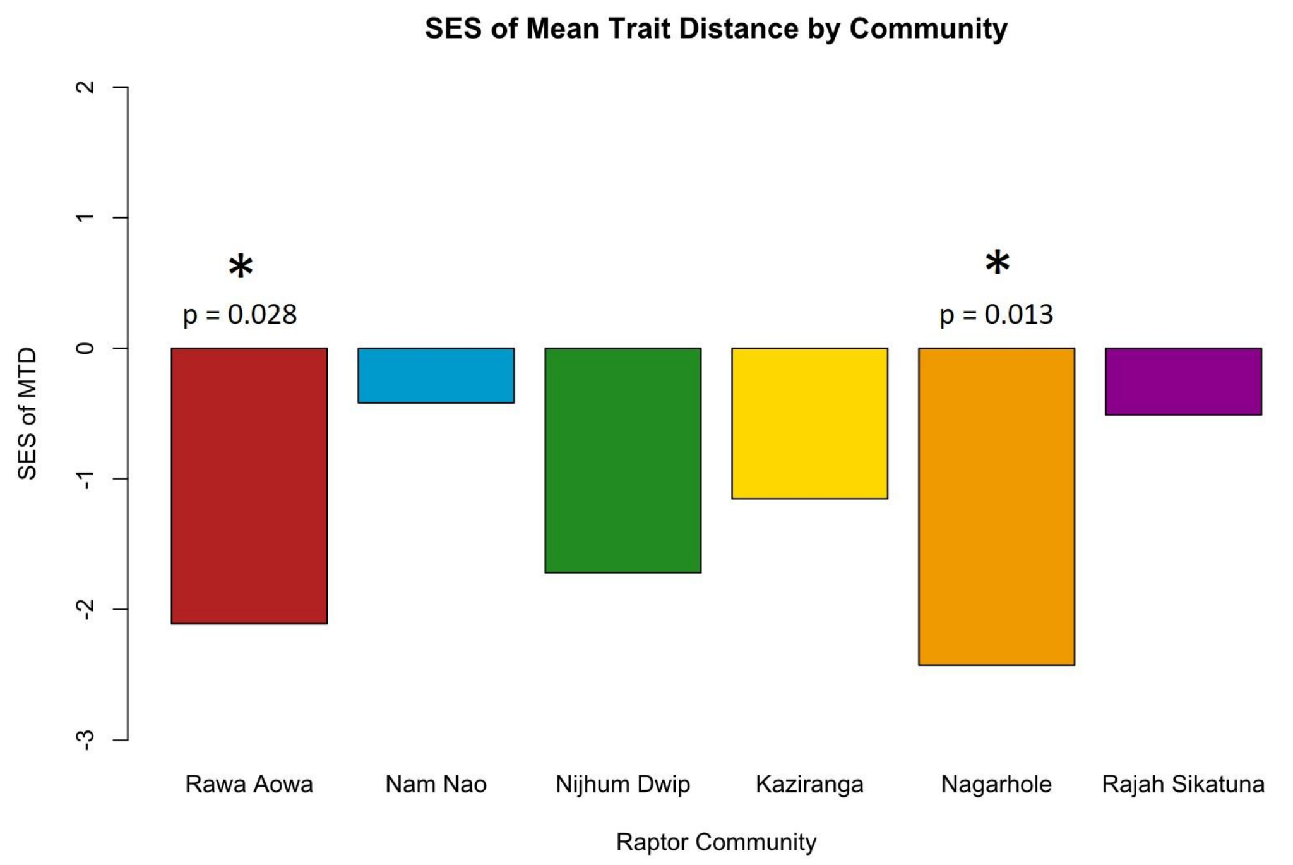


Phylogenetic Dispersion

Figure 3: Plot of the standardized effect size (SES) of the mean phylogenetic distance by community. Positive SES values indicate phylogenetic evenness and negative values indicate phylogenetic clustering. None of the SES.MPD values were statistically different from expected values under random assembly.

Functional Dispersion

Figure 4: Plot of the standardized effect size (SES) of the mean trait distance by community. Positive SES values indicate functional evenness and negative values indicate functional clustering. Bars with an asterisk above them are statistically significant. Rawa Aopa and Nagarhole communities were significantly more clustered than expected under model of random assembly.



Discussion

Our results indicate that phylogenetic dispersion in these communities is consistent with random assembly, and that functional dispersion is clustered in Rawa Aopa and Nagarhole National Park, and is consistent with random assembly in other communities. However, as pointed out by Pigot & Etienne[16], this approach did not account for historical community assembly, so the results of significant clustering in the MTD may be exaggerated by our model. Likewise, the model may also have understated the phylogenetic evenness (positive SES.MPD) in Rajah Sikatuna National Park. Our next steps include repeating the same analyses using different approaches to simulating null communities[16]. The Jetz tree used in this analysis has up to one-third of species placed by taxonomy with simulated branch lengths, which has the potential to skew these results. The issues with the Jetz tree will necessitate repeating these analysis with a complete, sequence-based, species-level phylogeny when one becomes available. Not only that, this approach is our first pass at designating an appropriate species pool, which can drastically affect the outcome of the analysis[17]. Finally, future analyses will formally correlate morphological data with functional ecology, to determine which measurements are the best indicators of functional divergence.

This research lays the groundwork for an ongoing study on global raptor diversity and community assembly, which will calculate these variables over the entire world. Future directions for this research will synthesize the results with comprehensive phylogenies, studies of trait evolution, and studies of biogeographic history to describe how macroevolutionary community assembly has unfolded in global raptor communities, and relate that assembly to real-world conservation issues.

Conclusions

In short, phylogenetic dispersion of these 6 communities is not significantly different from a random model of assembly. The functional dispersion of Rawa Aopa and Nagarhole National Park are significantly more clustered than random expectation. The tree we used, the simulation method, and the species pool we used may have contributed artifactual results to these analyses.

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