

**Title: Investigating marine biodiversity patterns and drivers at the global epicenter using environmental DNA (eDNA) metabarcoding**

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**Abstract**

Marine ecosystems provide important socio-economic and ecological services both at local and global scales, and regions with high marine biodiversity are often designated as focal areas for management and conservation. The marine ecosystems with the greatest biodiversity, those in the tropical Indo-Pacific region which include the Coral Triangle and the centers of reef and shore fish diversity, are also much less studied than other more depauperate regions, such as the temperate Atlantic and Pacific regions. The center of marine biodiversity is predicted to be in the Indo-Malay-Philippines Archipelago by evolutionary models based on the centers of overlap, origin, and survival hypotheses, and data on both shore and reef fish species range overlap predicts that the center of diversity is in the Central Visayas (CV) region of the Philippines. Observational surveys of fishes, however, found the CV to have the lowest species richness. Further, across the Philippines, fishes commercially exploited for food and the aquarium trade exhibited the lowest species richness. This highlights the potentially ephemeral nature of biodiversity patterns, the impact that anthropogenic activities can have on biodiversity in relatively short periods of time, and the importance of observational data in assessing biodiversity patterns. Further, it highlights the need for more rigorous study of the factors affecting marine diversity – commercially exploited fish might exhibit lower richness because there are fewer species that are commercially fished. More rigorous study is necessary to associate biodiversity patterns with their drivers.

To advance our knowledge about patterns of biodiversity in the hottest hotspot of marine biodiversity, we propose to collaborate with four Philippine universities to conduct a pilot study to rapidly assess the biodiversity of not only fishes, but also other eukaryotic metazoa such as invertebrates, eukaryotic zooplankton, photosynthesizers, and microbes in a latitudinal transect through the Philippines using use environmental DNA (eDNA) metabarcoding. Sampling will include the “center of fish diversity” (Central Visayas, Verde Island Passage) as well as locations outside of this region (West Philippine Sea, Celebes Sea). We plan to leverage existing data on (1) geographical location, (2) sea surface temperature, (3) chlorophyll-a concentration, (4) human population density, and (5) fishing effort to test for statistically significant relationships with observed biodiversity and community composition in the broad taxonomic groupings listed above. We will also test for concordance in biodiversity among the taxonomic groups which will allow more and better comparisons with commercially exploited taxa.

Overall, this pilot study will help to shed light on both the biogeography of marine biodiversity and its drivers in the center of marine biodiversity. It can also help to inform spatial conservation priorities by providing more comprehensive information on marine biodiversity that is not limited to a narrowly-defined taxonomic group. Furthermore, this research will be done alongside local collaborators, thus improving scientific partnerships within the region, and bridging the technological gap between high-income and developing countries.

We plan to leverage the results of this study in a new proposal to the National Science Foundation (NSF) Biological Oceanography Program (PD 23-1650). The pilot will strengthen the proposal by helping us to demonstrate proof of concept with preliminary data, iron out methodological details, strengthen partnerships, and hone the hypotheses.