**Body of Proposal (3 pages max)**

*Project Overview*

Regions with high marine biodiversity are often designated as focal areas for conservation. The most comprehensive biodiversity information from tropical regions often comes from marine fishes, while other taxonomic groups are not fully accounted for. Consequently, focus on reef fishes bias biodiversity drivers towards anthropogenic factors (e.g., fishing pressure and overexploitation) while discounting the effects of ecological factors. Therefore, this project will use environmental DNA (eDNA) metabarcoding to fill in the knowledge gaps on whether the patterns and drivers of marine biodiversity are consistent across different taxonomic groups. We aim to conduct the research at the epicenter of marine biodiversity – the Philippines; spatiotemporal trends in fish biodiversity are well reported in the country, providing a good foundation with which hypotheses on other taxonomic groups can be tested. We plan to compare the biodiversity of different taxa within and among selected marine biogeographic regions. We also plan to determine which between anthropogenic and environmental variables contribute more to the observed patterns of diversity across taxa.

*Context*

Highly biodiverse regions provide important socio-economic and ecological services both at local and global scales; with the threats brought about by anthropogenic factors and climate change, identifying them are critical so that management and conservation measures can be put in place1. Developing and utilizing rapid biomonitoring methods in the Indo-Malay Pacific Archipelago (IMPA) are therefore necessary since this is where the highest concentration of global marine biodiversity is located, along with countries that are most vulnerable to biodiversity threats. One of the most vulnerable regions is the Philippines, which was identified as the epicenter of marine biodiversity and evolution and thus warrant special attention for conservation efforts2,3.

Spatial variation in biodiversity, geomorphology, and oceanography across the Philippine archipelago characterize its six marine biogeographic regions4–6 (Appendix Figure 1) which provide the geographical framework on which management and conservation of marine resources are implemented7,8. While historical records indicated that the greatest marine biodiversity in the Philippines was concentrated within the Visayas Region (VR), reef fish surveys suggested otherwise; intense fishing pressure and habitat degradation have resulted to biodiversity loss in VR, which underscores the need to refocus management and conservation efforts elsewhere5,9,10. However, there are knowledge gaps on which such recommendations were based on. First, these observations were limited only to commercially important reef fishes, and other taxonomic groups have not been fully accounted for. Observing similar patterns across a wide range of taxa would result in a more reliable estimate of biodiversity and thus provide a stronger support in identifying regions of conservation priority. Second, loss of biodiversity was primarily attributed to fishing pressure and other anthropogenic disturbances; however, patterns of biodiversity are likewise influenced by ecological factors (e.g., sea surface temperature) that should be considered when informing spatial management areas1. We therefore ask the following questions: (1) Is the low species richness of reef fishes observed in VR relative to other marine biogeographic regions concordant with other taxonomic groups? (2) Are the patterns of diversity (i.e., community composition) in the different marine biogeographic regions consistent across taxa? (3) Are the patterns of diversity driven not only by anthropogenic factors, but also by ecological factors?

Relying on conventional monitoring methods (e.g., underwater visual census, market surveys) to answer our questions would be difficult and resource intensive, but such limitations can be circumvented with the use of environmental DNA (eDNA) metabarcoding. eDNA metabarcoding is an emerging technology that utilizes DNA traces from organisms within their environment; coupled with high throughput sequencing, this allows for simultaneous identification of various taxa from an environmental sample11,12. Its advantages over conventional monitoring methods (e.g., less labor intensive, less invasive, more cost effective, higher throughput) led to increased use in recent years and pushed it to the forefront in marine conservation efforts12–14. It has been used widely used for biomonitoring marine systems to inform management14–18.

This research would investigate the pattern and drivers of marine biodiversity among the different marine biogeographic regions in the Philippines using eDNA metabarcoding. We will do so by simultaneously looking at the patterns observed across different taxonomic groups. First, we will compare the species richness of the different taxa among the biogeographic regions. Second, we will test whether the community composition of each taxon varies among biogeographic regions. Third, we will determine what factors shape the diversity recovered with eDNA. We hypothesize that (1) reef fish diversity in VR is relatively lower compared to other regions, as was previously observed, but other taxonomic groups may show different trends; (2) different marine biogeographic regions have different ecological regimes and experience varying degrees of anthropogenic disturbances, and thus community composition of each taxon will be different among regions; and (3) while observed patterns of biodiversity are influenced by both anthropogenic and ecological factors, the degree at which they shape biodiversity will be different among regions (e.g.,, anthropogenic factors will have more effect in densely population regions) and across taxa (e.g., fishes will be more strongly affected by anthropogenic factors, while plankton will be more affected by ecological factors). The methodology for this research proposal is detailed in Appendix I and Appendix Figure 2.

*Impact/Explanation of Innovative Nature of the Project*

The impact and innovative nature of the project is twofold. First, it will inform spatial management and conservation priorities by identifying regions of high biodiversity. eDNA metabarcoding simultaneously looks at the diversity patterns across different taxonomic groups, thus the inferences will be more comprehensive. It will be the first time that this will be done in the epicenter of marine biodiversity. Second, it fosters international scientific collaboration, especially in the emerging field of eDNA metabarcoding. The use of eDNA is still confined to high-income countries, and one way for developing countries to have access to this technology is through cohesive international collaboration with developed countries to encourage technical exchange, develop capacity, and share facilities and resources19. The partnerships formed from this seed grant will be instrumental for future research projects with Filipino collaborators.

*Expected Career Impact*

Securing funding from the National Science Foundation, and other federal sources, is a critical factor in earning Promotion and Tenure for Assistant Professors, such as Dr. Lin, and Associate Professors such as Dr. Bird. It will also help Ph.D. student, Kevin Labrador, conduct research for his dissertation. The work of Dr. Bird in the Philippines has led to career development opportunities for himself and his students such as invited presentations, membership in the Philippines Fishes Genomics Working Group, a collaborative proposal to NSF DEB, and consistently being selected to represent TAMUS LSAMP since 2017 at the Louis Stokes Alliance for Minority Participation – NSF International Center of Excellence meetings, which was instrumental in securing funding from the NSF IRES program. This seed grant will develop the framework for our eDNA research in the Philippines, which can be leveraged in a grant proposal to the National Science Foundation (NSF) Biological Oceanography Program (BioOce) where international collaboration is highly encouraged. In this project, we will foster and expand existing collaborations with Silliman University and University of the Philippines (UP) – Mindanao as well as establish collaborations with the UP-Marine Science Institute, Batangas State University, and the Philippines National Fisheries Research and Development Institute. Collaborations with Filipino institutions are mandatory to secure the collection permits required to complete the proposed work. Demonstrating that TAMU-CC can lead such an effort will be an important consideration by NSF program officers and reviewers in making funding decisions.

*Timeline of Deliverables*



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