**Introduction**

The Philippines is the marine biodiversity capital of the world making it extremely important to protect. However, due to anthropogenic factors, the species living there are under threat of degradation and need immediate protective action ([Carpenter & Springer, 2005](#_ENREF_1)). The PIRE (Partnerships in International Research and Education) project is an educational program promoting outreach to students in hopes that the Philippines will continue to grow in marine research and education so the environment can prosper ([Carpenter, 2017](#_ENREF_2)). By studying the species in the Philippines and understanding what factors makes them vulnerable, scientists will then be able to understand how to protect the species there.

This project is a puzzle piece in the PIRE project and will focus on the effect of the type of habitat inhabited on demography inference in Philippine fishes. There has been little research done on how various habitats have affected populations over time, but there has been research done on how the habitats are used and/or affected. The habitats of interest for this project are reef-associated, estuarine/brackish, and near-shore semi-pelagic; each habitat is affected differently by humans or other impacts; therefore, each habitat should affect each population differently.

Coral reefs have the highest biodiversity of any of the three habitats, but coral bleaching which is caused by climate change, exploitation, sedimentation, pollution, and habitat modification threaten the effectiveness of this habitat ([Honda et al., 2013](#_ENREF_4); [Pratchett et al., 2011](#_ENREF_5)). Estuaries are dynamic, transitional habitats that connect the surface water from landmasses to oceans. It is vitally important for both fishes and humans, but because of large human populations established near estuaries, human impacts such as habitat modification, pollution, eutrophication, altered hydrodynamics, water extraction, and overexploitation greatly damage the important habitat ([Feyrer et al., 2021](#_ENREF_3)). Near-shore semi-pelagic habitats are defined as water depths shallower than 30 m but are not directly next to the coast and fish inhabiting spend some time on the seafloor and sometime in the water column. It is among the most productive habitats and is usually utilized as feeding and nursery grounds; however, habitat is mainly affected by overfishing, pollution, and habitat modification ([Seitz et al., 2013](#_ENREF_6); [Sichum et al., 2013](#_ENREF_7); [Wen et al., 2010](#_ENREF_8)). These three habitats are usually intertwined with no real barrier separating them and have similar threats that put them in danger, but the question prevails how do the populations that inhabit each habitat vary in their population histories?

This project hypothesizes that the type of habitat inhabited does have an effect on the population history of Philippine fishes. Between these three habitats, twelve species will be analyzed as listed in Table 1.

Table 1: List of species and their corresponding habitats

|  |  |
| --- | --- |
| Habitat | Species |
| Reef-associated | *Ostorhinchus chrysopomus*  *Sphaeramia nematoptera*  *Stethojulis interrupta*  *Taeniamia biguttata*  *Taeniamia kagoshimanus* |
| Estuarine/brackish | *Ambassis urotaenia*  *Ambassis kopsii*  *Atherinomorus duodecimalis*  *Leiognathus leuciscus* |
| Coastal/semi-pelagic | *Atherinomorus duodecimalis*  *Herklotsichthys quadrimaculatus*  *Hypoatherina temminckii*  *Spratelloides gracilis* |

To test the hypotheses, sub-sampling and DNA extraction will be done to the selected species. The extracted DNA will then be processed through the PIRE SSL (shotgun sequencing library) pipeline to develop a genome sequence to perform PSMC (pairwise sequentially Markovian coalescent) demographic analyses of the species to assess whether the type of habitat inhabited can be associated with historical population trends. The PSMC output can also test whether different habitats affect the differences between the genomes of different species. Those outputs can relate to effective population size, average effective population size, maximum, minimum, etc. Those outputs will be analyzed through R to produce statistical computing and graphics.

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