**Effect of Species Distribution on Demography Inference in Philippine Fishes**

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**Abstract** (250 words)

The Philippines is the center of marine biodiversity of the world, however it is not the center of marine biology research. This project aims to question how distribution levels, population history, and biodiversity of reef fishes impact each other. This is accomplished using shotgun sequencing and a Pairwise Sequential Markovian Coalescence (PSMC) program. Shotgun sequencing was used to generate the genome sequence of the fish *de novo*, and the PSMC program was used to infer current population size and history of the fish species using either coalescent simulation. The Spotted Gill Cardinalfish (*Ostorhinchus chrysopomus*) is distributed from the Indo-Malay region to New Guinea and the Solomon Islands, and is considered shortly distributed.  This methodology has been applied to 19 other fish species, 14 with long distributions (Africa to the West Pacific region), and 5 with short distributions (West Pacific region). It is hypothesized that fish species with longer distributions will have larger populations, and that fish biodiversity has decreased with an increase in anthropogenic impacts. This research will consolidate the relationship among the three parameters: distribution, population, and biodiversity, in order to create predictions about how human pressures will affect future population levels and marine biodiversity.

**Introduction**

The Philippines is the epicenter of marine biodiversity, but it is not the epicenter of marine biology research (Panga et al.) The Philippine Islands are in the Coral Triangle (Sanciangco et al.) with distribution data for 2983 fish species (Carpenter and Springer). As an island nation, the Philippines relies on fish for food, which has a nutritional value due to the high concentration of protein, amino acids, fatty acids, vitamins, and minerals (Wahyuningtyas et al.) Fish is also important due to its use for means of income, with 1.6 million Filipinos employed in fisheries-related occupations (Anticamara and Go; BFAR). However, overfishing has caused a rapid decline in marine biodiversity (Silvestre et al.); its conversation is critical to the interests of all humans, nations and governments (Dudgeon et al.). Biodiversity is important to resisting environmental changes, and the goal of the PIRE Project is to assess how human interference has affected biodiversity (PIRE 2022). One example of this kind of study is the Great *Albatross* Philippine Expedition, which assessed the aquatic resources of the Philippines by exploring fish, invertebrate specimens, and hydrographic and fish data (Smith and Williams) . This research centering on distribution and population history will contain contemporary data that will be collected as temporal duplicates of the Albatross locations from 1907 to 1909.

Distribution is the geographical range a species can survive in. This project will look specifically at latitudinal and longitudinal values of fish species. There are 2 groups, short distribution and long distribution. There are 5 species that are labeled as short distribution, which are localized to the West Pacific: Indo-Malay to New Guinea and the Solomon islands. There are 14 species that are labeled as long distribution, which range from Africa to the West Pacific. For the purpose of this study, population history will be viewed through the effective population (NE) which is defined as the portion of the overall population that can breed and produce viable offspring.

The goal of this project is to assess how distribution history affects demography inference, such as population history. This will be completed by using the Philippine International Research Experience (PIRE) Shotgun Sequencing Library (SSL) pipeline, and Pairwise Sequential Markovian Coalescence (PSMC) program. More specifically, researchers will be utilizing *Ostorhinchus chrysopomus* as an example to generate the genome *de novo* through the SSL pipeline. This species is used for exploration of the pipeline because it will generate contemporary data only, since there is no current genome sequence data. From there, the PSMC program is used to infer population history of this species and 19 other ones between current day and the past 10,000 years. If the association between the two parameters can be identified, then this can be used to make predictions about future populations of fish species.

**Methods: Field Collection and Laboratory Methods?**

* Fish collection methods
* DNA lab extraction methods (proprietary process)

**Methods: Data Analyses**

Shotgun sequencing is used to build the genome of *O. chrysopomus.* X amount of coverage was completed using a second-generation sequencing program, Illumina. This sequence was then pushed through the PIRE SSL Pipeline.

The Pairwise Sequential Markovian Coalescence program uses the genome from the contemporary species (all 20 studied) to infer population history from the last 10,000 years. This is done through using markers from loci positions and analyzing heterozygosity. A decrease in heterozygosity is associated with a coalescence event, which takes two species and traces it back to its most recent common ancestor (MRCA). This is likely to happen with a decline in population size.

**Results: Shotgun Sequencing of *Ostorhinchus chrysopomus***

Below is a diagram example with confidence bands of the SSL pipeline using Illumina:

The following is the contemporary genome of *O. chrysopomus* that has been generated:

**Results: PSMC**

* Current population of short distribution fish chart
* Population history of short distribution fish
* Current population of long distribution fish chart
* Population history of long distribution fish
* Include in diagrams confidence band/percent error

**Discussion**

* Paragraph on general result findings
* Everything else on results

**Conclusion**

* Tie to intro
* Future direction/implication of results findings/how can it be applied to other things/why was it important

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