Introduction Draft

The Indo-Malay-Philippines Archipelago is widely regarded as the most species-rich area of the world. Within this range, central Philippines has been found to contain the most biodiversity (Carpenter & Springer 2004).

The Philippines Partnerships for International Research and Education (PIRE) program is a multi-university effort led by Old Dominion University. The program aims to answer questions about historical and contemporary population dynamics of fish species in the Philippines. This paper will help determine if reproductive modes of fish are correlated with population size, and therefore genetic diversity.

Previous research suggests that life history influences population structure. The Mandarinfish *(Synchiropus splendidus)* is a pelagic egg producer native to the Philippines. While abundant, the population tends to be localized. Leung et al (2020) studied population structure at six locations. Population genomic analyses revealed strong connectivity among all localities. These results were unexpected as *Synchiropus splendidus* is a demersal species with no known migration patterns and a short 14-day larval life, suggesting that both adults and offspring do not travel between localities. The authors suggest two possible causes of this population structure. The researchers claim it could be due to *Synchiropus splendidus* year- round spawning pattern- while the larvae do not usually travel far, the fish spawns frequently enough that a number of larve make it into stronger currents each year. Alternatively, the connectivity may be attributed to range expansion to due ice melt 14,000 years ago.

The Crosshatch Triggerfish (*Xanthichthys mento)* also has localized populations in the Pacific Ocean. Multiple females establish territories within a single male territory. Eggs are spawned over sand and the eggs adhere to the sand particles. Eggs are maintained and protected by the females while the male defends the larger territory. Unlike pelagic eggs, the eggs of *Xanthichthys mento* do not travel outside of the localized population. While population structure of these localities was not analyzed, it is likely that there is not high connectivity within these populations. With restricted population size and gene flow this species may be more sensitive to pressures- particularly climate change, as *Xanthichthys mento* times spawning events with narrow temperature ranges (Kawase 2003).

Other species categorized as mouthbrooders or tailbrooders will guard eggs on the body instead of laying them in the water column or on a surface. One such fish is the messmate pipefish (Corythoichthys haematopterus). This syngnathid’s life history has sex-reversed roles- during spawning, the female lays an egg sheet on the male’s ventral brood pouch. The male then carries the eggs for up to nineteen days. It has been observed that members of this species have a small individual range, with males traveling smaller distances than females. Because egg movement is restricted to the male’s movement, it is likely that offspring populations are localized in the range of their parents. There has also been documented reaction to disturbance of this species, suggesting it may be delicate: water swells cleared a study area, resulting in the disappearance of over 60% of local males and abandonment of the spawning area (Masumoto & Yasunobu 2000).

This paper associates large population size with high genetic diversity and assumes a correlation between the two. After contemporary samples were processed via the PIRE SSL Pipeline (provided by the PIRE Program), the resulting genomes were analyzed using Pairwise Sequentially Markovian Coalescent (PSMC). PSMC is capable of estimating ancient population size from a sample size as small as 1. The program searches chunks of 100 base pairs at a time for the presence of at least one heterozygous locus in the chunk. PSMC is then able to detect events of coalescence- points where two genes share a common ancestor in time. Higher heterozygosity is an indicator for larger populations. More frequent coalescence events indicate that the ancient population is smaller. In studies of historical populations in humans, two people from the same village shared a more recent common ancestor than two people from different countries would.

In this study, the historical population sizes of twenty species – eight demersal egg producers, five mouthbrooders, one tailbrooder, and \_\_ pelagic egg producers were estimated using PSMC. \*Hypothesis: species with non-guarding, non-demersal egg producing life histories will have larger ancient population sizes.