The Population Genomics of Pacific Herring in the Bering Sea using mtDNA

Isabelle Nicoller1, Sydney Almgren2, J. Andrés López2.3, Jessica Glass2
1. University of Alaska Fairbanks, College of Natural Science & Mathematics
2. University of Alaska Fairbanks, College of Fisheries and Ocean Sciences
3. University of Alaska Museum

Research Question:
What is the geographic distribution of genetic diversity in the eastern Bering Sea of Pacific herring, Clupea pallasii?

Introduction:
Herring are culturally important to many Indigenous groups in Alaska as well as commercial fisherman, and have been for many centuries (1). Studies performed throughout the Pacific Coast have found that there are genetic differences between populations in the Bering Sea and the rest of the Pacific Ocean (2). Research has also shown that Pacific herring populations in Alaska may be genetically distinct from other Pacific populations (3). This research will provide a cursory analysis of genetic diversity in the eastern Bering Sea using mitochondrial DNA (mtDNA). Better understanding the genetic diversity of Pacific herring in the Bering Sea will lead to better fisheries management decisions, which are vital to the productivity of Pacific herring stocks to prevent population collapses and preserve genetic diversity.

Methodology:

1. Processing Samples
   - Weight
   - Length
   - Gonad size
   - Tissue sample

2. DNA Extraction
   - DNA was extracted from heart tissue for 96 samples
   - Primers from Lui (2011) (CO1) of mitochondrial control region.

3. Amplification
   - The control region (COI) of mitochondrial genome was amplified with herring specific primers from Lui (2011)

4. Sequencing & Analyses
   - Sanger Sequencing
   - Analysis with Geneious Prime

Preliminary Results:

Early analysis shows herring sampled from the eastern Bering Sea may have greater genetic diversity compared to herring samples from the Northern Bering Sea. However, an increased in sample size will provide more data.

Next Steps:
Continue with the remaining samples and compare the genetic diversity from these regions in the Bering Sea to each other.

To follow this and the larger project, use this link to see the project website: icnicoller@alaska.edu

References:

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