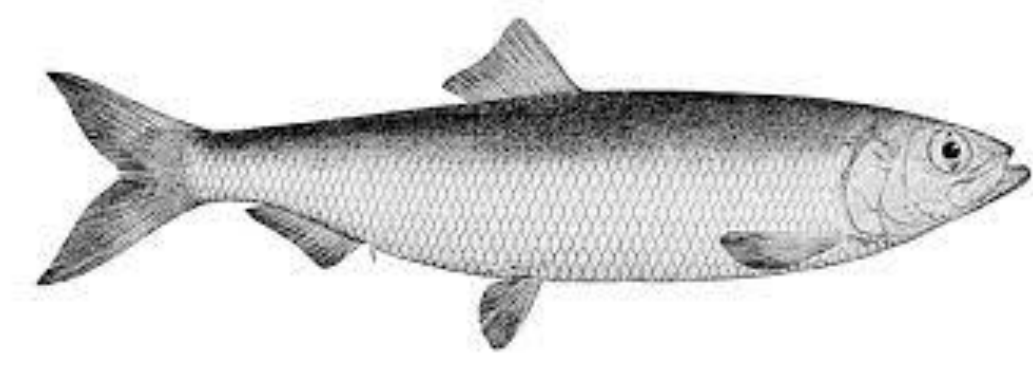


# The Population Structure of Pacific Herring in the Bering Sea and GoA using mtDNA

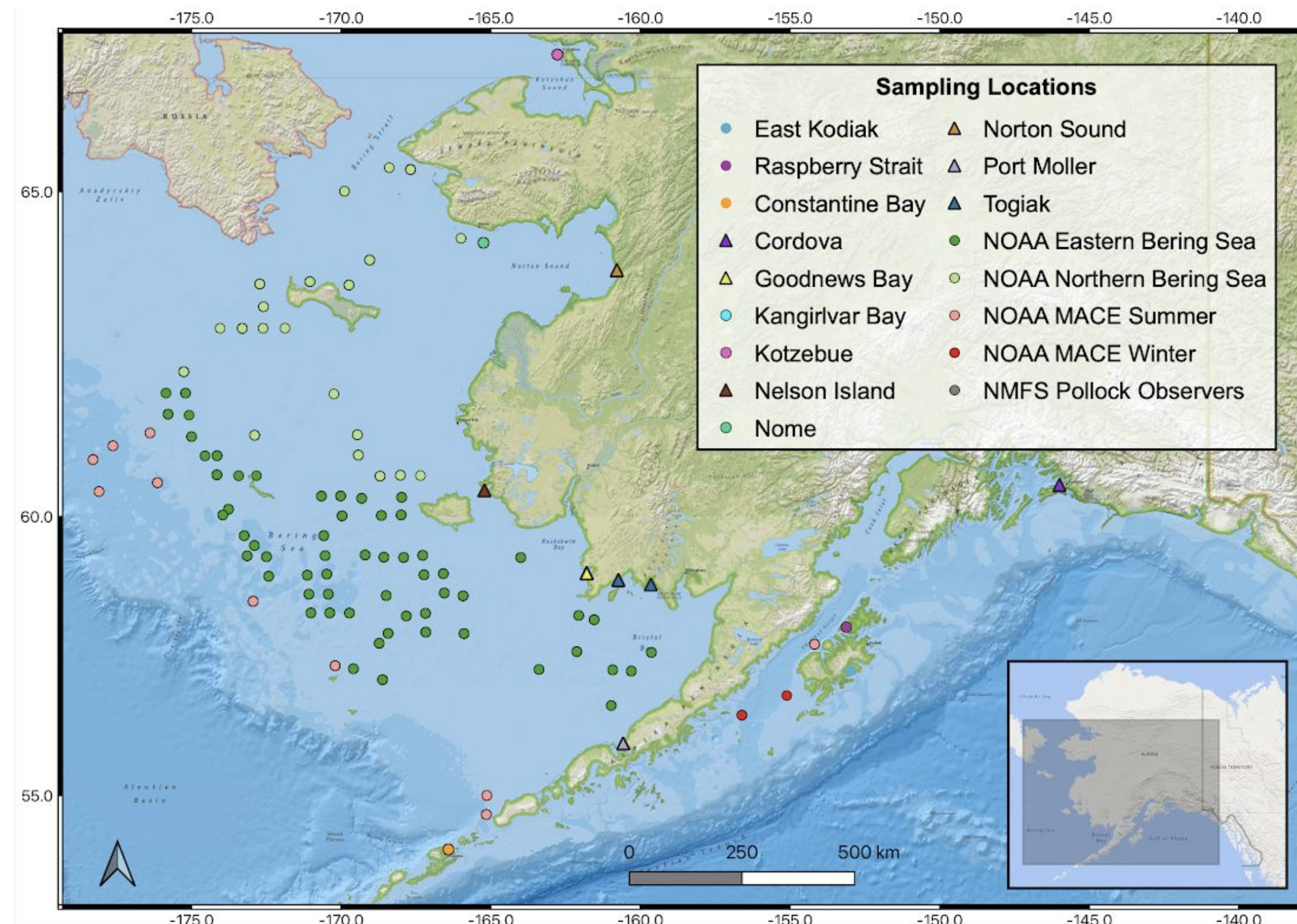


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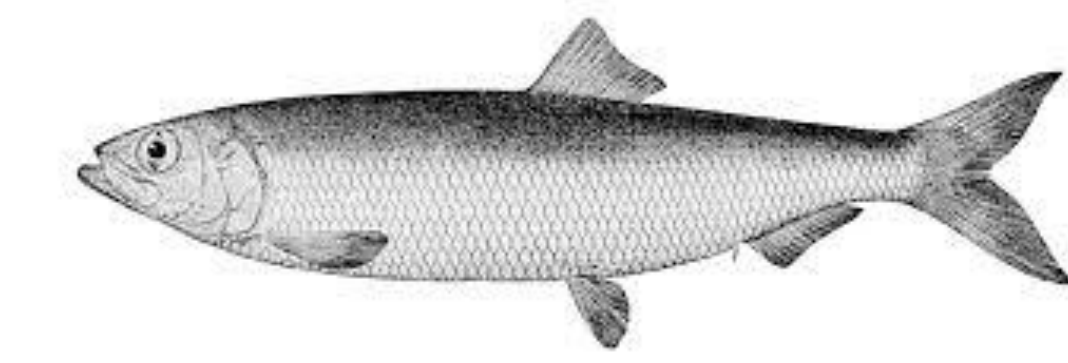


## Research Questions:

What is the geographic distribution of genetic diversity in the eastern Bering Sea of Pacific herring, *Clupea pallasii*?  
 How does it compare to spawning populations in the Gulf of Alaska?



Sample area. Courtesy of Sydney Almgren MS



## Next Steps:

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



Logan Ito, Sydney Almgren, Isabelle Nicolier  
 Photos courtesy of J. R. Ancheta; JR-22-G11088-155.jpg

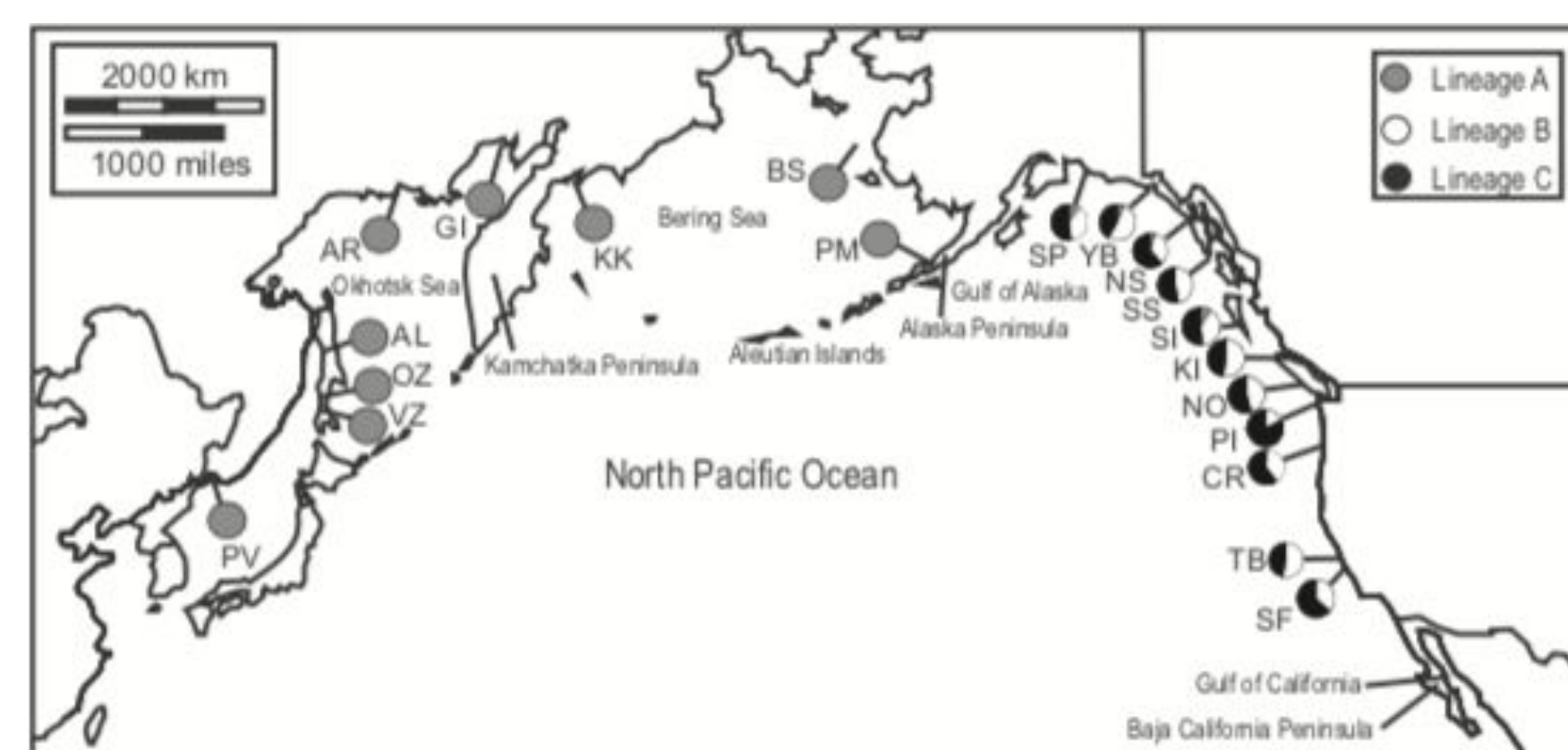
JR-22-G11088-103.jpg

To follow this and the larger project, use this link to see the project website.  
[icnicolier@alaska.edu](mailto:icnicolier@alaska.edu)



## Introduction:

Pacific Herring are a foundational foraging fish whose annual spawn affects multiple trophic levels. Including humans whether that be the harvesting of their roe from kelp or hemlock branches or fisherman pulling them up in their nets. Culturally herring can be described as keystone to many indigenous groups, highlighting Tlingit and Haida.



Map from Liu et al. (2011)

## Background:

Some studies done along the Pacific Coast have found that there are differences between populations in the Bering Sea and the rest of the west coast (Hay et al. 2008). Research has also shown that Pacific herring populations in Alaska may be genetically distinct from each other (O'Connell et al. 1998). However, a fine scale analysis of herring population structure in the eastern Bering Sea has not yet been achieved. Better understanding the population genomics of Pacific herring in the Bering Sea will lead to better fisheries management decisions.

## Methodology:

### 1 Processing Samples

- Weight
- Length
- Gonad size
- Tissue sample



Photos courtesy of J. R. Ancheta; JR-22-G11088-14.jpg

### DNA Extraction

2 DNA was extracted from heart tissue for 96 samples

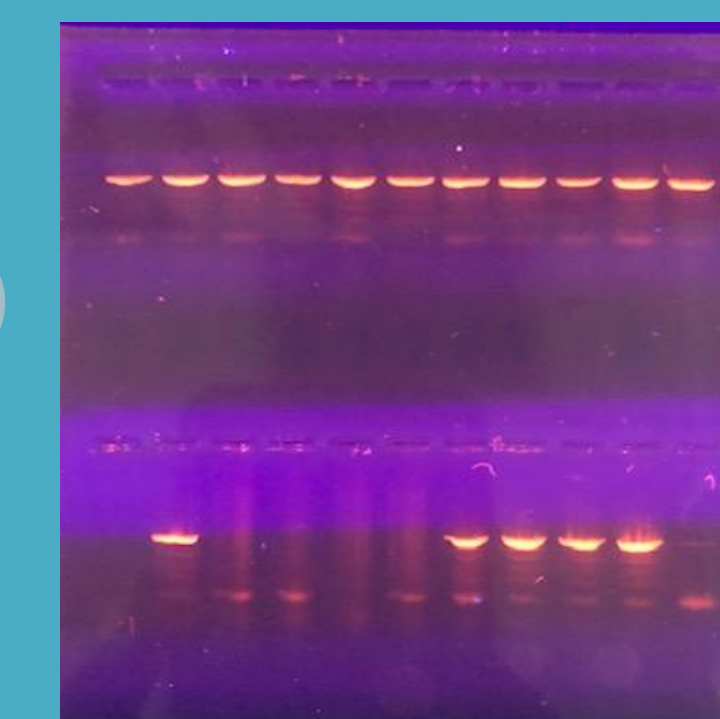


Tissue samples, photo courtesy of J. R. Ancheta; JR-22-G11088-133.jpg

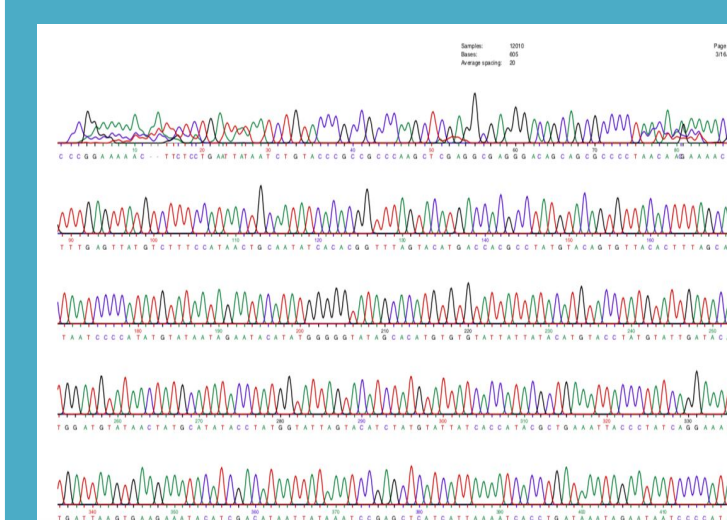
### Amplification

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

3



Gel electrophoresis of amplified control region



Chromatogram of control region from Sanger sequencing

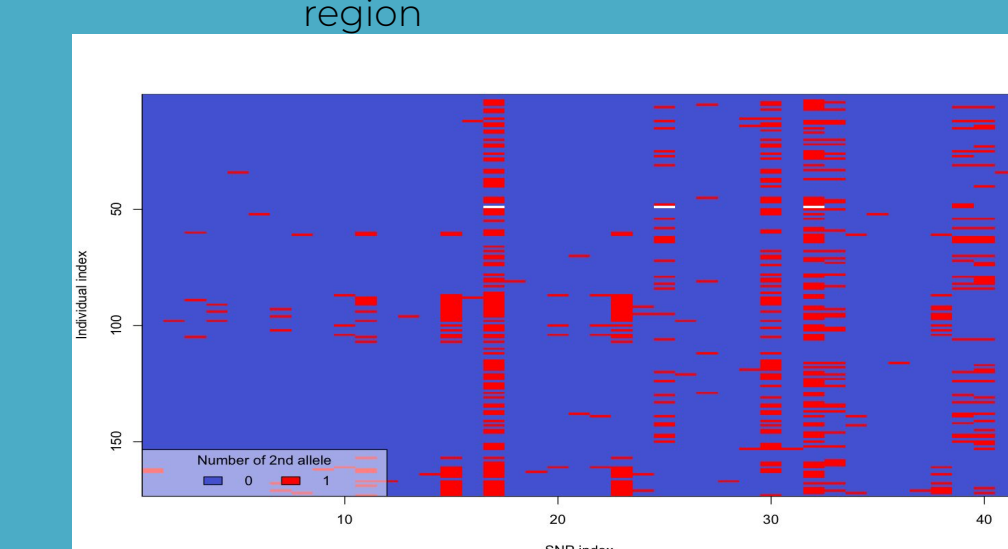
### 4 Sequencing

Sanger Sequencing

Analysis with Geneious Prime

### 5 Statistical Analysis

Analysis with R Studio



Map of the COI region highlighting the SNPs

## References:

1. Thornton, T. F., & Hebert, J. (2015). Neoliberal and neo-communal herring fisheries in Southeast Alaska: Reframing sustainability in marine ecosystems. *Marine Policy*.
2. Hay, D. E. et al., (2008). Geographic variation in North Pacific herring populations: Pan-Pacific comparisons and implications for climate change impacts. *Progress in oceanography*.
3. O'Connell, M., et al. (1998). Genetic structuring among Alaskan Pacific herring populations identified using microsatellite variation. *Journal of Fish Biology*.
4. Grant, W.S. et al. (2012). Limits of Bayesian skyline plot analysis of mtDNA sequences to infer historical demographics in Pacific herring (and other species). *Mol Phylogenet Evol*.
5. Liu, J. X., Tatarenkov, A., Beacham, T. D., Gorbachev, V., Wildes, S., & Avise, J. C. (2011). Effects of Pleistocene climatic fluctuations on the phylogeographic and demographic histories of Pacific herring (*Clupea pallasii*). *Molecular ecology*.

## Acknowledgements:

Would like to recognize that we work on the unceded lands of the lower Tanana and Dene people. A big thank you goes out Logan Ito, for time in the lab. Laura Timm for aid in analyzing data. Huge thank you to URSA for funding this project.