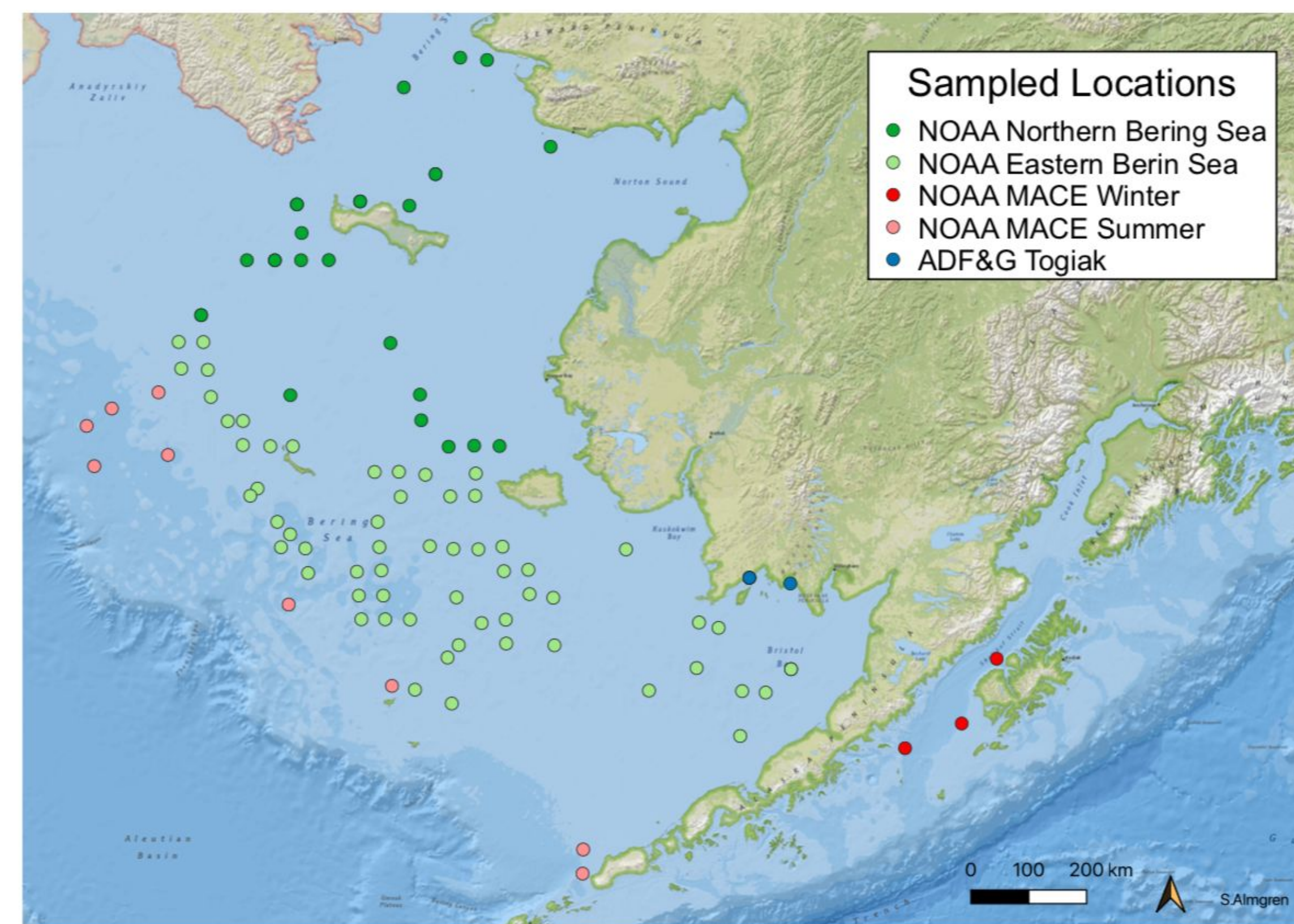


Research Question:

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



Photos courtesy of J. R. Ancheta; JR-22-G11088-14.jpg (Left) JR-22-G11088-127.jpg (Right)



Sample area. Courtesy of Sydney Almgren MS



Fig. 2. Map showing historical distribution of Pacific herring (blue) across the North Pacific and locations of samples for molecular analysis. Populations along the coast of southern California appear to be extinct. Geographic distributions compiled from Miller and Schmidtke (1956), Lassy (1989), Alaska Department of Fish and Game (www.adfg.alaska.gov/index.cfm?adfg=herring_rangemap), and NOAA Fisheries (www.nmfs.noaa.gov/pr/species/fish/pacific_herring.htm). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.) Previously sampled areas using mtDNA (4).

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

Preliminary Results:

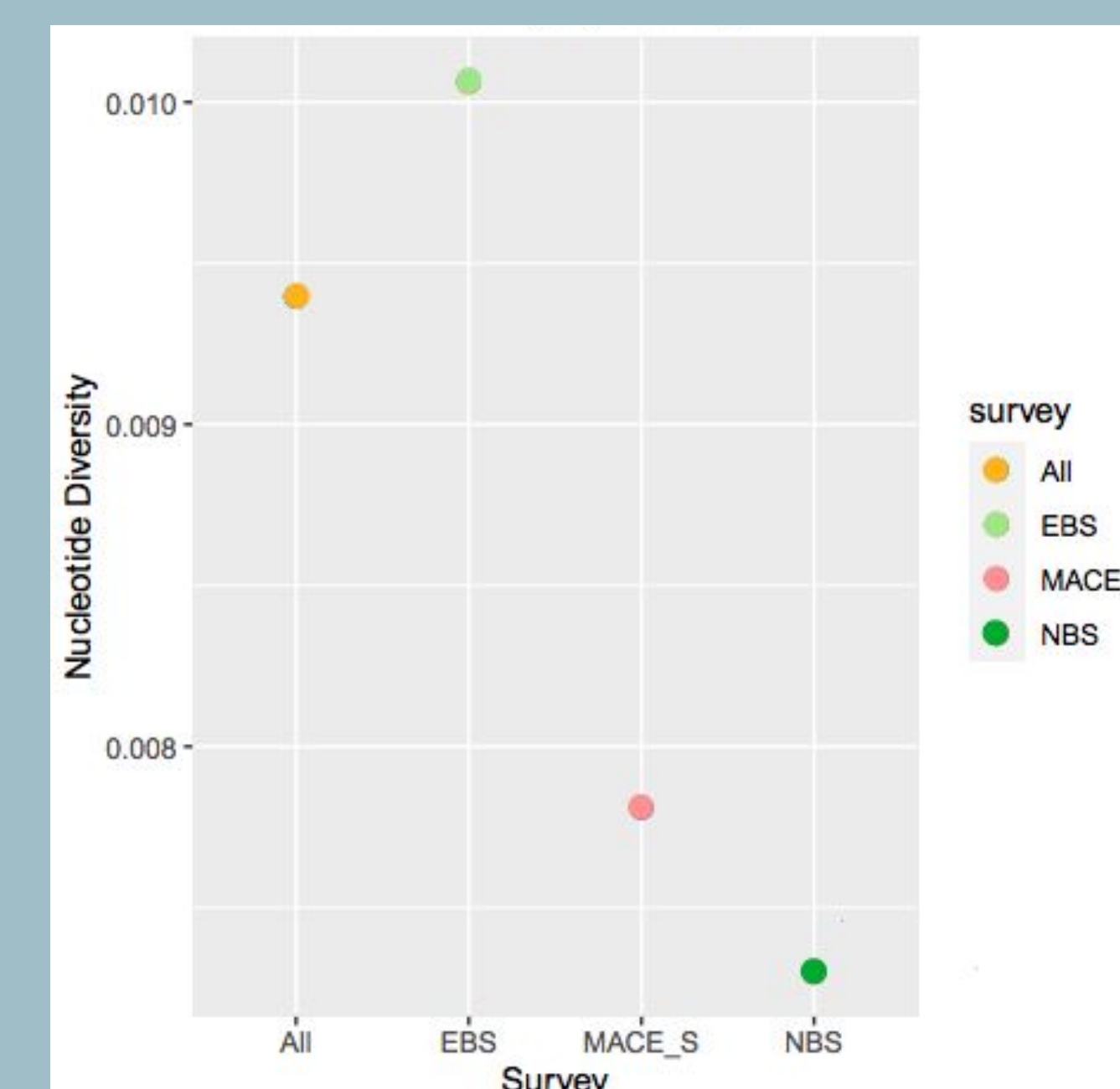


Figure 1. Nucleotide diversity by survey.

Sample Survey	Current Sample Size	Nucleotide Diversity
Eastern Bering Sea	31	0.010063
Northern Bering Sea	8	0.0073
MACE Summer	2	0.00781
Togiak	1	NA
All Samples	42	0.00934

Table 1. Nucleotide diversity and current sample sizes pictured in Figure 1.

Figures courtesy of Sydney Almgren

Sample Area	Nucleotide Diversity	Source
Bering Sea	0.011	Lui et al. (2011)
Togiak	0.0125	Grant et al. (2012)

Table 2. Nucleotide diversity results from other Bering Sea research for mitochondrial control region.

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.

Methodology:

1 Processing Samples

- Weight
- Length
- Gonad size
- Tissue sample



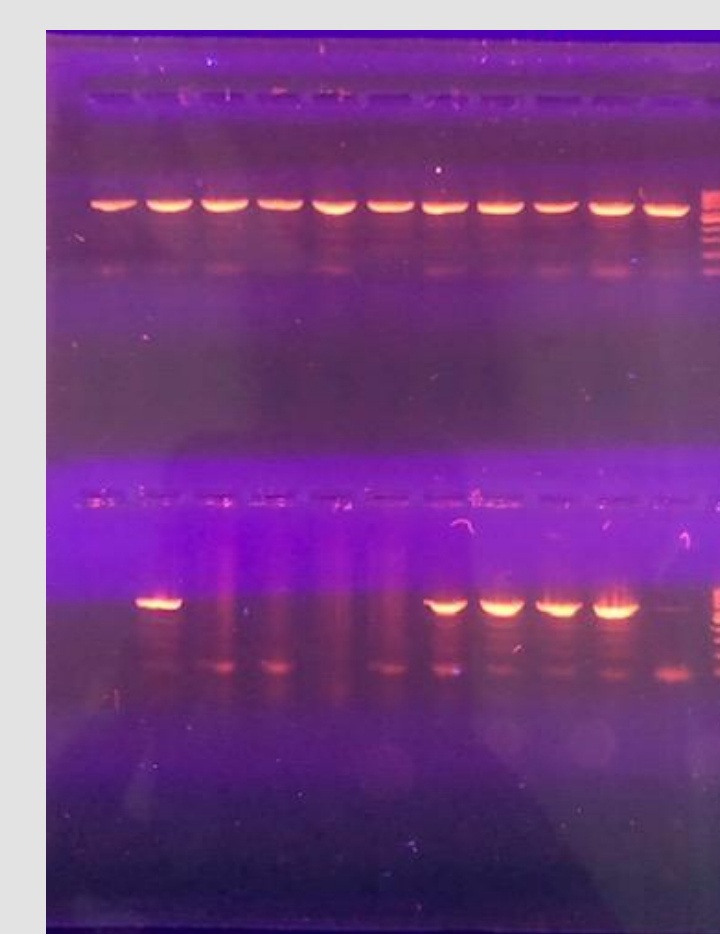
Herring Roe, photo courtesy of Sydney Almgren



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

2 DNA Extraction

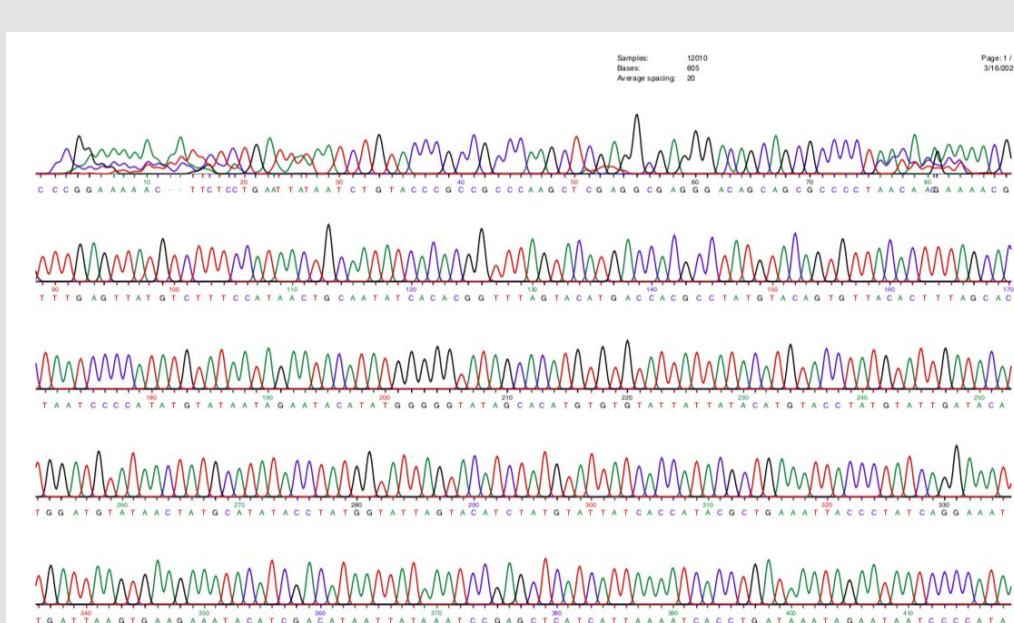
- DNA was extracted from heart tissue for 96 samples



Gel electrophoresis of amplified control region

3 Amplification

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



Chromatogram of control region from Sanger sequencing

4 Sequencing & Analysis

- Sanger Sequencing
- Analysis with Geneious Prime

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.



Clupea pallasii, photo courtesy of Sydney Almgren

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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:

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