



Using eDNA to Determine Humpback Whale Prey Rhayne Loggins¹, Jessica Glass^{1,2}, Chris Gabriele³

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Introduction

Glacier Bay National Park and Preserve have monitored its humpback whale population since 1985 via photo identification. One of the main concerns of the park is to ensure that the habitat, prey, and feeding activity of humpbacks are not disturbed by anthropogenic forces, which include rising ocean temperatures and noise pollution. To better understand humpback prey patch composition, this study is utilizing environmental DNA (eDNA) to confirm current understanding of prey patch makeup. We decided to test for Pacific Herring (Clupea pallasii), Walleye Pollock (Gadus chalcogrammus), Capelin (Mallotus villosus), and Sand Lance (Ammodytidae), as these are know to be common prey of humpback whales.

Objective

The purpose of this study is to identify the prey of humpback whales in Glacier Bay National Park and Preserve.

Methods

- Collect water samples
- Two samples, each two liters, per collection site
- Filter eDNA from Collected Water Samples
- Extract eDNA from filters
- Perform PCR with MiFish and a species-specific PCR
- Perform Digital PCR (dPCR) on samples



Image 1. Water sample collection. Photo: Chris Gabriele



Image 2. Filtering water samples Photo: Rhayne Loggins



Image 3. Extracting eDNA from filters Photo: Rhayne Loggins







Image 5.Gel electrophoresis of PCR with MiFish and Pacific Herring PCR Photo: Rhayne Loggins

Results/Discussion

- Found indication of high DNA concentration from PCR
- Next steps:
 - Create primers for Walleye Pollock, Capelin, and Sand Lance
 - Continue with species-specific PCR
 - dPCR of samples for detection and quantification of specific species.
 - Collect more samples during the 2024 season
- dPCR less expensive than metabarcoding

References

Fisheries, N. (n.d.). Preliminary results of E-DNA study shows promise for improving understanding of nearshore habitats for fish and crabs in Alaska.

https://www.fisheries.noaa.gov/feature-story/preliminary-results-e-dna-st udy-shows-promise-improving-understanding-nearshore

MiFish, a set of universal PCR primers for metabarcoding ... (2015, July 1). https://royalsocietypublishing.org/doi/10.1098/rsos.150088

Quantifying impacts of an environmental intervention using ... (n.d.). https://esajournals.onlinelibrary.wiley.com/doi/abs/10.1002/eap.2914

Stoeckle, M. Y., Mishu, M. D., & Charlop-Powers, Z. (2018, December 11). GoFish: A versatile nested PCR strategy for environmental DNA assays for marine vertebrates. PLOS ONE.

https://journals.plos.org/plosone/article?id=10.1371%2Fjournal.pone.01 98717

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