Integrating Steller Sea Lion Archaeogenomics with Archaeological Data to Understand Human-Marine Ecosystem Interactions and Demographic Shifts in the Kuril Islands

Report Prepared for the UW Quaternary Research Center

Introduction

The goal of this project was to understand how people inhabiting the Kuril Islands used the coastal resources available to them and how they may have shaped these marine ecosystems. The Kuril archipelago stretches from Hokkaido to Kamchatka and is prone to earthquakes, eruptions, and tsunamis, providing challenges to the hunter-gatherers who lived there throughout the late Holocene. In this challenging environment, people still managed to sustain themselves on a wide variety of food resources including marine mammals, fish, birds, and shellfish.

Elsewhere in the Pacific, researchers have argued that even a small group of hunters over a sustained period of time can deplete a marine mammal population, while others argue that at a metapopulation level, some marine mammal populations may be resilient to sustained hunting at low levels. In the Kurils, the Steller sea lion population has been declining since at least the historic period, from approximately 100,000 individuals to around 16,000, almost an order of magnitude. To provide more context for this decline and to learn more about the sea lion population prior to the colonial fur trade era, we attempted to sequence the mitogenomes of 14 archaeological, 14 historical, and 20 modern sea lions. This data was analyzed and placed in the context of other coastal fauna exploited at the site.

Methods

Ancient DNA

We originally tried to sequence part of the nuclear genome of our samples, but due either to poor preservation or other unknown reasons, this was unsuccessful and we did not obtain enough data to move forward with analysis. We then decided to switch gears and try to sequence the mitogenomes; mitochondria are present in higher copy numbers within cells and are relatively short at only ~16600 bp, so we predicted that we would have higher success.

To sequence the mitogenomes, we first extracted the DNA from our samples. For the ancient and historical museum samples, this was completed in the Ancient DNA Lab at the Smithsonian's Museum Support Center in Suitland, Maryland. Modern DNA extractions were performed in the pre-PCR room of the Laboratories for Analytical Biology at the Smithsonian's National Museum of Natural History in Washington, D.C. We then made and quantified libraries following established protocols for degraded DNA. We captured mitogenomes using custom *Eumetopias jubatus* probes following the myBaits High Sensitivity protocol (v. 5.02), but without two-round enrichment. Finally, libraries were pooled in equimolar ratios and sent for sequencing.

We used the PopArt program to visualize Steller sea lion haplotypes and diversity and TempNet to visualize any continuity in haplotypes through time. Bayesian skyline plots were used to reconstruct population size of the Steller sea lions throughout the late Holocene.

Faunal Data Analysis

We further analyzed a faunal dataset from the Kuril Biocomplexity Project. Previously, the data was analyzed to identify biogeographic patterns in faunal exploitation; we added a temporal component to this by assigning cultural periods to each context in the dataset as determined by associated, published radiocarbon dates and confirming intact stratigraphy from site reports and stratigraphic drawings.

(Preliminary) Results & Discussion

Results (as of April 2023) are not yet published and data is still being analyzed.

Unfortunately, we were only able to successfully sequence three of the fourteen archaeological samples, but had success with the historical and modern samples. Mitochondrial diversity was high during all three periods; this is noteworthy particularly from the historic to modern period when there was a major population decline. We also found there was limited continuity in haplotypes between time periods, or at least in the population we sampled. A Bayesian skyline analysis revealed that the historic population estimates of around 100,000 individuals held true throughout the late Holocene as well. This suggests that despite millennia of sustained hunting, as demonstrated by the archaeofaunal record, human populations in the Kurils did not cause a decline in this species of marine mammal until the historic period.

Briefly, our diachronic faunal analysis showed that during the Okhotsk period, there was a decreased reliance on marine mammal hunting. This was a surprising result because elsewhere in the northern Japanese archipelago, the Okhotsk people were recognized for their marine mammal hunting practices.

Further Funding Obtained

This QRC grant served as a pilot for a project where I successfully obtained an NSF Doctoral Dissertation Research Improvement Grant.

This research was presented at the March/April 2023 Society for American Archaeology conference in Portland, Oregon.

Marine Mammal Hunting in the Kuril Islands: Zooarchaeological and Genetic Insights

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Introduction

People have inhabited the NW Pacific & Kuril Islands for millennia, supported by the productive marine and coastal environments. Here, we build upon previous faunal analyses that examined biogeographical patterns in faunal exploitation by conducting a chronological analysis, grouped by cultural period (Epi-Jomon, Okhotsk, Ainu and Colonial) to investigate the importance of marine mammals in the diets of people through time. We selected one species, Steller sea lions, to interrogate further using ancient DNA analyses with the goal of better understanding their demographics prior to Russian and Japanese colonial expansion into the region during the fur-trade. Ultimately, we aim to establish a historical ecological baseline for marine mammal communities in the region and to understand the dynamic relationships between humans and pinnipeds more broadly.



Methods & Results

Ancient DNA

- We sampled archaeological, historic (1800s museum specimens), and modern (2000s museum specimens) Steller sea lions (Eumetopias jubatus) from the Kurils, Sakhalin and the Commander Islands
- Mitogenome capture was performed
- Haplotype networks and analyses using PopArt and TempNet



Figure 1
Median joining network of archaeological, historic and modern Steller sea lions showing extremely high mitochondrial diversity.

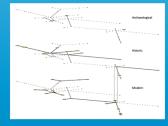


Figure 2
TempNet analysis to identify any shared haplotypes between archaeological, historic, and modern Steller sea lions. Very few shared haplotypes are seen even among the same time period; there is one shared haplotype between the historic and modern period.



Faunal Analysis

- We further analyzed a faunal dataset from the Kuril Biocomplexity Project, building upon Gjesfjeld et al. (2019)
- Analysis of Otariid hunting by time period
- Application of Modified Meat Utility Index to Otariid elements (following Savelle et al. 1996)

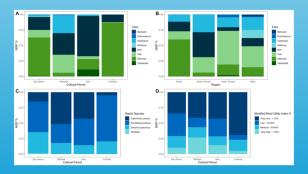


Figure .

regions of the Kurils. There is a significant decrease in the amount of mammal hunted during the Okhotsk period and an increase in the amount of shellfish. C: Three different Otariid species were found in the Kurils and hunted (one now extinct). There was a slight decrease in the amount of Steller sea lion hunted in the Okhotsk period versus others, but this could be due to regional trends or the amount of unidentified Otariid elements.

D: The decreased amount of mammal found in Okhotsk sites does not appear

D: The decreased amount of mammal found in Okhotsk sites does not appear to be due to butchering/transport decisions since both high and low-ranking elements are present in about equal numbers.

Conclusions

Despite millennia of sustained hunting by people throughout the Kurils, Steller sea lion populations remained stable until their decline in the historic furtrade era. Although there was a major population decline in both the historic and modern periods as noted through surveys (Burkanov & Loughlin 2005), their mitochondrial diversity remains high to this day. Interestingly, we noted a sharp decrease in the importance of mammals to the Okhotsk people, a group traditionally associated with marine mammal hunting.

Acknowledgements

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