Foraging Ecology of Black Oystercatchers (*Haematopus bachmani*) in the Gulf of Alaska

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Background

- The goals of this study are to determine diet composition of black oystercatchers, possible regional variability in diet in Alaska populations, and temporal variability over the last 100 years.
- Here, we present results from year one of a two year study on the foraging ecology of black oystercatchers in the Gulf of Alaska.
- This study uses a Bayesian analysis of stable isotopes of oystercatcher feathers and blood to identify the proportional contribution of major prey groups to black oystercatcher diet.
- Potential implications of this study include a greater understanding of the species' ability to shift its diet based on available prey.

Methods

- In year one, sampling of oystercatchers and their prey was conducted in Kenai Fjords National Park and northern Prince William Sound—areas with historic data on the location of nesting pairs.
- Blood and feather samples were collected from each captured bird. A minimum of five specimens of each target invertebrate species were collected opportunistically from each sampling location.
- All samples were dried and ground to a homogenous powder for processing. Stable isotope analysis was conducted using a continuous flow isotope ratio mass spectrometer (CF-IRMS) at the Environment and Natural Resources Institute (ENRI) Stable Isotope Lab at the University of Alaska Anchorage (UAA).

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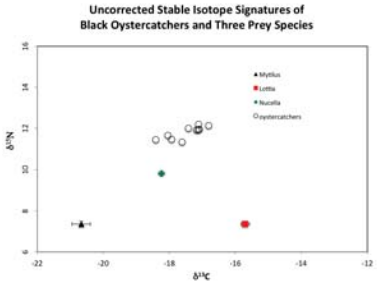
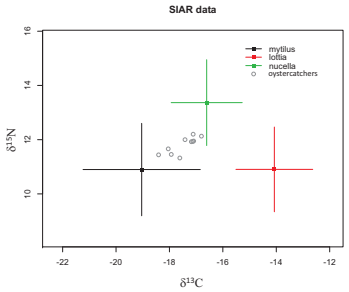
Preliminary Results

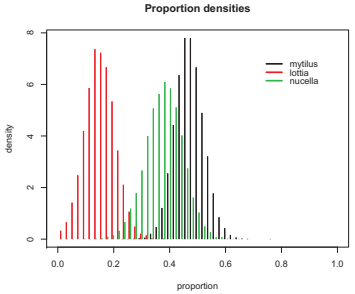
- As expected, prey signatures are isotopically distinct and oystercatcher signatures reflect a diet composed of the three groups.
- The diet composition of black oystercatchers in the northern Gulf of Alaska is approximately 49% *Mytilus*, 38% *Nucella*, and 15% *Lottia* based on stable isotope analysis.
- Interestingly, previous observational studies of prey delivered to chicks have shown a relatively higher proportion of limpets (*Lottia*) in the diet.
- Based on limited initial data, signatures show little spatial variation between two locations in the northern Gulf of Alaska.

Next Steps

- Complete analysis of 2012 samples (feathers and remaining invertebrates).
- Obtain and analyze archived black oystercatcher blood collected in 2004 – 2007 in several locations throughout the GOA.
- Obtain and analyze archived feathers from museum specimens, which were collected between 1910 and 1945.
- Conduct controlled diet study on captive oystercatchers at the Alaska SeaLife Center to obtain more accurate estimates for rates of turnover and fractionation values.
- Conduct season two of field work in Aialik Bay and Harriman Fjord (Prince William Sound).







	Low 95% hdr	High 95% hdr	mode	mean
mytilus	0.38	0.58	0.49	0.47
lottia	0.05	0.25	0.15	0.15
nucella	0.24	0.50	0.38	0.37

Figures 1 and 2

- Stable isotope signatures ($\delta^{13}C$ and $\delta^{15}N$) are presented for three isotopically distinct prey species—mussels (*Mytilus trossulus*), limpets (*Lottia* spp.), and dogwinkle (*Nucella lamellosa*) as well as for oystercatcher whole blood, which reflects diet three-four weeks before the date of collection.
- Carbon values reflect primary production sources. Limpets (*Lottia*) feed on benthic algae while mussels (*Mytilus*) filter feed on pelagic plankton.
- Nitrogen values reflect trophic levels, and dogwinkles (*Nucella*) prey on other intertidal invertebrates while mussels (*Mytilus*) and limpets (*Lottia*) are primary consumers.
- Figure 1 shows uncorrected consumer values and standard error bars around mean prey values.
- Figure 2 is produced by running the data through a Bayesian model using SIAR (Stable Isotope Analysis in R). Here, correction values are applied to source values. Error bars show the probability error associated with the Bayesian mixing model and incorporate error values from sources, trophic position correction values, and residual error.
- Trophic correction values used in Figure 2 are taken from the literature (3.54 for N and 1.63 for C).

Figure 3

- Figure 3 shows the relative proportion of the diet for an average oystercatcher signature.
- The range of bars for each prey item represent the posterior probability distribution based on 200,000 iterations of the SIAR model.
- The highest bar is the most likely proportion (mode) and the spread of the bars represent the 95% credibility intervals for each source. Density is a measure of model confidence.