

# Comparison of Three Diet Analysis Methods within Individual Bearded Seals

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#### Introduction

Analysis of stomach contents, stable isotopes, and fatty acids are three common methods used to analyze the diet of marine mammals. How these methods compliment each other is poorly understood. To learn how these methods compare with each other, we applied all three methods to the same sample of bearded seals (*Erignathus barbatus*) because they have a mixed diet including benthic and pelagic species.



**Figure 1.** Map of Alaska including Point Hope; seal tissue collection location.

# Methods

# **Field Collections**

In 2007 and 2008 stomach contents, muscle, and blubber samples were collected from 8 (4 female, 4 male) adult (>5years) bearded seals harvested for subsistence use in Point Hope (*Figure 1*) and kept frozen at -20°F until analysis.

# Stomach Content Analysis

Stomachs were thawed in the Alaska Department of Fish and Game laboratory and the contents were rinsed with freshwater through two sieves and prey items were indentified to the lowest taxonomic level.

## Stable Isotope Analysis

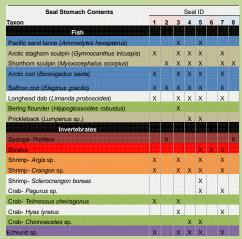
Freeze-dried muscle was analyzed for  $\delta^{13}$ C and  $\delta^{15}$ N at the Alaska Stable Isotope Facility at University of Alaska Fairbanks on a IRMS-EA following the methods described in Dehn et al. 2007.

#### Fatty Acid Analysis

Lipids were extracted from full thickness blubber and analyzed at Dalhousie University following the methods described in Budge et al. 2007.

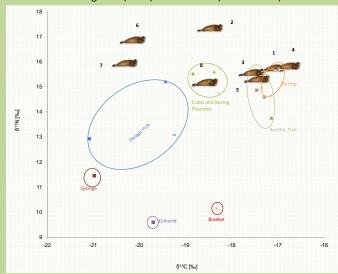
## Results

Stomach Content Analysis is the gold standard for diet analysis because the data do not require additional interpretive analysis/modeling, but the data are limited to recent feeding only.



**Table 1.** Stomach contents from 8 bearded seals. "X" represents presence of prey item. Colored rows represent the same color scheme as prey highlighted in the stable isotope Figure (2). Seal ID cells colored in pink represent female and blue represent male. Note that stomachs from seals 6 & 8 were mostly empty and most of the stomachs included both pelagic and benthic prey species.

<u>Stable Isotope Analysis</u> can be run on most tissues and only require small quantities for analysis. Depending on tissue analyzed, stable isotopes yield information on long term (bone) or short term (blood & liver) diet.

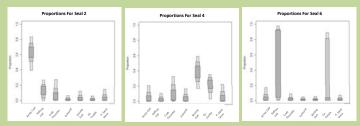


**Figure 2.** Stable isotopes for seal muscle and some representative prey species trophic guilds. Seals are numbers as in Table 1. Prey Isotope signatures are used with permission from Dehn et al. 2007, Iken et al. 2010, and Sara Carroll unpublished.

Stable isotope analysis **does not** reveal individual prey consumed, but can **indicate trophic level and carbon source**. For example, in Figure 2 seals 2 & 6 were eating at a higher trophic level and seals 2 & 8 were eating more pelagic prey. Seals 1, 3, 4, & 5 were eating mostly benthic species.

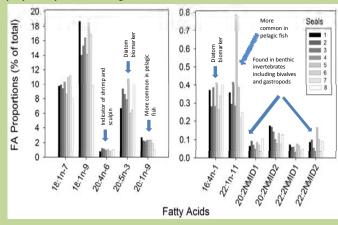
Carbon isotope signatures for seals 6 & 7 are erroneous due to sample impurity from seal oils on the muscle. If these samples were lipid extracted and reanalyzed they would likely have carbon values similar to the other seals.

Mixing models, Figure 3, require an accurate prey library and accurate tissue fractionation factors to interpret the predator's isotope signatures. Isotopes may differ regionally (Iken et al. 2010), so prey need to be collected in the same area.



**Figure 3.** Examples of SIAR Mixing model for seals 2, 4, and 6. Mixing models for stable isotopes are designed to provide the most likely proportions of prey consumed, however the results will differ depending on what prey species were included in the model. Also too many sources can cloud the interpretation (See Carroll et al. presentation).

<u>Fatty Acid Analysis</u> requires interpretive analysis/modeling (i.e., QFASA) and an accurate prey library for the specific region of study. **Currently there is no prey library for the Bering/Chukchi seas!** 



**Figure 4.** Fatty acid signatures provide a cumulative diet over time and can indicate prey species and proportions to the diet. However, the exact allocation of fats from prey to the seal blubber is unknown and fatty acid deposition may differ by position of blubber core on the body and vertical stratification (Budge et al. 2006).

#### Discussion

Limiting diet analysis to only one of these three methods will not result in a complete dietary picture.

#### For example:

- Seal 2 included shorthorn sculpin and saffron cod in the stomach, but stable isotope mixing models showed more Arctic cod
- Seal 4 both stomach content and stable isotopes agreed on a wide variety of benthic invertebrates, and benthic and pelagic fishes
- Seal 6 had a mostly empty stomach providing limited dietary information.
   Mixing models indicated a diet high in saffron cod, but lipids skewed analysis

Although our interpretation is limited for fatty acid data due to lack of a prey library, we conclude that shrimp, sculpins, pelagic fish, and benthic invertebrates were likely part of the diet

# Conclusions

- For the greatest understanding of diet, combining methods with an understanding of their strengths and weaknesses is necessary
- Stomach contents provide actual prey items, so that prey libraries can be developed
- Stable isotopes and fatty acids can add an expanded view, but species resolution is limited and metabolic physiology is not clearly understood

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Budge, S. M., et al. 2006. Studying Trophic ecology in marine ecosystems using fatty acids: a primer on analysis and interpretation. Marine Mammal Science. 22(4): 759-801.

Bodgs, S. M., et al. 2007. Ferry and thormaries reveal inche separation in a Activitieshelds food web. Maries Excluse Progress Series. 136: 325-330.

Mallys, S. M., M. J. Wooller, A. M. Springer, S. I. Inverso, C. P. Molloy and G. I. Divoley, 2008. Tracing carbon flow in an arctic marine food web using letty acid-stable inotrops enalysis. Occologis, 137(1): 117-129.

Coper, M. S., St. Bodgs, A. M. Springer, and G. Sheffield. 2009. Resource partitioning by ynepark pupping sails in Adalast monitoring effects of climate variation with listy acids. Paler Biology (20): 1137-1145.