UNIVERSITY OF MIAMI ROSENSTIEL SCHOOL of MARINE & **ATMOSPHERIC SCIENCE**

COMPOUND-SPECIFIC ISOTOPE ANALYSIS OF PERIOSTRACUM GROWTH BANDS FROM BATHYMODIOLUS CHILDRESSI: POTENTIAL TEMPORAL ARCHIVE OF ECOLOGY AT METHANE SEEPS

Abstract

The extensive methane seeps of the U.S. Atlantic Margin (USAM) are home to mussel communities that use endosymbiotic methanotrophic bacteria as their primary dietary source. Here we present results of compound-specific isotope analysis of amino acids (CSIA-AA) of the shell periostracum, or "shell skin", of the ubiquitous mussel species at these seeps, *Bathymodiolus childressi*, to assess organismal trophic position and methane reliance over mussel lifetime. We compare periostracum CSIA-AA data relating to mussel dietary sources over the individual lifespan to recently reported data from adductor and gill tissues of the same individuals in order to assess the reliability of the periostracum as an isotopic record.

Introduction

Objective

- Examine the trophic ecology of *B. childressi* using isotopic evidence from periostracum samples, as the periostracum forms in sequential bands, and can be analyzed after mussel death (unlike soft tissues)
- Does the periostracum represent a reliable temporal archive of methane seep ecology?

<u>Background</u>

- USAM: tectonically inactive passive margin that runs along the eastern U.S.
- Bathymodiolus childressi: mussels host bacterial symbionts that oxidize methane as an energy source, while retaining a digestive system and the ability to filter-feed [1,2]
- The periostracum: A thin protein layer that forms along the shell edge in continuous growth bands [3].



Methods

- 1. Mussels collected from the Chincoteague (925m) and Baltimore Canyon (395m) seep fields by investigators from the U.S. Geological Survey
- 2.Periostracum was excised at % lengths using a scalpel and forceps
- 3.A Growth Curve was developed using existing *B. childressi* mark-recapture data from a different methane seep site and used to age periostracum samples
- 4.The absolute abundance of individual amino acids in each periostracum sample of two mussels was determined using gas chromatography-mass spectrometry (GC-MS) at the UM Close Lab
- 5. δ^{15} N values of amino acids were determined using gas chromatography-isotope ratio mass spectrometry (GC-IRMS) for two mussels at the UM Lab



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→ Adductor Trophic Position (troph-sourc) → Adductor Trophic Position (Glu-Phe)

Conclusions

Mussel periostracum is a reliable archive of *B. childressi* isotopic patterns

Periostracum 0% sections (most recent) compare well to adductor muscle samples

The periostracum records variation in amino acid composition over lifetime

These variations are likely due in part to the quinonetanning (hardening) process of the periostracum protein

imitations

Processing time and analytical time

- only two individuals were analyzed via the Close Lab GC-IRMS
- Degradation of the periostracum with age

• Sections 0-30% are preferentially excised for analysis Analyses are time-intensive, but eventual analysis of more individuals will allow for statistical replication

Future Research

- Mark-recapture surveys of USAM B. childressi would improve growth curves
- Characterizing the effect of distance from the seep on methane energy-sourcing
- Characterize methanotrophic symbiont specifically Refined periostracum excision, increased
- replicability
- δ^{13} C analysis
- Examination of archived shells from museums, etc.

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Background: Image courtesy of Deepwater Canyons 2013 - Pathways to the Abyss, NOAA-OER/BOEM/USGS.

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Gill Trophic Position (Glu-Phe)

Adductor Trophic Position (troph-sourc) Adductor Trophic Position (Glu-Phe)

Gill Trophic Position (troph-source)

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