Bay of the Living Dead: 
Preservational Bias and Historical Ecology of Holocene Mollusks in the Chesapeake Bay

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Talk outline

I. Introduction
II. Preservation of Bay mollusks
   ▪ Methods and results
III. Amino acid geochronology and time averaging of Holocene mollusks
   ▪ Methods and results
IV. Historical ecology of Holocene mollusks
   ▪ Methods and preliminary results
V. Conclusions
Introduction: coastal ecosystems

- threatened by human disturbance
- millions spent on restoration
- what’s the baseline?

Currently relying on short-term ecological and historical data, but what about the fossil and geological record?

Introduction: Chesapeake Bay

- anthropogenic problems include over-fishing and nutrient pollution
- Holocene record of mollusks may provide a baseline for restoration
- effects of preservational bias must first be assessed
Fossils to the rescue?

Holocene record does exist, but is it complete enough to use?

Live-dead comparison

Live community
- death
- scavenging
- decay
- disarticulation
- burial

Death assemblage
- fossilization
- exposure
- diagenesis

Fossil record

Live-dead comparison

Does the death assemblage accurately represent the living community?

- Species composition
- Richness
- Abundance
Time averaging

- multiple generations of organisms are preserved together in a single stratigraphic unit
- effect is to set limits on temporal resolution by obscuring ecological and environmental change

What is the magnitude of time averaging?

Metrics
- maximum shell age
- age range
- standard deviation
- shell half-life

Behrensmeyer et al. (2000)

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Taphonomy of CBay mollusks

Questions addressed
1. How well does the death assemblage record live species composition, richness, and abundance?
2. What types of taphonomic damage occur in the molluscan death assemblage?
3. Does this taphonomic damage vary according to intrinsic factors such as life habit and shell mineralogy?

Methods: live-dead comparison
- 4 sites in main channel
- collaboration with CBP
- 2 boxcore samples/yr
- live: 20 yrs, dead: 1 yr
- temperature, salinity, pH, & grain-size
- sieved to 0.5mm
Methods: live-dead comparison

- sorted and ID’d to species level
- ~4000 dead
- ~24,000 live from CBP data
- calculated species richness and abundance

Species composition
1. % species in the live found dead
2. % species in the dead found live
3. % individuals of species found in the dead also found in the live

following Kidwell & Bosence 1991

Results: species composition

Across all sites, compiling 20 years of live data

- 77% species in the live found in the dead
- 71% species in the dead found in the live
- 99% individuals of species found in the dead also found in the live

Missing taxa: rare, patchy, thin-shelled, hard to ID

Lockwood & Chastant (2006)
Results: species richness

- live almost = dead with 20 years of live data

\[ r_4 = 0.11-0.94 \]
\[ p = 0.89-0.06 \]

Lockwood & Chastant (2006)

Results: abundance

- live = dead with 1-20 years of live data
- past work: \( R = 0.45 \) (coastal mud), 0.32 (sand)

\[ R_{24-29} = 0.47-0.68; \ p = 0.01-0.0001 \]

Lockwood & Chastant (2006)
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Amino acid geochronology and time averaging of Holocene mollusks

Amy Edwards Simonson
M.S., University of Delaware, 2007

Goals of research
1. Establish a radiocarbon-calibrated aminochronology for Holocene of the Chesapeake Bay
2. Quantify time averaging of Holocene molluscan deposits
Methods: aminochronology and time averaging

- 3 cores collected by giant piston corer, RV Marion-Dufresne (June 2003)
- selected cores with greatest amount of molluscan material
- collaborators collected sediment and microfossil data and dated core material by AMS radiocarbon dating

**MD03 2661: (Kent Island)**

- Core length: 2448 cm
- 820 – 7660 BP
- *Mulinia lateralis*
- AAR performed at Kauffman lab (NAU)
- Glutamic (Glu), Aspartic (Asp) acids
- Screened using internal consistency & serine concentration
Methods: aminochronology and time averaging

- Radiocarbon performed at NOSAMS (WHOI)
  - Used CALIB 5.0.2, MARINE07 to convert to cal yrs
  - Used CBay correction of 365±143 yrs (Colman et al. 2002)
- AAR and $^{14}C$ calibration approaches
  1. Direct articulated ($n = 8$)
  2. Direct split ($n = 7$)
  3. Indirect ($n = 129$)
- Time averaging
  - Standard deviation at each core depth

Results: aminochronology

Direct articulated
- Controls for intrashell variability and time averaging
- Most accurate of calibrations
- Used to calculate time averaging

Direct split
- Controls for time averaging

Indirect
- Controls for intrashell variability

Simonson et al. 2013
Results: time averaging

- 5-52 specimens per core depth, 25 core depths
- assigned ages based on direct articulated calibration
- Standard deviation
  - avg 720 yrs
  - 12 - 2700 yrs

Canuel et al. (in press)

Results: time averaging

- both time averaging and effects of nonlinearity of racemization kinetics increase with depth, severely limiting temporal resolution
- suggests that CBay mollusks may not be useful tools for high resolution paleoestuarine reconstructions
- in process of trying another approach using all three calibrations to parse sources of AAR variability

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<th>Articulated</th>
<th>Paired</th>
<th>Indirect</th>
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<td>Analytical error</td>
<td>2%</td>
<td>2%</td>
<td>2%</td>
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<tr>
<td>Intrashell variability</td>
<td>0%</td>
<td>Total deviation minus analytical error</td>
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<tr>
<td>Intershell variability (inherent)</td>
<td>Total deviation minus analytical error</td>
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<td>Time averaging (age mixing)</td>
<td>0%</td>
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Simonson et al. (2013)
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Historical ecology of Holocene mollusks

Questions addressed

1. What species occur in the Holocene record of the Chesapeake Bay?
2. How does molluscan richness and abundance shift throughout the Holocene?
3. Do these changes correspond to climate changes?
Methods: historical ecology of Holocene mollusks

Two cores collected by RV Marion-Dufresne

MD03 2661: (Kent Island)
- 14 samples
- 820 – 7660 BP
- mollusks sieved (0.5mm), sorted, and ID’d
- calculated richness (number of species)
- calculated abundance (proportional/rank)

Results: sp. composition

- 3410 individuals, 33 species

<table>
<thead>
<tr>
<th>Common</th>
<th>Rare</th>
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<tbody>
<tr>
<td>Mulinia lateralis</td>
<td>Macoma balthica</td>
</tr>
<tr>
<td>Acteocina canaliculata</td>
<td>Littoridinops tenuipes</td>
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<tr>
<td>Boonea impressa</td>
<td>Urosalpinx cinerea</td>
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<td>Crassostrea virginica</td>
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</table>
Results: species richness

Late Holocene
~2500-0 BP
- richness decreases

Early Holocene
~7600-6000 BP
- richness increases

Results: % abundance

- *Mulinia* dominant throughout

Early Holocene
- greater richness, lower % of *Mulinia*

Late Holocene
- lower richness, higher % of *Mulinia*
Results: salinity

Early Holocene
- taxa with high salinity requirements present

Late Holocene
- taxa with high salinity requirements absent

Corresponds with interval of climate change

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Conclusions I

1. A live-dead comparison documented strong agreement between living community and death assemblage estimates of species composition and abundance

Results strongly suggest that death assemblage data can be used as an accurate proxy for the live Chesapeake Bay community

Conclusions II

2. Established a radiocarbon-calibrated Holocene aminochronology applicable throughout the Bay

3. Time averaging estimates for Holocene Mulinia range from 12-2700 years

CBay mollusks may not be useful for high resolution reconstructions

5. Preliminary results indicate that mollusks responded to changes in bay salinity from the Early to Late Holocene
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Results: shell organic content

**Low >**
- external FSA

**High >**
- disart
- encrustation
- fragmentation
- edge mod

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Lockwood & Work (2006)