Connecting Heterotrophic Microorganisms to the Ocean C cycle at the Sargasso Sea Microbial Observatory

Craig Carlson

Objectives

1. Identify temporal and spatial patterns of dissolved organic carbon and significant bacterioplankton lineages

2. Discovery.... High throughput culturing in low nutrient media as a means to bring some of the uncultured bacterioplankton into culture and sequence their genomes

3. Connect important microbial plankton groups to the remineralization of specific DOM compounds

4. Identify key organisms, proteins and DOM compounds to target for automated, high frequency monitoring
Core Measurements

**Continuous**
- Temperature
- Dissolved Oxygen
- Beam Attenuation
- PAR

**Discrete**
- Salinity
- Total CO$_2$ (TCO$_2$)
- Nitrate
- Phosphate
- POC/PON
- Pigments (HPLC)
- Oxygen
- Alkalinity
- Nitrite
- Silicate
- DOC/DON
- Bacteria

**Rates**
- Primary Production
- Bacteria Production
- Particle Fluxes

1988 - present
15 cruises / yr

BATS core data
Episodic events tied to mixing

BATS Primary Production

- spring bloom - summer low
- Interannual variability

DOC (µM) dynamics at BATS

Adapted from Hansell and Carlson 2001
Relationship between the maximum depth of convective overturn and DOC export from the BATS euphotic zone

DOC export (mol C m$^{-2}$ y$^{-1}$)

Max Mixed Layer Depth (m)

Adapted from Hansell and Carlson 2001

DOC (μM) dynamics at BATS

Adapted from Hansell and Carlson 2001
Bacterioplankton cell abundance (E8 L⁻¹)

Whole community response …

BATS CDOM Cruise Aug 2001

Cells E8 / l

Bacterial LH-PCR 16s electropherograms
Microbial communities in the surface layer at BATS are highly structured in time and space!

Publications from BATS showing vertical and temporal patterns in community structure:

- Gordon et al 1996.
- Giovannoni et al. 1996.
- Wright et al. 1997
- Morris et al. 2002
- Morris et al. 2005

Do surface and deep bacterioplankton assemblages respond differently to DOC that accumulates in the surface waters?

Mixing Experiments

Controls
Microbes growing in their own filtrate

Mixing treatments
Microbes growing in a mixture of surface and deep water

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### HS 893 Mixing Experiment

#### Experiment Table

<table>
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<th>Experiment</th>
<th>Inoc. Source</th>
<th>0.2 Filtrate Source</th>
<th>ΔCell Cells E8/l</th>
<th>ΔDOC 1 week</th>
<th>ΔDOC &gt; month</th>
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</table>
Characterization of DOC pool in northwestern Sargasso Sea

- Contribution of specific compounds like DCNS to total DOC can be used as an index of diagenetic state

- Quality of DOC in surface water is more bioreactive than DOC present in the upper mesopelagic zone

Diagenetic Index of DOC quality at BATS

Goldberg et al in revision
**MLD and Integrated Prokaryotic Biomass in the Upper Mesopelagic at BATS**

**Bacterioplankton cell abundance (E8 L⁻¹)**

Is the mesopelagic bloom a entire community response or lineage specific?
16S rDNA community diversity

81 - surface samples
83- 200 m samples
HAE III digest

Community fingerprint

Nonmetric multidimensional scaling

Members of the SAR11 clade demonstrate temporal shift

Marine actinobacteria

<table>
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<th>Clone ID</th>
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Summary

• The accumulated Surface water DOC is resistant to rapid microbial degradation by surface consortium

• Mixing deep microbial consortium and nutrients with surface DOC results in DOC drawdown and diagenetic alteration

• Relative increases in T-RFLP fragments of OCS 116, SAR11, SAR202 and Actinobacteria following convective overturn suggest that members of these groups may be important in DOC dynamics

MO objective: Identify temporal and spatial patterns in specific bacterioplankton populations quantitatively

SAR11 (E8/L) at BATS

Carlson et al submitted
Bifurcated SAR11 maximum

- Spring max: coincident with mixing and Spring PP bloom
- Summer max: After water column is stratified

Do these observations represent a shift between SAR11 Ecotypes???

Evolution Within the SAR11 Clade

- SAR11 IA
- SAR11 IB
- SAR11 II
- Brackish (III)
- Freshwater (IV)

T-RFLP fingerprints (HAE III)

- Relative contribution of each fragment = % contribution of each ecotype to total SAR11
  - 97 separate cast 0 & 200 m
  - Additional 32 cast 0-300 m

Monthly mean contribution of SAR11 Ecotypes

- 1 m samples
- 200 m samples

SAR 11 ecotype variability based on T-RFLP data

- 1 meter
- 200 meter
We constructed an annual composite matrix describing the relative contribution of each ecotype at each depth for each month.

<table>
<thead>
<tr>
<th>Depth (m)</th>
<th>Fragments length (bp)</th>
<th>SAR11 1b</th>
<th>SAR11 1a</th>
<th>SAR11 1l</th>
<th>Modeled partitioning over 80 m</th>
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<tr>
<td>0</td>
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<td>40 (1)</td>
<td>38 (3)</td>
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<td>20 (17)</td>
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Carlson et al. submitted
Summary

• DOC dynamics is of significant importance to the oceanic C-cycle

• Understanding how microbes are linked to these dynamics is still in a primitive phase

• Bulk DOC dynamics at BATS have been resolved and there are apparent relationships between temporal and spatial patterns of specific microbial populations

• BIG UNANSWERED QUESTION: How do specific microbes interact with specific compounds?

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Meredith Meyers

OSU
Giovannoni Lab group
Kevin Vergin

Microbial Observations