Microbial processes in the mesopelagic

Alyson Santoro
CMORE Summer Course 2014
Some of my best friends hang out in the mesopelagic

Santoro et al. 2010
Burd et al. 2010
Outline

• Importance of microbial activity in the mesopelagic to the biological pump

• Problems with quantifying microbial activity in the mesopelagic

• Toward a biogeography of the mesopelagic
What fuels microbial metabolism in the mesopelagic?

Why is there a mismatch between estimates of microbial carbon demand and particulate organic carbon supply?

Can a better understanding of nitrogen remineralization inform this problem?

Can the microbes themselves tell us anything?
Epipelagic 0 – 200 m  
Mesopelagic 200 – 1000 m  
Bathypelagic 1000 – 4000 m  
Abyssopelagic below 4000 m

I prefer the definition that the mesopelagic starts at the base of the euphotic zone.
POC Flux ambiguously related to primary production

ThE is the ratio of POC flux to NPP

Buesseler, 1998
Net community production =
Gross primary production – respiration

NCP = GPP - R
Diverse approaches to a common problem

Incubation independent or ‘in situ’ methods

• $O_2$:Ar (Gives NOP, convert to NCP)

• AOUR – Deviation from $O_2$ equilibrium compared with an independent ‘clock’ (like $^3$He)

• $\Delta^{17}O$ – uses unique stable isotopic signature of atmospheric $O_2$ to separate it from photosynthetic $O_2$ (GOP, convert to GPP)
But even these methods also appear to give conflicting results.

Incorporating DOC export resolves some of the discrepancy, but not all.
Buessler and Boyd 2009, as shown in Herndl and Reinthaler 2013
What is a young scientist to conclude?

• There is still uncertainty in how much carbon is exported from the euphotic zone, and whether this export occurs as POC or DOC.

• The fate of OC in the upper mesopelagic is also uncertain, and variable.
Estimates of bacterial carbon demand far exceed POC supply

VERTIGO data; Steinberg et al. 2008
Why is this so hard?

Assessing the apparent imbalance between geochemical and biochemical indicators of meso- and bathypelagic biological activity: What the @$#! is wrong with present calculations of carbon budgets?

Adrian B. Burd a,*, Dennis A. Hansell b, Deborah K. Steinberg c, Thomas R. Anderson d, Javier Arístegui e, Federico Baltar e, Steven R. Beaupré f, Ken O. Buesseler g, Frank DeHairs h, George A. Jackson i, David C. Kadko b, Rolf Koppelmann j, Richard S. Lampitt d, Toshi Nagata k, Thomas Reinthaler l, Carol Robinson m, Bruce H. Robison n, Christian Tamburini o, Tsuneo Tanaka p

Burd et al. 2010, Deep Sea Res II
Bacteria Respiration Rate

Calculate carbon respiration from oxygen consumption

\[
\frac{\text{grams O}_2}{L \times h} \times \frac{1 \text{ mol O}_2}{32 \text{ grams O}_2} \times \frac{1 \text{ mol C}}{1 \text{ mol O}_2} \times \frac{12 \text{ grams C}}{1 \text{ mol C}} = \frac{\text{grams C}}{L \times h}
\]

Collect and incubate in air-tight 'bacterial oxygen demand (BOD)'

Measure oxygen concentration

\[y = -0.0147x + 8.7127 \quad R^2 = 0.9983\]
Lots of assumptions in converting the measured quantity to the desired value

We want to know:

\[
\text{Org C} \quad \rightarrow \quad \text{CO}_2
\]

We measure:

\(^3\text{H} \text{ leucine uptake} \times \text{conversion factor} = \text{BP}

\[
\text{BCD} = \frac{\text{BP}}{\text{BGE}}
\]

\[
\text{BGE} = \frac{\text{BP}}{\text{BP} + \text{BR}}
\]

Further reading: Ducklow 2000, Del Giorgio and Williams 2005
BGE is related to BP, but there is a lot of scatter.

del Giorgio and Cole, 1998
**Microbial Biomass**

- **a:** Depth (m) vs. Microbial Biomass
- **b:** log$_{10}$ (µmol C m$^{-3}$ d$^{-1}$) vs. Microbial Biomass for BCD, 20% BGE
- **c:** log$_{10}$ (µmol C m$^{-3}$ d$^{-1}$) vs. Microbial Biomass for BCD, 2% BGE

Source: Herndl and Reinthaler, 2013
Giering et al. 2014
Evidence for autotrophy – cellular uptake of bicarbonate

Estimate flux of $6.5 \times 10^{13}$ mol C yr$^{-1}$
(0.8 Pg yr$^{-1}$)

Herndl et al. 2005
Single cell genomic data for carbon fixation in the mesopelagic

<table>
<thead>
<tr>
<th>Station</th>
<th>Depth (m)</th>
<th>Total SAGs*</th>
<th>Identified SAGs†</th>
<th>Metabolic gene screening results‡</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>RuBisCO</td>
</tr>
<tr>
<td>KN192-5-11</td>
<td>10</td>
<td>311</td>
<td>89 (29%)</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>800</td>
<td>1252</td>
<td>257 (21%)</td>
<td>21 (12%)</td>
</tr>
<tr>
<td>ALOHA</td>
<td>25</td>
<td>630</td>
<td>147 (23%)</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>770</td>
<td>630</td>
<td>245 (39%)</td>
<td>23 (12%)</td>
</tr>
</tbody>
</table>

*Total SAGs are the number with successfully amplified DNA product.
†SAGs for which high-quality SSU rRNA sequences were obtained.
‡Percentages based on the total number of identified bacterial SAGs only; ND, no data.

Single cell genome sequencing suggested that 12% of mesopelagic microbes have RuBisCO

What could the electron donors be?

Swan et al. 2011
Microautoradiography shows DI$^{14}$C uptake
Radiocarbon evidence for chemoautotrophy in the mesopelagic

Hansman et al. 2009
What does the nitrogen budget in the upper mesopelagic tell us?

Respiration: \( \text{CH}_2\text{O} + \text{O}_2 \rightarrow \text{CO}_2 + \text{H}_2\text{O} \)

Nitrification: \( \text{NH}_3 + 2\text{O}_2 \rightarrow \text{NO}_3^- + \text{H}^+ + \text{H}_2\text{O} \)

But unlike respiration, we can actually measure this directly.
Foster, Santoro, and Berelson unpublished
- $b$ compares well with JGOFS era $b$ for this region (0.76 versus 0.72).

- Depth integrated rates are in the right ball park if we convert JGOFS C flux to N flux.
“Our results suggest that a substantial fraction of sinking N flux may follow the pathway sinking N-urea-ammonium-nitrate. . . .”

Cho and Azam 1995, MEPS
Can the microbes themselves help us understand the mesopelagic?
Niche partitioning by temperature in *Prochlorococcus*

Johnson et al. 2006
We have a relatively good idea of ‘who’ is the surface ocean

Table 2  The most abundant genomes in the GOS data set

<table>
<thead>
<tr>
<th>Genome</th>
<th>GOS sequences recruited</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>90% Identity</td>
</tr>
<tr>
<td><strong>Prochlorococcus marinus AS9601</strong></td>
<td>163 465</td>
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<tr>
<td><strong>Prochlorococcus marinus MIT9301</strong></td>
<td>119 804</td>
</tr>
<tr>
<td><strong>Prochlorococcus marinus MIT9202</strong></td>
<td>48 213</td>
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<tr>
<td><strong>Prochlorococcus marinus MIT9312</strong></td>
<td>46 549</td>
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<tr>
<td><strong>Candidatus pelagibacter HTCC7211</strong></td>
<td>28 811</td>
</tr>
<tr>
<td><strong>SAR86A</strong></td>
<td>27 391</td>
</tr>
<tr>
<td><strong>Synechococcus sp. 9605</strong></td>
<td>26 071</td>
</tr>
<tr>
<td><strong>Ca. pelagibacter HTCC1062</strong></td>
<td>22 236</td>
</tr>
<tr>
<td><strong>Ca. pelagibacter HTCC1002</strong></td>
<td>20 901</td>
</tr>
<tr>
<td><strong>Prochlorococcus marinus MIT9215</strong></td>
<td>17 732</td>
</tr>
<tr>
<td><strong>Prochlorococcus marinus MED4</strong></td>
<td>9033</td>
</tr>
<tr>
<td><strong>SAR86B</strong></td>
<td>3579</td>
</tr>
<tr>
<td>Recruited by top 12 genomes</td>
<td>5.30%</td>
</tr>
<tr>
<td>Recruited by all the genomes</td>
<td>5.60%</td>
</tr>
<tr>
<td>(n = 1700)</td>
<td></td>
</tr>
<tr>
<td>Recruited by SAR86</td>
<td>0.31%</td>
</tr>
</tbody>
</table>

DuPont et al. 2012
But there are limited metagenomic data from the mesopelagic

Community Genomics Among Stratified Microbial Assemblages in the Ocean’s Interior

Edward F. DeLong,¹ Christina M. Preston,² Tracy Mincer,¹ Virginia Rich,¹ Steven J. Hallam,¹ Niels-Ulrik Frigaard,¹ Asuncion Martinez,¹ Matthew B. Sullivan,¹ Robert Edwards,³ Beltran Rodriguez Brito,³ Sallie W. Chisholm,³ David M. Karl³

Delong et al. 2006
Toward a biogeography of the mesopelagic

Giovannoni and Vergin 2012
Treusch et al. 2011; Giovannoni and Vergin 2012