Dissolved Organic Carbon Accumulation, Export and Microbial Transformation

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NPP ~ 54 Pg C y⁻¹... Dunne et al, 2007

~ 21 Pg C y⁻¹ is partitioned as DOC of which >90% is remineralized in the epipelagic (Williams, 2000; Hansell 2013)

• small fraction of the DOC production accumulates
• Early 1990’s - Observation of seasonal variability and redistribution of DOC via mixing

• DOC contributes to vertical export
DOC (µmol kg⁻¹) dynamics at BATS

- DOC Flux into mesopelagic zone: 0.2 – 1.4 mol C m⁻² y⁻¹
- Export flux “best” guess: 2-4 mol C m⁻² y⁻¹ at BATS

Adapted from Hansell and Carlson 2001
High Resolution DOC Data

> 50,000 DOC data points

2003-2014
Global Ocean Dissolved Organic Carbon (DOC)

~ 662 Pg C

DOC export is ~ 1.9 Pg C y\(^{-1}\) into the upper mesopelagic

Hansell, Carlson, Repeta and Schlitzer 2009
• DOC export ~ 77 Tg C y\(^{-1}\)

~ 10 – 20% of export production in the North Atlantic
Contribution of DOC oxidation to AOU in various neutral density layers in the North Atlantic

Slope = 0.14 ± 0.01

$r^2 = 0.52$

Labrador Sea Water

<table>
<thead>
<tr>
<th>Water mass</th>
<th>Contribution of DOC Oxidation to AOU-C$_{eq}$</th>
<th>Single end-member mixing</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$%$</td>
<td>$n$</td>
</tr>
<tr>
<td>UTCL</td>
<td>$28 \pm 2$</td>
<td>161</td>
</tr>
<tr>
<td>STMW</td>
<td>$9 \pm 1$</td>
<td>109</td>
</tr>
<tr>
<td>LTCL</td>
<td>$7 \pm 1$</td>
<td>332</td>
</tr>
<tr>
<td>LSW</td>
<td>$14 \pm 1$</td>
<td>464</td>
</tr>
<tr>
<td>ISOW</td>
<td>$19 \pm 1$</td>
<td>192</td>
</tr>
<tr>
<td>DSOW</td>
<td>$16 \pm 1$</td>
<td>487</td>
</tr>
</tbody>
</table>

Carlson et al 2010
Microbial perspective....

DOC (µmol kg⁻¹) dynamics at BATS

Deep Microbes grown on Surface DOC – Exp. HS893

Bacterioplankton

Carlson et al. 2004

Adapted from Hansell and Carlson 2001
Characterization of DOC pool at BATS

- Quality of DOC in surface water is diagenetically “fresher” than in the upper mesopelagic zone.

Decrease in DCNS % after stratification indicates DOC is diagenetically altered within the upper mesopelagic zone.

Goldberg et al. 2009
MLD and Integrated Bacterial Stocks in the Upper Mesopelagic (140-250m) at BATS

Bacteria Stocks (cells $E^{11}$ m$^{-2}$)

MLD (m)


0 100 200 300 400 500 600 700 800

50 100 150 200 250 300 350 400 450 500 550 600 650 700 750 800

MLD

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

Microbial communities are highly structured over depth

- Gordon et al 1996.
- Giovannoni et al. 1996.
- Wright et al 1997
- Giovannoni 2000.
- Morris et al. 2002
- Morris et al. 2005
- Carlson et al. 2009
- Treusch et al. 2009
Bacterial community is highly structured over depth: Molecular approaches reveal response of specific bacterial lineages in the mesopelagic zone after mixing.

- distinct mesopelagic microbial assemblages respond to mixing
- mesopelagic microbial response cued to the delivery of DOM
- DOM that persists at one depth horizon can become available to microbial degradation at another
Summary

- DOC can be an important export term in the biological pump. Global contribution is approximately 1.9 Pg C y\(^{-1}\) ~ 20\% of export production.

- Contribution of DOC as an export term varies in space and time.

- DOC that is persistent at one geographical location or depth horizon may be bioavailable at another.

- There are apparent responses by specific mesopelagic microbial lineages that coincide with DOM export, nutrient field, diagenetic state of exported DOM.

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