Biogeochemical effects of ringwater influence on the Mid-Atlantic Bight shelf: differences in microbially-driven carbon cycling along a shelf transect

C. Arnosti[1] , A. Hoarfrost[1], J.P. Balmonte[1], K. Ziervogel[2], S. Ghobrial[1], G. Gawarkiewicz[3]
[1]Univ. North Carolina-Chapel Hill; [2]Univ. New Hampshire; [3]Woods Hole Oceanographic Institution

Introduction

- Waters of the Mid-Atlantic Bight (MAB) are affected by interactions with offshore waters of the Gulf Stream[5]; these interactions can bring different organisms – including microbial communities – to the MAB. These microbial communities drive key biogeochemical processes.

- Surface and bottom water was sampled at four stations along a shelf transect at 71 ºW to compare microbial carbon-cycling capabilities and water mass characteristics at distinct depths and locations in the MAB.

- We measured bacterial abundance and activities, focusing on microbial enzyme activities, because these activities differ among microbial communities[1]; the rates and substrate specificities of extracellular enzymes help determine the rate and location of carbon remineralization in the ocean.

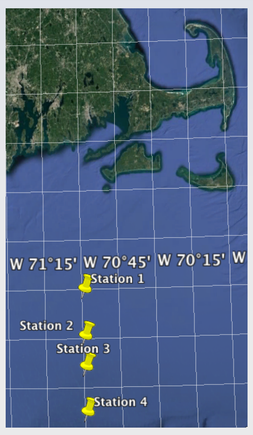


Fig. 1: stations along 71 W

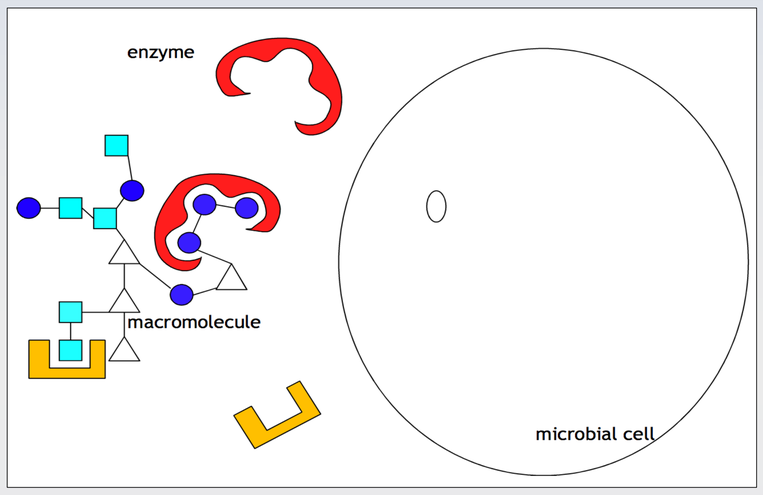
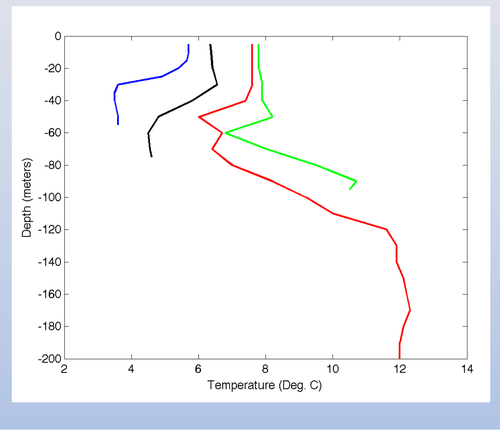


Fig. 2: High molecular weight substrates must be hydrolyzed by extracellular enzymes prior to substrate uptake. The activities and structural selectivity of these enzymes helps determine which substrates are accessible for a microbial community. The nature and types of substrates that are hydrolyzed by microbial extracellular enzymes varies markedly in ocean waters, with difference in hydrolysis patterns with depth, latitude, and distance from the coast.[1,2]



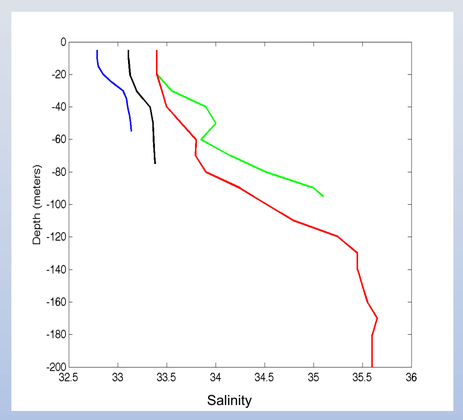


Fig. 3: Temperature and salinity at Stn. 1 (blue line; bottom depth 60 m), Stn. 2 (black; bottom depth 80 m), Stn. 3 (green; bottom depth 100 m), and Stn4 (red; bottom depth 200m). **Bottom waters of Stns. 1 and 2 were characteristic of shelf water, while the bottom water of Stn. 3 showed features characteristic of a mixture of slope and shelf water, and the bottom water of Stn. 4 was characteristic of ring water.**

	cells (L-1)	bact prod, pmol/cell	Chl a (ug/L)	NO2+NO3 (uM)	NH4 (uM)	PO4 (uM)	DOC (uM)
Stn 1 surface	6.90E+07	1.80E-07	0.142	0.39	0.63	0.396	135
Stn 1 bottom	9.80E+07	2.00E-07	0.281	0.85	1.81	0.413	137
Stn 2 surface	2.00E+08	1.00E-07	0.445	0.11	0.60	0.419	120
Stn 2 bottom	6.20E+07	3.40E-07	0.110	1.50	1.99	0.399	81
Stn 3 surface	6.80E+07	6.20E-07	0.845	0.16	0.24	0.322	90
Stn 3 bottom	4.10E+07	1.70E-07	0.079	5.51	1.48	0.659	78
Sn 4 surface	7.50E+07	1.20E-06	1.445	0.04	1.39	0.451	89
Stn 4 bottom	5.40E+06	5.40E-07	0.035	5.17	0.36	0.506	63

Table 1: Cell counts, per-cell bacterial protein production, DOC, and nutrients at all depths and stations.

Microbial enzymatic activities

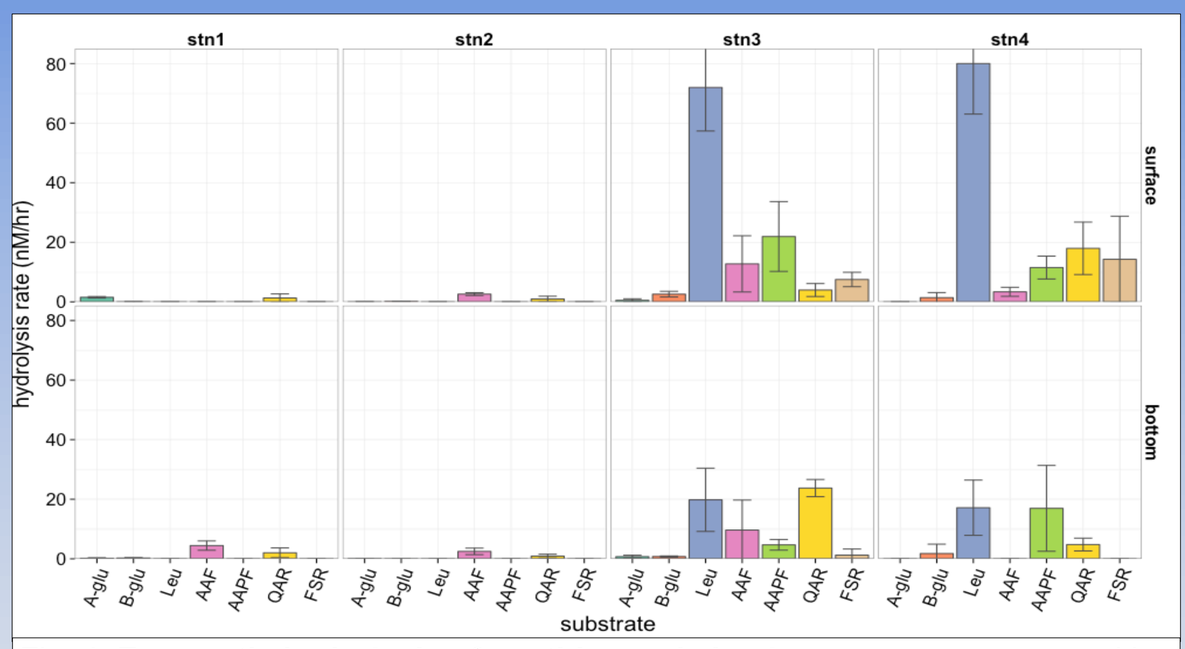


Fig. 4: **Enzymatic hydrolysis of peptides and simple sugars** was compared in using small substrate proxies[3,4]**. Rates and patterns of activities differed strongly by station and depth: at Stns. 1 and 2, hydrolysis rates were very low and only a narrow range of substrates was hydrolyzed**. **At Stns. 3 and 4, a much wider range of substrates was hydrolyzed, and at higher rates.** The hydrolysis pattern in Stn. 4 bottom water was quite distinct from Stn. 3 or Stn. 4 surface water: no α-glucose, AAF, or FSR were hydrolyzed.

Key: a-glu = α-glucose; b-glu = β-glucose. Leu = leucine amino peptidase. AAF and AAPF are chymotrypsin substrates; QAR and FSR are trypsin substrates (single letter AA codes)

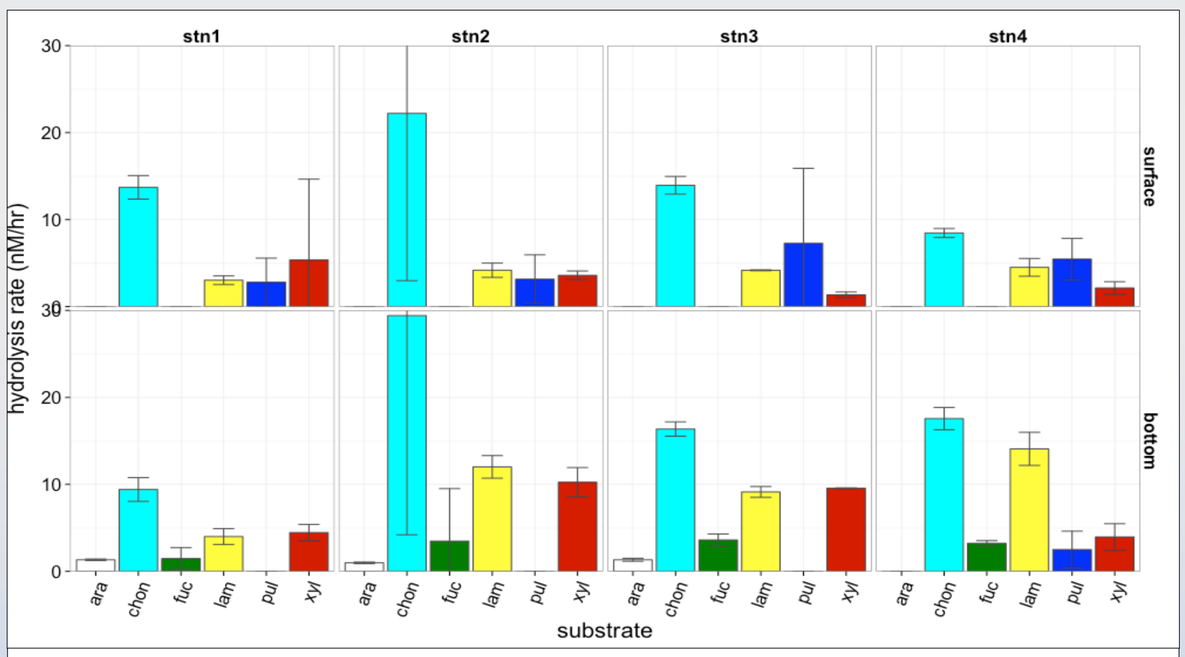


Fig. 5: **Enzymatic hydrolysis of 6 high molecular weight polysaccharides also showed substrate- and depth-related differences.** None of the microbial communities could hydrolyze all 6 substrates: the same 4 substrates were hydrolyzed in surface water; 5 of the substrates were hydrolyzed in bottom water. Pullulan was hydrolyzed only in surface waters – and in the bottom waters of Stn. 4. Fucoidan was hydrolyzed only in bottom waters. Arabinogalactan was hydrolyzed in bottom waters – except at Stn. 4.

Key: ara = arabinogalactan; chon = chondroitin sulfate; fuc = fucoidan; lam = laminarin; pull = pullulan; xyl = xylan. All are high molecular weight marine-related polysaccharides of differing chemical composition.

Implications

Bottom water of Stn. 4 is characteristic of Gulf Stream rings that impinge on the shelf of the MAB[5]. These waters clearly bring microbial communities with carbon-cycling capabilities distinct from communities associated with other water masses. The nature and extent of organic carbon cycled in the MAB will depend in part on the frequency and extent to which ring-associated water is brought into the MAB.

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