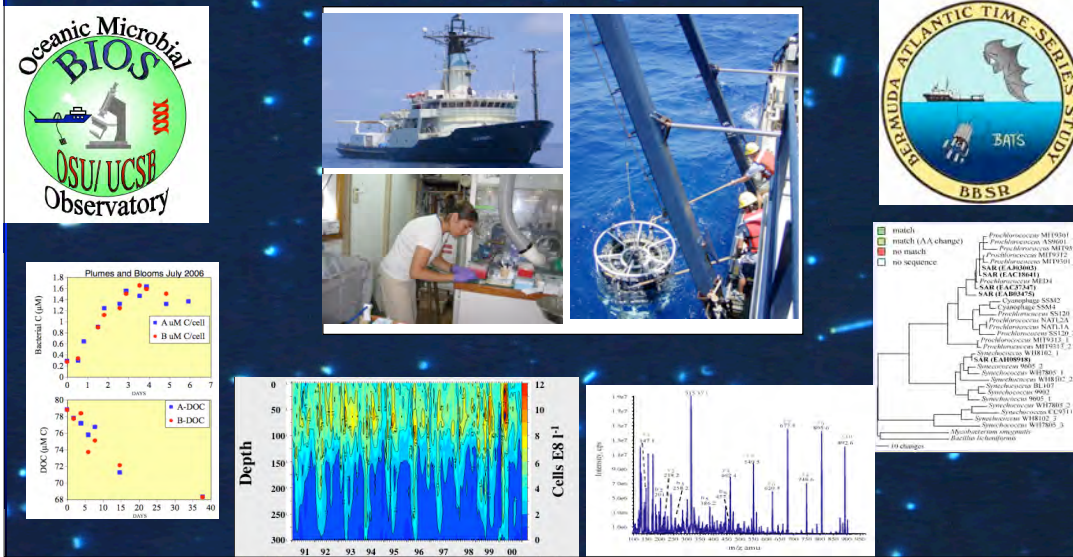


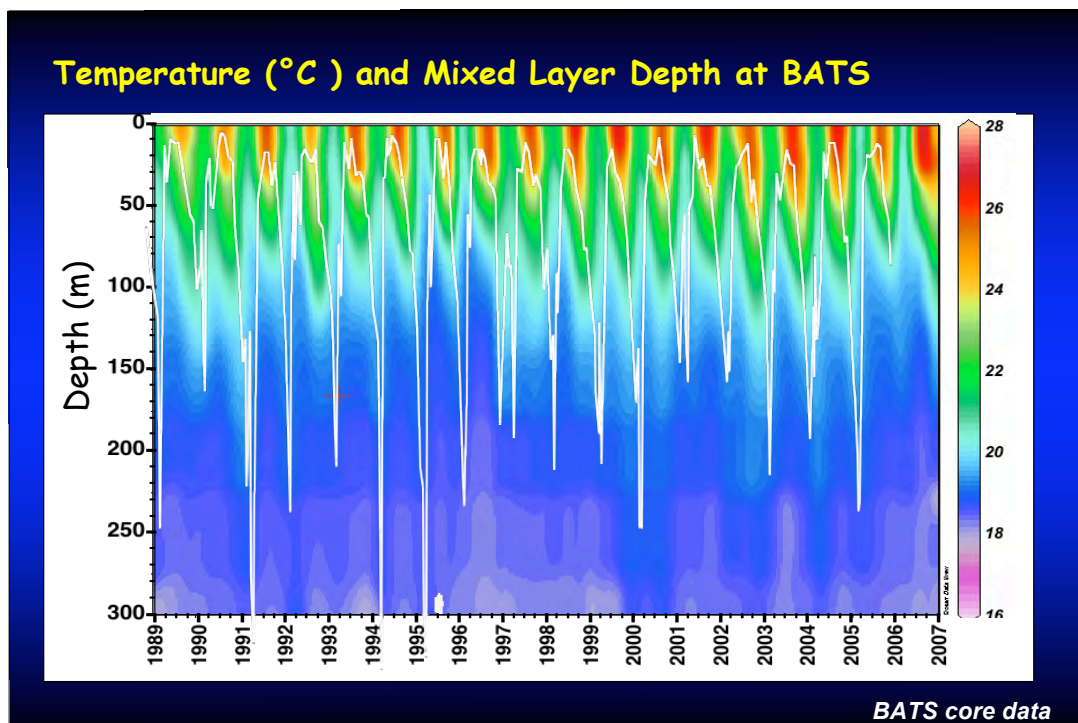
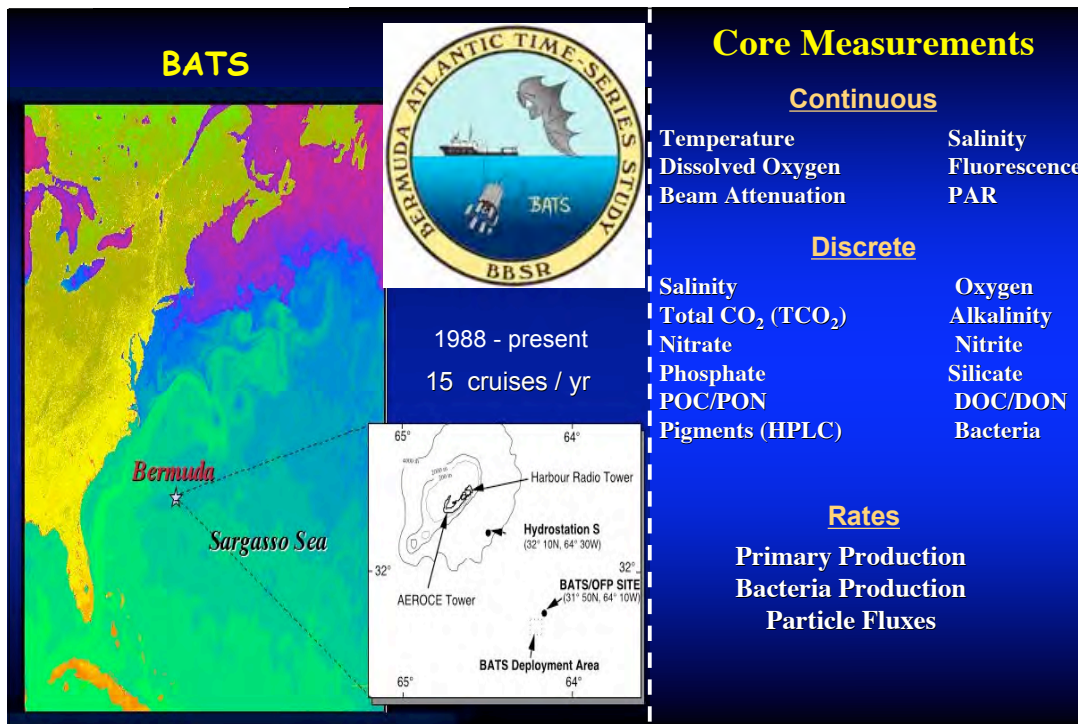
Connecting Heterotrophic Microorganisms to the Ocean C cycle at the Sargasso Sea Microbial Observatory

Craig Carlson

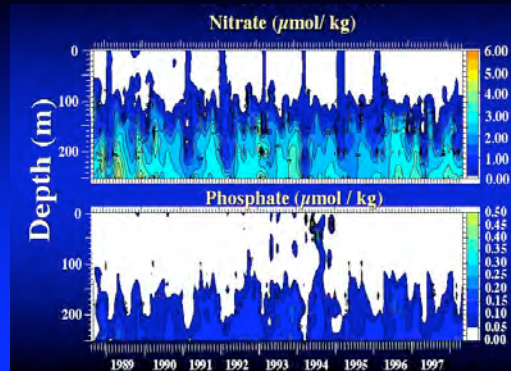


Oceanic Microbial Observatory Objectives

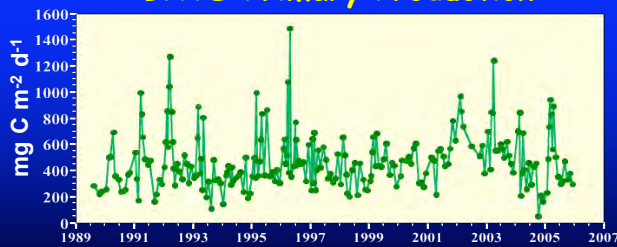
1. Identify temporal and spatial patterns of dissolved organic carbon and significant bacterioplankton lineages
2. Discovery.... High throughput culturing in low nutrient media as a means to bring some of the uncultured bacterioplankton into culture and sequence their genomes
3. Connect important microbial plankton groups to the remineralization of specific DOM compounds
4. Identify key organisms, proteins and DOM compounds to target for automated, high frequency monitoring



Episodic events tied to mixing



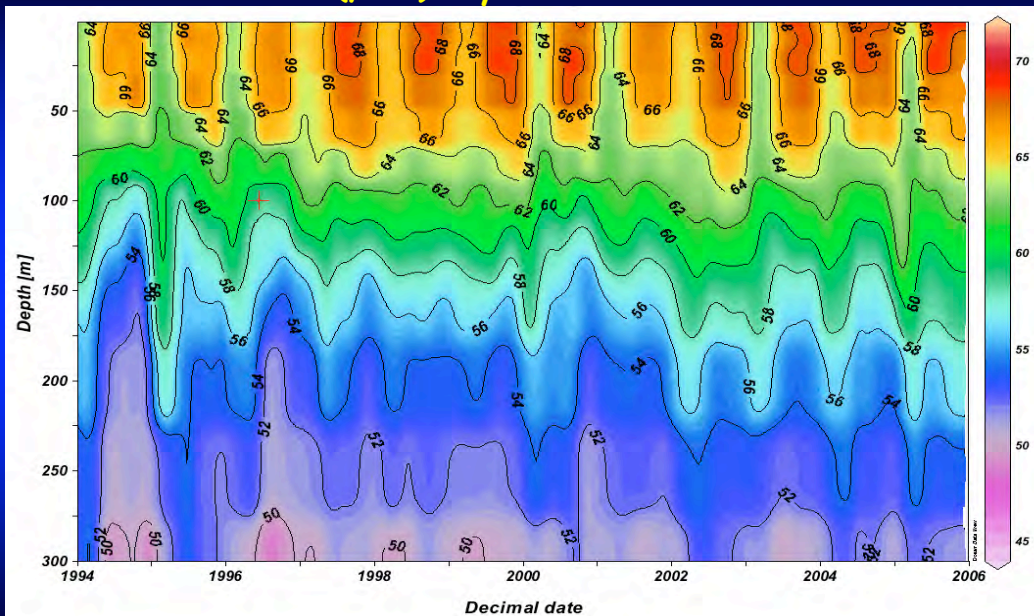
BATS Primary Production



- spring bloom - summer low
- Interannual variability

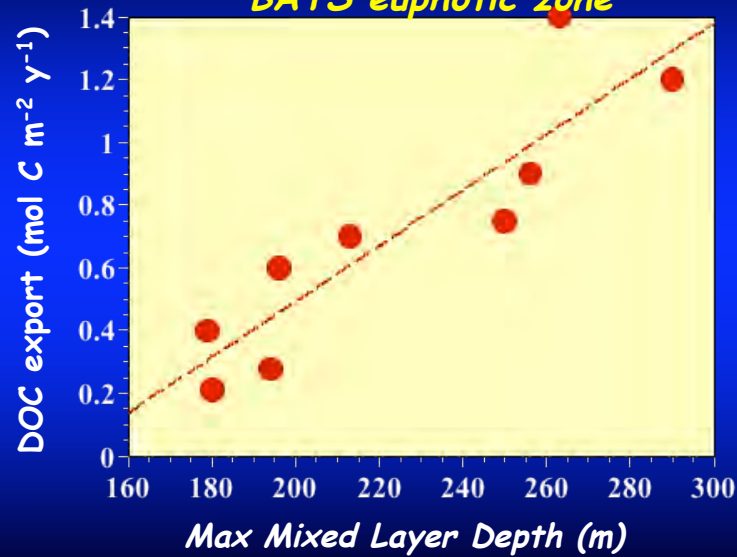
Steinberg, Carlson, Bates et al. 2001

DOC (μM) dynamics at BATS



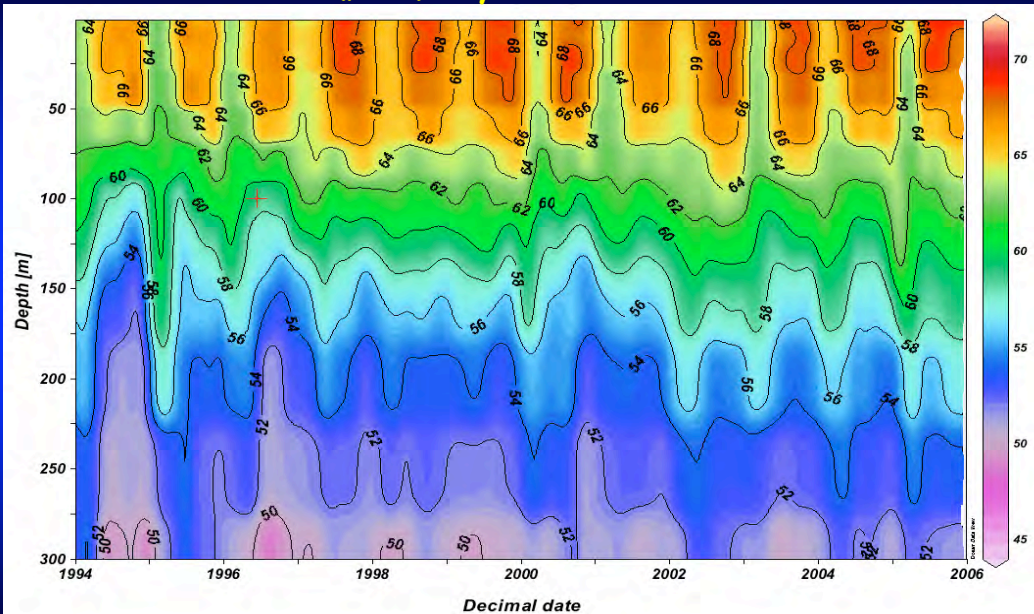
Adapted from Hansell and Carlson 2001

Relationship between the maximum depth of convective overturn and DOC export from the BATS euphotic zone



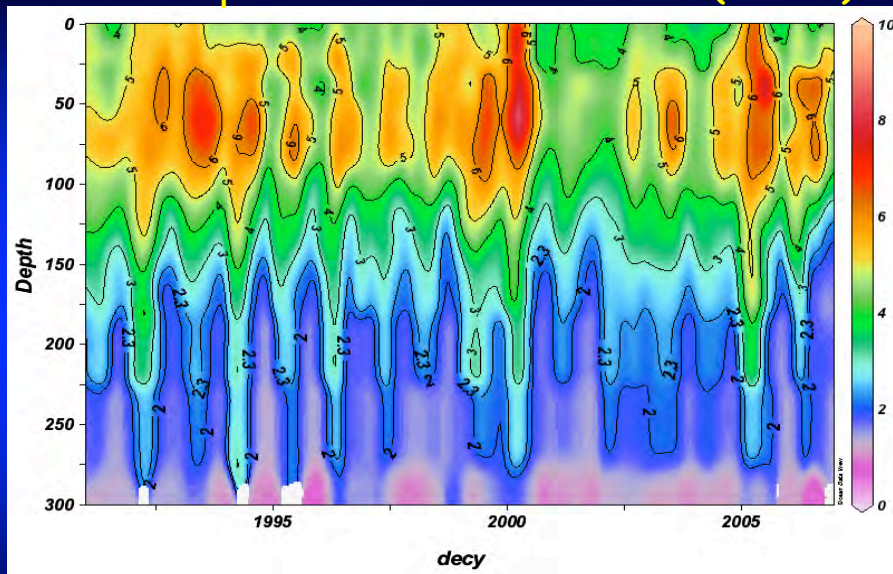
Adapted from Hansell and Carlson 2001

DOC (μ M) dynamics at BATS



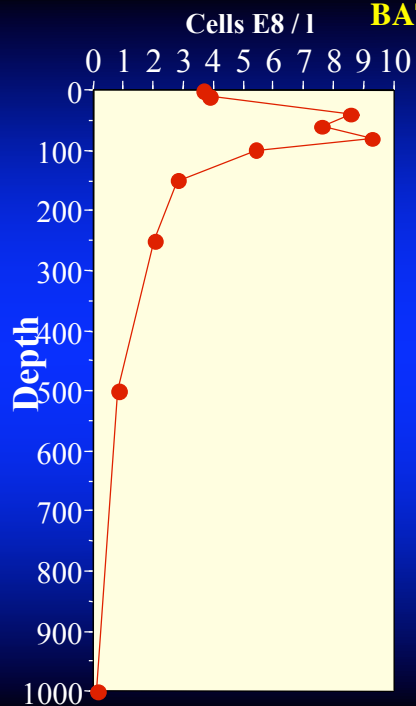
Adapted from Hansell and Carlson 2001

Bacterioplankton cell abundance (E8 L⁻¹)

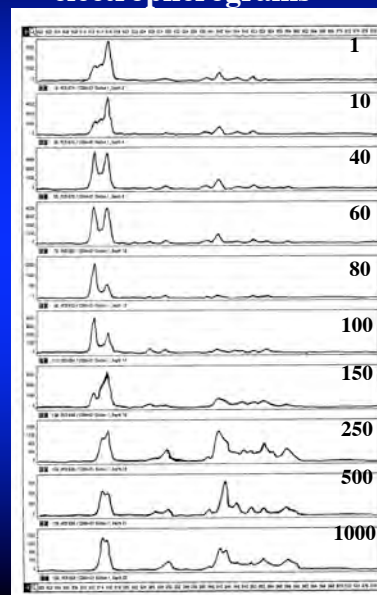


Whole community response ...

BATS CDOM Cruise Aug 2001



Bacterial LH-PCR 16s electropherograms



Microbial communities in the surface layer at BATS are highly structured in time and space!

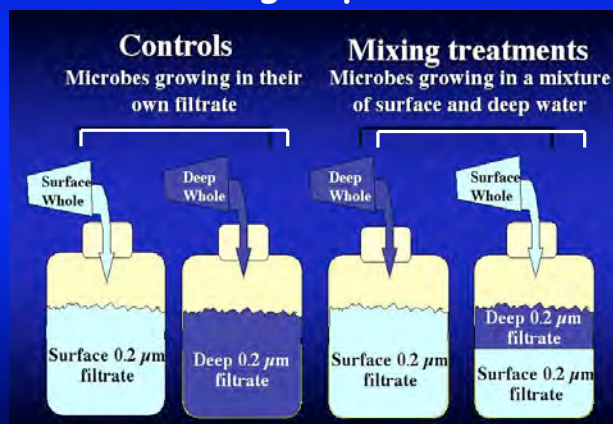
Publications from BATS showing vertical and temporal patterns in community structure:

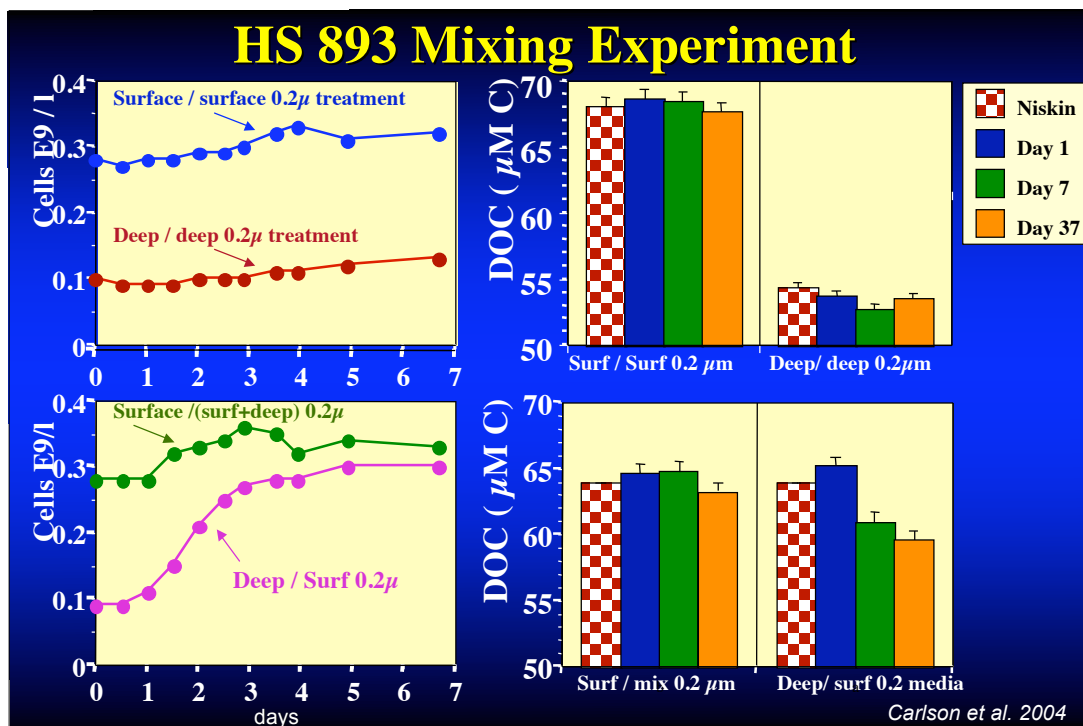
- Gordon et al 1996.
- Field et al. 1997.
- Giovannoni 2000.
- Morris et al. 2004.
- Giovannoni et al. 1996.
- Wright et al 1997
- Morris et al. 2002
- Morris et al. 2005

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



Mixing Experiments



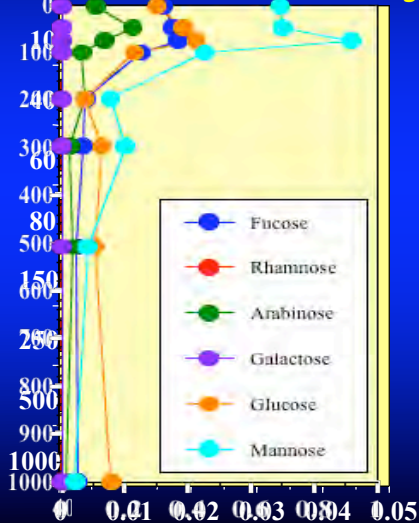


Experiment	Inoc. Source	0.2 Filtrate Source	ΔCell Cells E8/l	ΔDOC 1 week	ΔDOC > month
HS 852 (Aug-97)	Surf	Surf	0.75	-	-
	Deep	Surf	2.85	1.9	3.5
HS 875 (Aug-98)	Surf	Surf	0.75	-	-
	Deep	Surf	2.5	3.1	3.1
HS 893 (Aug-99)	Surf	Surf	0.5	-	-
	Deep	Surf	2.1	3.7	5.1
	Deep	Deep	0.25	-	-
	Surf	mix	0.9	-	1.3
BATS 155 (Aug-01)	Surf	Surf	0.5	-	-
	Deep	Deep	-	-	-



Characterization of DOC pool in northwestern Sargasso Sea

Dissolved + Combined Neutral Sugars



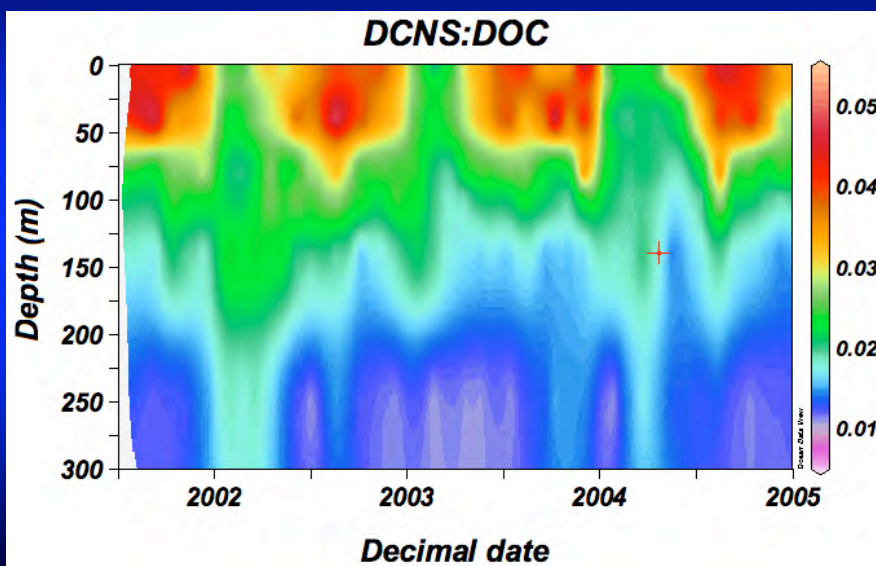
- Contribution of specific compounds like DCNS to total DOC can be used as an index of diagenetic state

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

Goldberg et al in revision

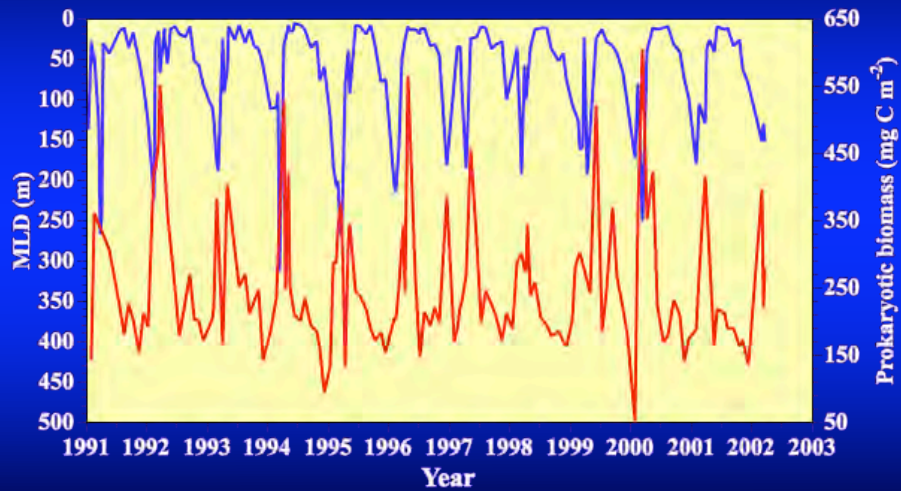


Diagenetic Index of DOC quality at BATS

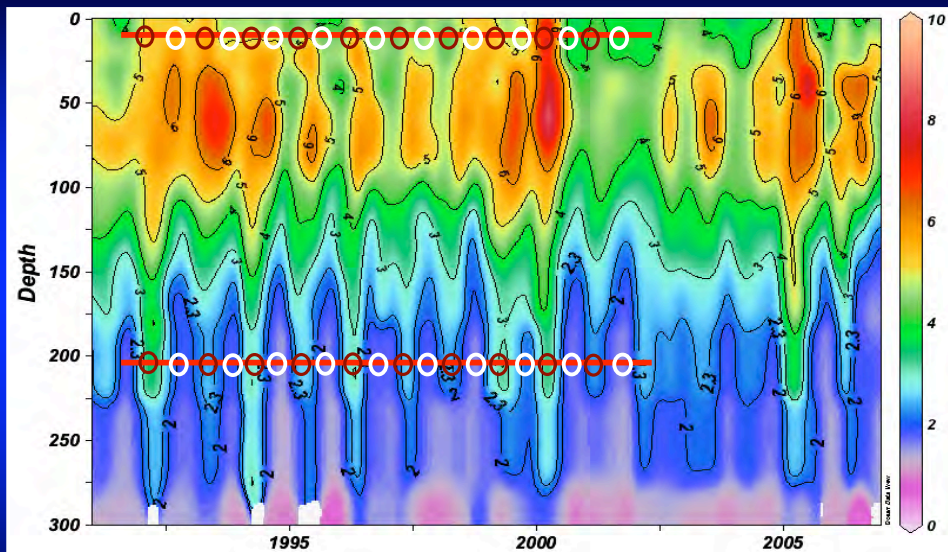


Goldberg et al in revision

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?

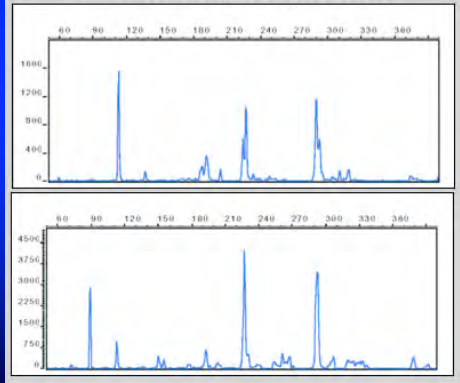
16S rDNA community diversity

81 - surface samples

83- 200 m samples

HAE III digest

Community fingerprint

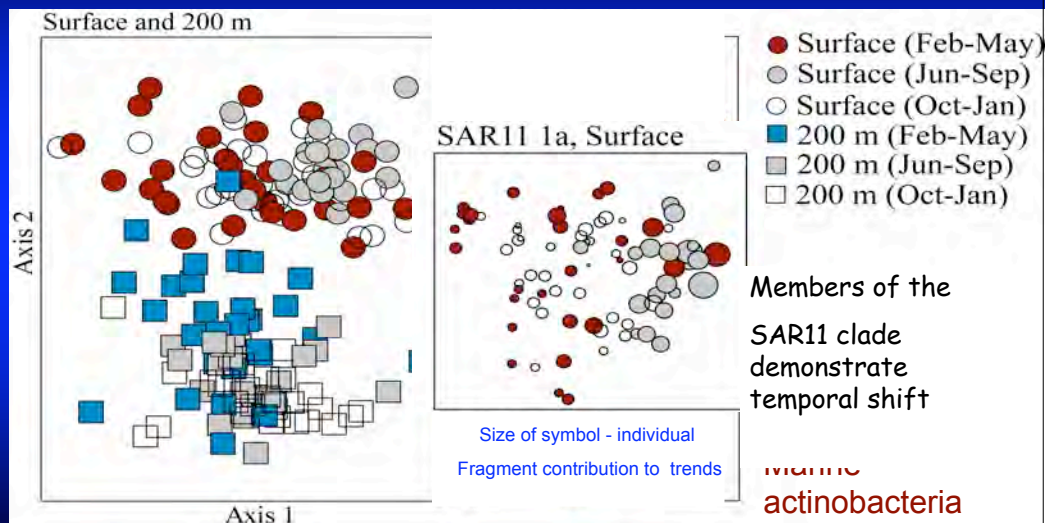


Clone ID	T-RFLP Fragment designation	Fragment length		Total
		A	B	
D92_09	SAR11	ND	39	7
D92_20	Uncultured <i>gamma</i>	ND	39	1
D92_33	<i>Alteromonas</i>	ND	39	1
D92_11	SAR11 subgroup Ia	113	117	7
D92_72	SAR86	187	188	1
D92_37	SAR86	188	189	2
D92_82	SAR116	192	193	2
D92_17	Uncultured <i>gamma</i>	193	193	2
D92_84	<i>Roseobacter</i>	194	195	1
D92_26	SAR316	202	203	1
D92_04	SAR11 subgroup Ib	227	228	10
D92_46	SAR11 subgroup Ib	228	230	1
D92_22	SAR202	257	258	1
D92_36	SAR202	260	263	1
D92_53	<i>Cytophaga</i>	286	287	2
D92_01	SAR11 subgroup II	291	293	11
D92_34	SAR11 subgroup II	291	293	1
D92_31	SAR11 subgroup Ib	292	294	5
D92_03	OCS116	302	303	5
D92_63	OCS116	302	303	1
D92_65	OCS116	302	303	1
D92_92	OCS116	302	303	1
D92_25	<i>Prasinophyte</i> chloroplast	303	304	1
D92_02	<i>Alcanivorax</i>	311	311	1
D92_74	Uncultured <i>gamma</i>	325	326	1
D92_32	Marine <i>Actinobacteria</i> cluster	328	330	2
D92_10	<i>Prasinophyte</i> chloroplast	388	390	1
D92_78	SAR324	405	405	2

Morris, Cho, Rappé, Vergin, Carlson, and Giovannoni, 2005

Ordination of T-RFLP Fragments (1992-2002)

Nonmetric multidimensional scaling



Morris, Cho, Rappé, Vergin, Carlson, and Giovannoni, 2005

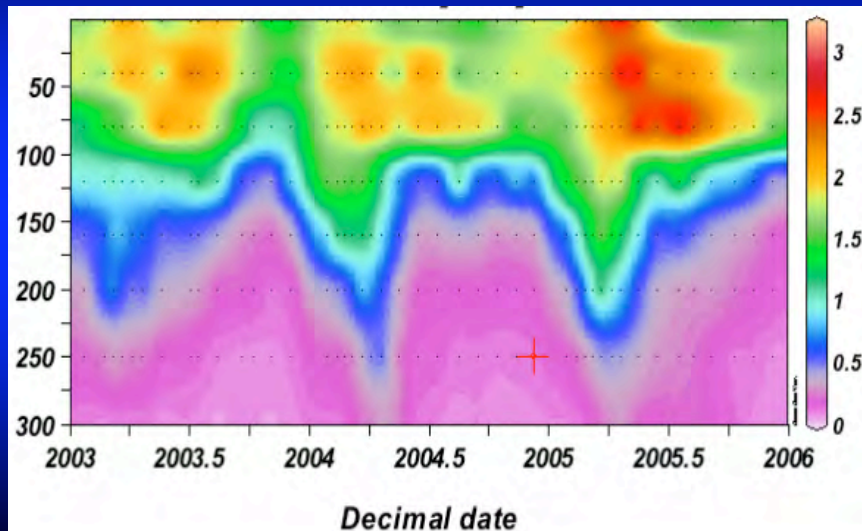
Summary

- 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

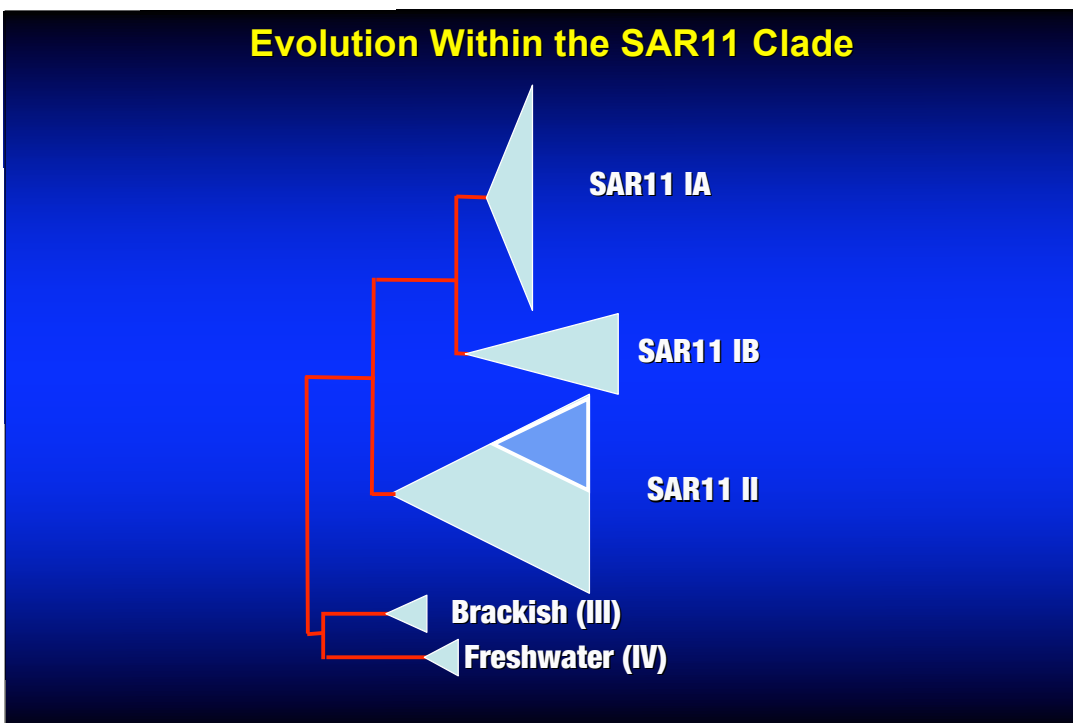
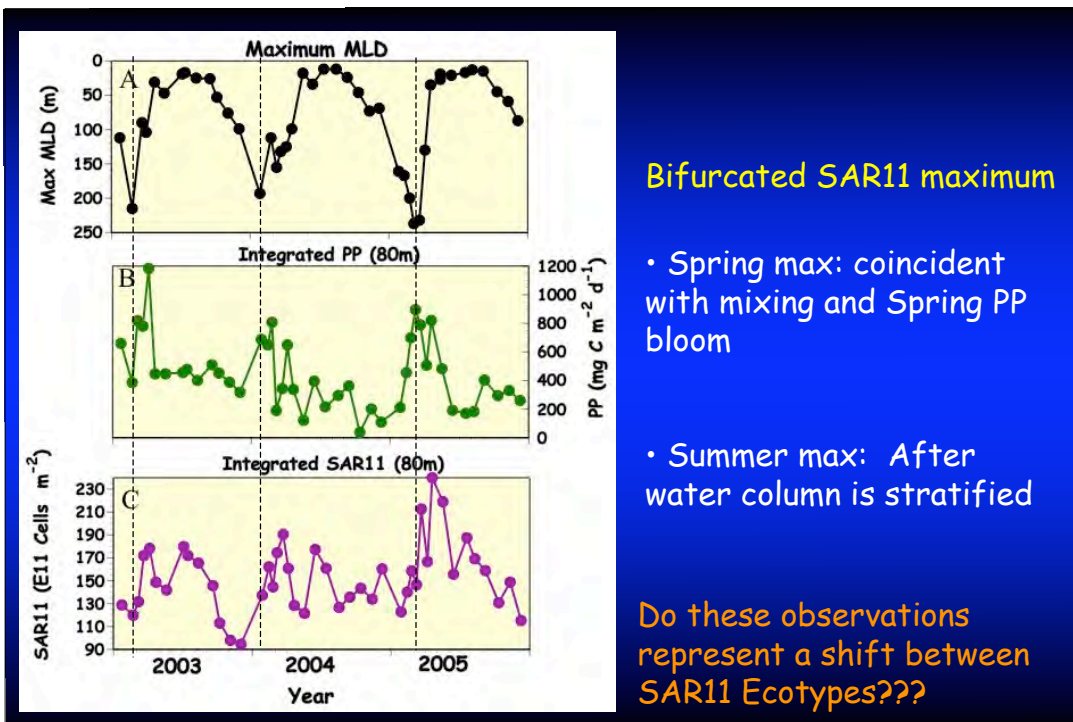
MO objective: Identify temporal and spatial patterns in specific bacterioplankton populations quantitatively



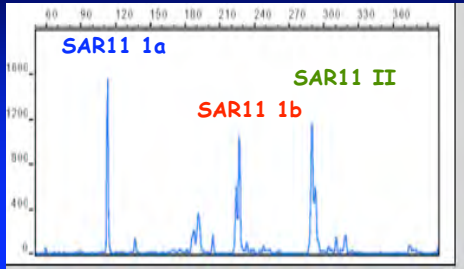
SAR11 (E8/L) at BATS



Carlson et al submitted



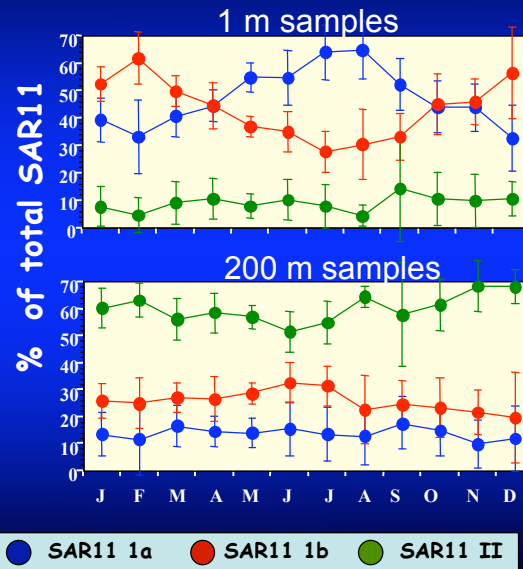
T-RFLP fingerprints (HAE III)



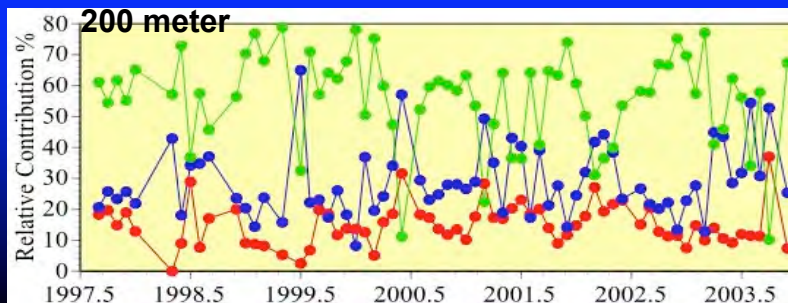
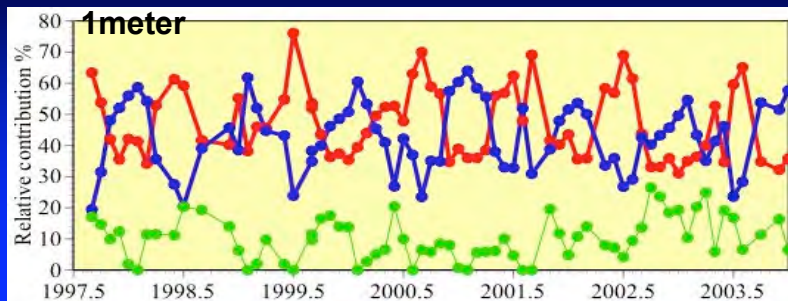
relative contribution of each fragment
 \approx % contribution of each ecotype to
 total SAR11

- Total of 372 samples (1991- 2003)
 - 97 separate cast 0 & 200 m
 - additional 32 cast 0-300m

Monthly mean contribution of SAR11 Ecotypes

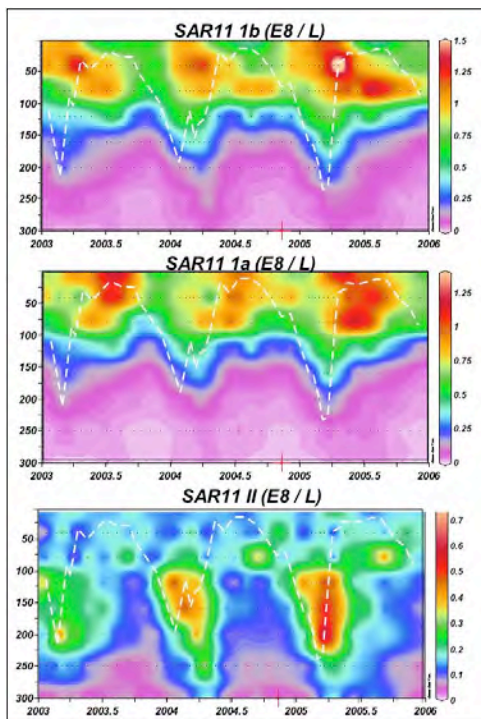


SAR 11 ecotype variability based on T-RFLP data

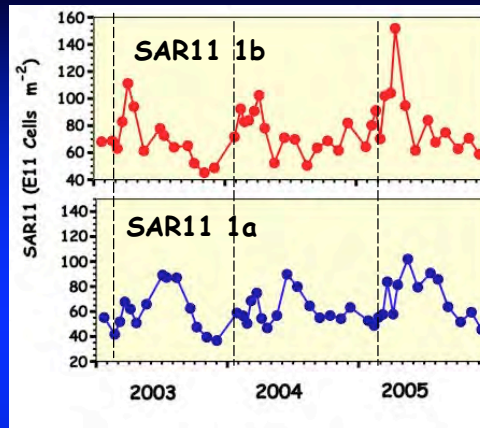


We constructed an annual composite matrix describing the relative contribution of each ecotype at each depth for each month

Depth m	Observed T-RFLP Fragment length (bp)	Putative SAR11 Subclade	Mean Relative Contribution for Each Month											
			Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
0	113	Ia	40 (8)	38 (5)	41 (8)	45 (6)	55 (5)	55 (10)	64 (10)	65 (11)	52 (9)	44 (9)	44 (9)	36 (4)
40			44 (3)	36 (4)	39 (7)	39 (12)	45 (15)	47	49 (4)	53 (10)	48 (5)	44	41 (7)	42
80			45 (12)	35 (7)	39 (11)	42 (12)	43 (10)	43 (10)	40 (10)	37 (4)	41	38	35 (2)	40
120			17 (11)	34 (11)	31 (9)	34	36 (14)	38 (11)	37 (12)	37 (9)	42 (3)	34	27 (9)	22
160			13 (2)	20 (6)	32 (10)	28	24 (7)	20 (13)	25 (17)	20 (7)	27 (3)	24	21 (10)	17
200			14 (9)	15 (3)	17 (9)	17 (3)	14 (9)	16 (10)	14 (10)	13 (5)	17 (3)	17 (9)	10 (4)	13 (4)
250			4 (5)	10 (1)	19 (15)	16 (11)	16 (6)	17 (6)	17 (6)	17 (7)	13 (5)	12	10 (1)	7
300			20 (17)	8 (1)	13 (7)	15	16 (8)	18 (6)	17 (4)	16 (3)	15 (8)	13	11 (5)	16



Modeled partitioning over 80 m



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?

Acknowledgements

BIOS

Rachel Parsons
The BATS Team past and present

UCSB

Bob Morris
Stu Goldberg
Courtney Ewart
Elli Wallner
Aubrey Cano
Meredith Meyers

OSU

Giovannoni Lab group
Kevin Vergin

RSMAS

Dennis Hansell

