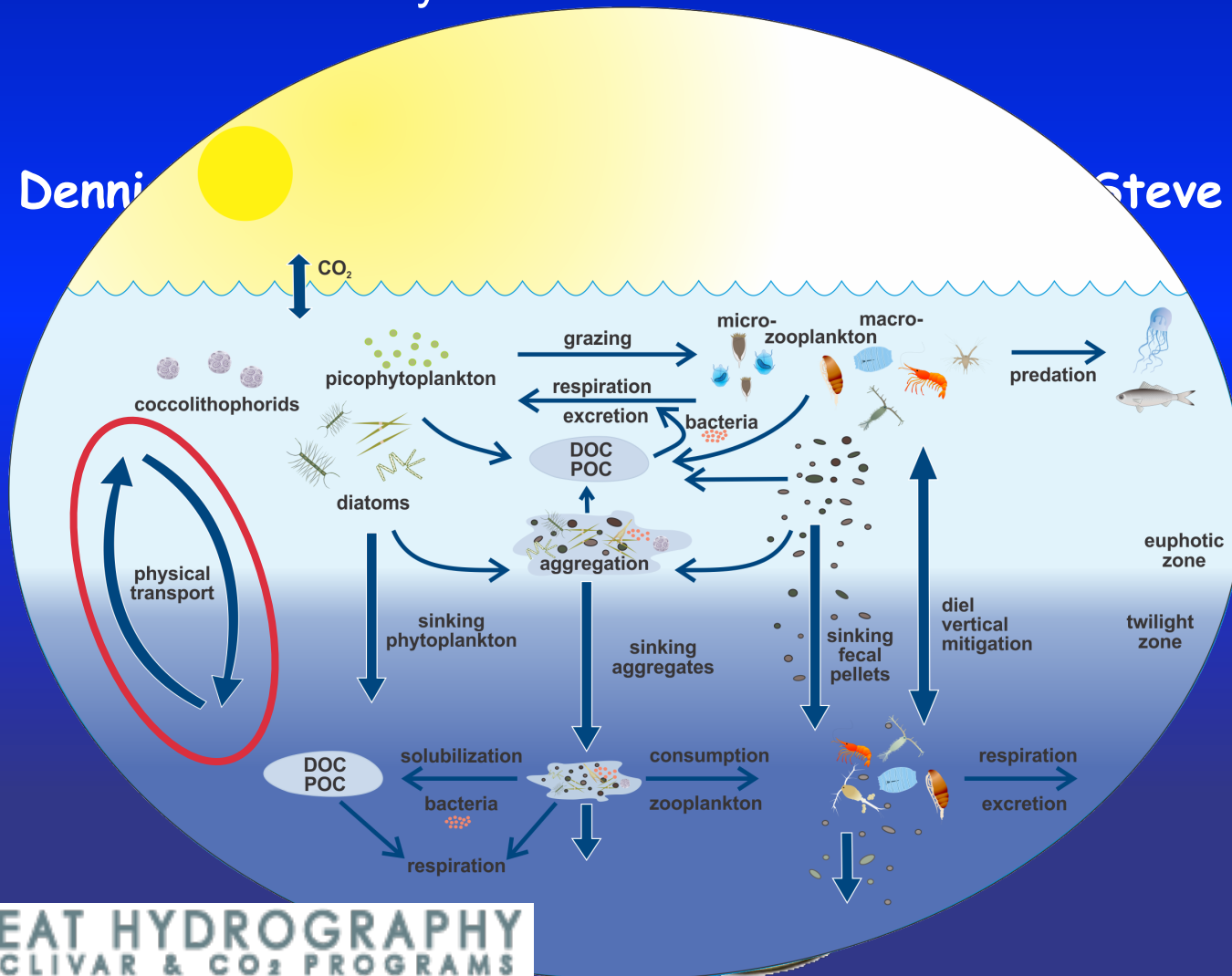


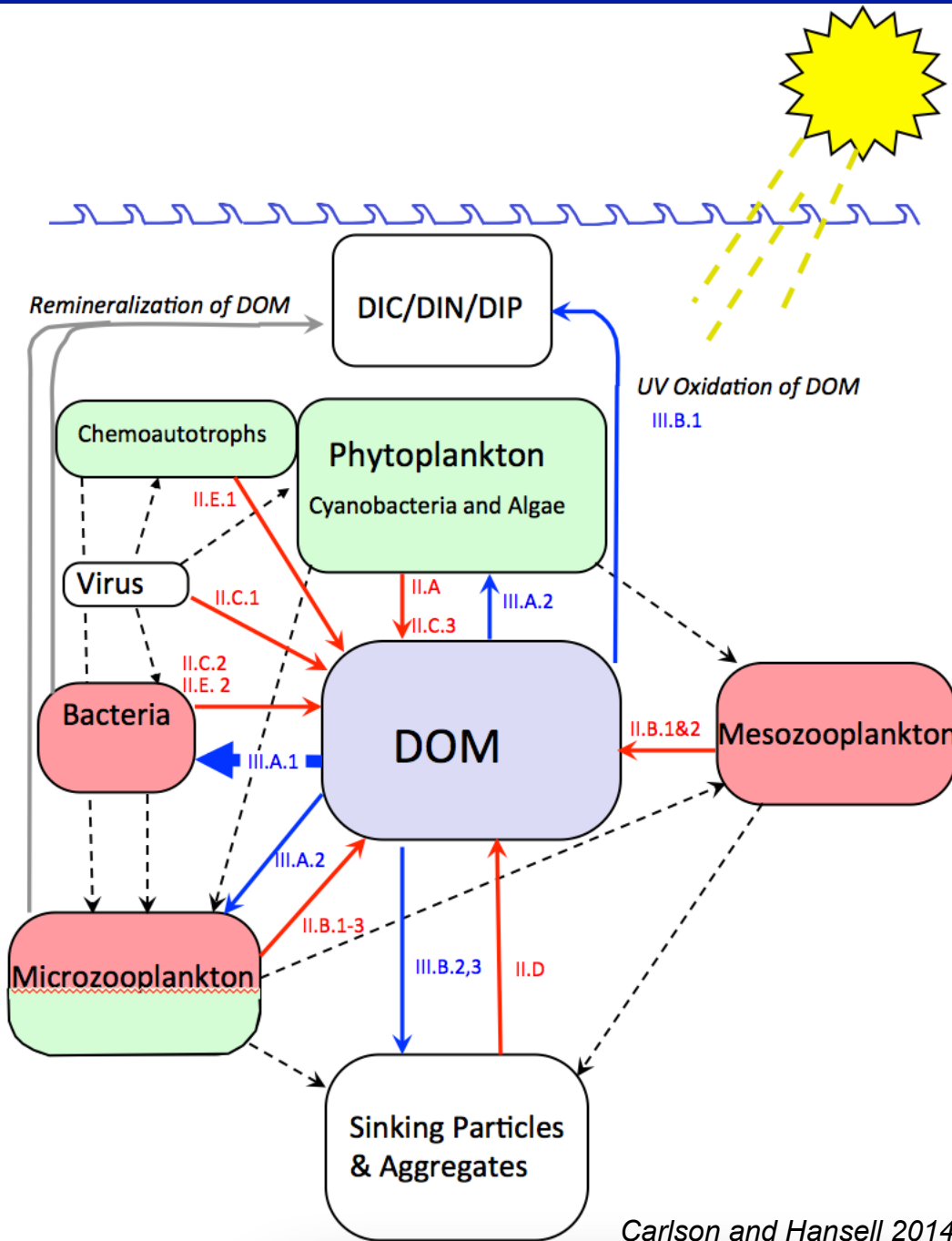
Dissolved Organic Carbon Accumulation, Export and Microbial Transformation

Craig Carlson

University of California at Santa Barbara



DOC production and removal mechanisms



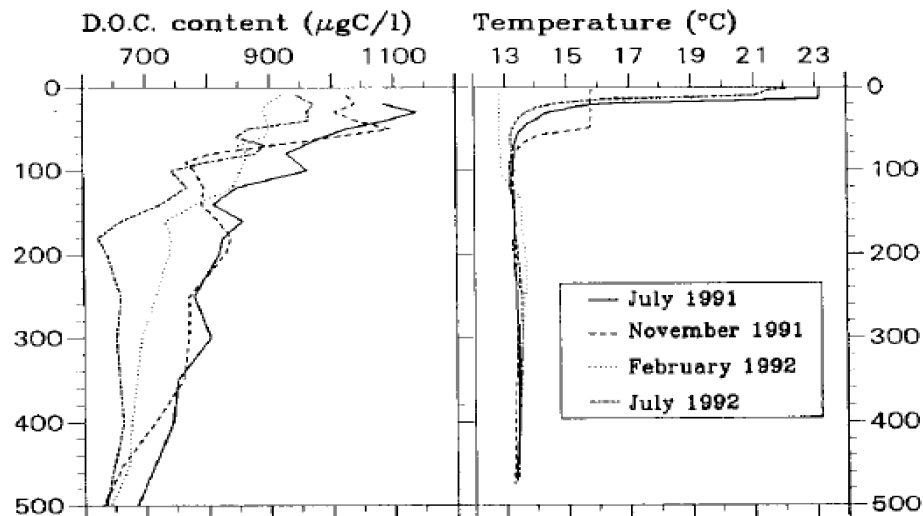
NPP $\sim 54 \text{ Pg C y}^{-1}$... Dunne et al, 2007

$\sim 21 \text{ Pg C y}^{-1}$ is partitioned as DOC of which $>90\%$ is remineralized in the epipelagic (Williams, 2000; Hansell 2013)

- small fraction of the DOC production accumulates

Mediterranean Sea

DOC in the Mediterranean Sea

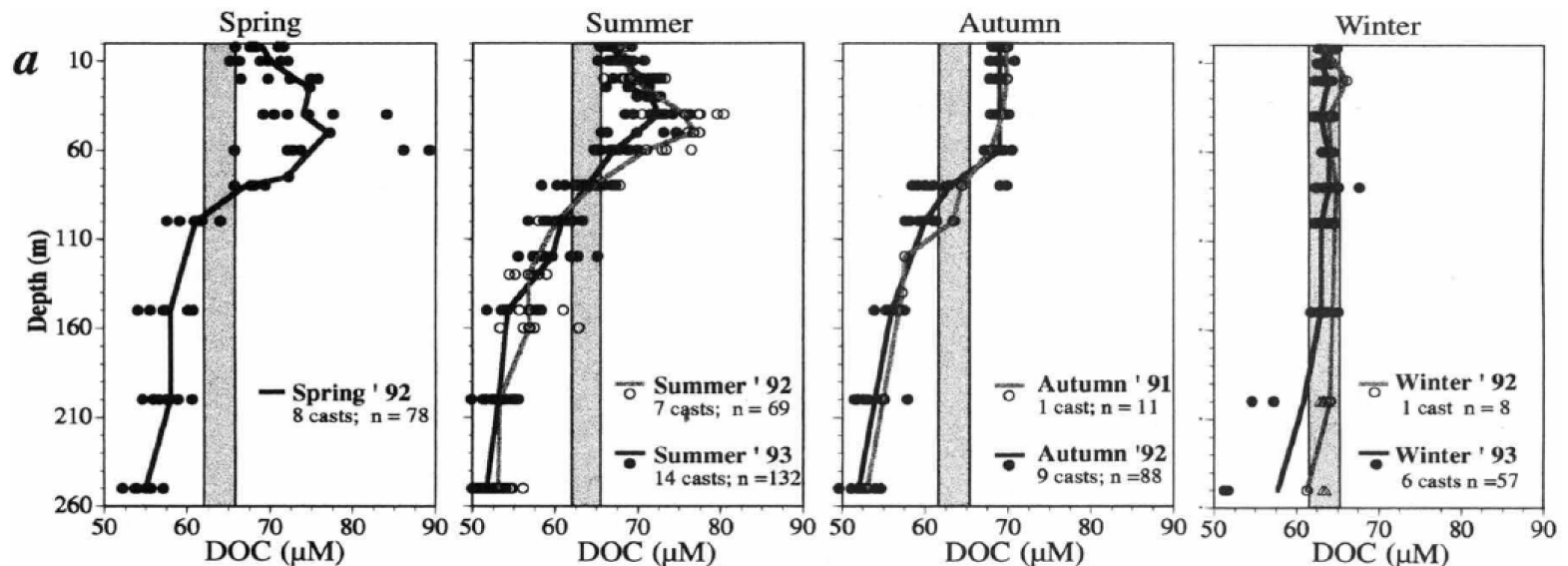


- Early 1990's - Observation of seasonal variability and redistribution of DOC via mixing

- DOC contributes to vertical export

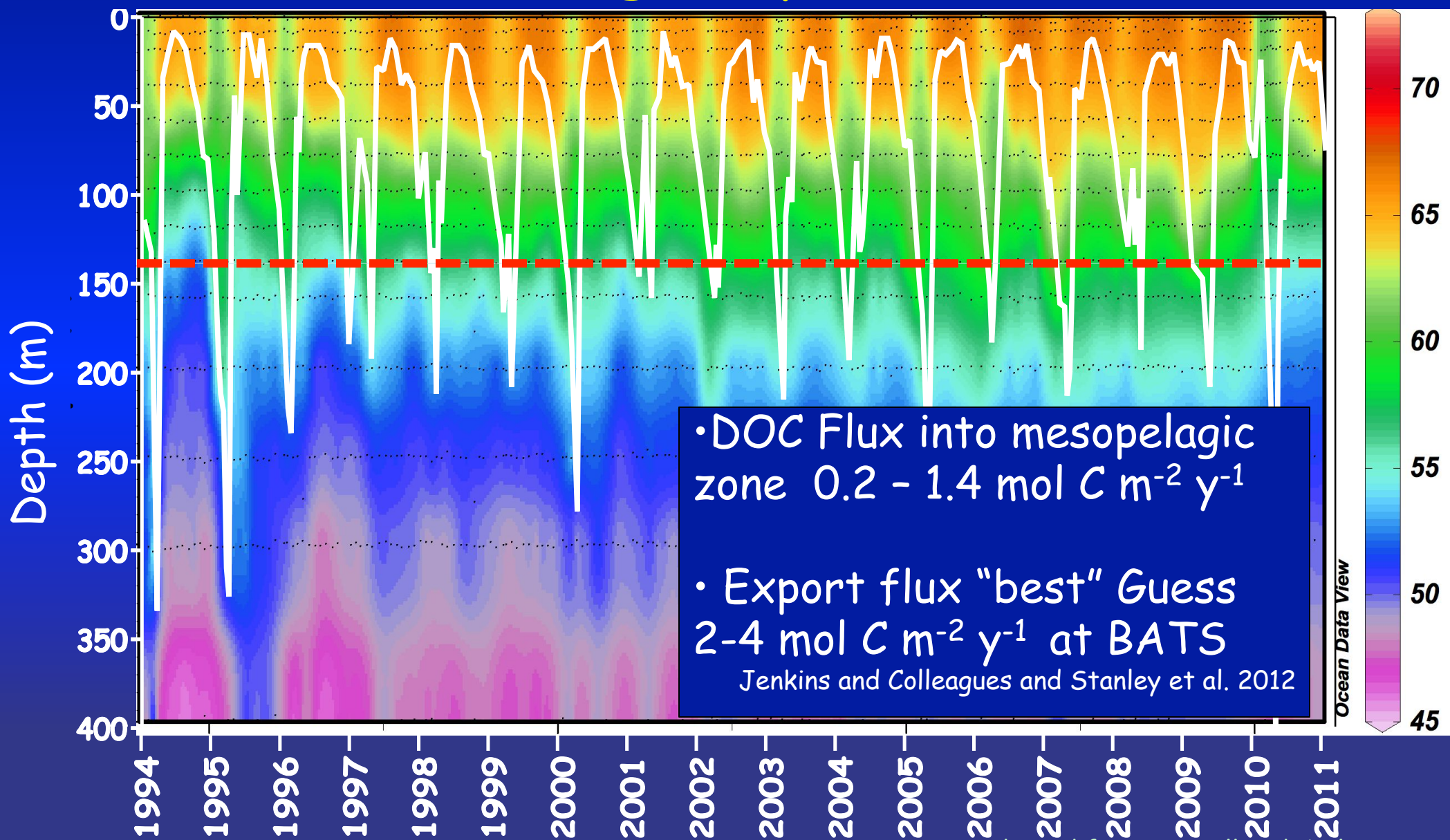
Copin-Montegut and Avril 1993

Sargasso Sea



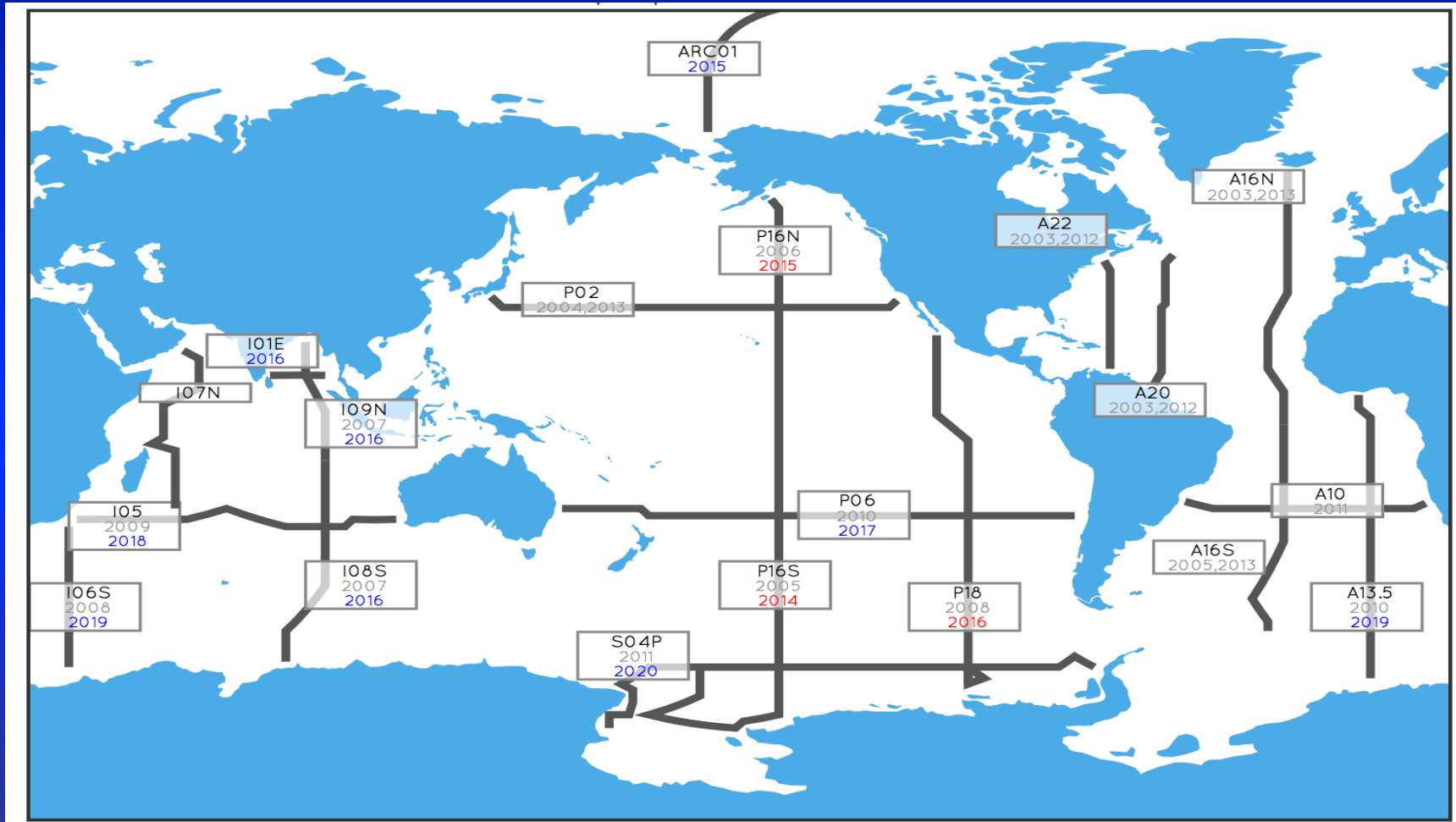
Carlson et al. 1994

DOC ($\mu\text{mol kg}^{-1}$) dynamics at BATS



2003- 2014

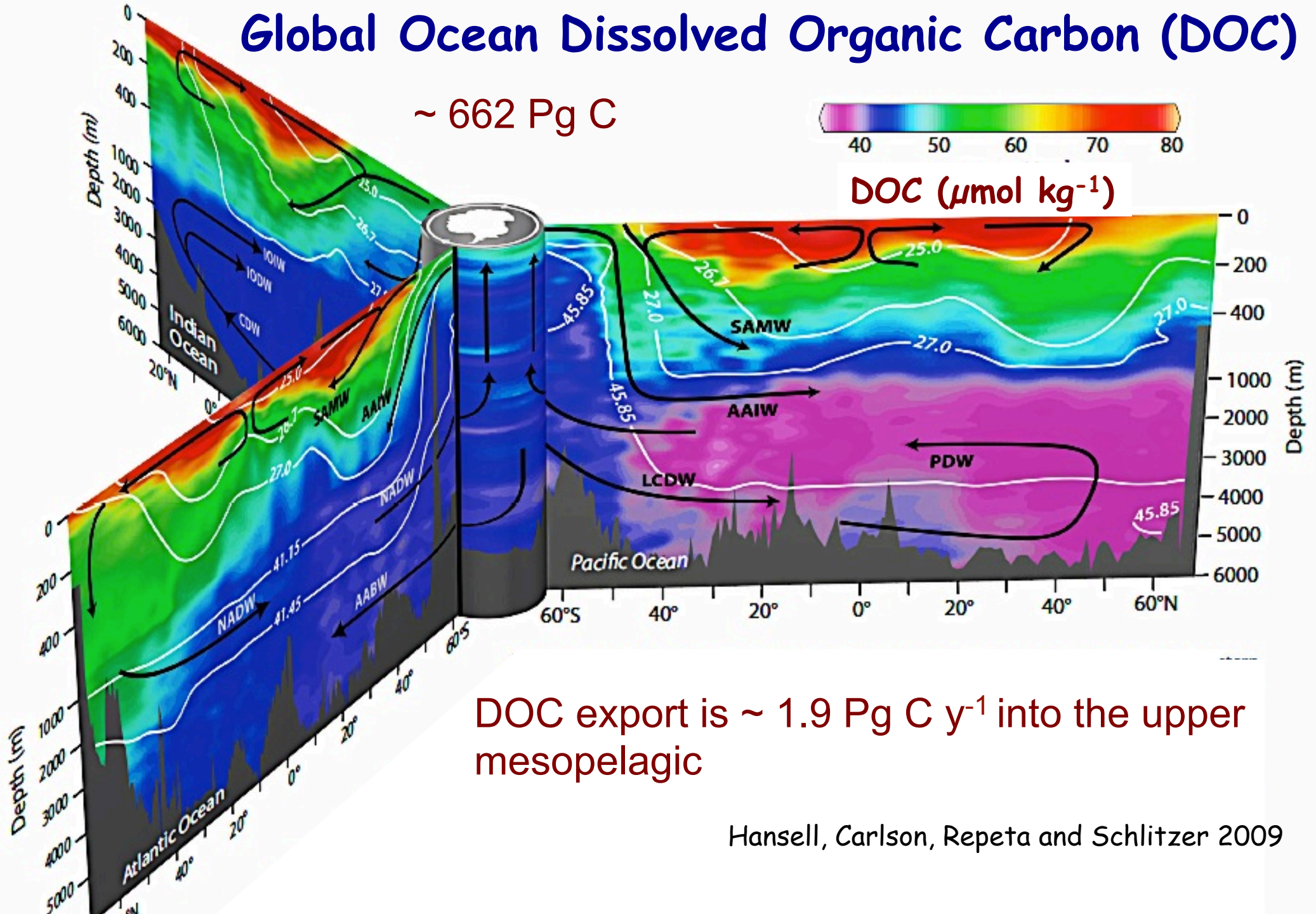
High Resolution DOC Data



> 50,000 DOC data points

Global Ocean Dissolved Organic Carbon (DOC)

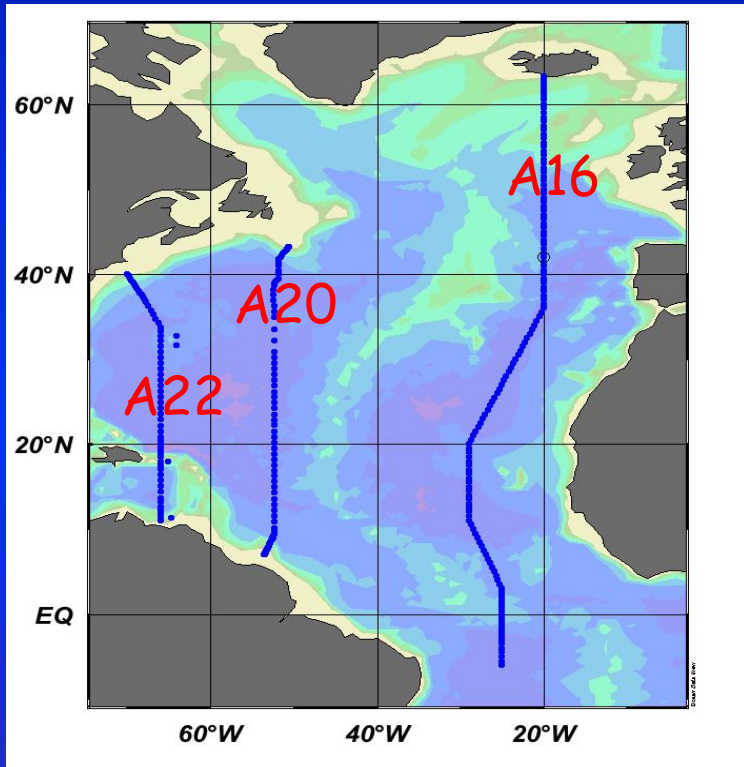
~ 662 Pg C



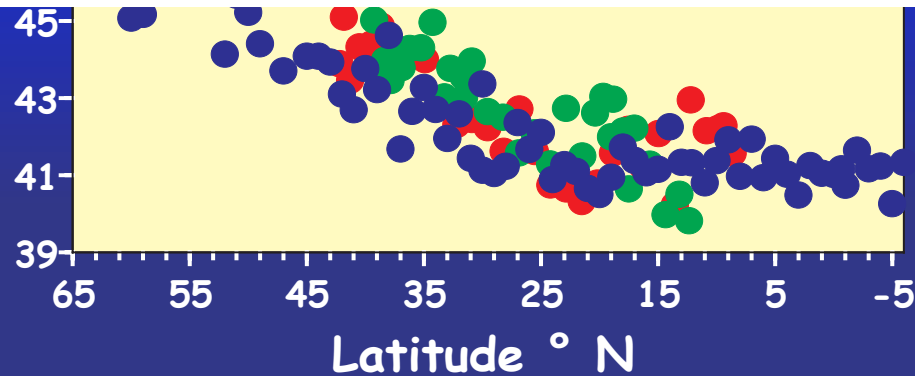
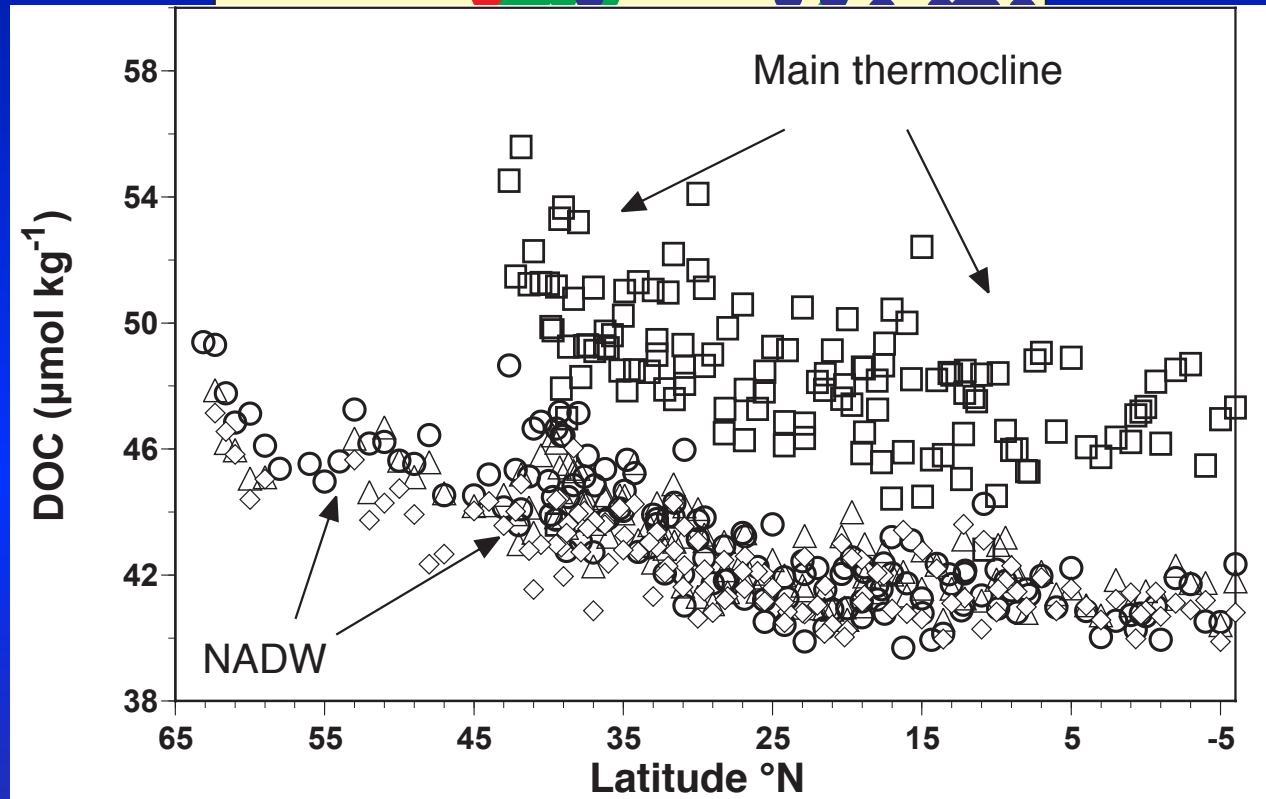
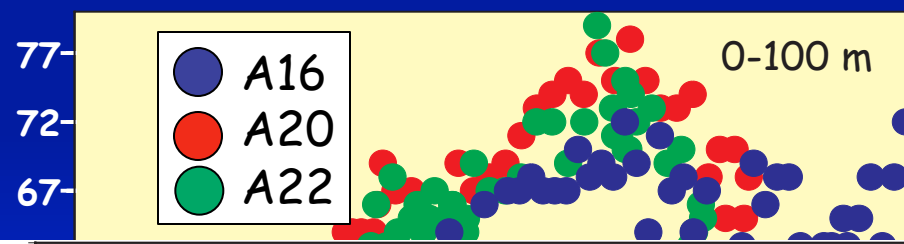
DOC export is ~ 1.9 Pg C y^{-1} into the upper mesopelagic

Hansell, Carlson, Repeta and Schlitzer 2009

Meridional Distribution of Mean DOC Concentrations

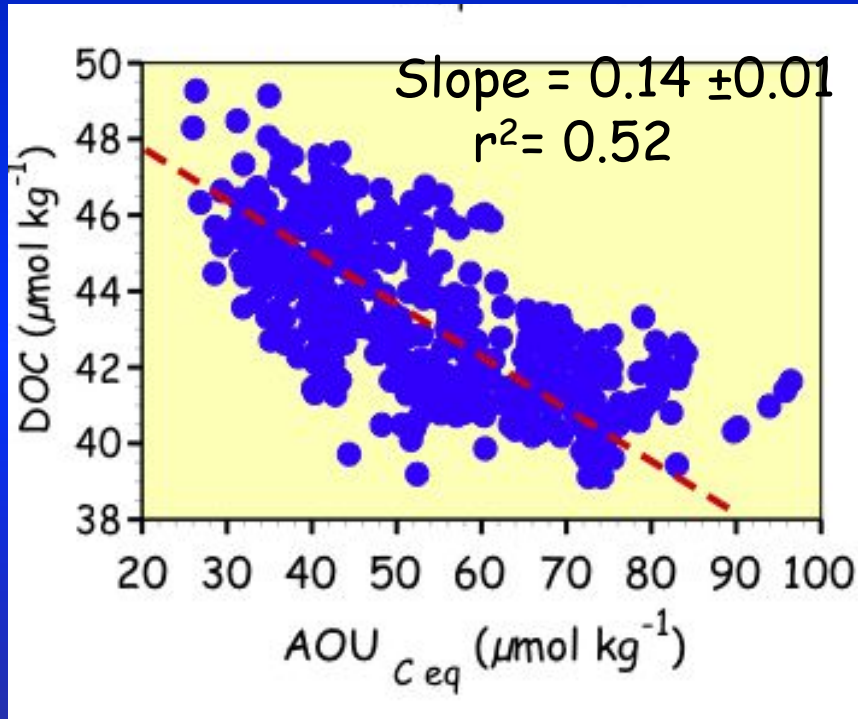


- DOC export $\sim 77 \text{ Tg C y}^{-1}$
- $\sim 10 - 20\%$ of export production in the North Atlantic



Contribution of DOC oxidation to AOU in various neutral density layers in the North Atlantic

Labrador Sea Water

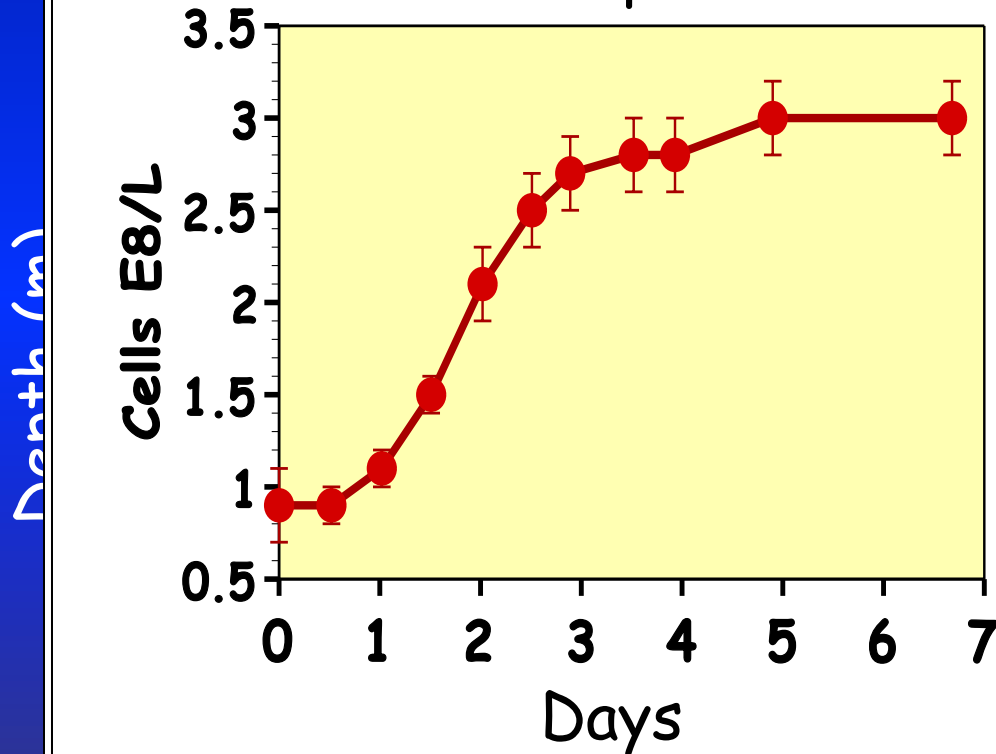


Water mass	Contribution of DOC Oxidation to AOU- C_{eq}			
	Single end-member mixing			
	%	<i>n</i>	r^2	
UTCL	28 ± 2	161	0.24	
STMW	9 ± 1	109	0.17	
LTCL	7 ± 1	332	0.34	
LSW	14 ± 1	464	0.52	
ISOW	19 ± 1	192	0.55	
DSOW	16 ± 1	487	0.35	

DOC ($\mu\text{mol kg}^{-1}$) dynamics at BATS

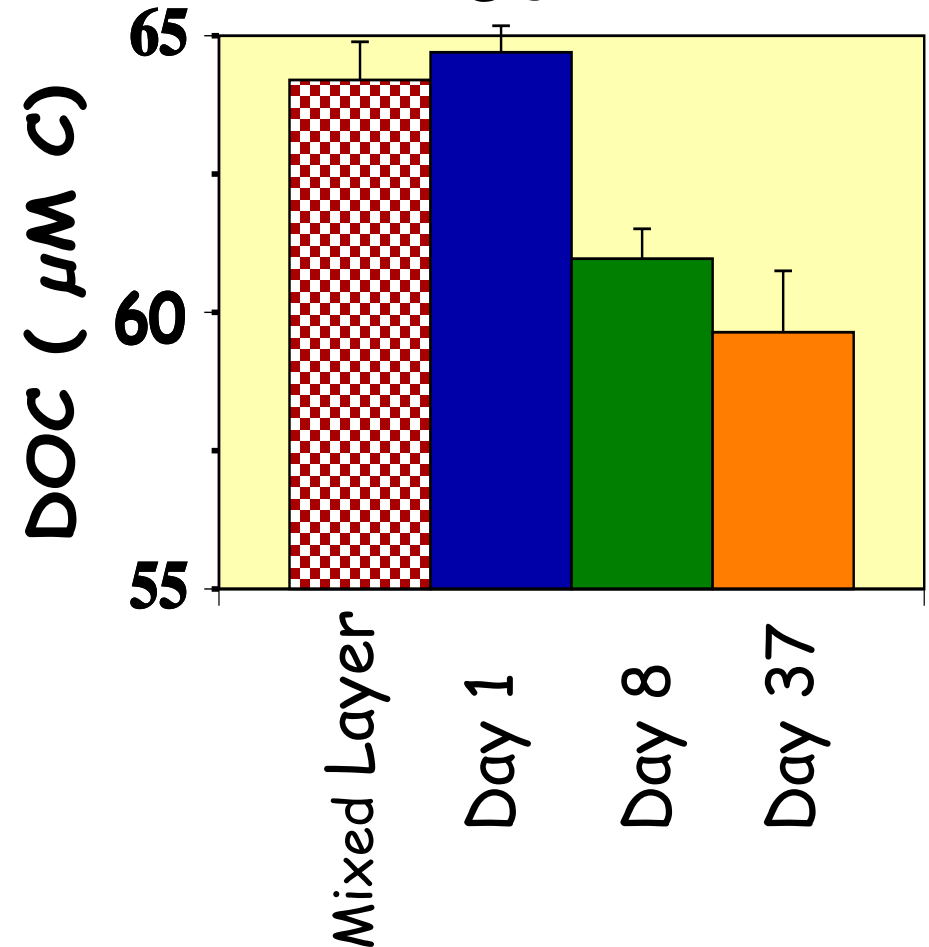
Deep Microbes grown on Surface DOC - Exp. HS893

Bacterioplankton

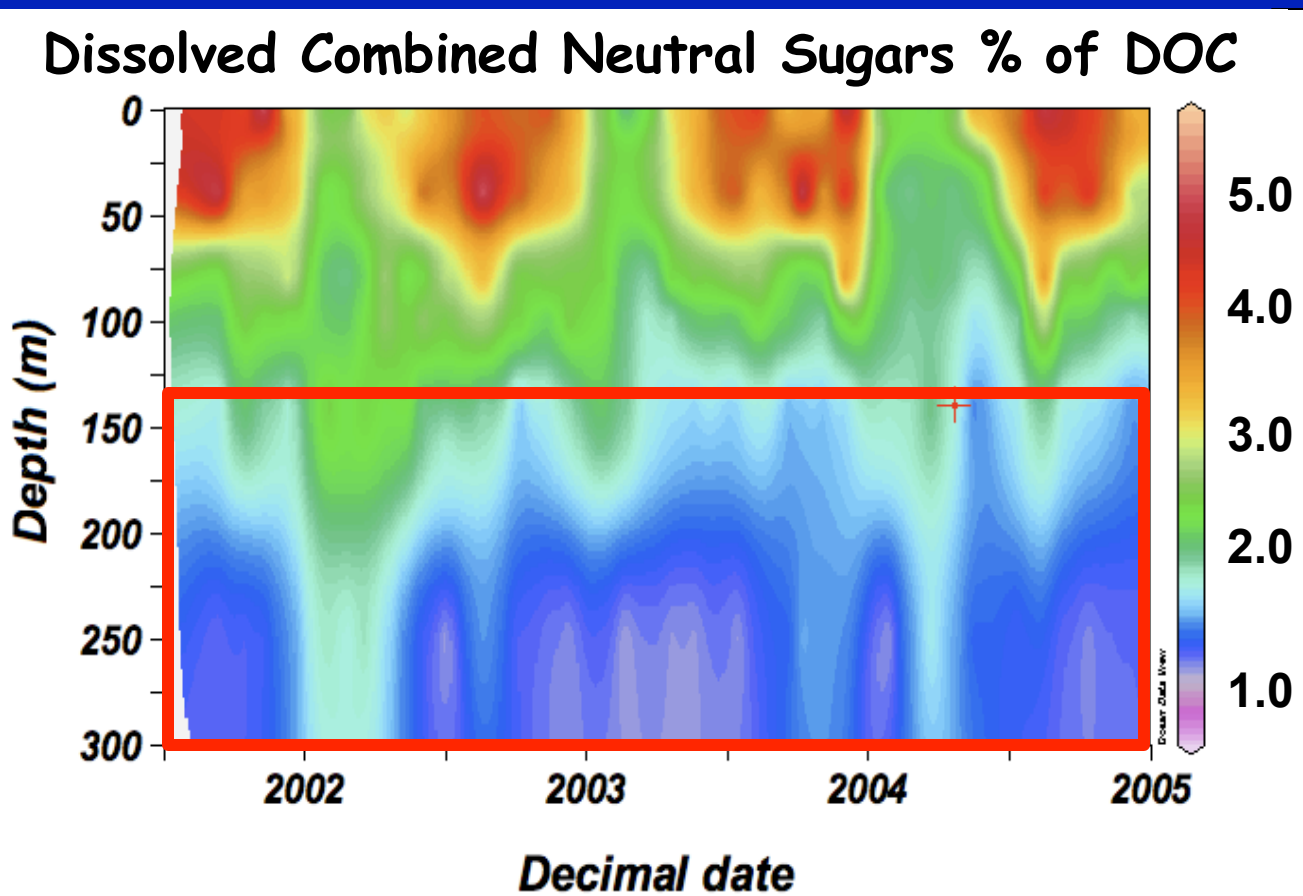


Carlson et al. 2004

DOC



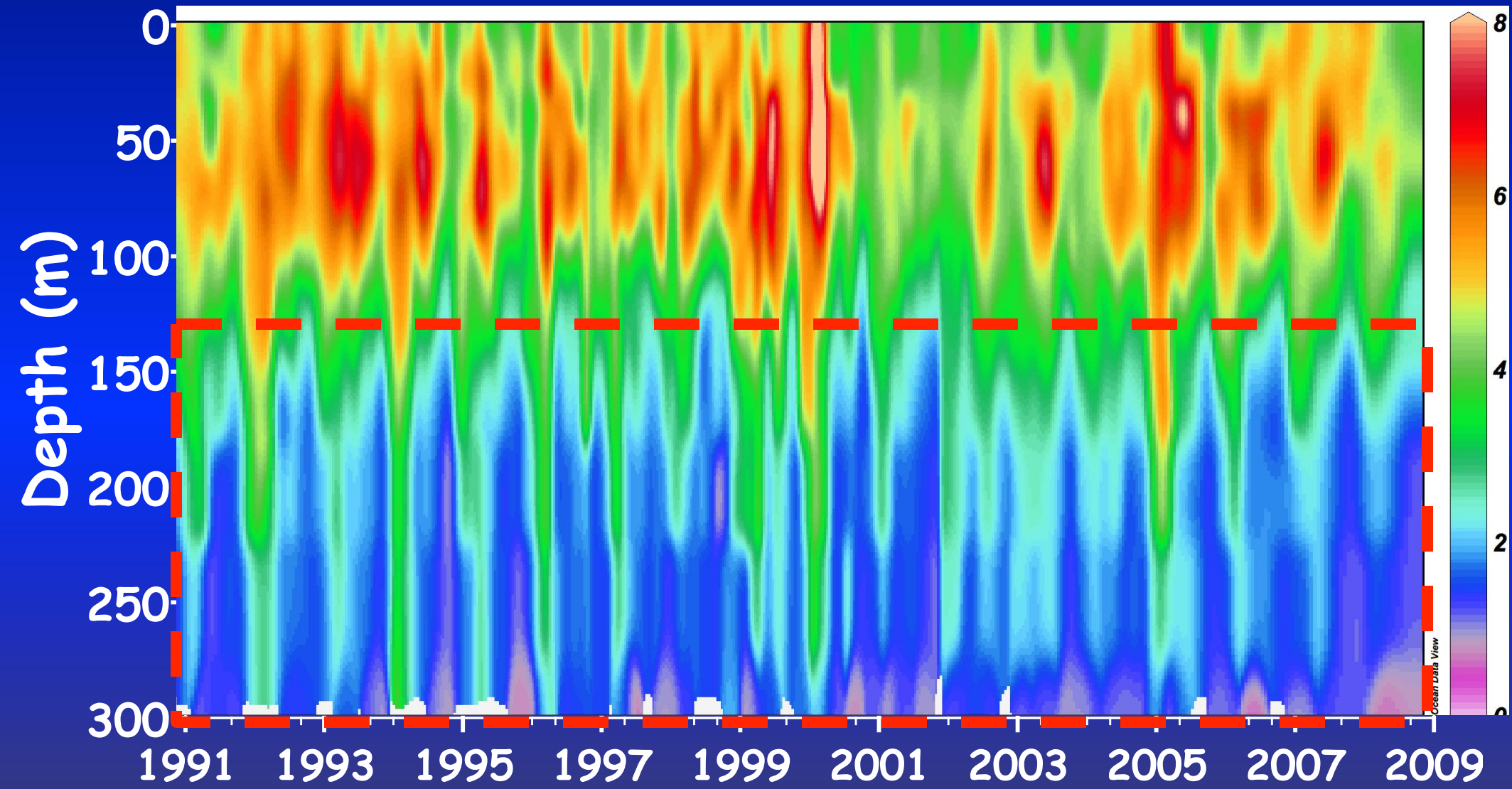
Characterization of DOC pool at BATS



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

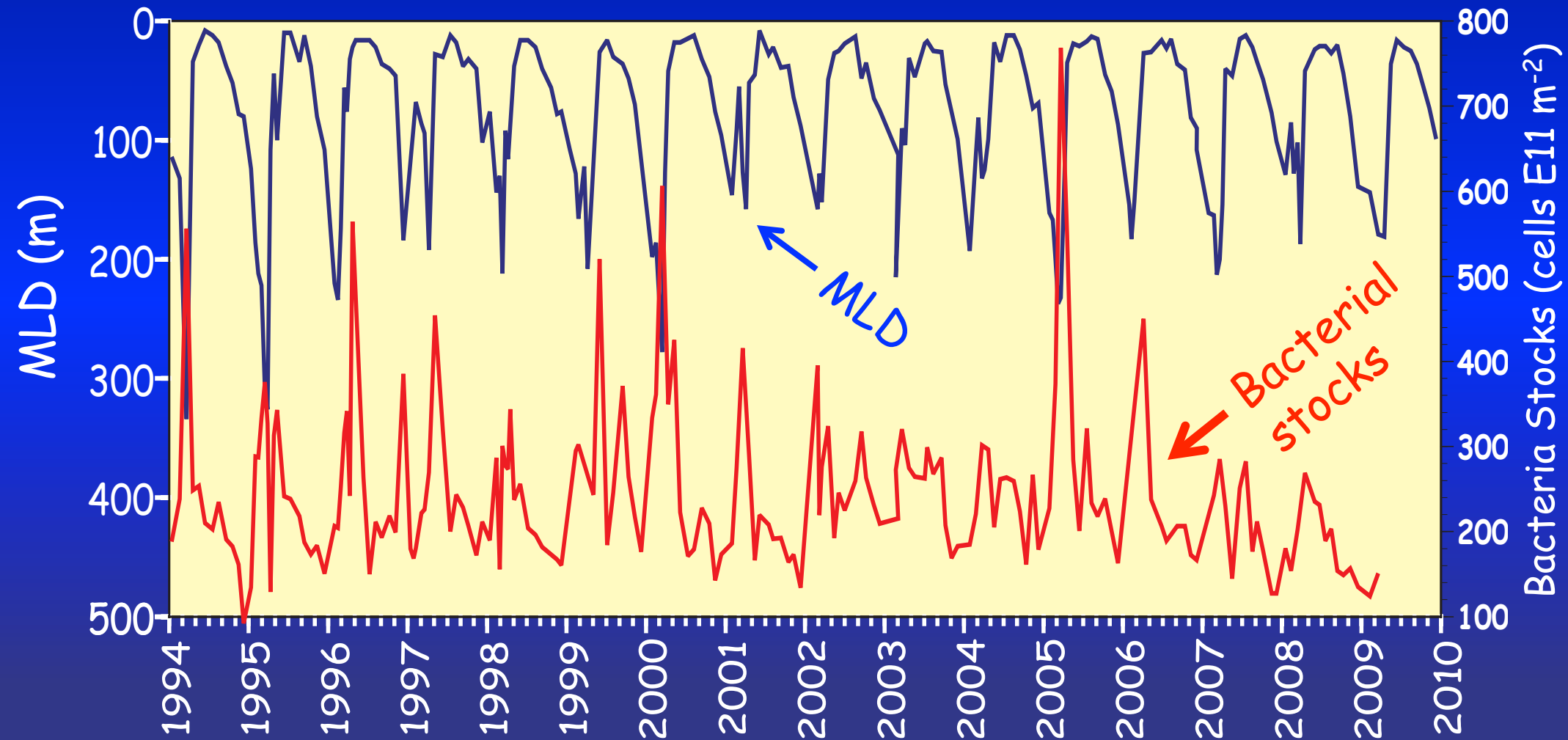
Decrease in DCNS % after stratification indicates DOC is diagenetically altered within the upper mesopelagic zone

Bacterioplankton cell abundance (E8 L⁻¹)



BATS Core data

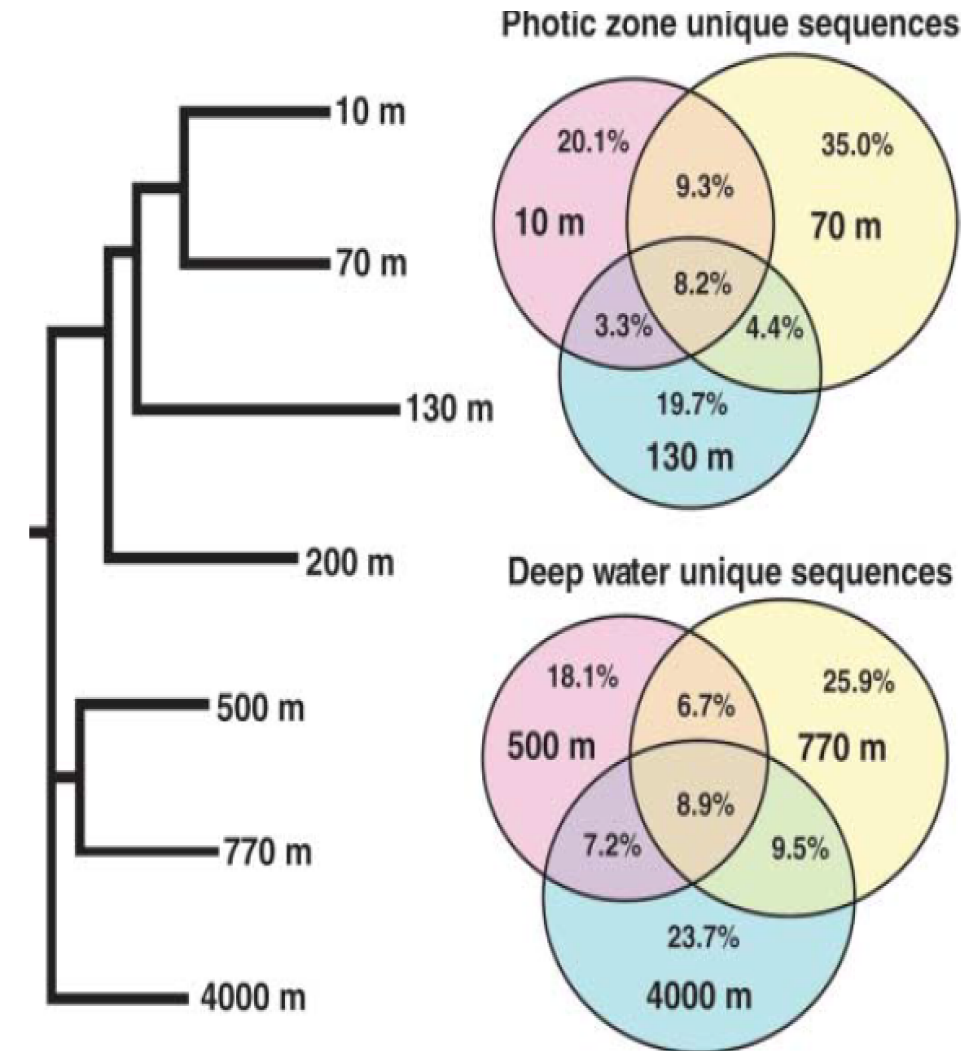
MLD and Integrated Bacterial Stocks in the Upper Mesopelagic (140-250m) at BATS



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

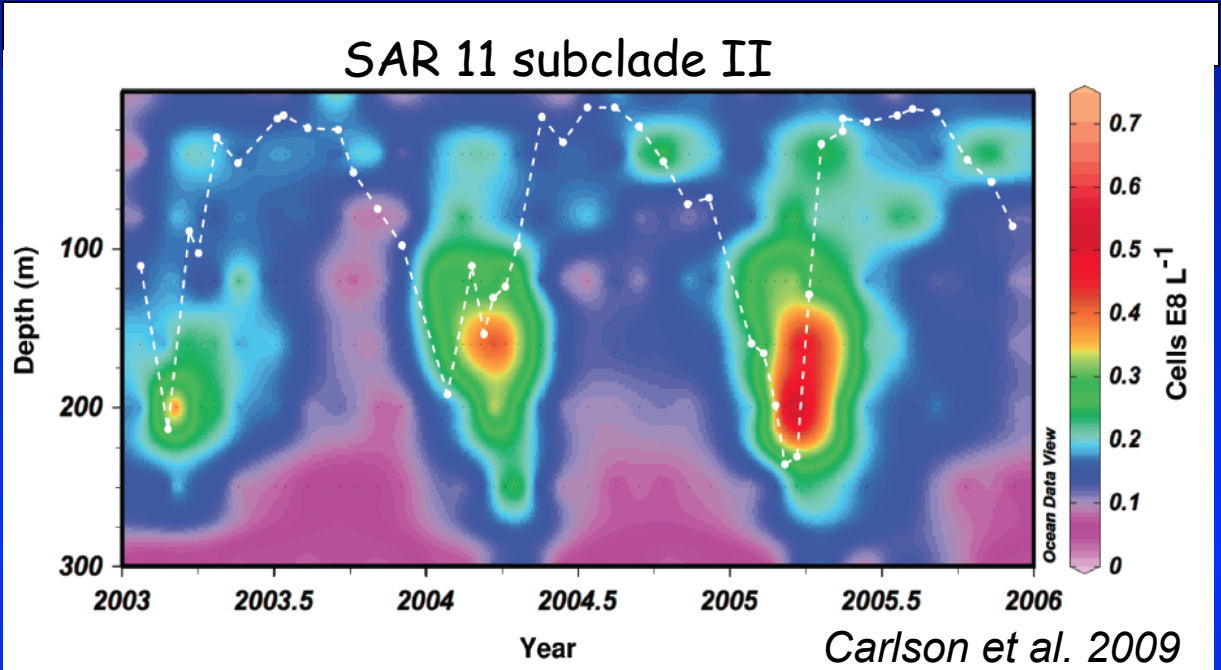
Edward F. DeLong,^{1*} Christina M. Preston,² Tracy Mincer,¹ Virginia Rich,¹ Steven J. Hallam,¹ Niels-Ulrik Frigaard,¹ Asuncion Martinez,¹ Matthew B. Sullivan,¹ Robert Edwards,³ Beltran Rodriguez Brito,³ Sallie W. Chisholm,¹ David M. Karl⁴

Microbial communities are highly structured over depth

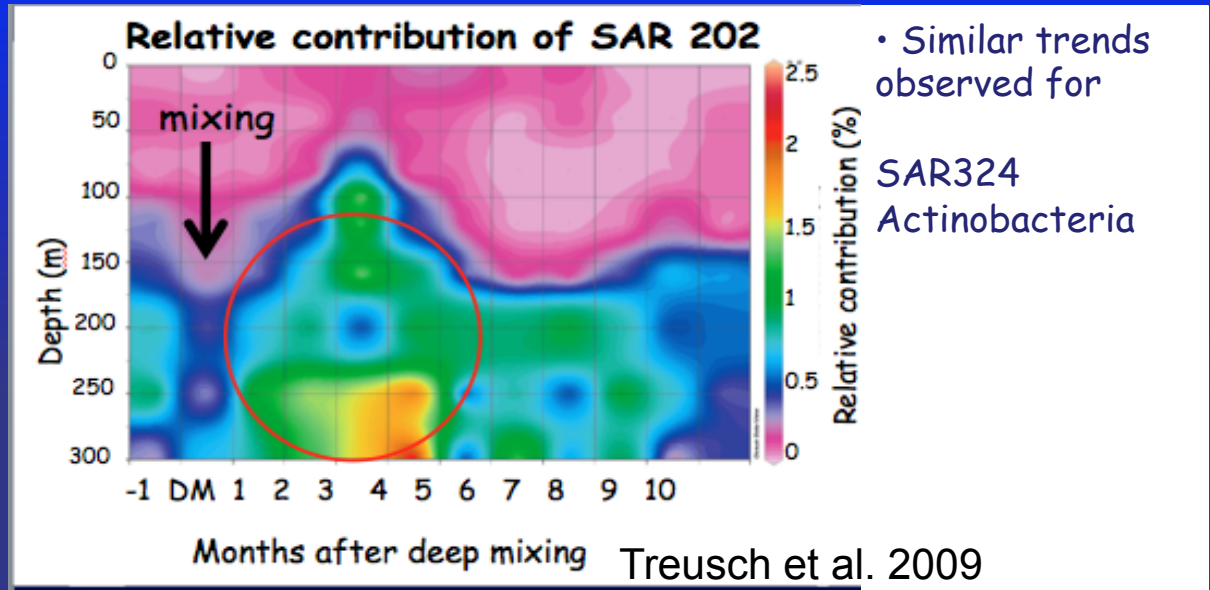


- Gordon et al 1996.
- Giovannoni et al. 1996.
- Field et al. 1997.
- Wright et al 1997
- Giovannoni 2000.
- Morris et al. 2002
- Morris et al. 2005
- Carlson et al. 2009
- Treusch et al. 2009

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?