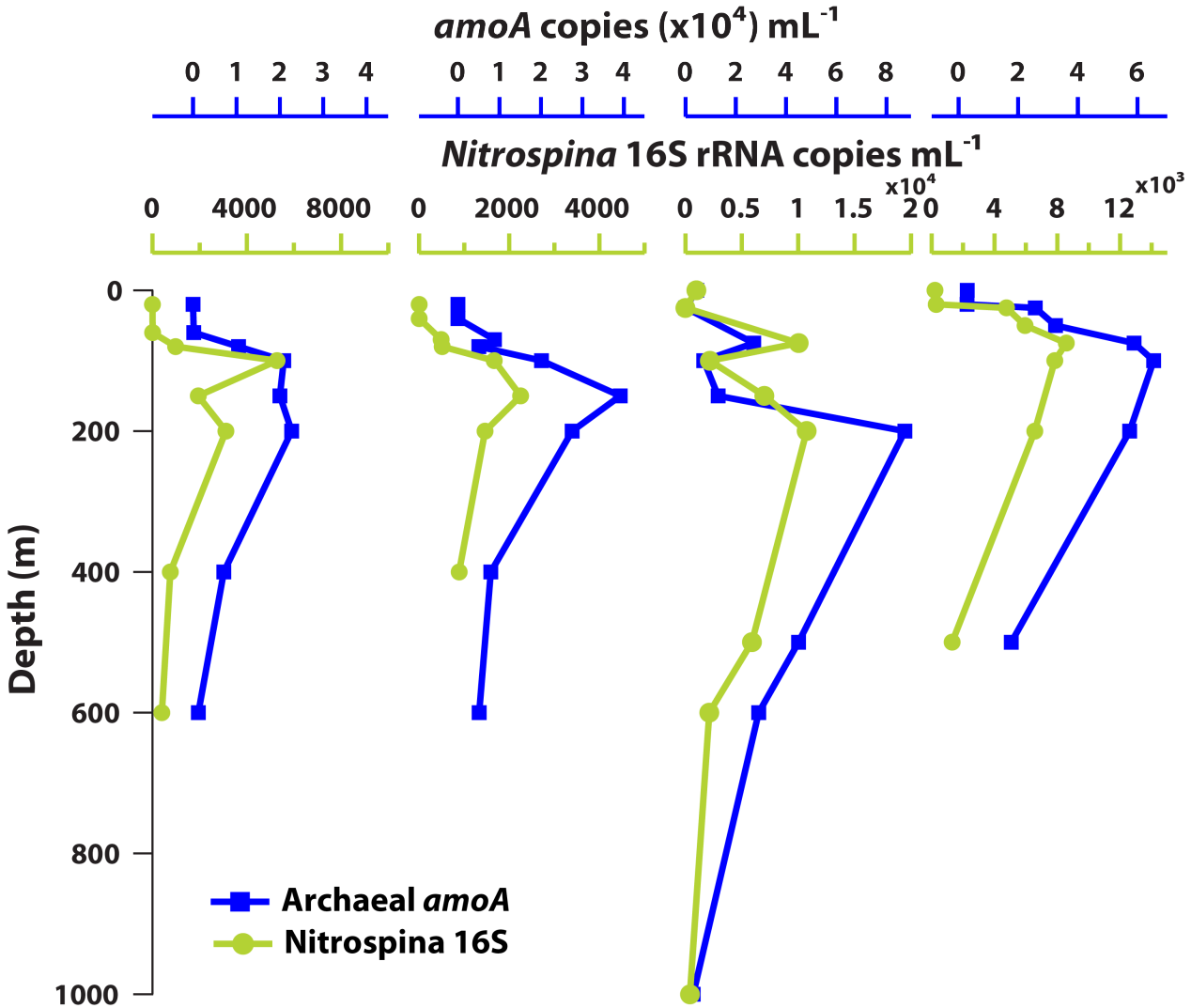
Microbial processes in the mesopelagic

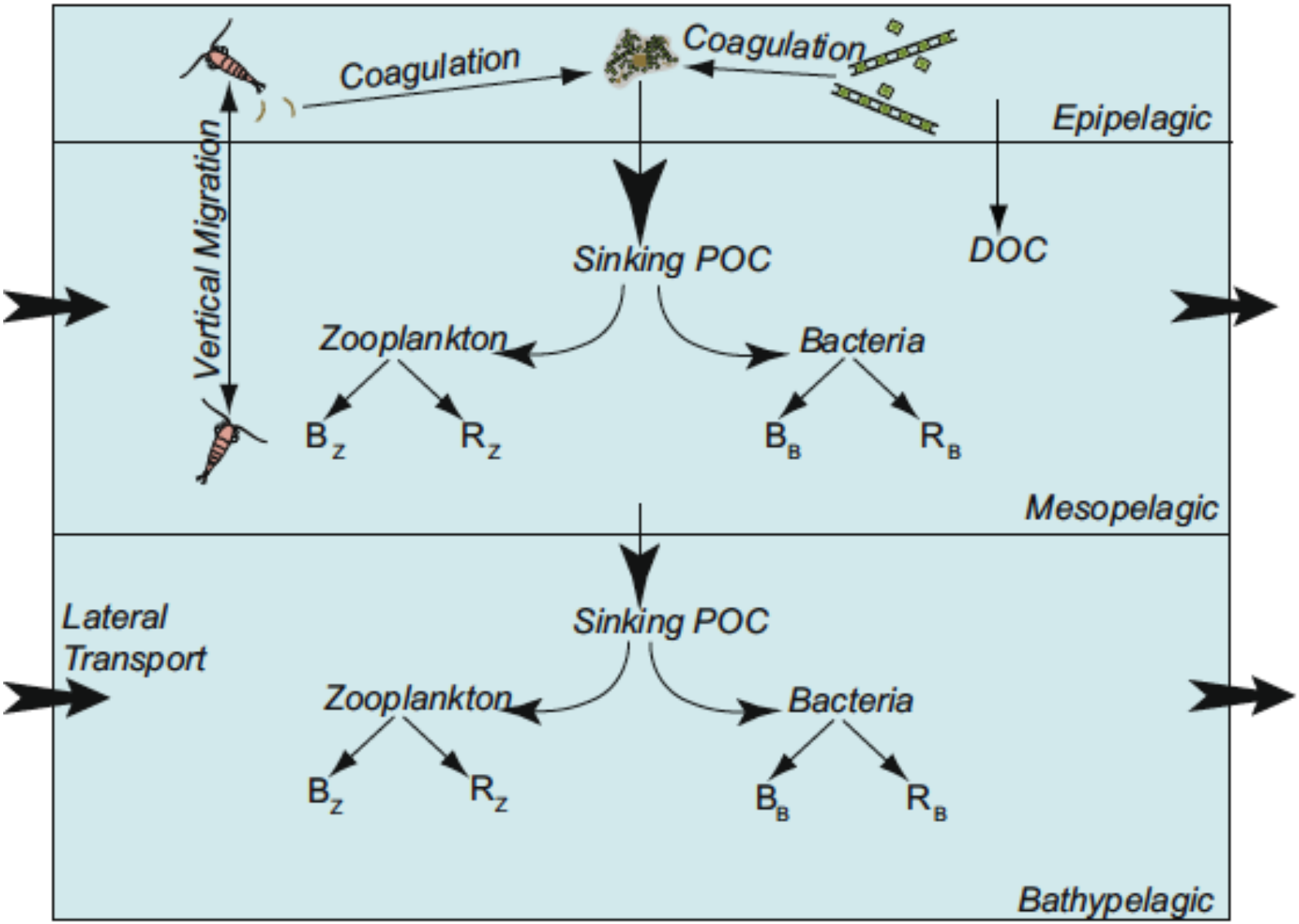
Alyson Santoro

CMORE Summer Course 2014

Some of my best friends hang out in the mesopelagic



Santoro et al. 2010



Burd et al. 2010

Outline

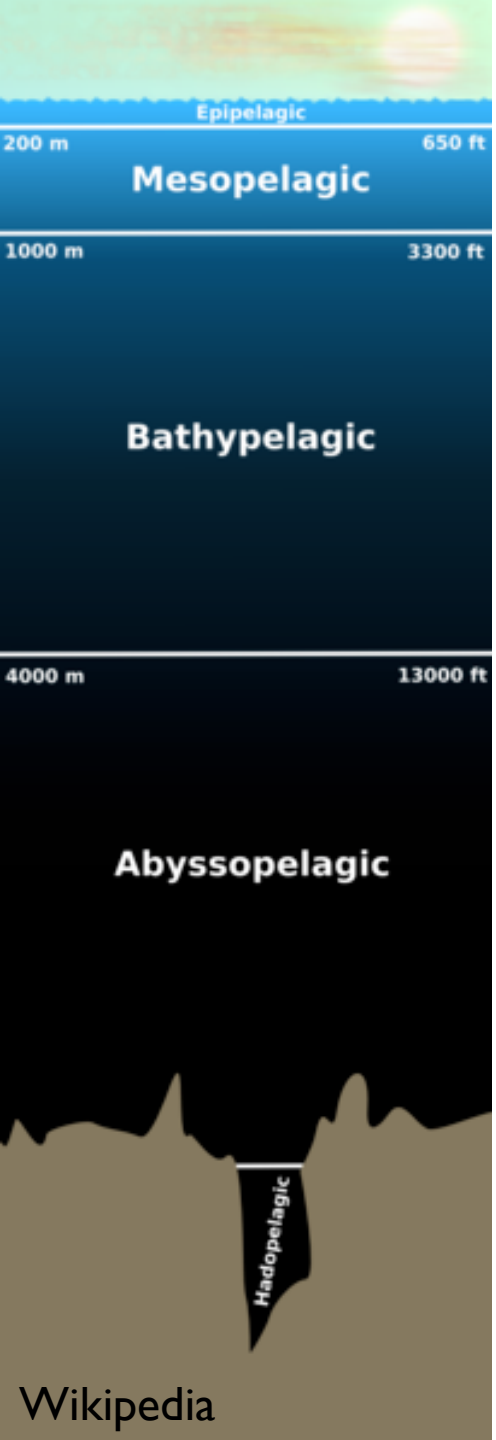
- Importance of microbial activity in the mesopelagic to the biological pump
- Problems with quantifying microbial activity in the mesopelagic
- Toward a biogeography of the mesopelagic

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?

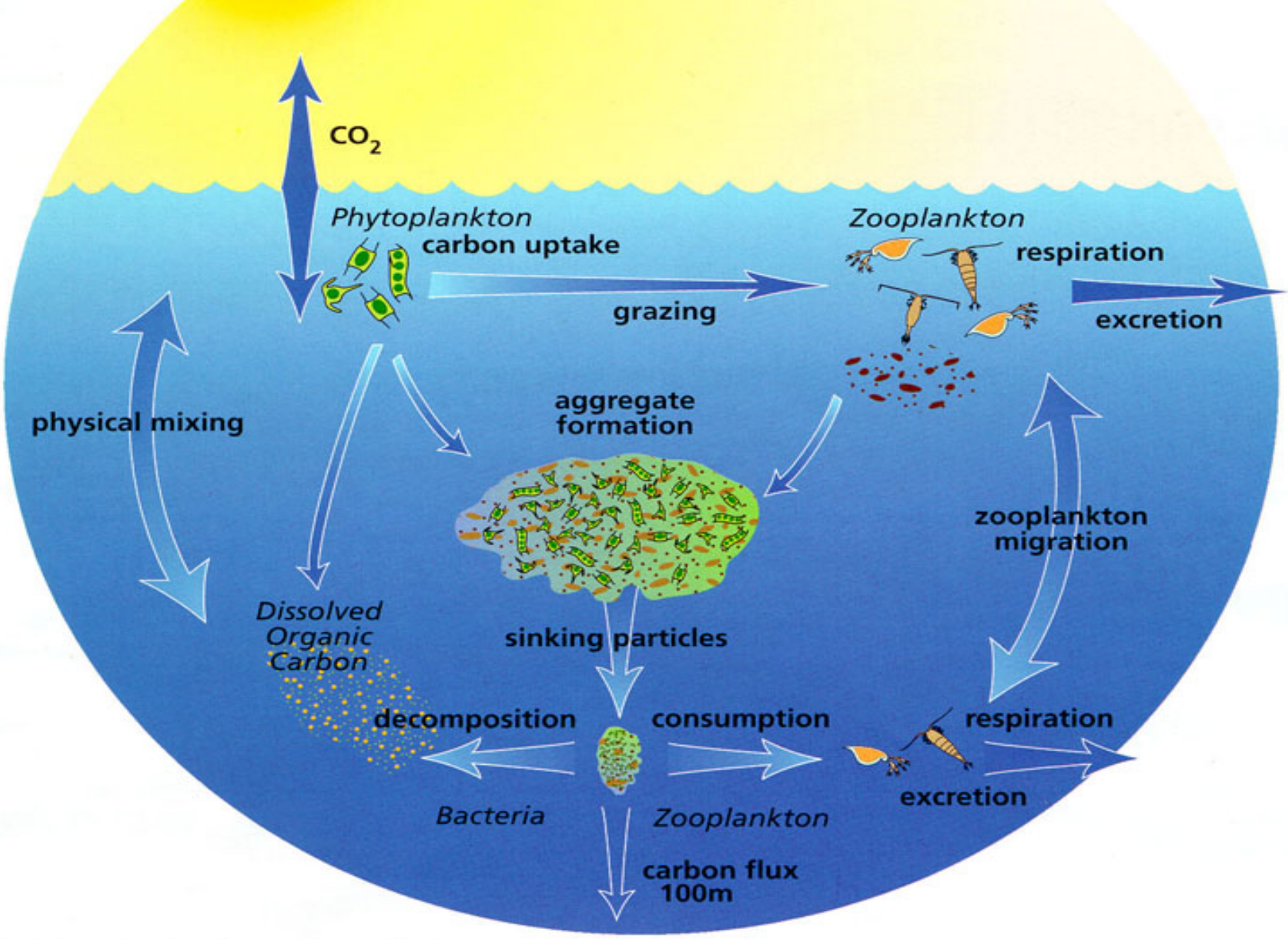
Can the microbes themselves tell us anything?



Wikipedia

Epipelagic	0 – 200 m
Mesopelagic	200 – 1000 m
Bathypelagic	1000 – 4000 m
Abyssopelagic	below 4000 m

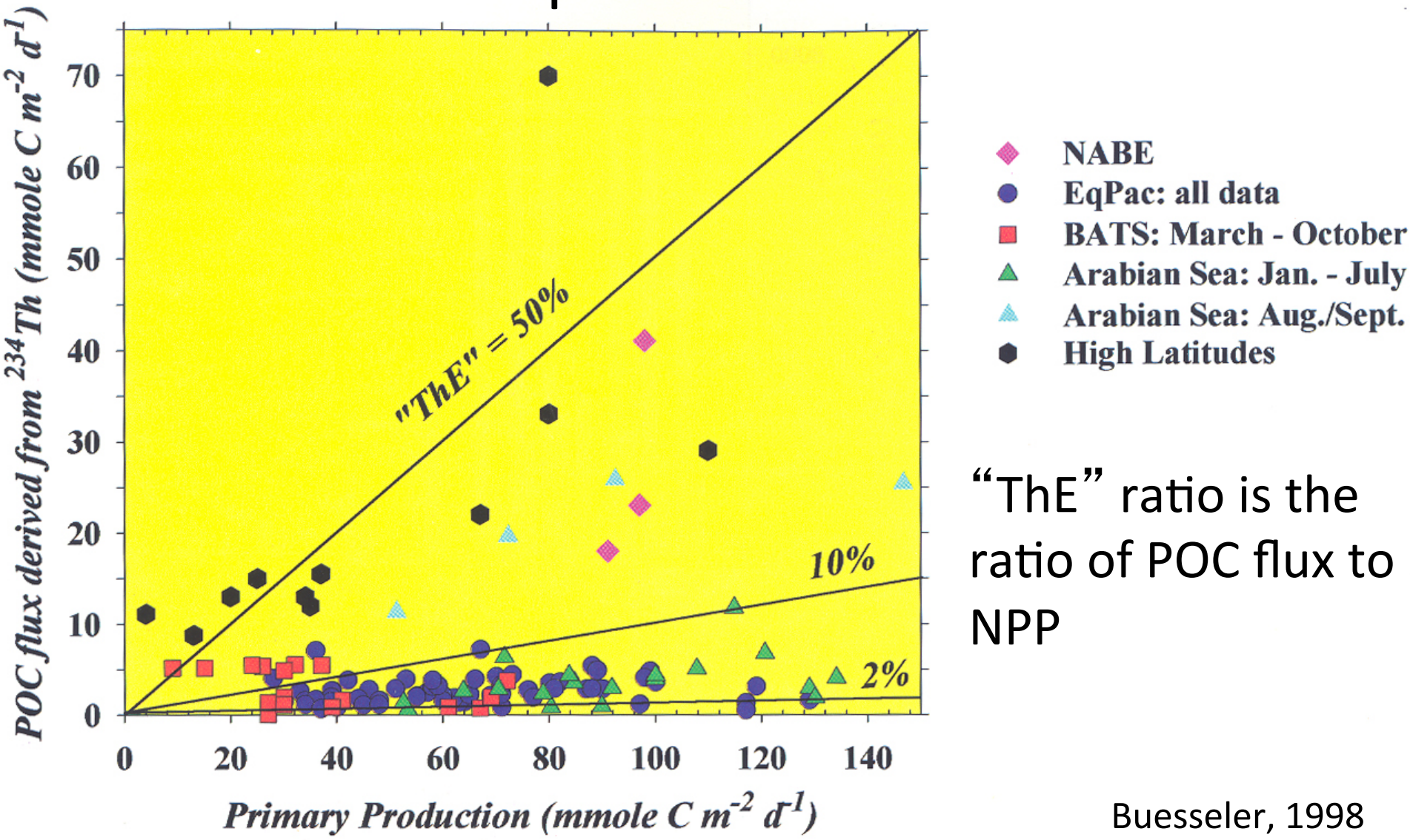
I prefer the definition that the mesoplegic starts at the base of the euphotic zone.



The Biological Pump

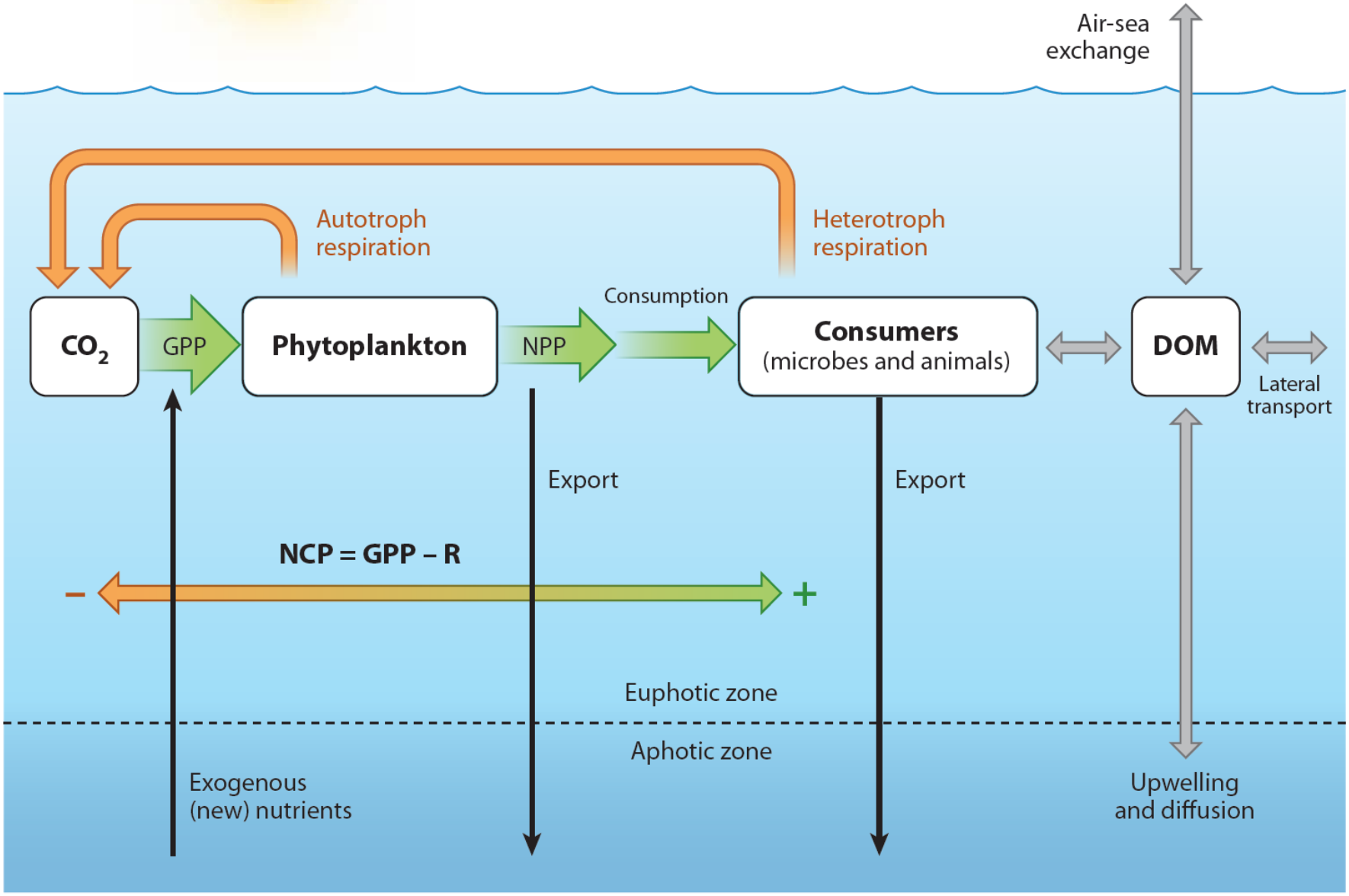
JGOFS

POC Flux ambiguously related to primary production



"ThE" ratio is the ratio of POC flux to NPP

Buesseler, 1998

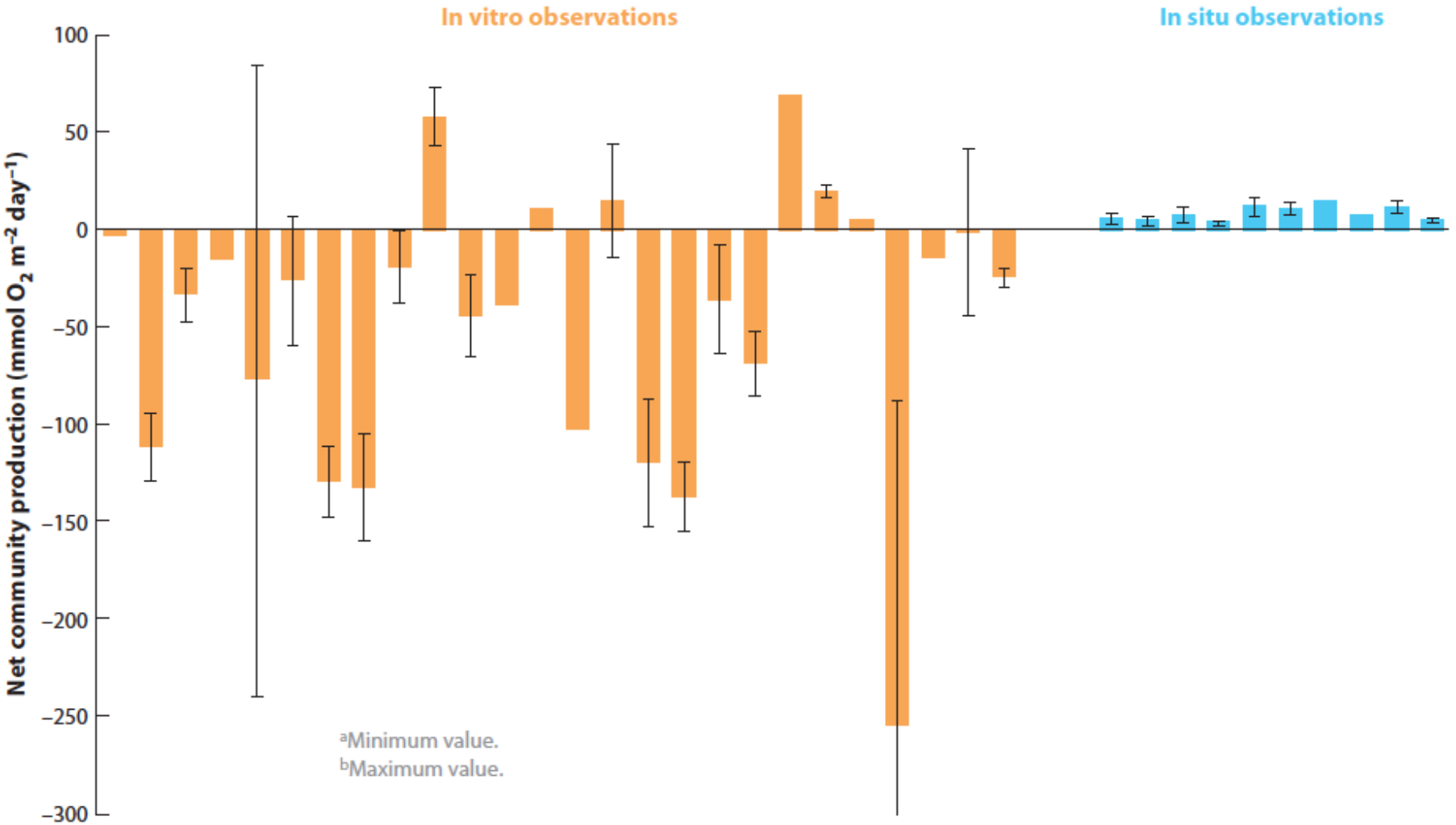


Ducklow and Doney 2013

Net community production =

Gross primary production – respiration

$$NCP = GPP - R$$



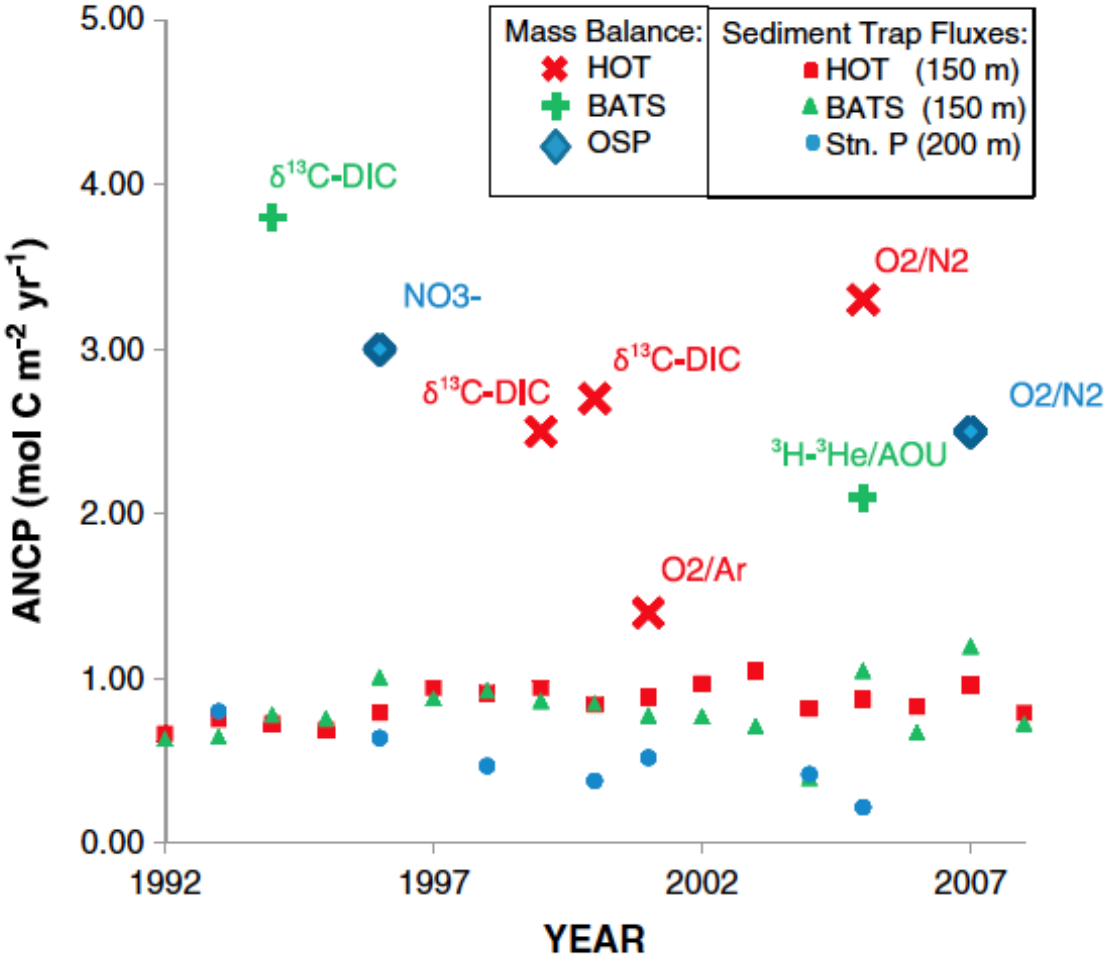
Williams et al. 2013

Diverse approaches to a common problem

Incubation independent or 'in situ' methods

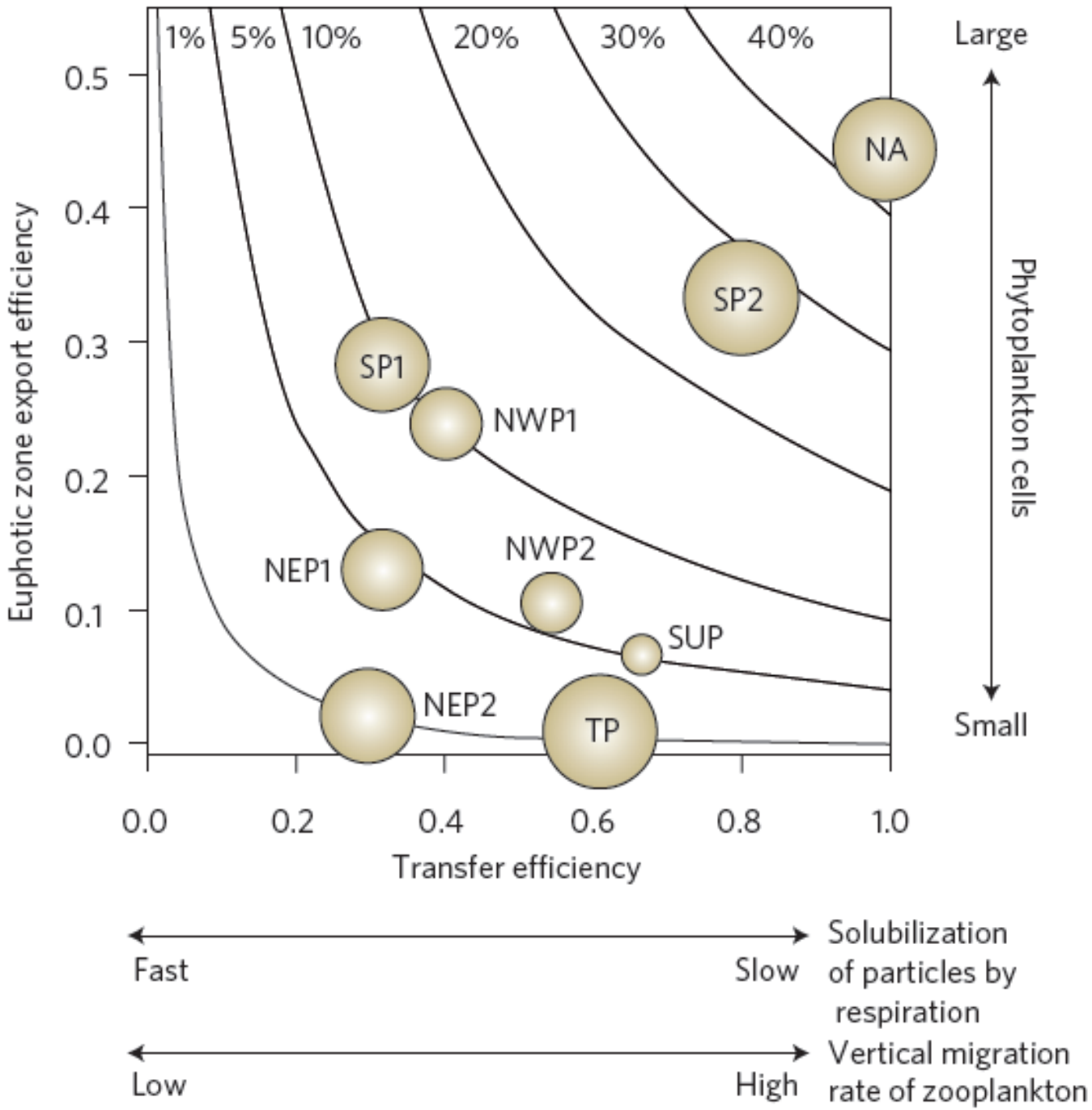
- O_2:Ar (Gives NOP, convert to NCP)
- AOUR – Deviation from O_2 equilibrium compared with an independent 'clock' (like ^3He)
- $\Delta^{17}O$ – uses unique stable isotopic signature of atmospheric O_2 to separate it from photosynthetic O_2 (GOP, convert to GPP)

But even these methods also appear to give conflicting results



Incorporating DOC export resolves some of the discrepancy, but not all.

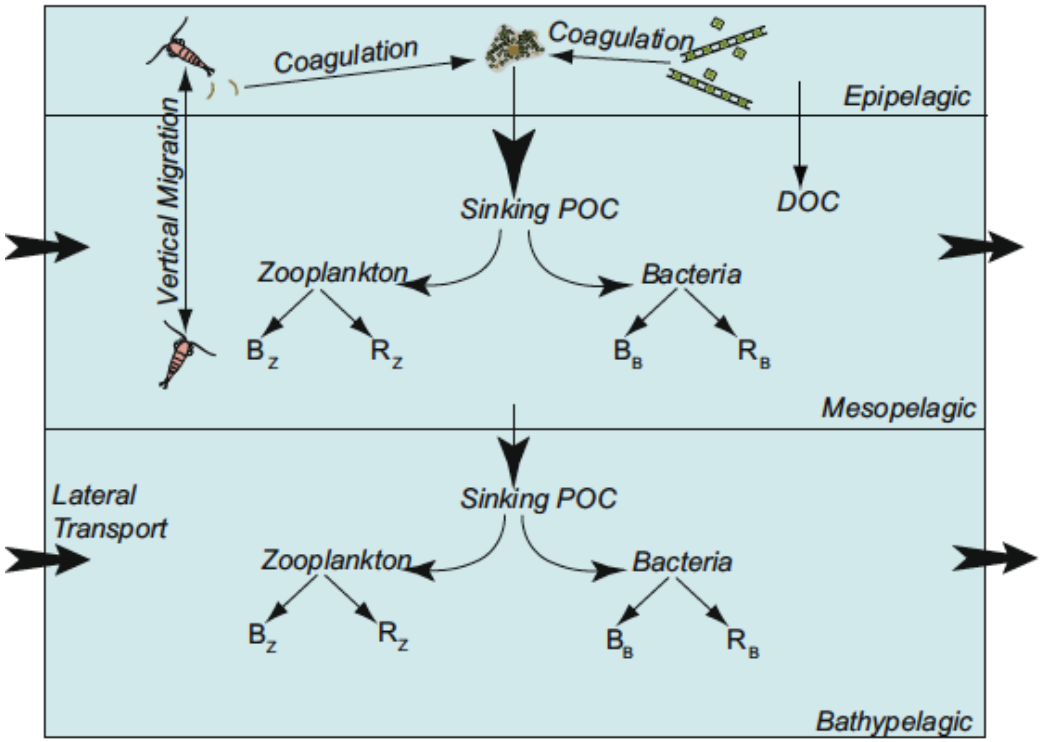
Emerson 2013



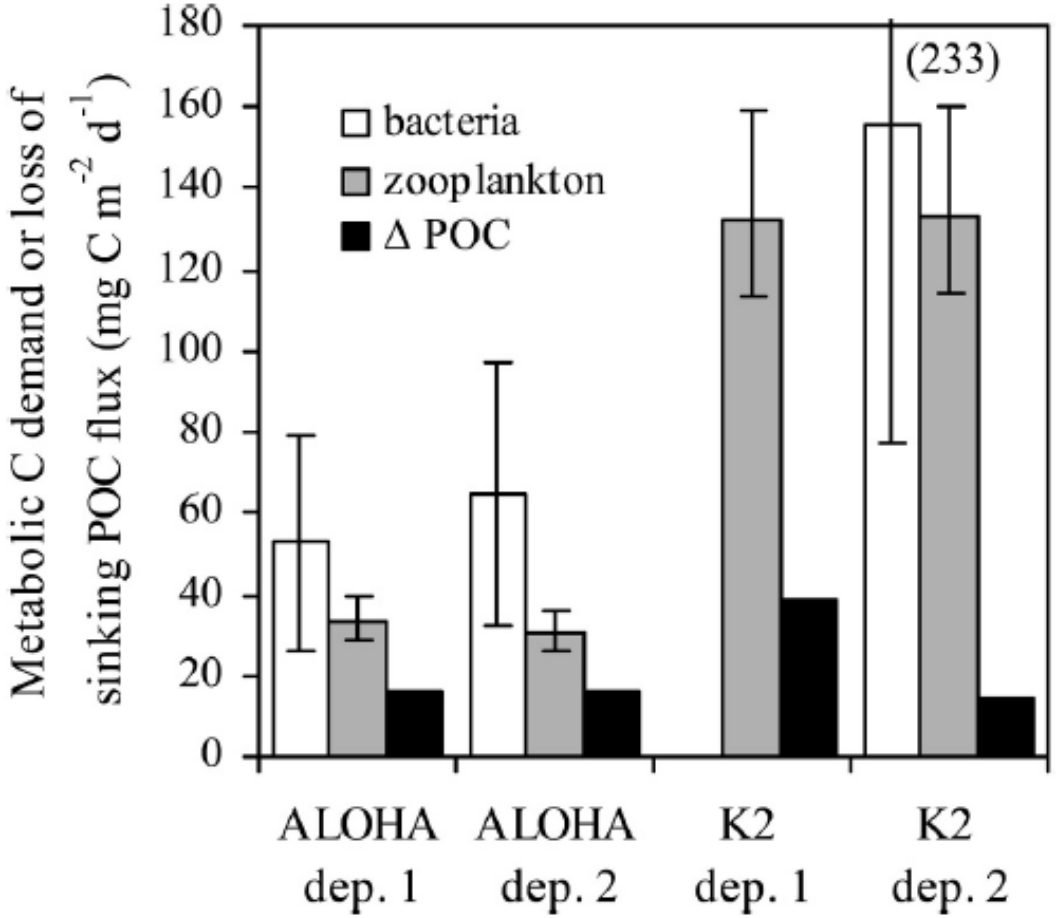
Buessler and Boyd 2009, as shown in Herndl and Reinthaler 2013

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

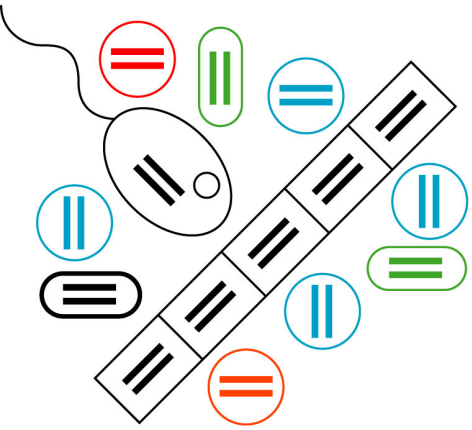
Why is this so hard?

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]

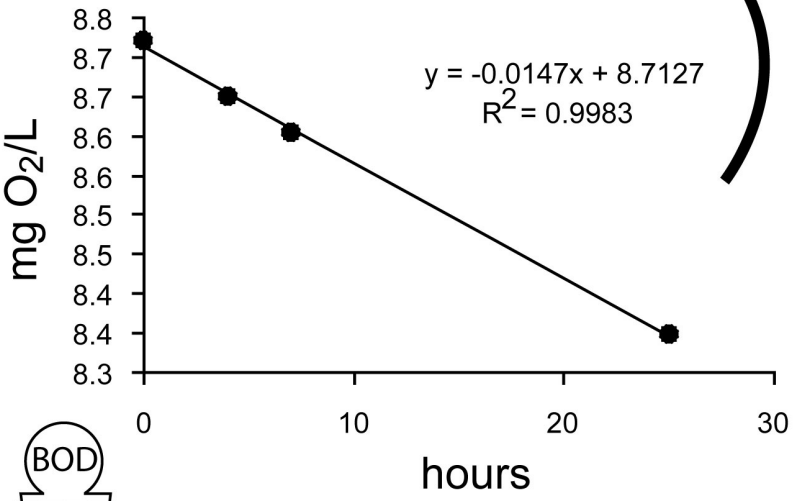
Burd et al. 2010, Deep Sea Res II

Bacteria Respiration Rate

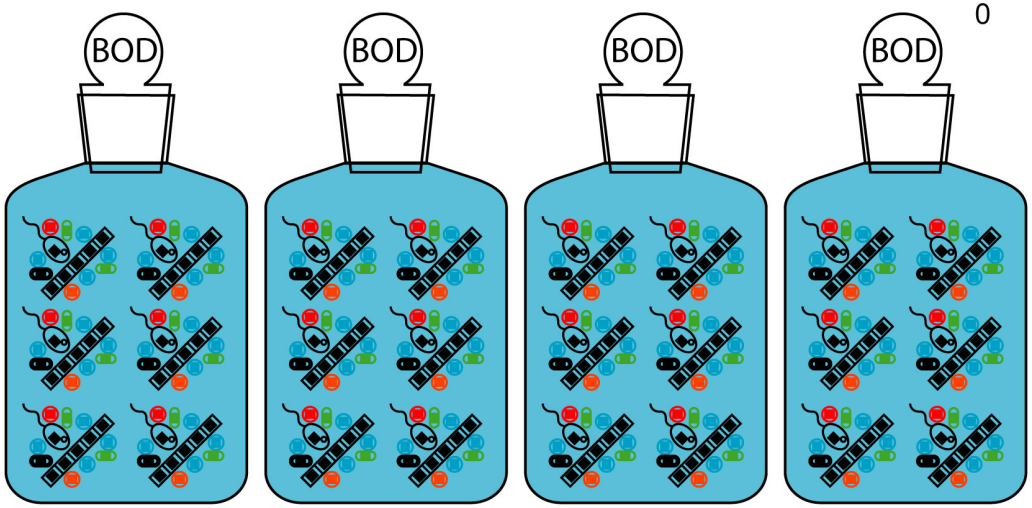


$$\frac{\text{grams } O_2}{\text{L x h}} \times \frac{1 \text{ mol } O_2}{32 \text{ grams } O_2} \times \frac{1 \text{ mol C}}{1 \text{ mol } O_2} \times \frac{12 \text{ grams C}}{1 \text{ mol C}} = \frac{\text{grams C}}{\text{L x h}}$$

Calculate carbon respiration from oxygen consumption



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



Measure oxygen concentration

Lots of assumptions in converting the measured quantity to the desired value

We want to know:

Org C $\longrightarrow$ CO_2

We measure:

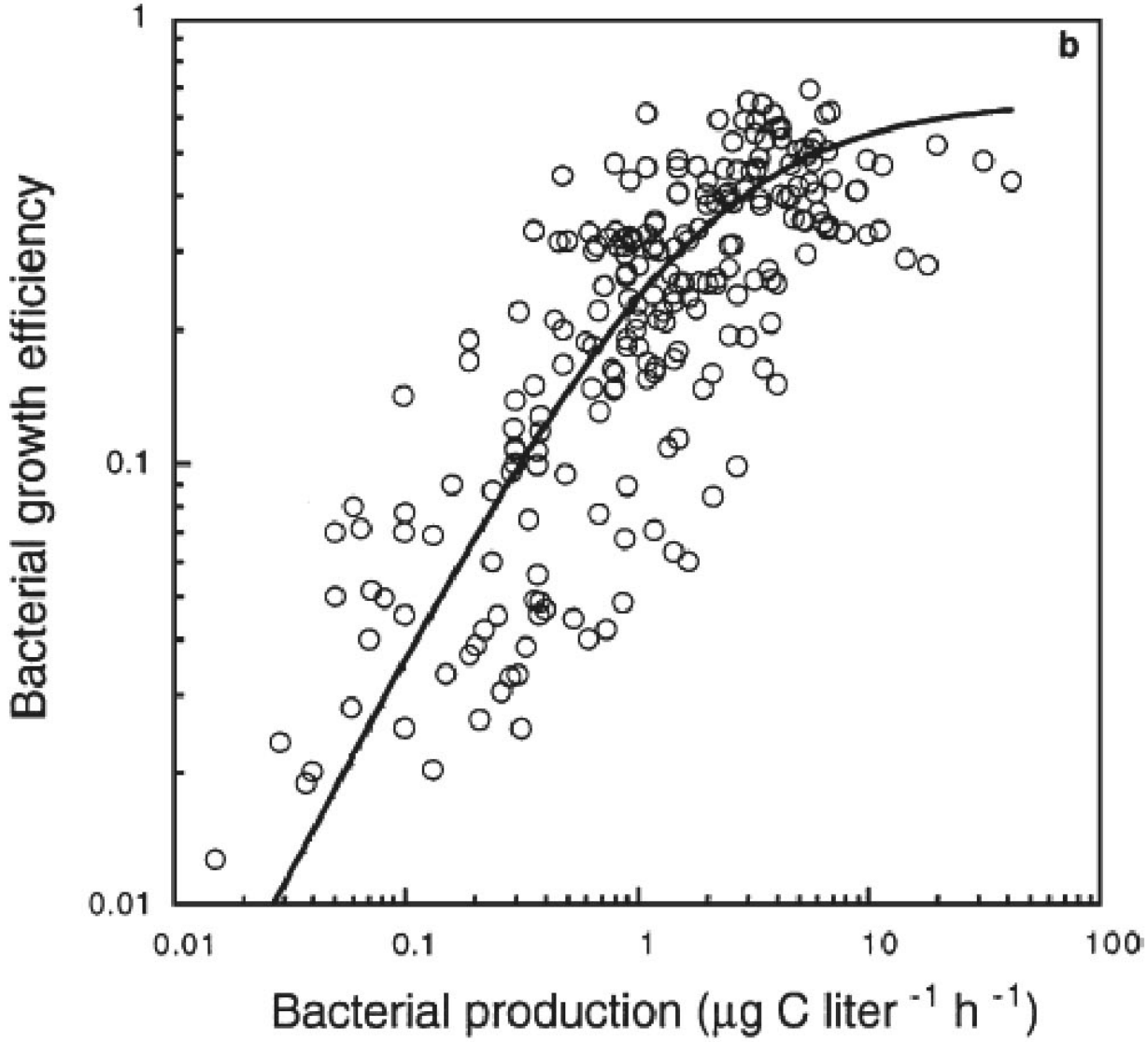
^{3}H leucine uptake x conversion factor = BP

BCD = BP/BGE

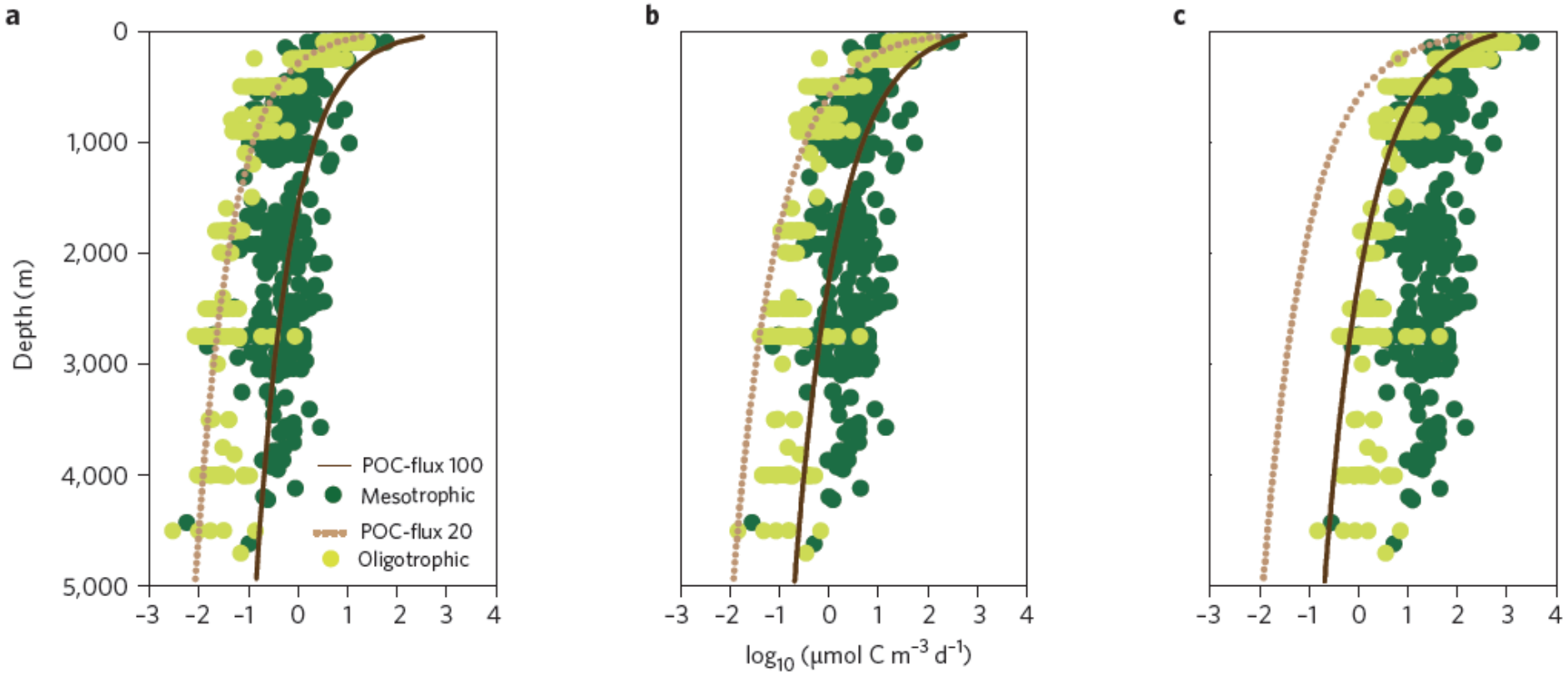
BGE = BP/(BP+BR)

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

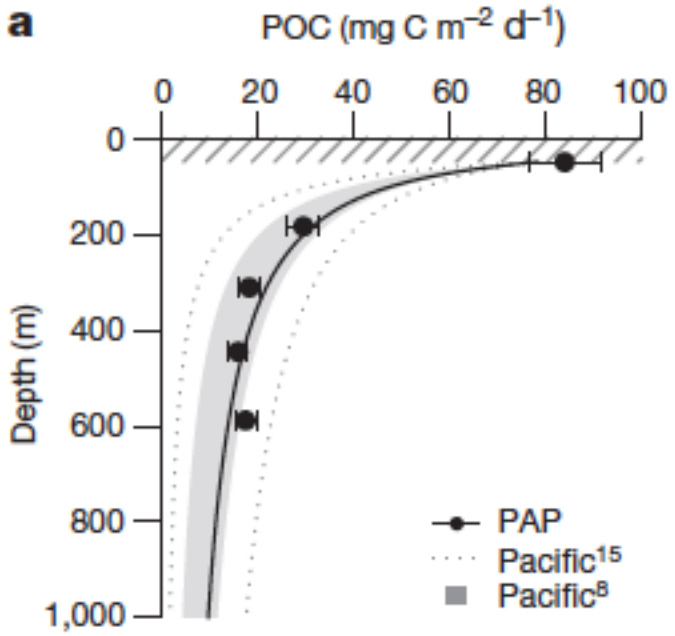


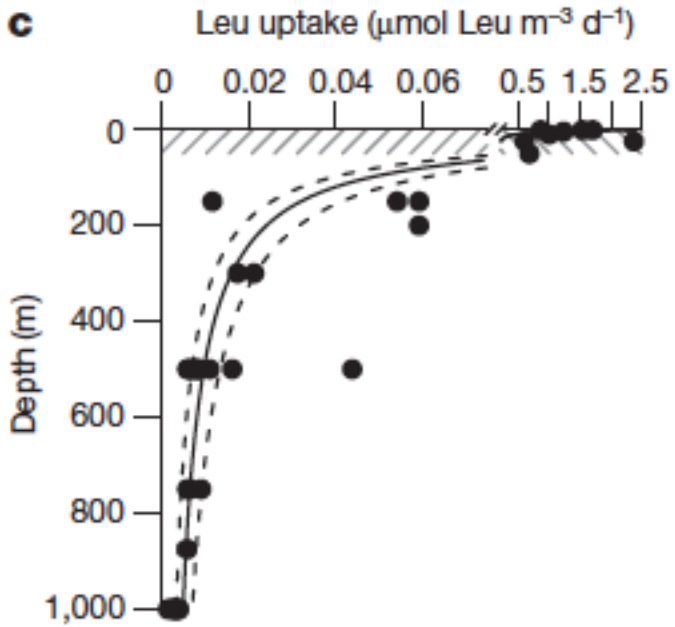
Microbial Biomass

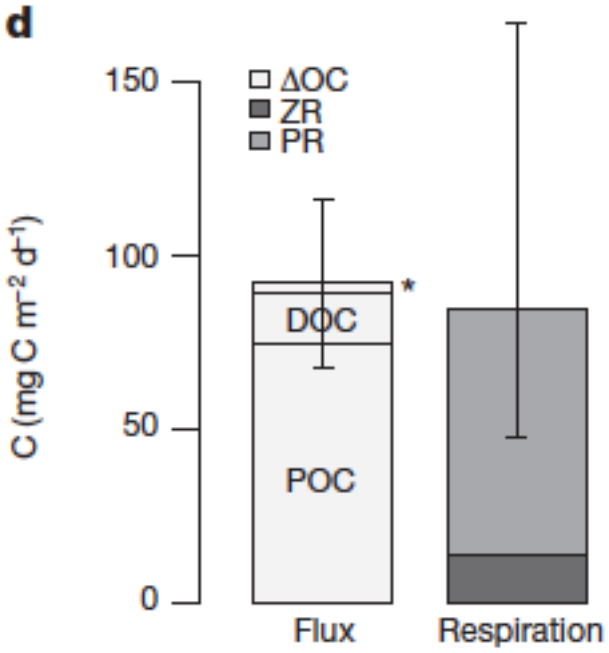
BCD, 20% BGE

BCD, 2% BGE

Herndl and Reinthaler 2013

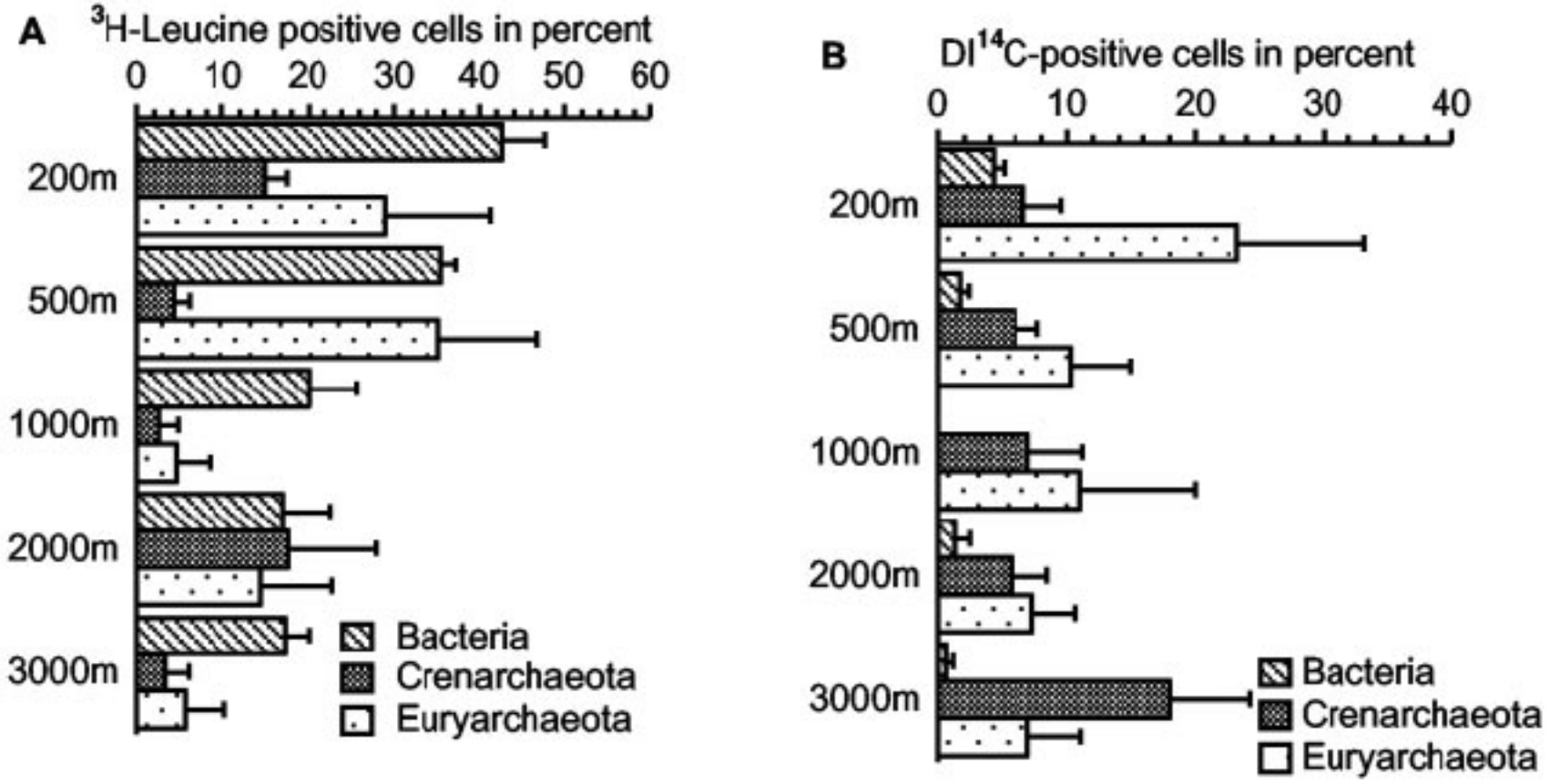






Giering et al. 2014

Evidence for autotrophy – cellular uptake of bicarbonate



Estimate flux of 6.5 x 10^{13} mol C y^{-1} (0.8 Pg y^{-1})

Herndl et al. 2005

Single cell genomic data for carbon fixation in the mesopelagic

Station	Depth (m)	Total SAGs*	Identified SAGs†	Metabolic gene screening results‡		
				RuBisCO	*aprA*	*rdsrA*
KN192-5-11	10	311	89 (29%)	ND	ND	ND
	800	1252	257 (21%)	21 (12%)	15 (8%)	1 (0.6%)
ALOHA	25	630	147 (23%)	ND	ND	ND
	770	630	245 (39%)	23 (12%)	17 (9%)	2 (1%)

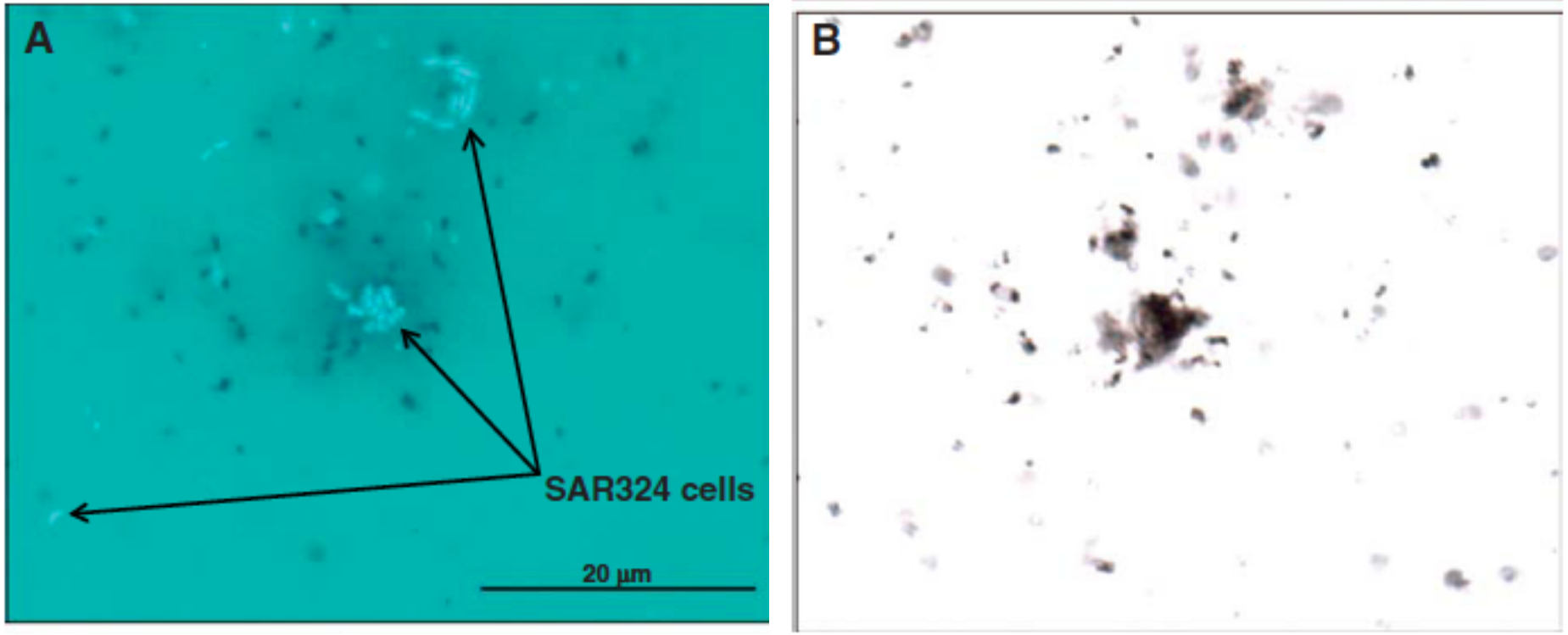
*Total SAGS are the number with successfully amplified DNA product. †SAGs for which high-quality SSU rRNA sequences were obtained. ‡Percentages based on the total number of identified bacterial SAGs only; ND, no data.

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

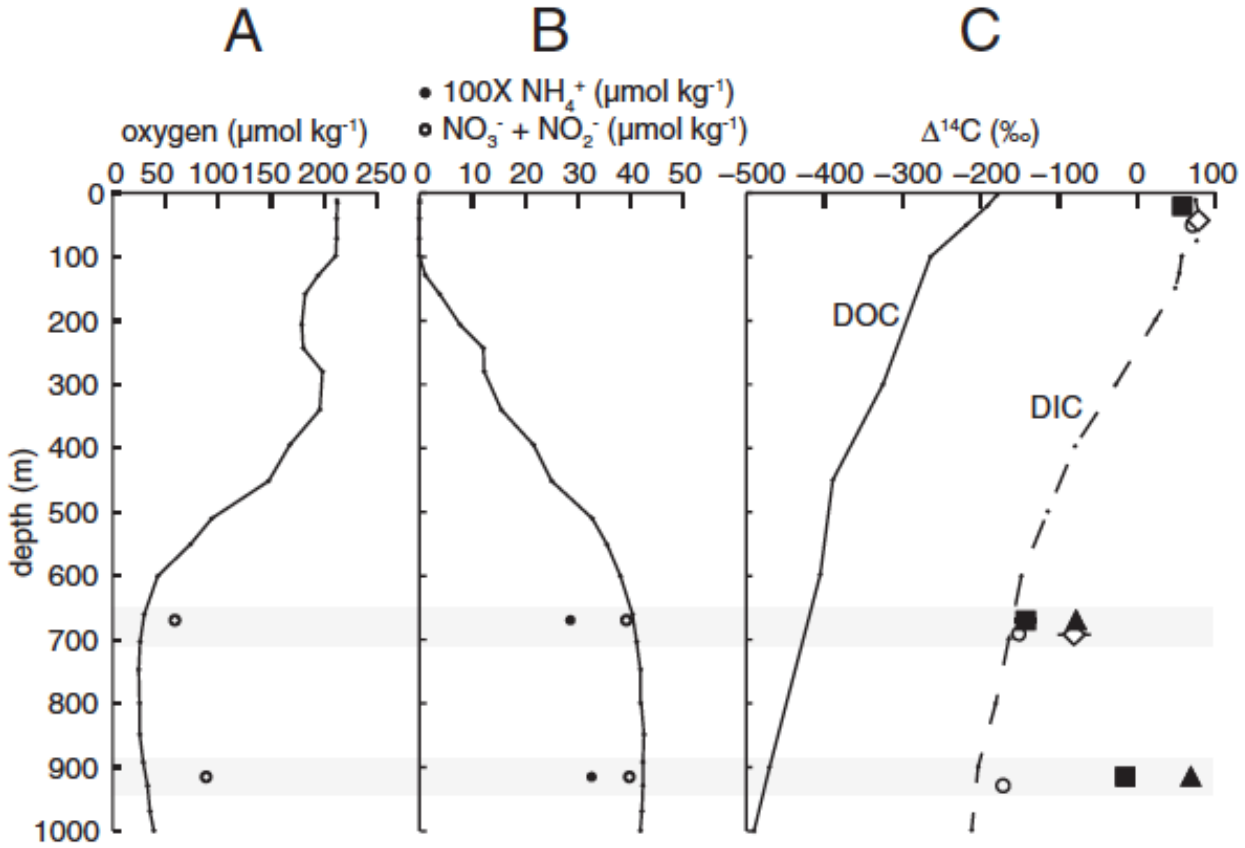
What could the electron donors be?

Swan et al. 2011

Microautoradiography shows DI^{14}C uptake



Radiocarbon evidence for chemoautotrophy in the mesopelagic



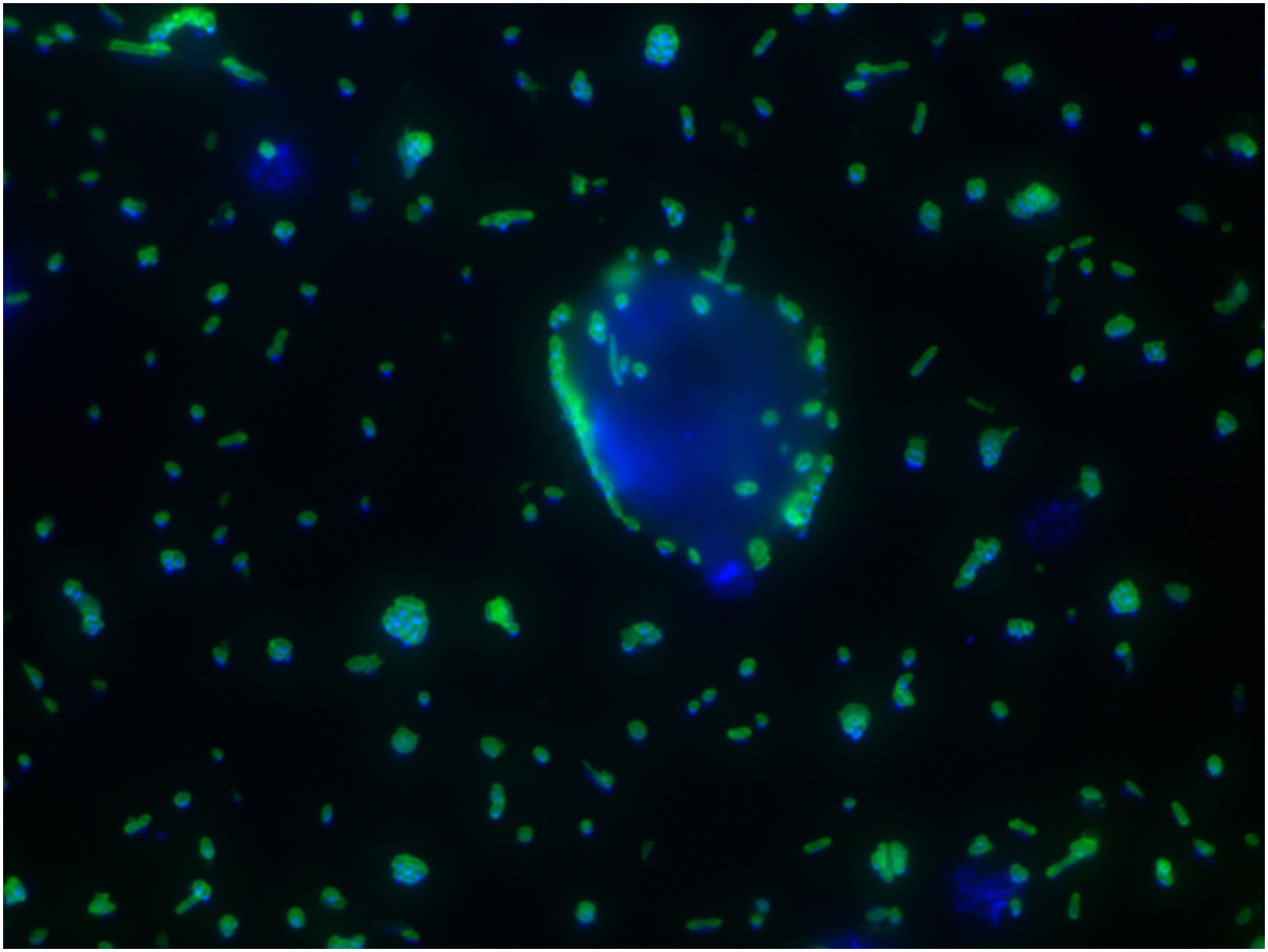
Hansman et al. 2009

What does the nitrogen budget in the upper mesopelagic tell us?

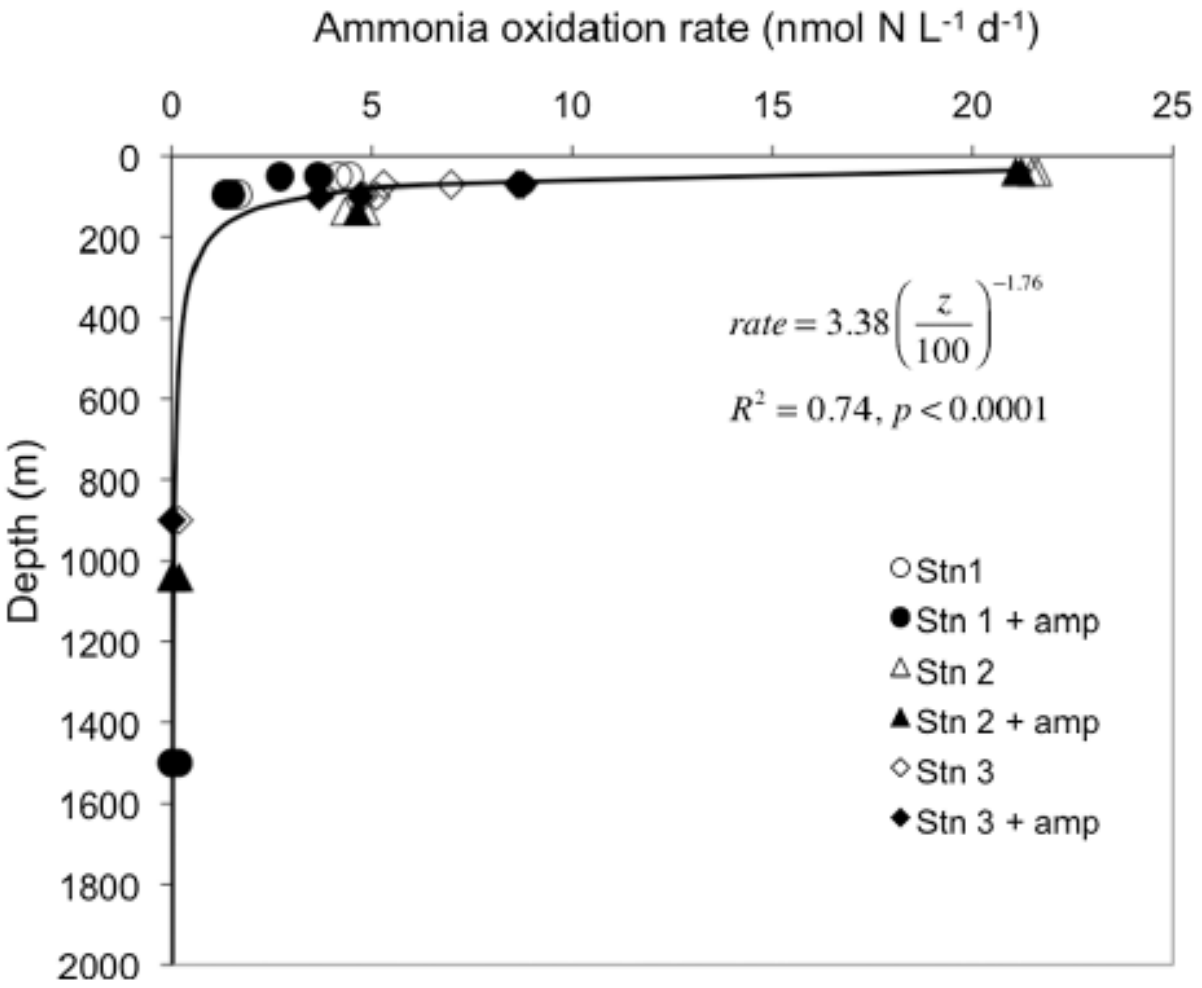
Respiration: $CH_2O + O_2 \longrightarrow CO_2 + H_2O$

Nitrification: $NH_3 + 2\ O_2 \longrightarrow NO_3^- + H^+ + H_2O$

But unlike respiration, we can actually measure this directly.



Foster, Santoro, and Berelson unpublished



Arabian Sea

- *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.

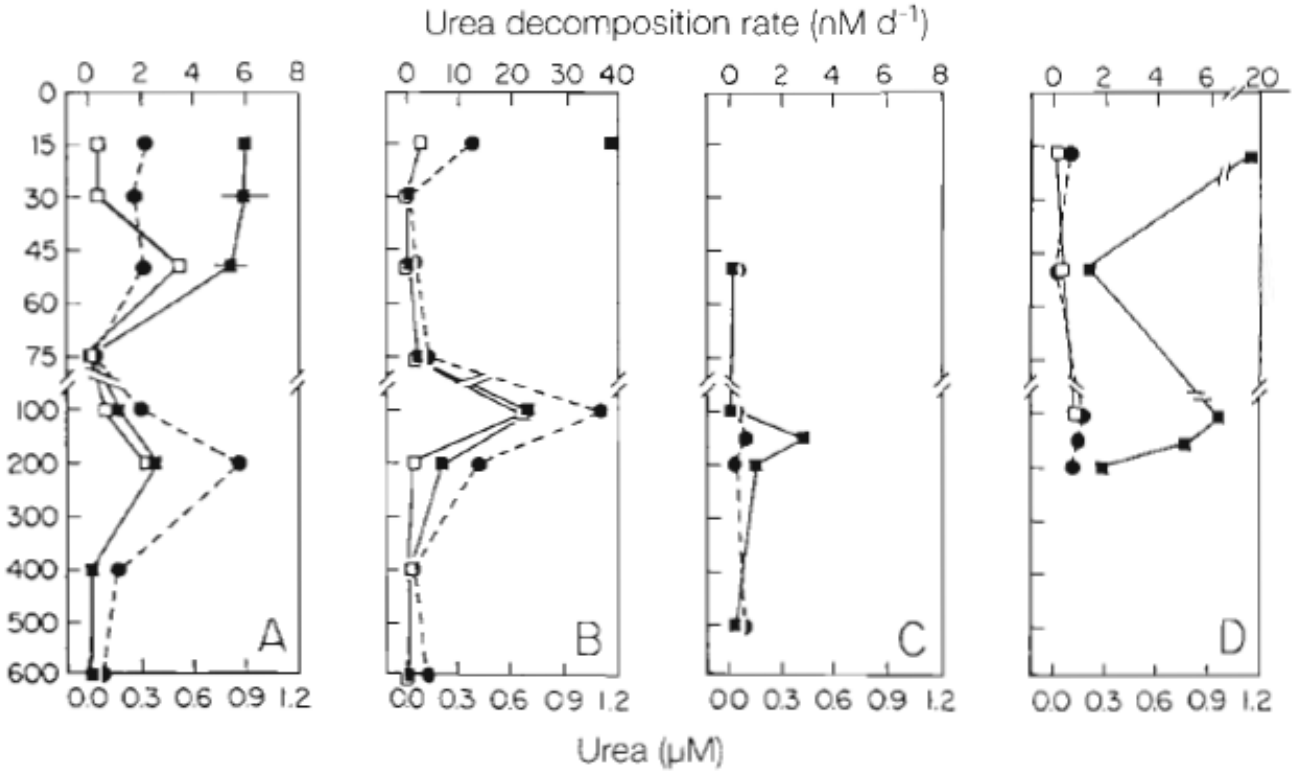
Newell et al. 2011

Urea decomposition by bacteria in the Southern California Bight and its implications for the mesopelagic nitrogen cycle

Byung C. Cho*, Farooq Azam

Marine Biology Research Division, Scripps Institution of Oceanography, UCSD, La Jolla, California 92093-0202, USA

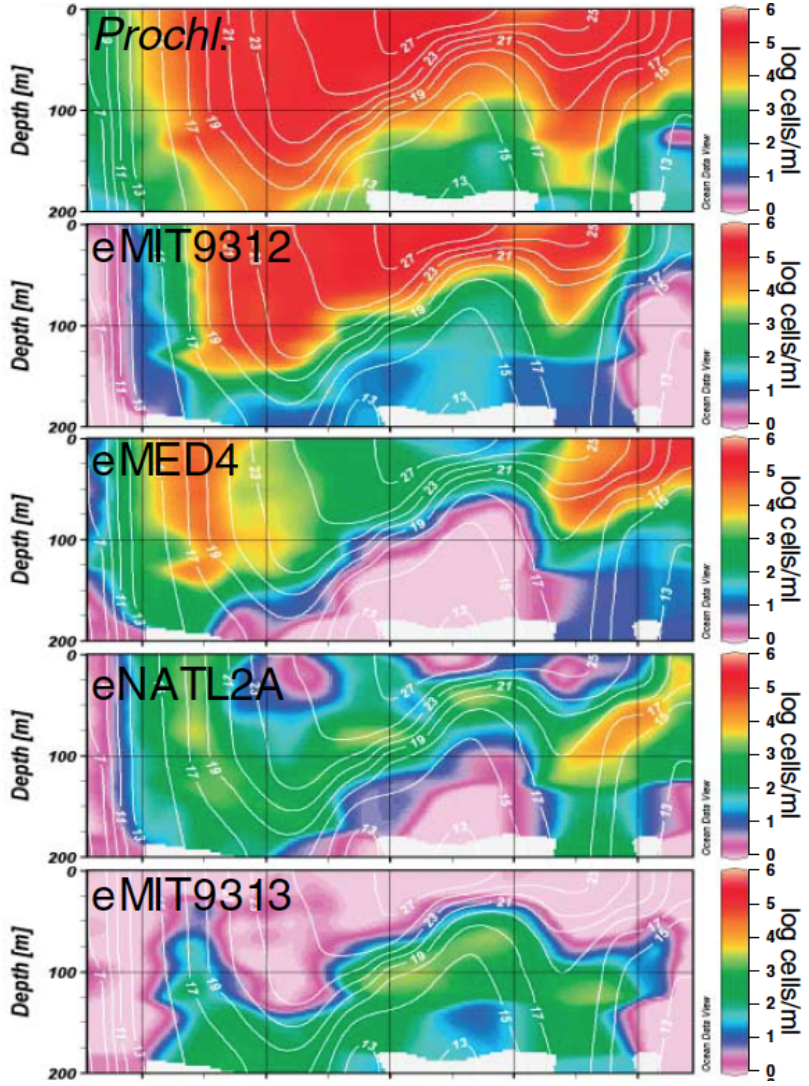
"Our results suggest that a substantial fraction of sinking N flux may follow the pathway sinking N-urea-ammonium-nitrate. . . ."



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

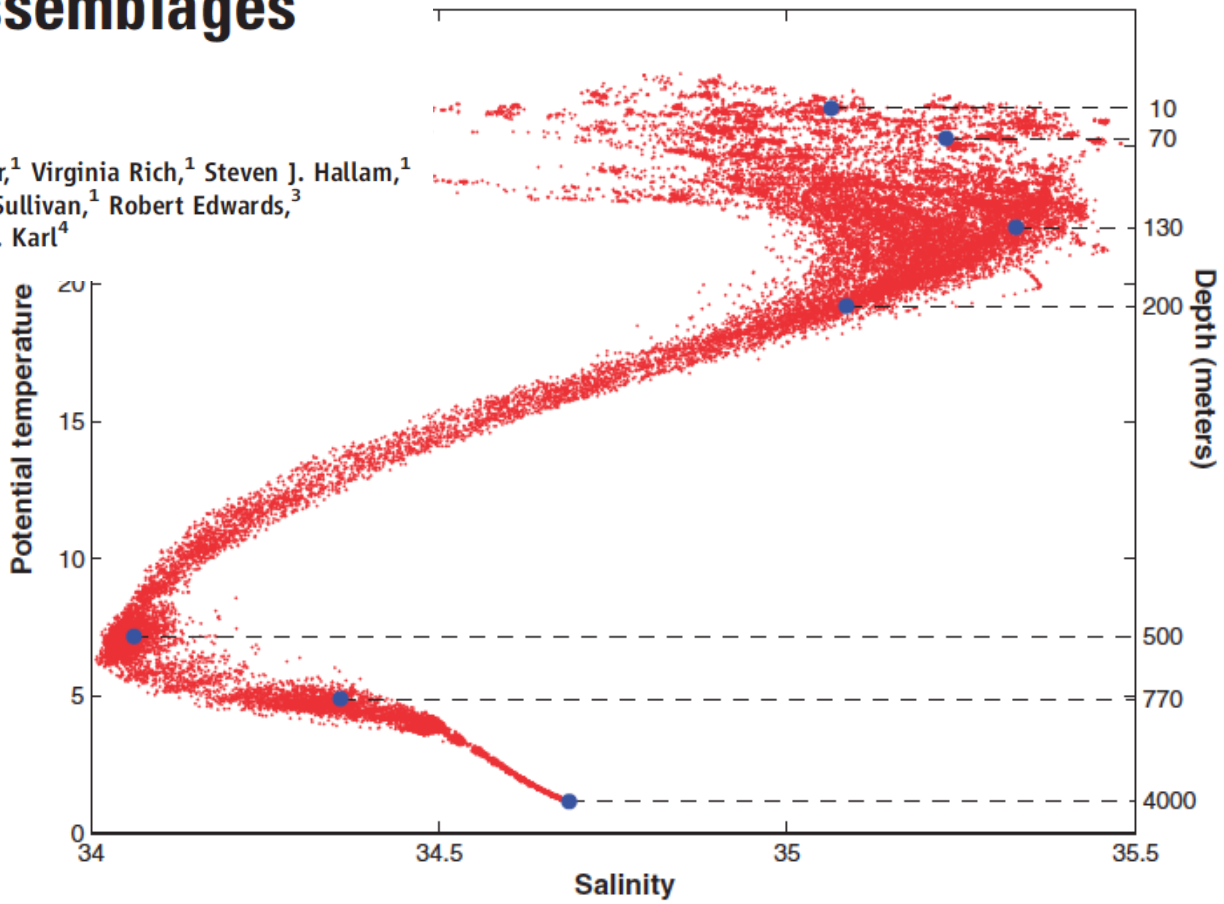
Genome	*GOS sequences recruited*		
	90% Identity	*50% Identity*	*% Difference*
Prochlorococcus marinus AS9601	163 465	192 515	18
Prochlorococcus marinus MIT9301	119 804	145 096	21
Prochlorococcus marinus MIT9202	48 213	70 083	45
Prochlorococcus marinus MIT9312	46 549	93 811	102
Candidatus pelagibacter HTCC7211	28 811	1 128 240	3816
SAR86A	27 391	200 708	633
Synechococcus sp. 9605	26 071	35 269	35
Ca. pelagibacter HTCC1062	22 236	38 2680	1621
Ca. pelagibacter HTCC1002	20 901	373 189	1686
Prochlorococcus marinus MIT9215	17 732	29 402	66
Prochlorococcus marinus MED4	9033	36 462	304
SAR86B	3579	84 868	2271
Recruited by top 12 genomes	5.30%	27.90%	
Recruited by all the genomes ($n = 1700$)	5.60%	35.20%	
Recruited by SAR86	0.31%	2.80%	

DuPont et al. 2012

But there are limited metagenomic data from the mesopelagic

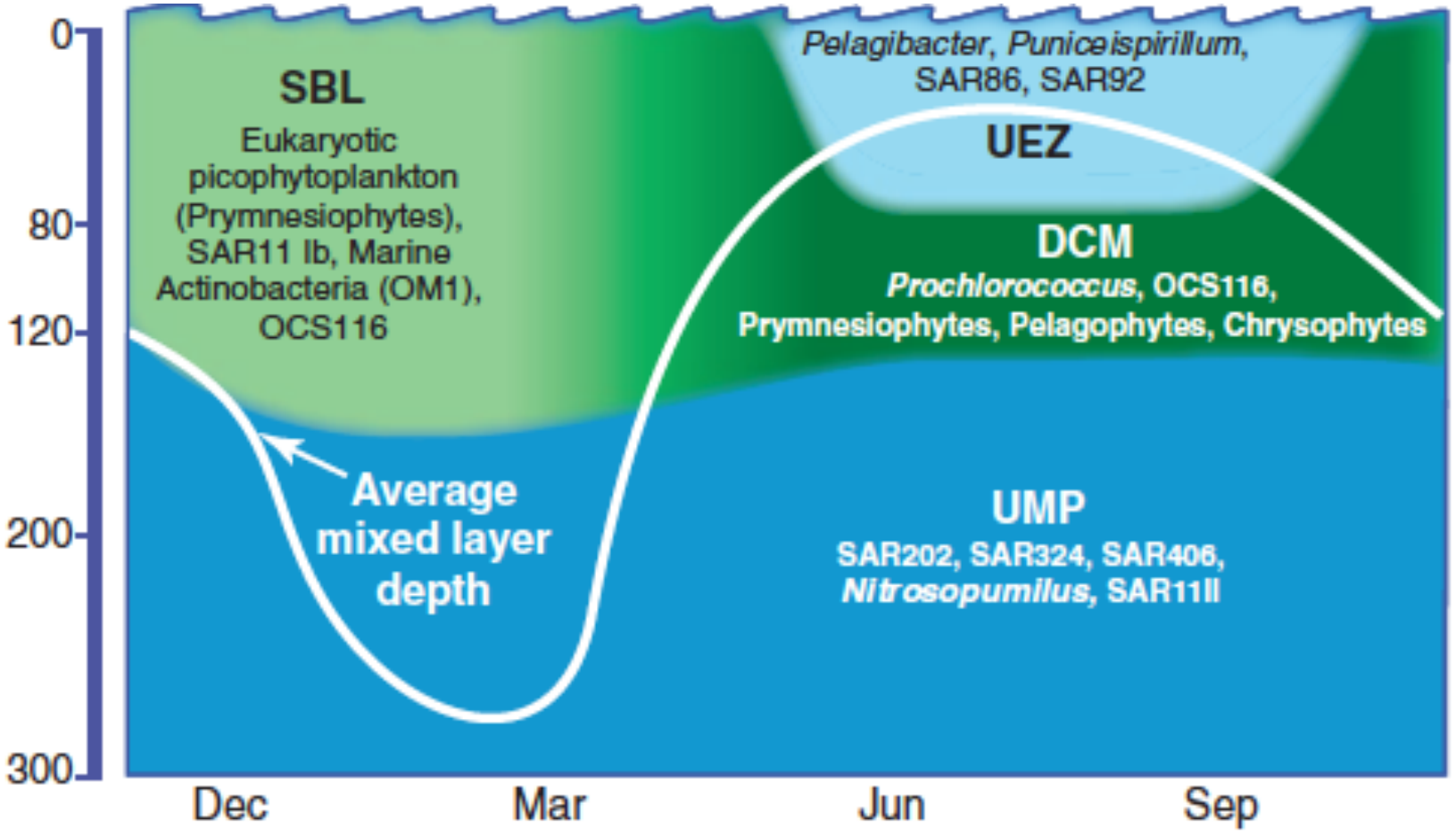
Community Genomics Among Stratified Microbial Assemblages in the Ocean's Interior

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,[1] David M. Karl[4]

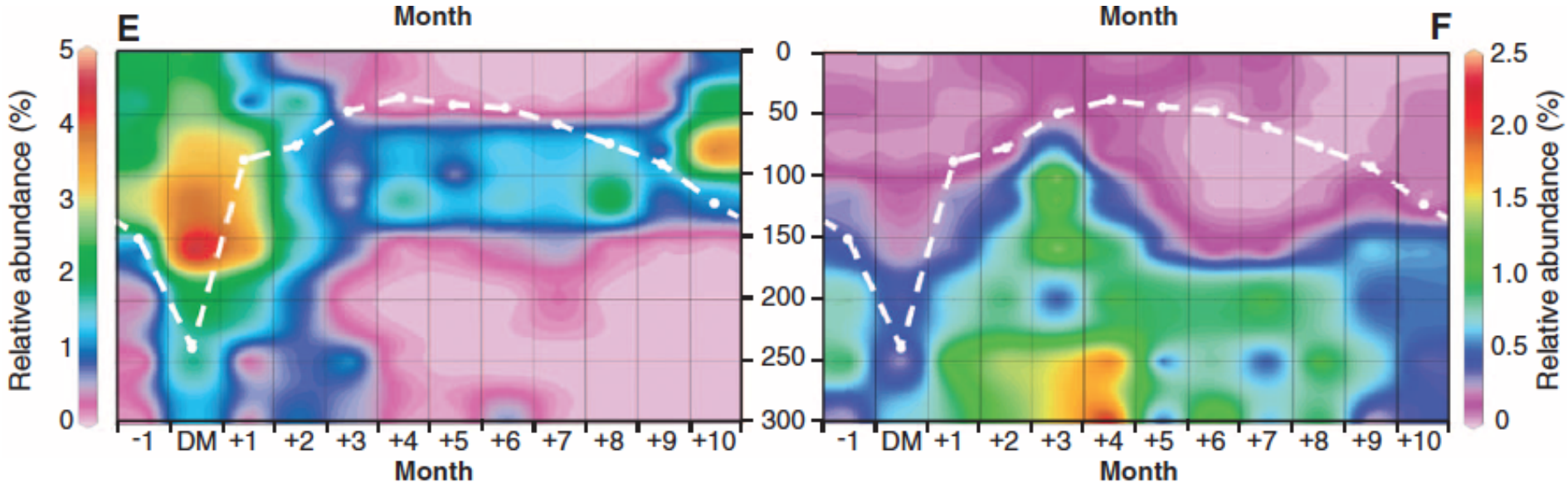


Delong et al. 2006

Toward a biogeography of the mesopelagic



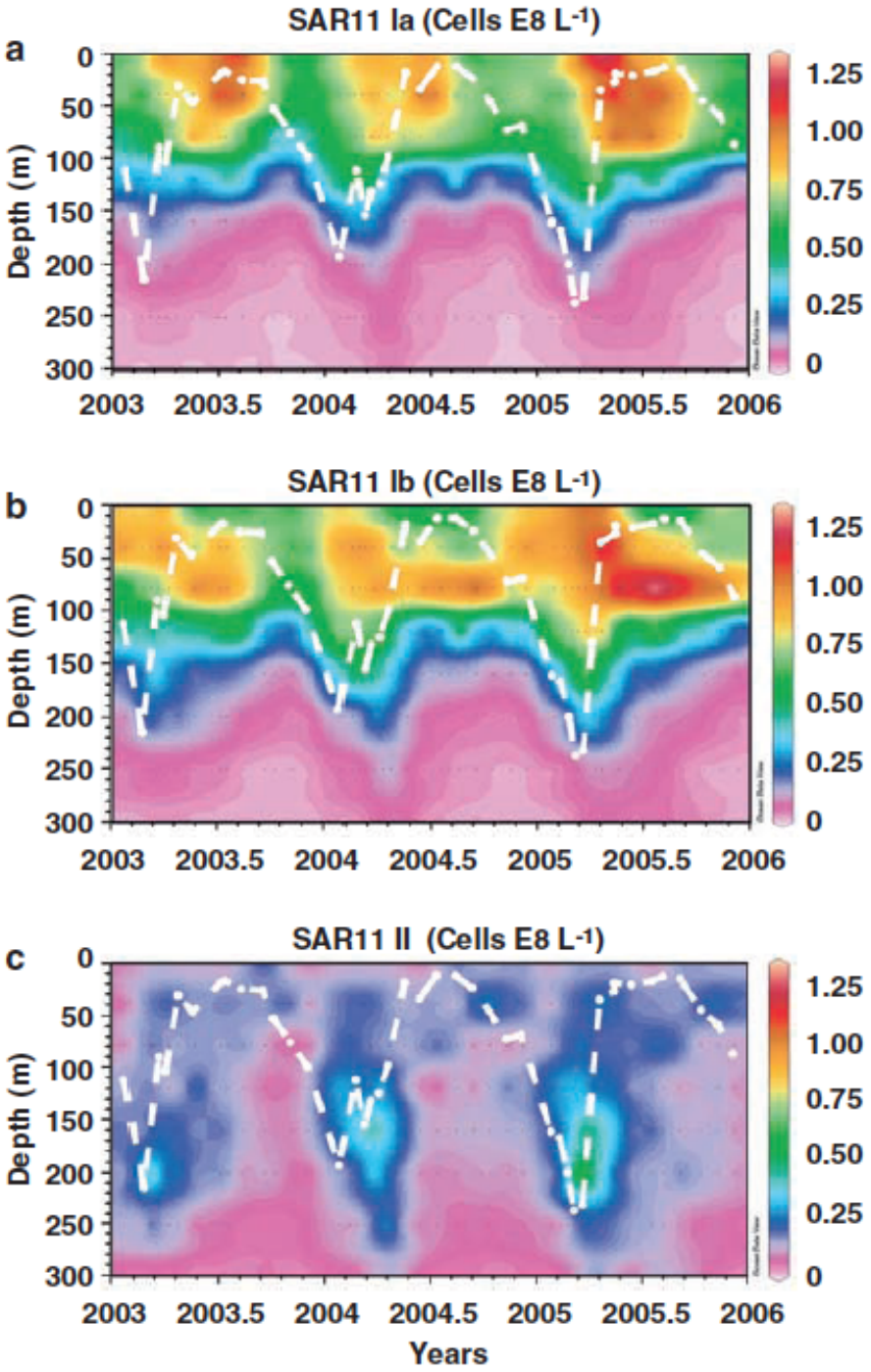
Giovannoni and Vergin 2012



OCS116

SAR202

Treusch et al. 2011; Giovannoni and Vergin 2012



Carlson et al. 2009