Evolution of marine microbial ecology

James Christian

Fisheries and Oceans Canada
Institute of Ocean Sciences
Sidney, BC

and

Canadian Centre for Climate Modelling and Analysis
University of Victoria

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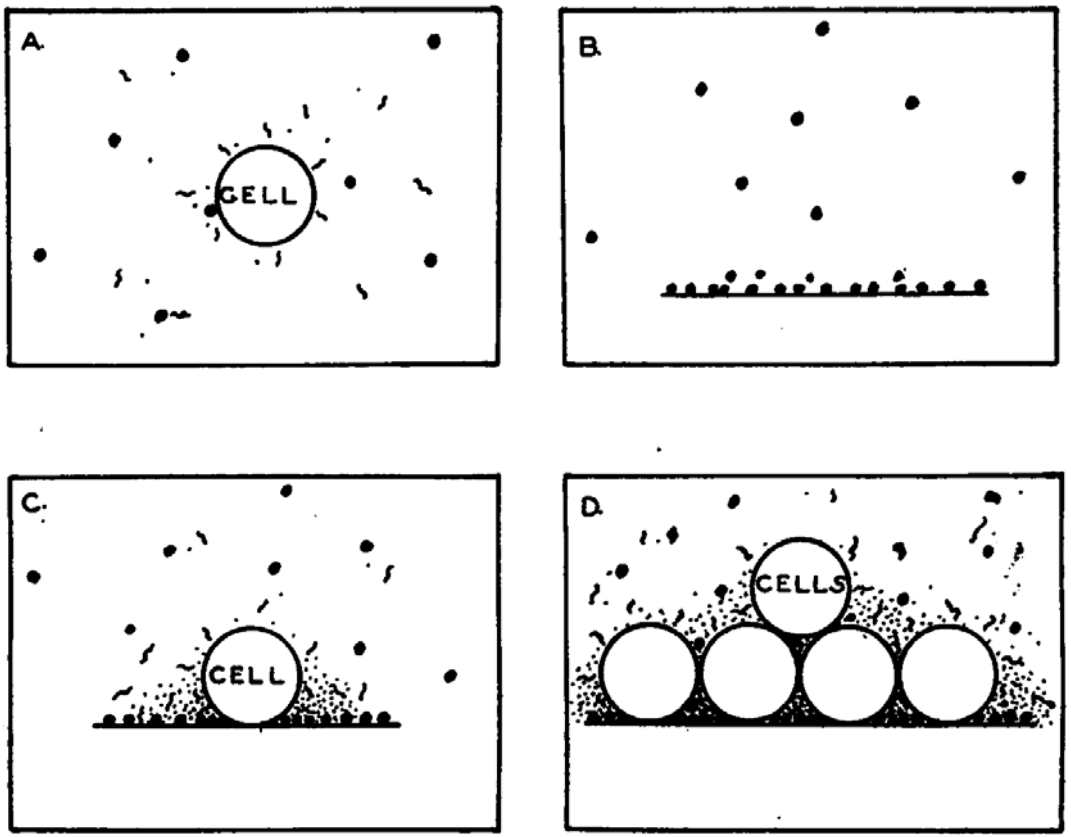
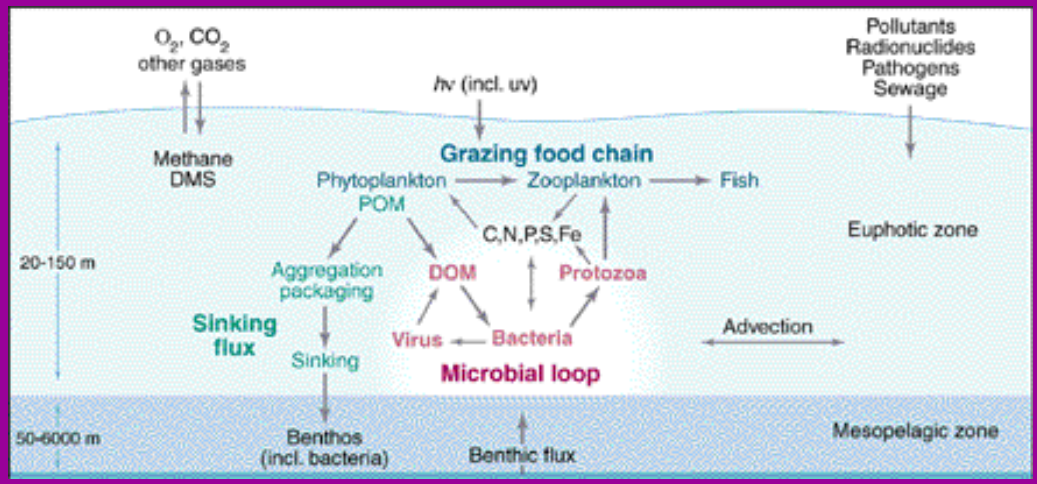
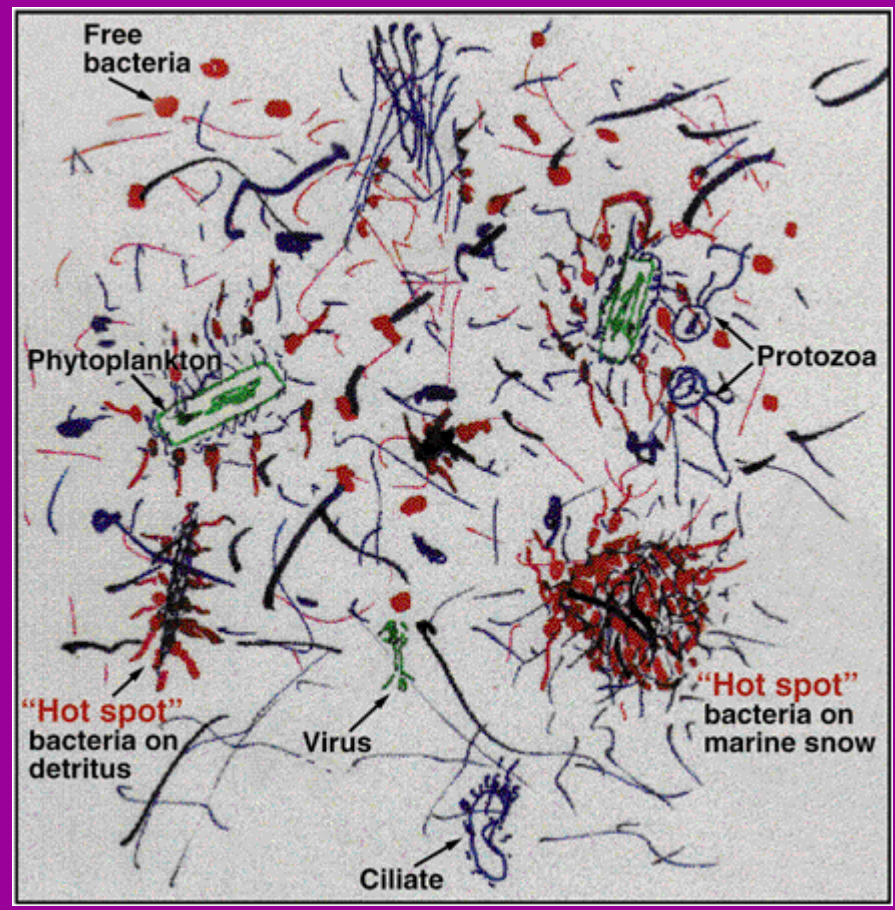


FIG. 2. A, A free-floating bacterial cell surrounded by a few suspended particles of food (dark circles) which must be hydrolyzed by the exoenzyme (helicoidal lines) before the resulting hydrolyzates (dots) can be ingested and assimilated. B, Particles of food concentrated in a monomolecular layer on a solid surface. C, Food particles are more available to the cell on the solid surface where the interstices at the tangent of the bacterial cell and the solid surface retard the diffusion of exoenzymes and hydrolyzates away from the cell. D, Multiple cells form additional interstitial spaces.

from CE Zobell J. Bact. 46: 39-56 (1943)





from F Azam Science 280: 694 (1998)

Timeline of significant methodological advances

1975 - bacterial direct counts
1980 - ^{3}H-thymidine bacterial production
1982 - low-level nitrate (chemiluminescence)
1982 - Fe ‘clean’ techniques
1982 - dilution method for microflagellate grazing
1983 - hydrolytic enzyme activity
1983 - phytoplankton pigments by HPLC
1988-1993 HTCO method for dissolved organic matter
1989 - RNA probes
1989 - dissolved DNA
1990 - FDM model
1990 - tangential flow filtration
1992 - bacterial direct counts by flow cytometry
1995 - individual proteins by electrophoresis
1996 - first complete genome sequence
2001 - capillary electrophoresis zymography
2002 - acylated homoserine lactones
2004 - metagenomics
2005 - proteomics
2009 - eukaryotic genomics

Timeline of introduction of some significant new ‘players’

1977 - free living bacteria

1979 - *Synechococcus*

1988 - *Prochlorococcus*

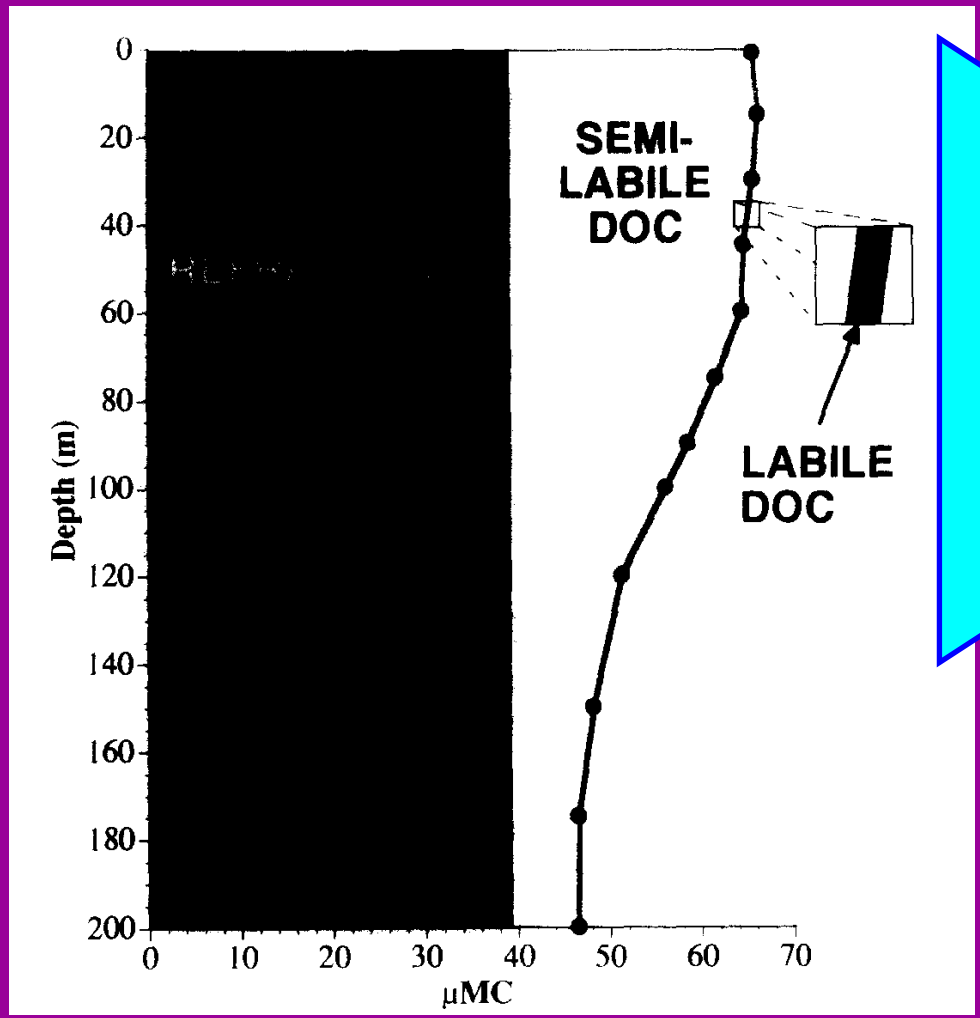
1990 - SAR 11

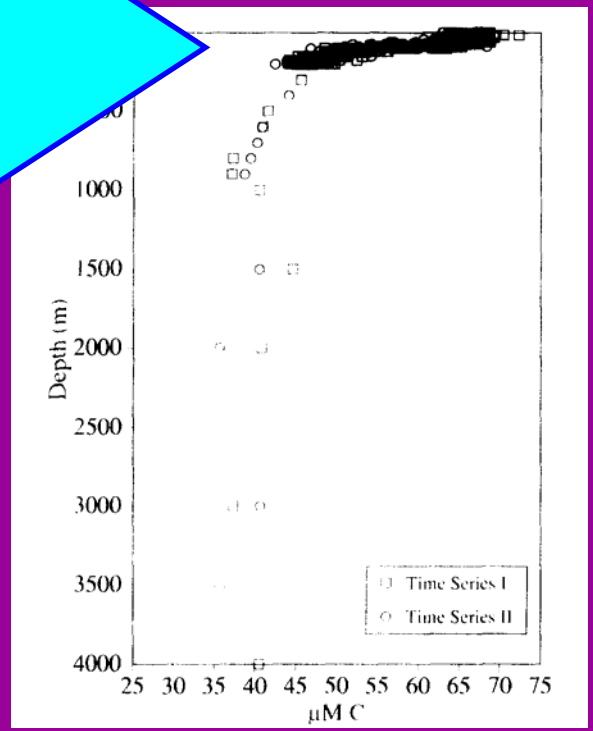
1989 - viruses

1992 - *Archaea*

1993 - IronEx !!!

2001 - proteorhodopsin





Division of DOM into 3 now ‘canonical’ fractions (Carlson and Ducklow 1995 DSR II 42: 639)

Inferences about net elemental budgets can often be made more reliably by looking at total pools than by extrapolating from microbiological rates

Table 2. Precision and accuracy estimates for direct chemical measurements of microbial loop elements at Station ALOHA

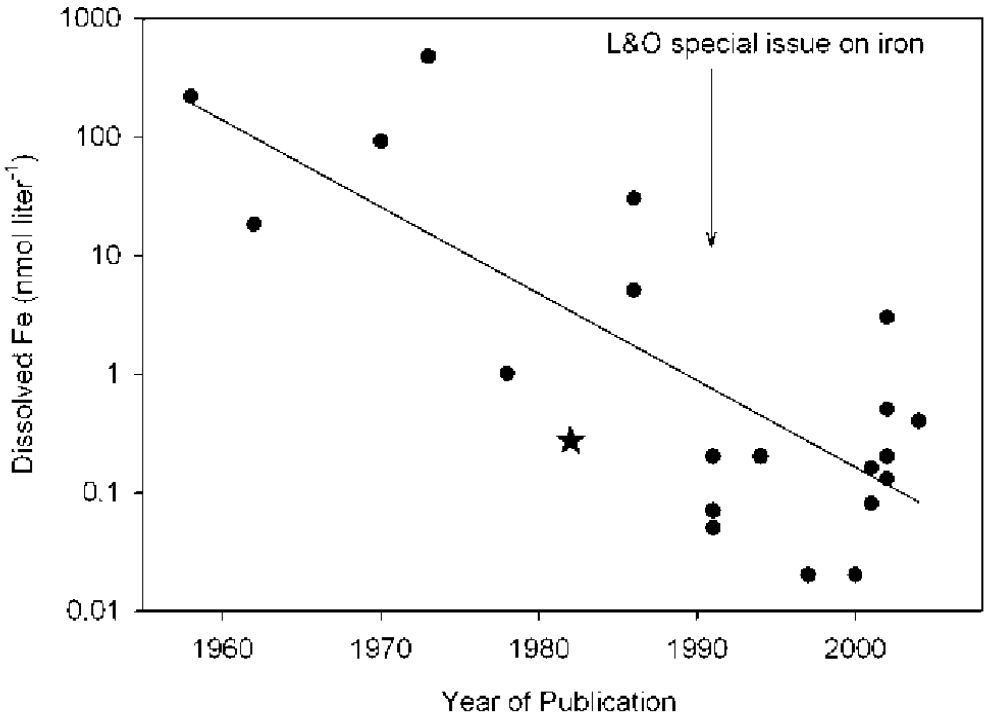
Parameter	Method	Ambient concentration (0–100 m)	Precision[a]	Certified standards available
ΣCO_2	coulometry (SOMMA)	~2,000 μmol kg^{-1}	0.05% (±1 μmol kg^{-1})	yes
DOC	high temp. catalytic oxidation	80–120 μmol kg^{-1}	1% (±1 μmol kg^{-1})	no
O_2	computer-assisted micro-Winkler	~225 μmol kg^{-1}	0.07% (±0.15 μmol kg^{-1})	yes
NO_3	chemiluminescence	1–10 nmol kg^{-1}	1% (<1 nmol kg^{-1})	yes
PO_4	MAGIC	5–50 nmol kg^{-1}	1–3% (<0.5 nmol kg^{-1})	yes

[a] Numbers in parentheses indicate typical concentrations that are able to be reliably measured using the currently available methods

Karl 1994 Microb Ecol 28: 147

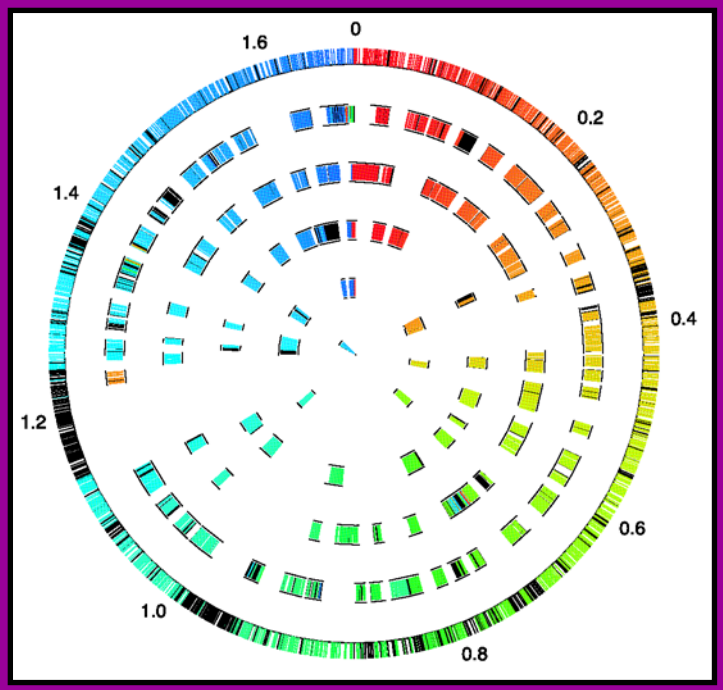
Dissolved iron concentration has declined over time due to analytical advances but has been stable for over a decade

Figure 2. Total dissolved Fe concentrations in marine waters reported by papers published in *L&O* since 1958. The star is Fitzwater et al. (1982), which has been cited 307 times.

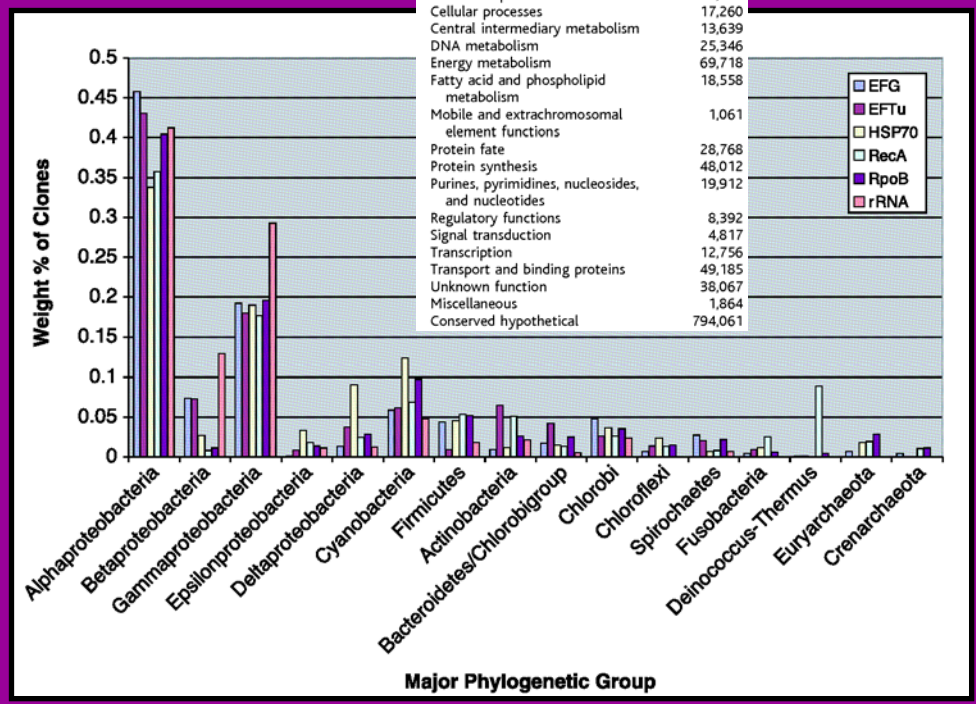


Kirchman, L+O Bulletin, June 2005

The genome ‘sequence’ of an entire microbial community can now be determined



“These data are estimated to derive from at least 1800 genomic species based on sequence relatedness, including 148 previously unknown bacterial phylotypes.”



“We have identified over 1.2 million previously unknown genes”

Venter et al 2004 Science 304: 66

Microbial nitrogen metabolism involves many biogeochemically important reactions catalyzed by enzymes for which gene sequences are known

TABLE 1. Nitrogen cycle gene probes

Transformation	Gene(s)[a]	Protein
N_2 fixation	*nifHDK*	Nitrogenase
Nitrite assimilation	*nir*	Nitrite reductase
Nitrate assimilation	*narB, nasA*	Assimilatory nitrate reductase
Ammonium assimilation	*glnA*	Glutamine synthetase
Nitrate respiration and denitrification	*nirS*	Nitrate reductase
	nirK	Nitrite reductase
	norB	Nitric oxide reductase
	nosZ	Nitrous oxide reductase
Organic N metabolism	*ure*	Urease
Ammonium oxidation/nitrification	*amo*	Ammonia monooxygenase
Nitrogen regulation (cyanobacteria)	*ntcA*	Nitrogen regulatory protein

[a] Nitrogen cycle genes for which probes or PCR primers have been designed.

Zehr and Ward 2002 AEM 68: 1015

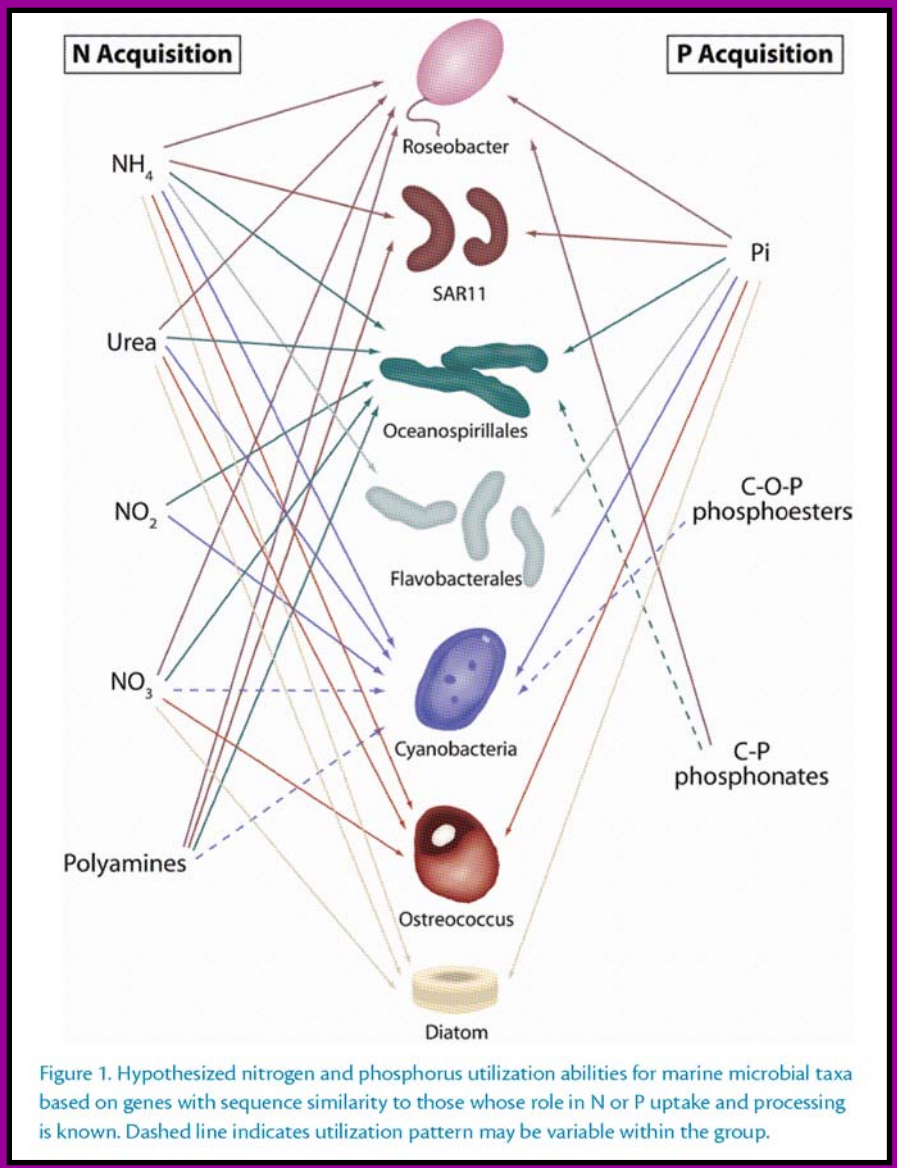


Figure 1. Hypothesized nitrogen and phosphorus utilization abilities for marine microbial taxa based on genes with sequence similarity to those whose role in N or P uptake and processing is known. Dashed line indicates utilization pattern may be variable within the group.

"Pure-culture genomics has indeed begun to fundamentally change our understanding of who is doing what in the ocean, and how they are doing it."

Known gene sequences for specific metabolisms can be used to identify specific groups of microbiota that possess that metabolic ability (Moran and Armbrust, Oceanography Magazine, June 2007)

Conclusions

- **methodology drives perception, perception establishes paradigms, paradigms guide further research**

- **new and innovative methods can spread rapidly, sometimes more rapidly than the context for their interpretation evolves**

- **progress has been made in large part through the dissemination of standard methods, and through the unification of chemistry and biology**