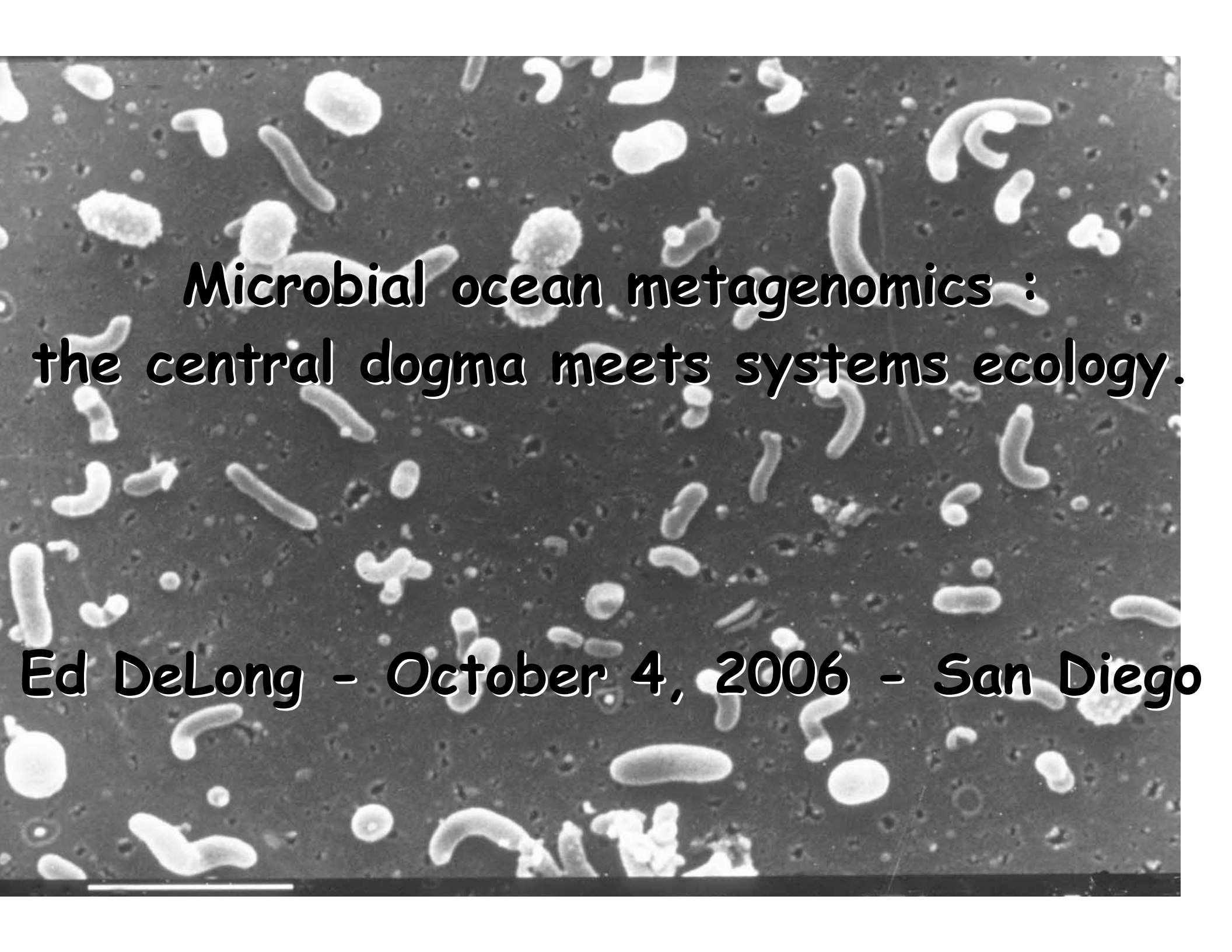


A black and white micrograph showing a dense population of marine microorganisms. The organisms vary in shape, including rod-shaped, comma-shaped, and spherical forms. Some appear to have flagella. The background is dark, and the organisms are brightly lit, creating a high-contrast image. The text is overlaid on the center of the image.

**Microbial ocean metagenomics :
the central dogma meets systems ecology.**

Ed DeLong - October 4, 2006 - San Diego

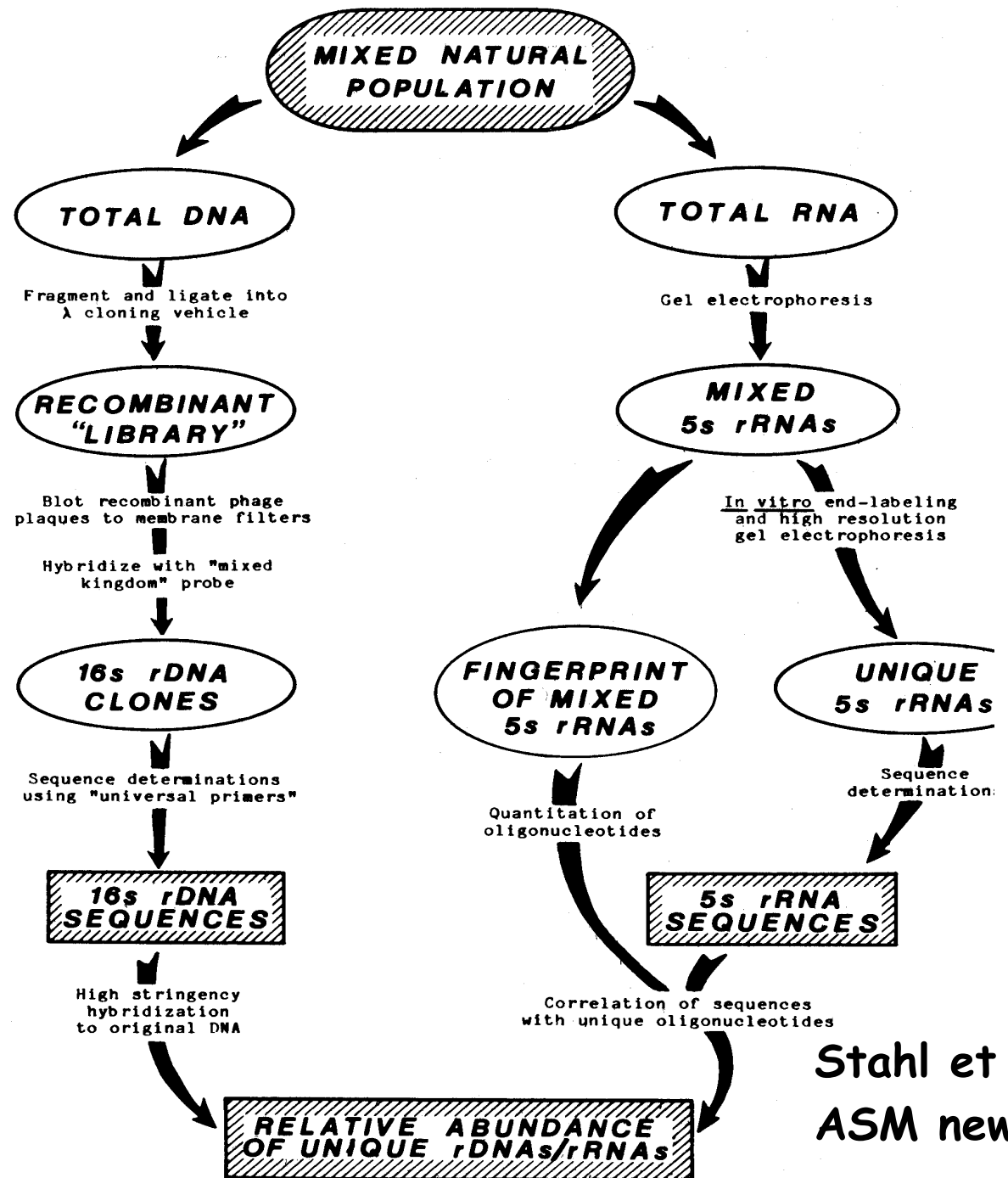
CULTIVATION INDEPENDENT SURVEYS

A la Pace et al., 1986

(Stahl, Olsen, Lane, et al.)

1986 ISME-4 in Ljubljana

Perspectives in Microbial Ecology

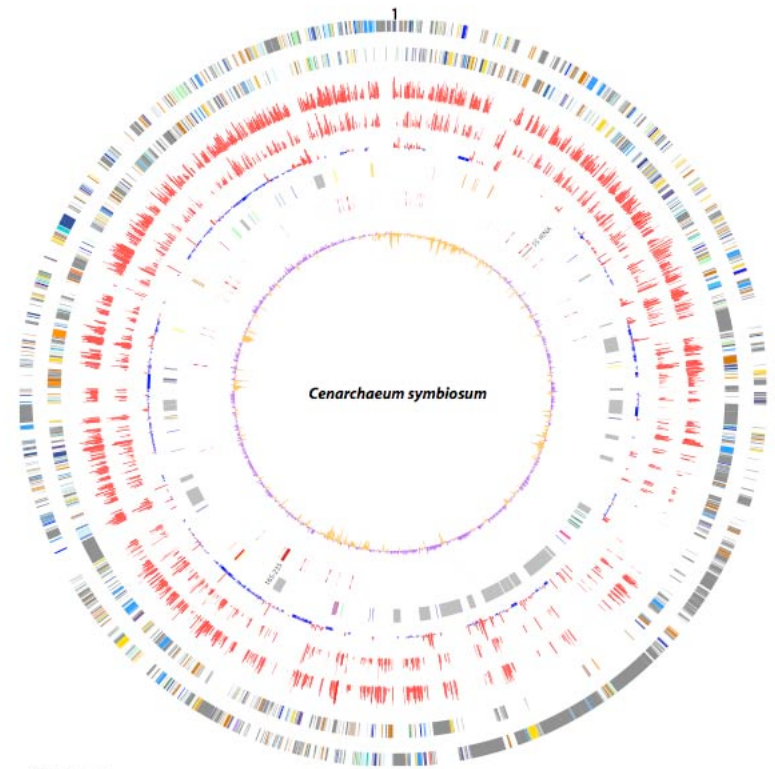
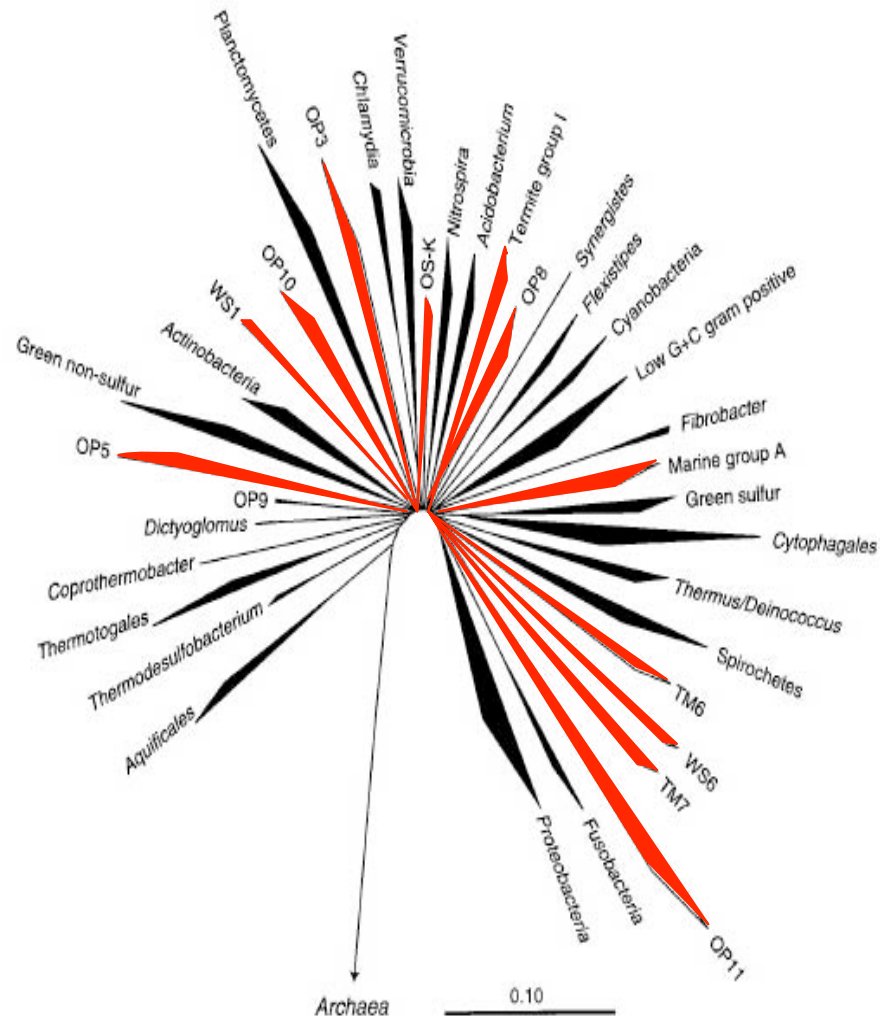


Stahl et al.
ASM news

UNCHARACTERIZED NATIVE TAXA

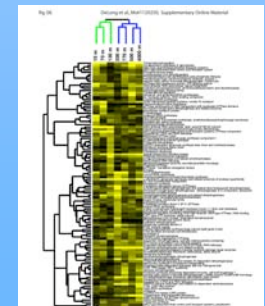
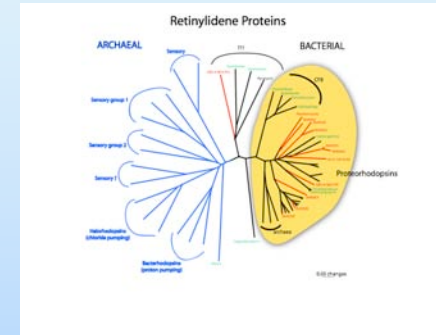


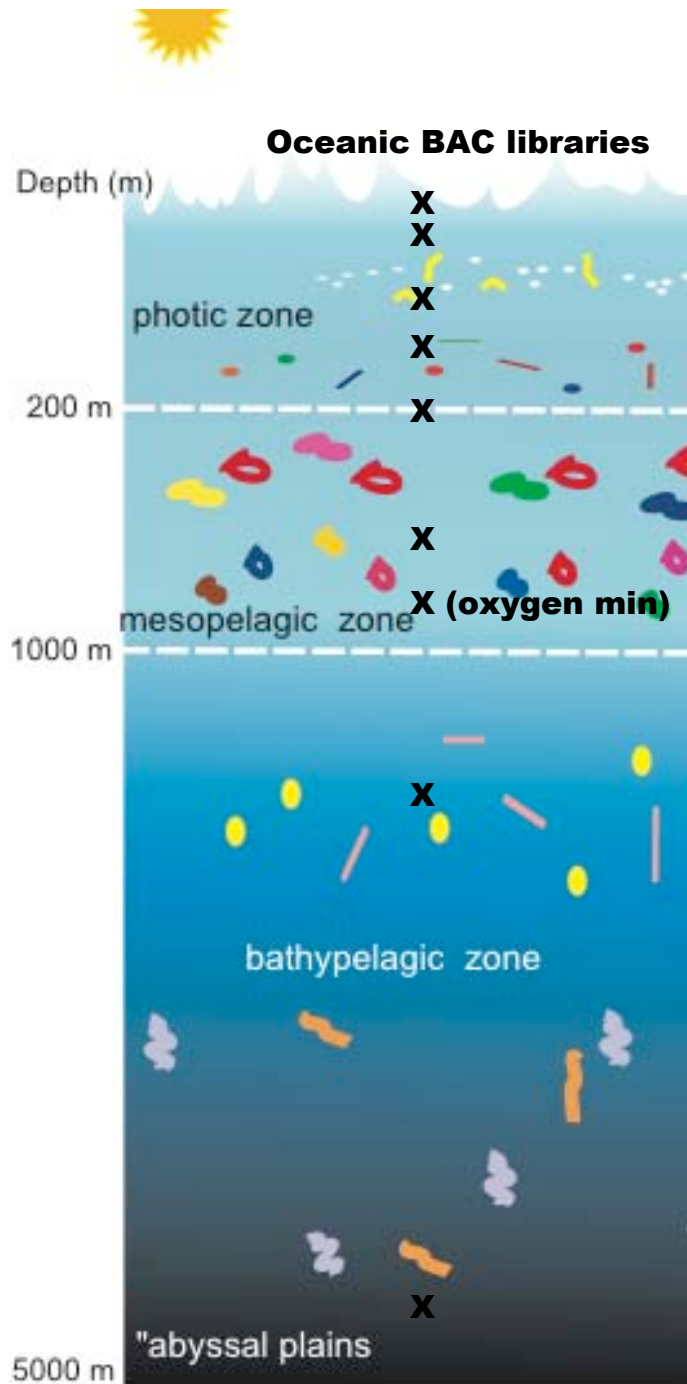
GENOMIC ANALYSES



Microbial Community Genomics & Ecology

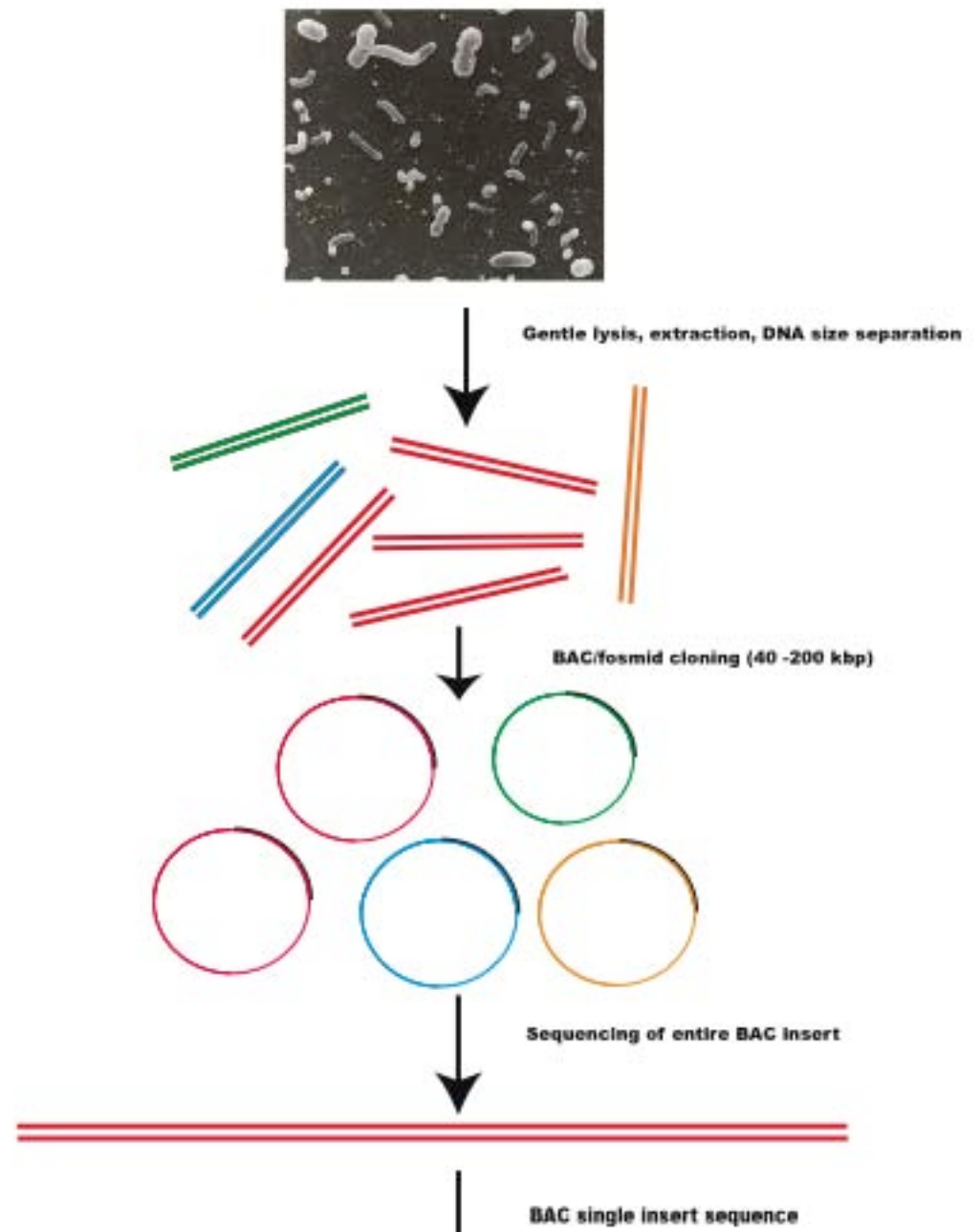
- Philosophical underpinnings
- Proteorhodopsin ecology
- Archaeal metagenomics
- Comparative community genomics



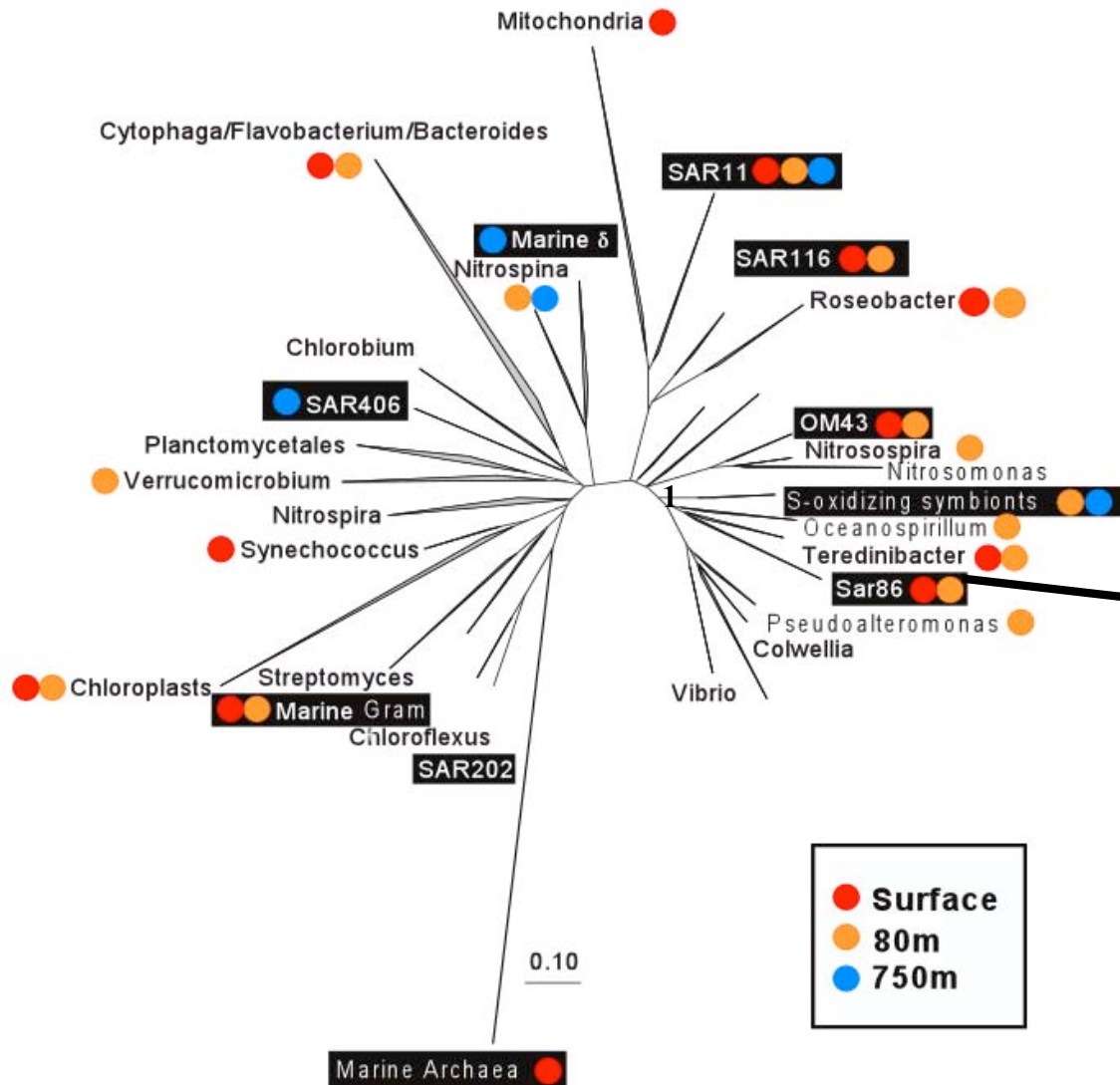


B

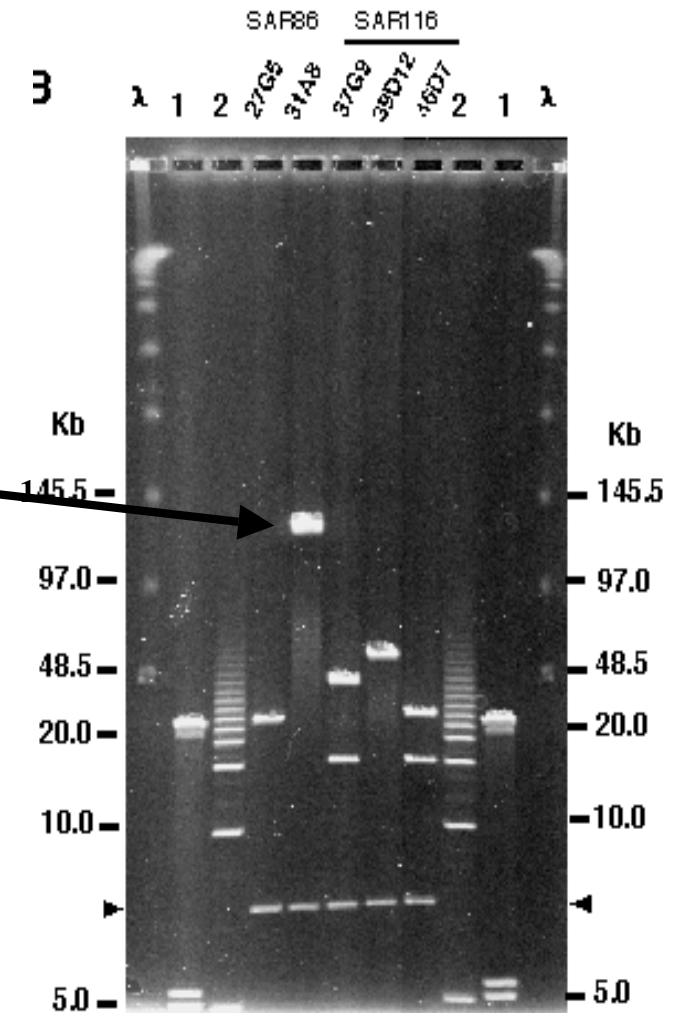
Large Insert Cloning & Sequencing

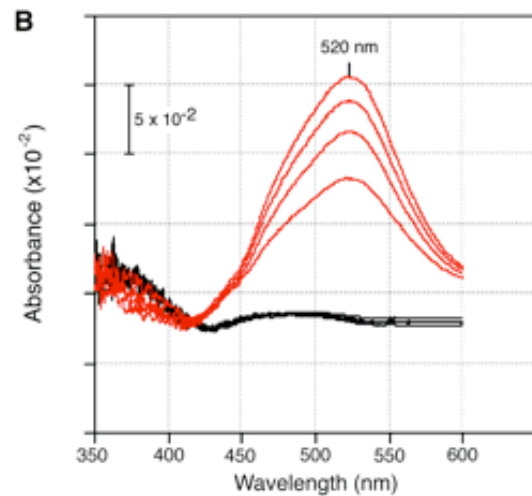
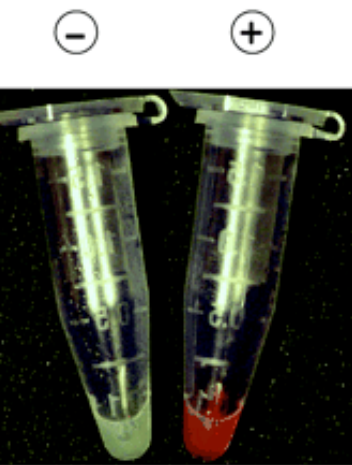


Monterey Bay BACs



SAR86 130 kbp BAC



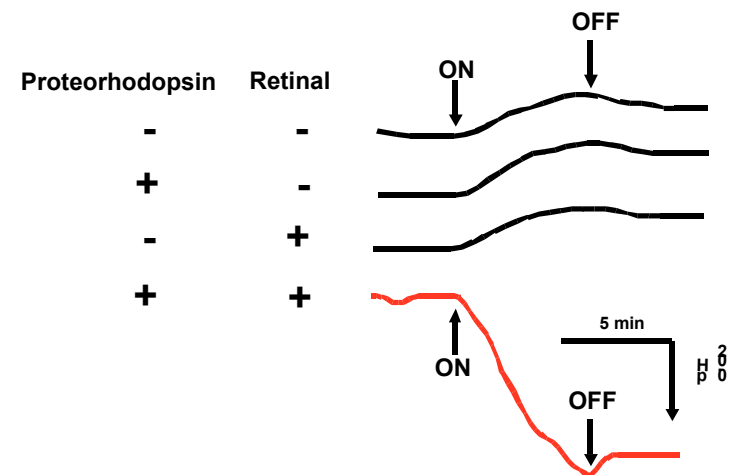


Expression of proteorhodopsin in *E. coli*

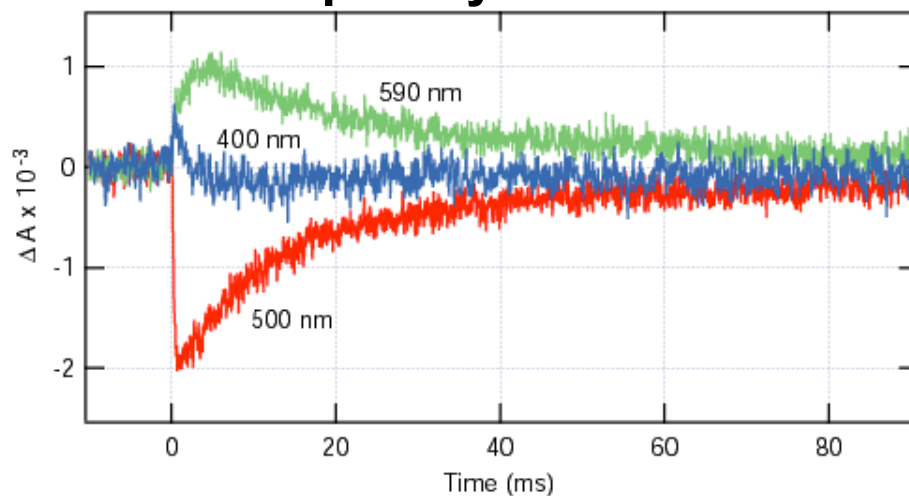
Béjà et al. Science 289: 1902-1906 (2000)

LIGHT-DRIVEN PROTON PUMPING IN *E. COLI* (via “SAR86” PROTEORHODOPSIN)

Oded Beja



Fast photocycle kinetics



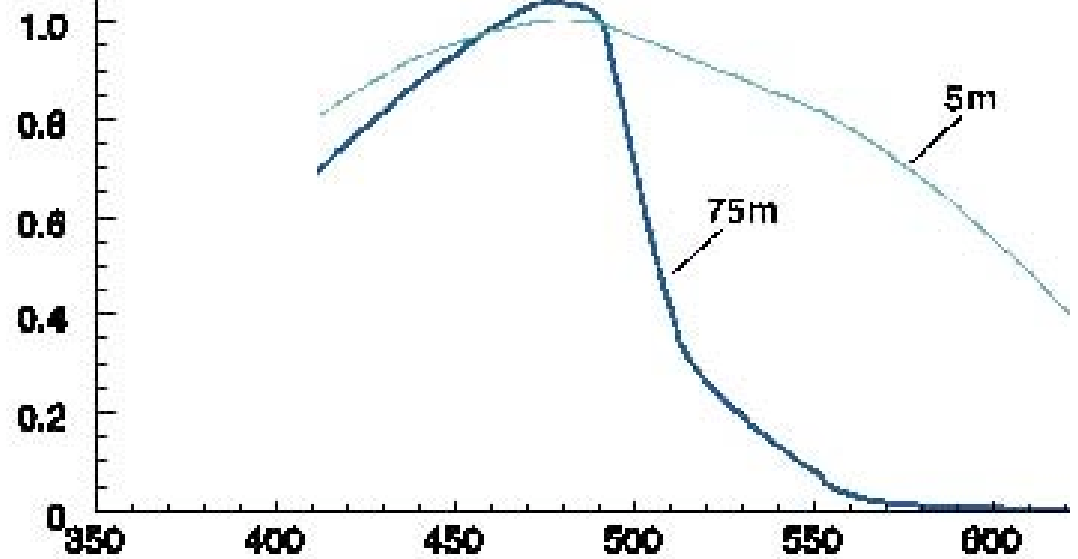
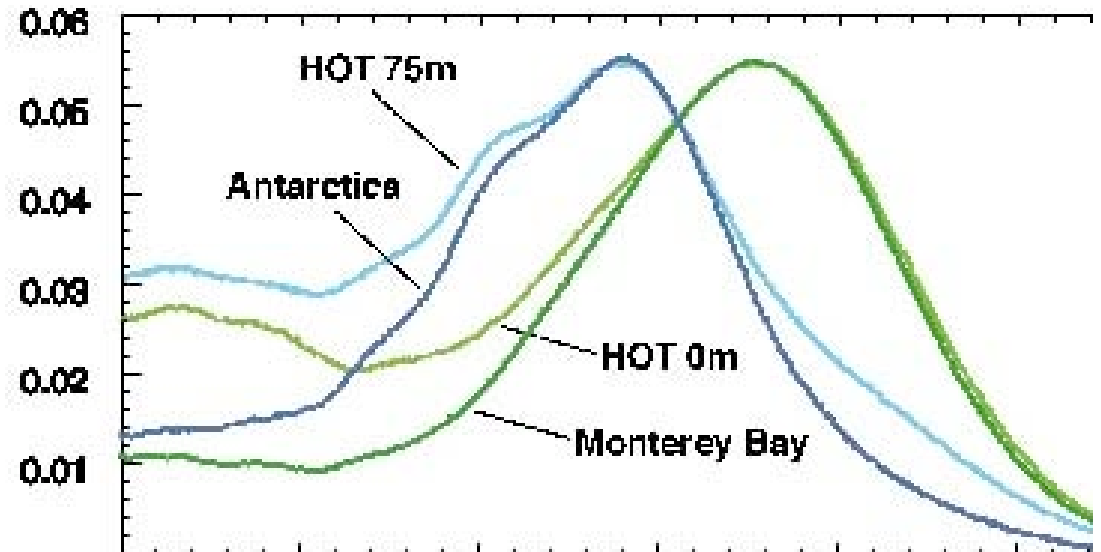
Depth-specific differences in proteorhodopsin variants

MB 0m 2
MB 40m 5
BAC 40E8
HOT 0m1
MB 20m 2
MB 40m 12
MB 100m 10
MB 20m 12
BAC 31A8
MB 40m 1
MB 100m 5
MB 20m 5
BAC 64A5
MB 100m 7
MB 0m 1
MB 100m 9

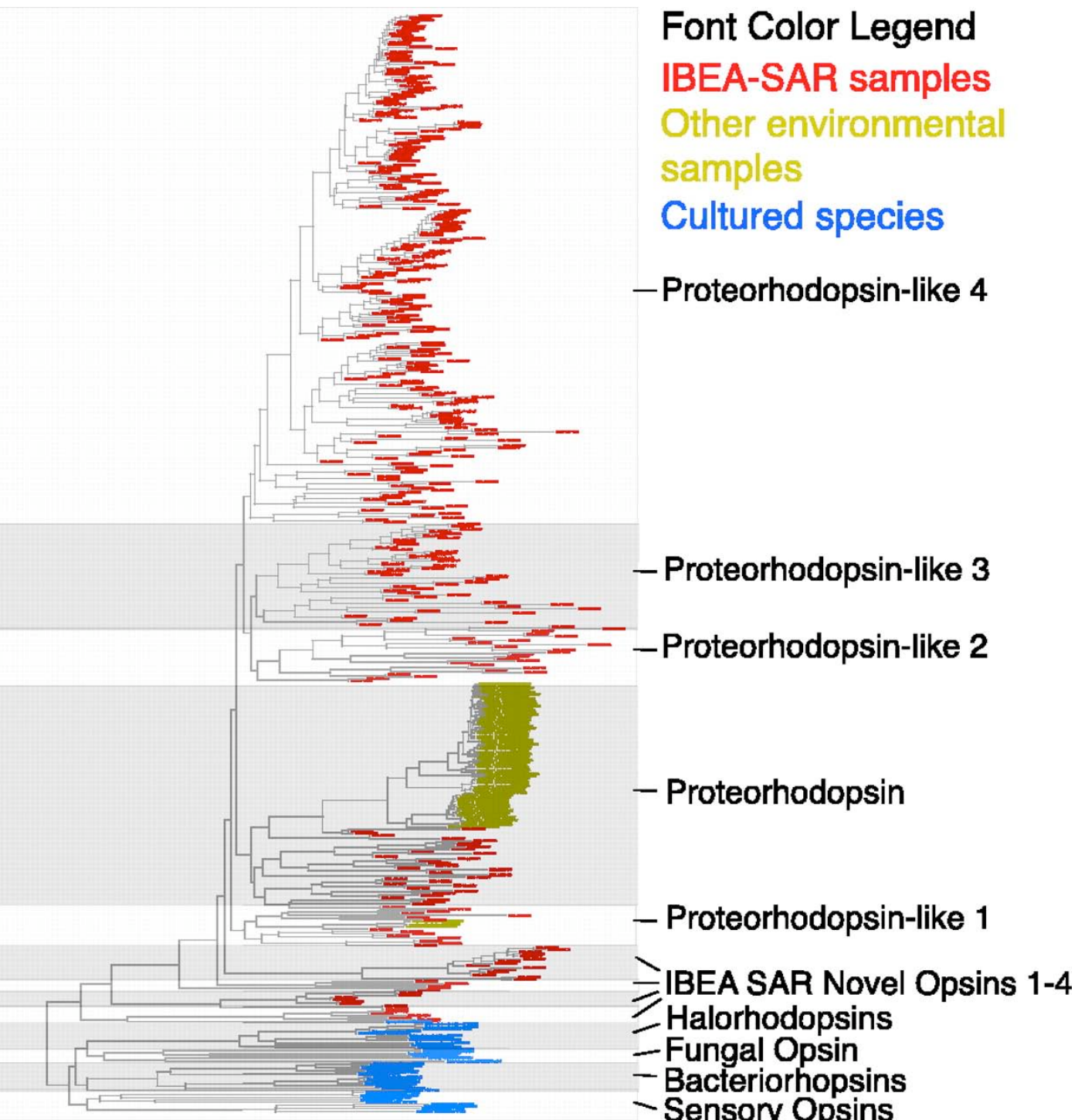
Monterey Bay &
shallow HOT

PAL E6
HOT 75m 3
PAL B1
PAL E7
PAL B2
PAL B8
HOT 75m 1
PAL B7
PAL E1
HOT 75m4
PAL B5
PAL B6
HOT 75m 8

Antarctica &
deep HOT



Béjà et al. Nature 411:786-789 (2001)

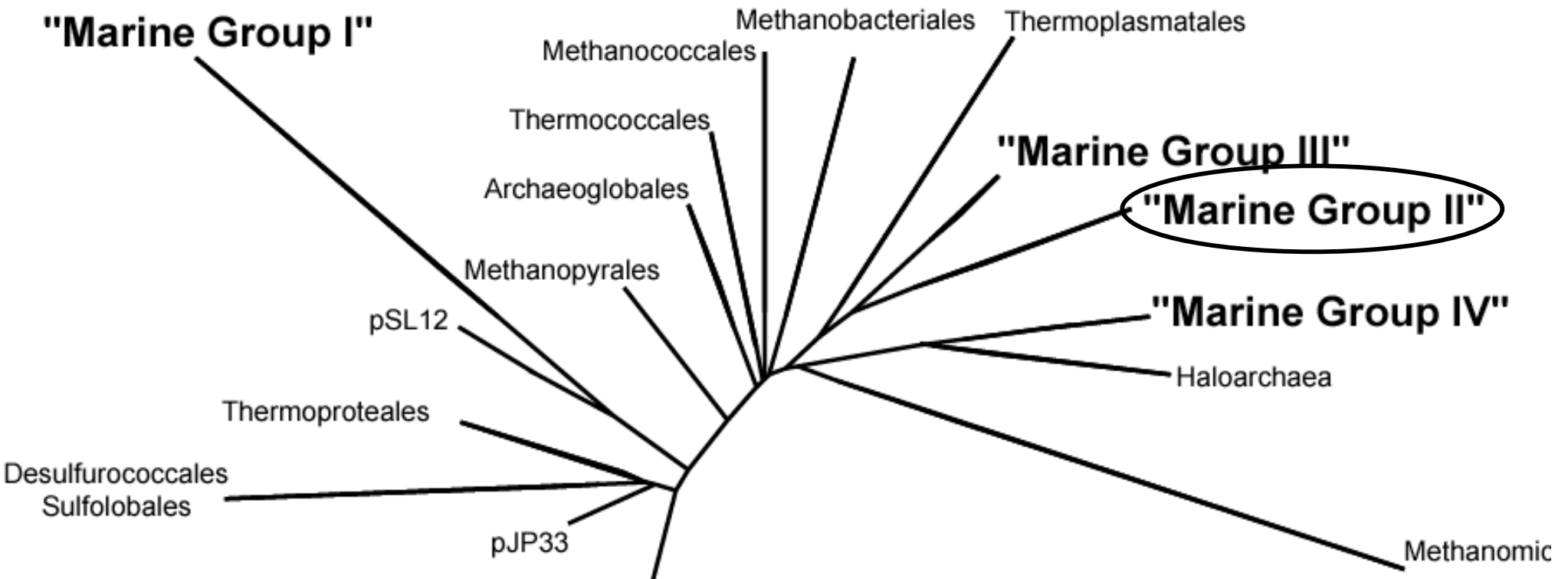


Venter et al., Environmental Genome Shotgun Sequencing of the Sargasso Sea, Science 394:66-74 (2004)

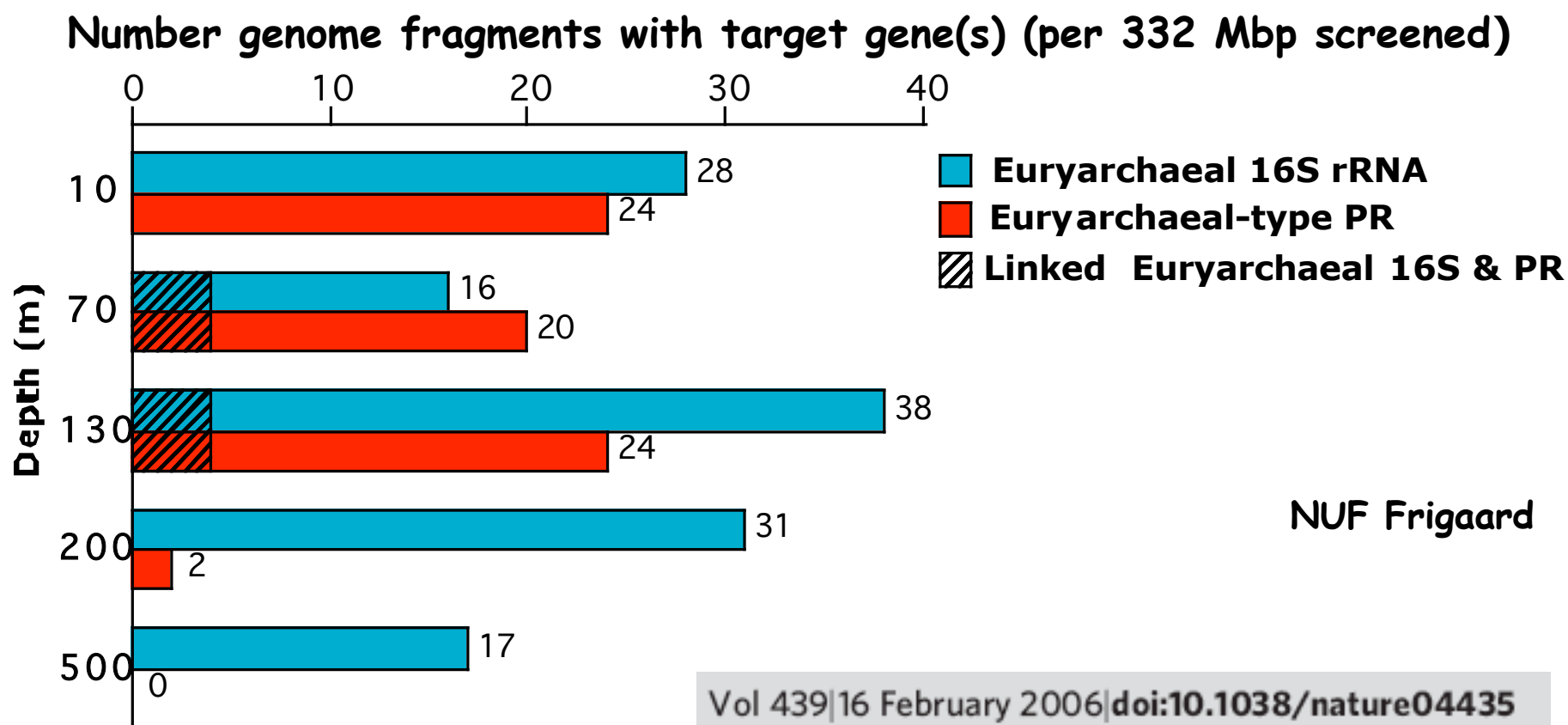
PLANKTONIC ARCHAEA

CRENARCHAEOTA

EURYARCHAEOTA



Archaeal PR gene distributions track the light gradient



Vol 439|16 February 2006|doi:10.1038/nature04435

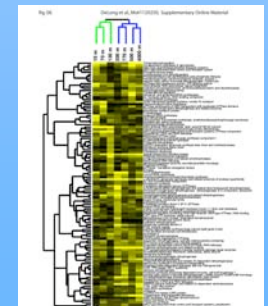
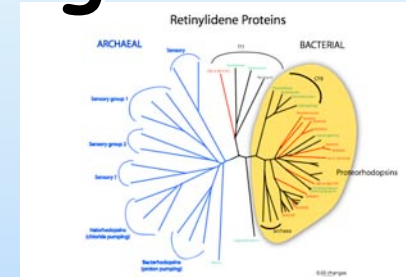
nature

Proteorhodopsin lateral gene transfer between marine planktonic Bacteria and Archaea

Niels-Ulrik Frigaard^{1†}, Asuncion Martinez¹, Tracy J. Mincer¹ & Edward F. DeLong¹

Microbial Community Genomics & Ecology

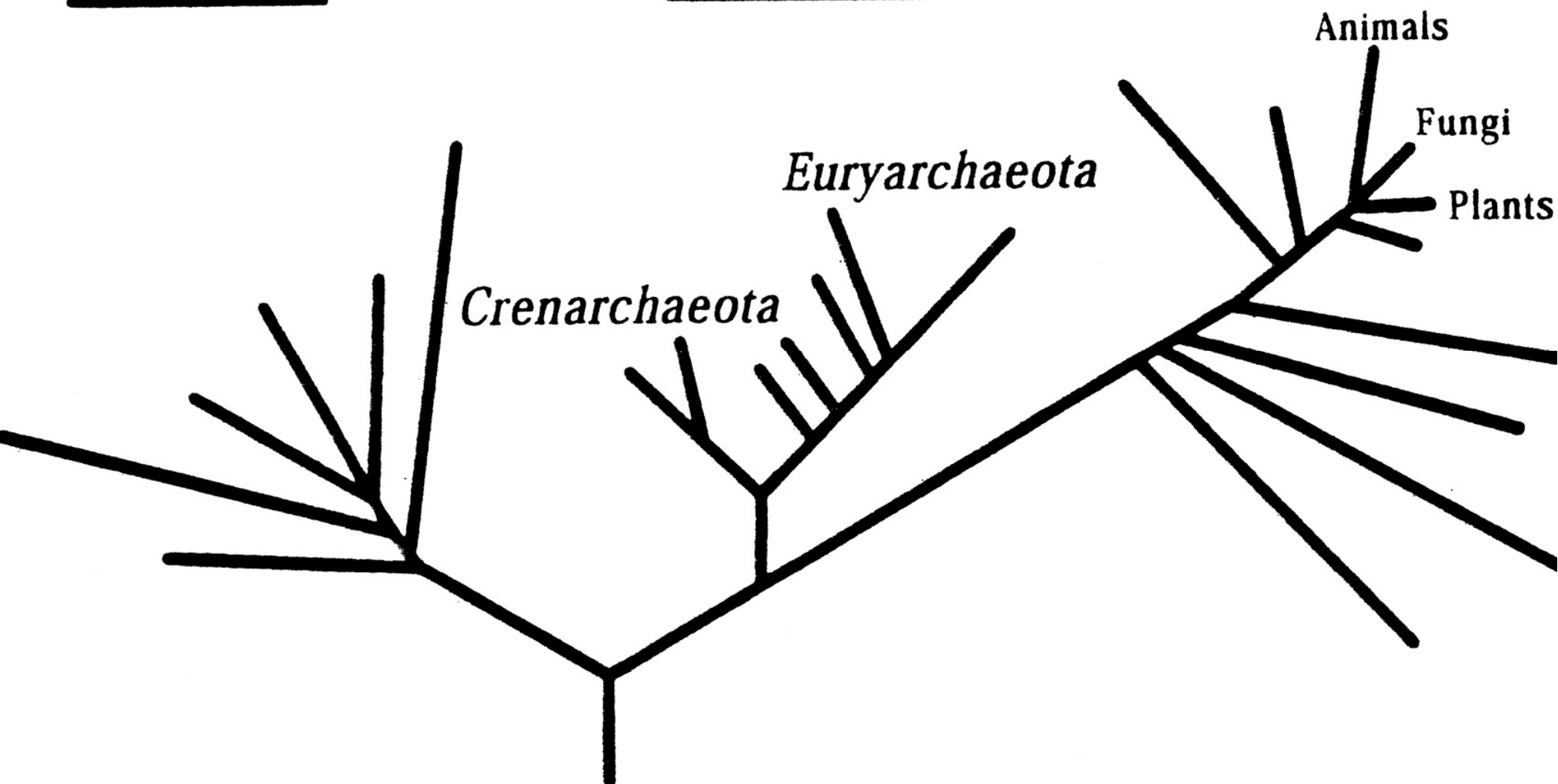
- Background/Philosophical underpinnings
- Proteorhodopsin ecology
- Crenarchaeal metagenomics
- Comparative community genomics



Bacteria

Archaea

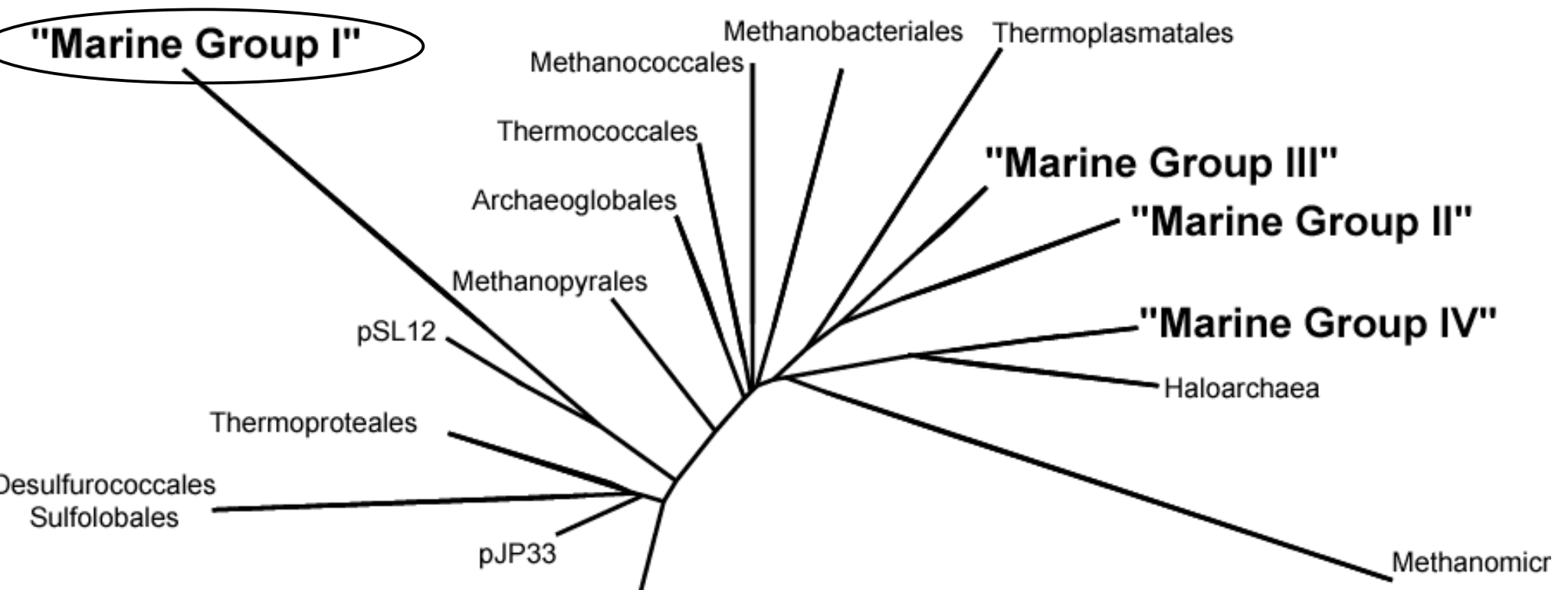
Eucarya

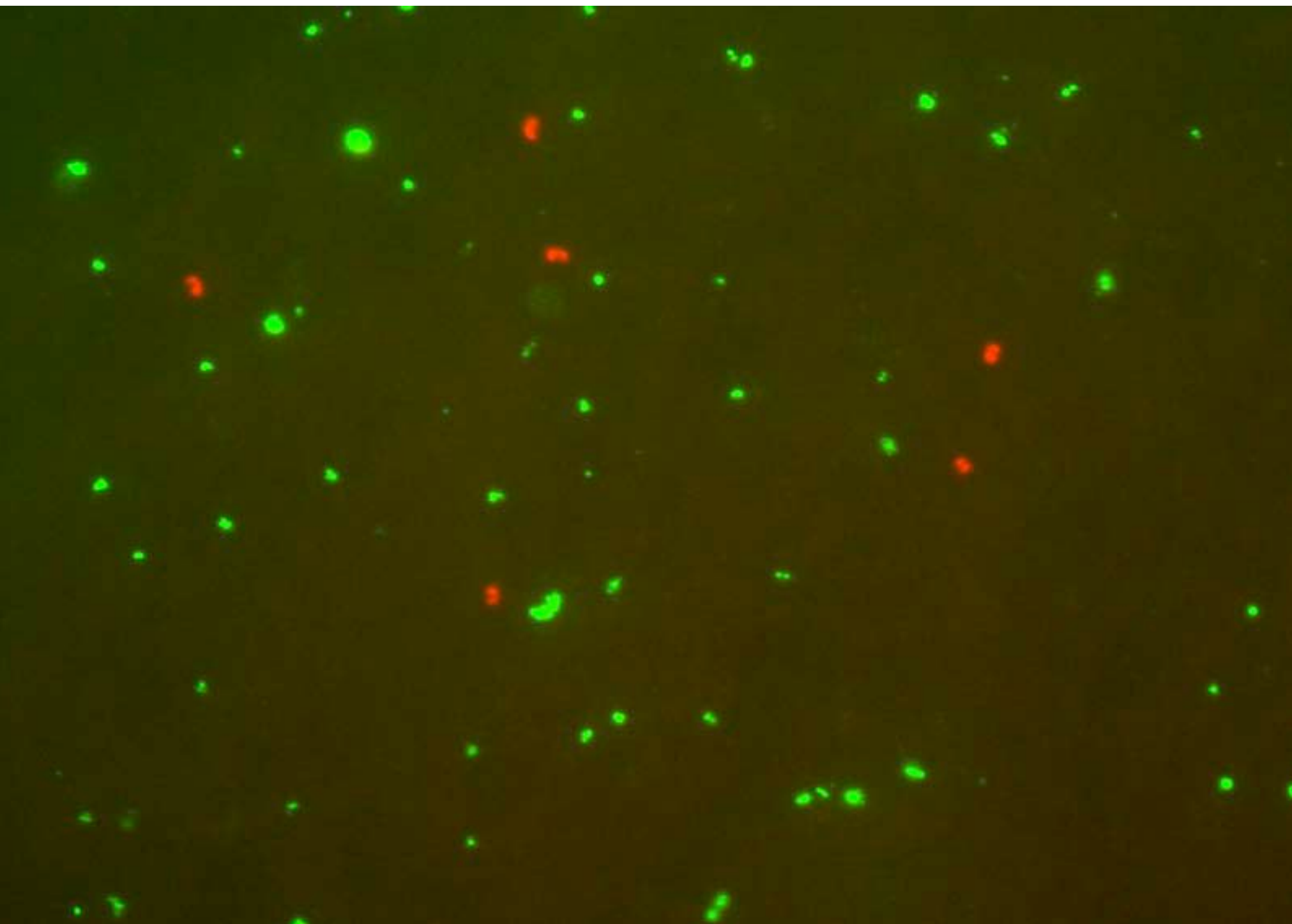


PLANKTONIC MARINE ARCHAEA

CRENARCHAEOTA

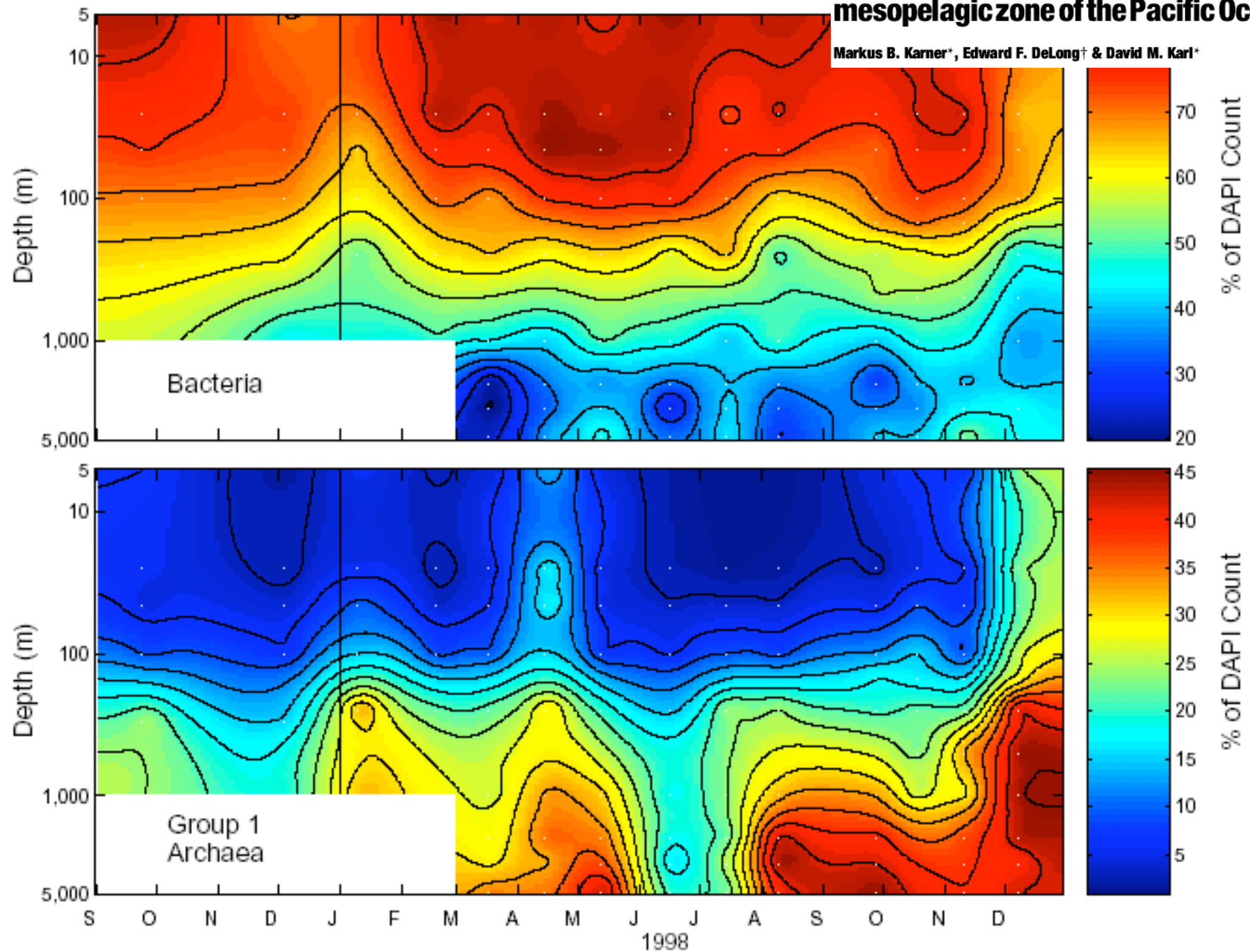
EURYARCHAEOTA





Archaeal dominance in the mesopelagic zone of the Pacific Ocean

Markus B. Kärner^{*}, Edward F. DeLong[†] & David M. Karl^{*}



Crenarchaea fix CO_2 - what is the reductant ?

Reports of crenarchaeal-associated amoA-like gene fragments

Venter et al, Science 304: 66 (2004)

Schleper, Nat Rev Micro 3: 479 (2005)

Konneke et al., Nature 437: 543 (2005)

Truesch, Schleper et al., EM 7:1985 (2005)

Francis et al., PNAS 102:14683 (2005)

Hallam et al., PLoS 4: e95 (2006)

Wuchter et al., PNAS 103:12317 (2006)

Leininger, Schleper, et al. Nature 442: 806 (2006)

ARCHAEAL NITRIFICATION ????

Isolation of an autotrophic ammonia-oxidizing marine archaeon

Martin Könneke^{1*†}, Anne E. Bernhard^{1*†}, José R. de la Torre^{1*}, Christopher B. Walker¹, John B. Waterbury¹ & David A. Stahl¹

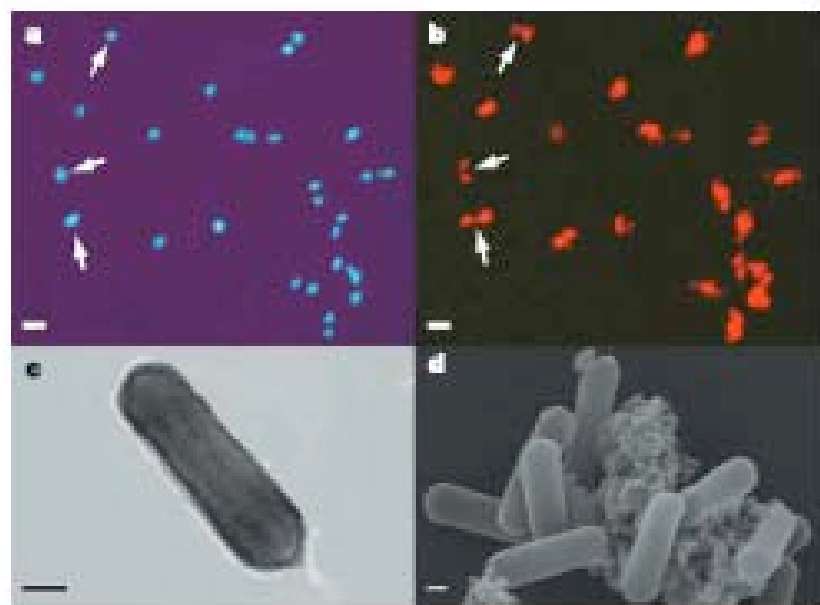


Figure 2 | Photomicrographs of SCM1. a, b, Fluorescence image of cells in identical fields of view stained with DAPI (a) and after hybridization with nucleotide polyp probes targeting SCM1 cells (b). Arrows indicate cells showing the characteristic peanut-like shape of marine *Crenarchaeota*^{14,15}. Scale bars represent 1 μm . c, Transmission electron micrograph of negative-stained cells. Scale bar represents 0.1 μm . d, Scanning electron micrograph of Au/Pd-sputtered cells. Scale bar represents 0.1 μm .

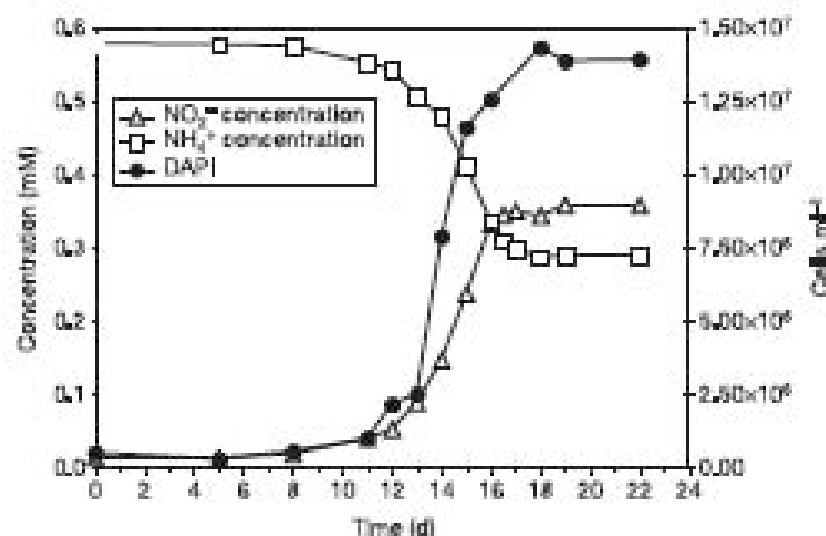
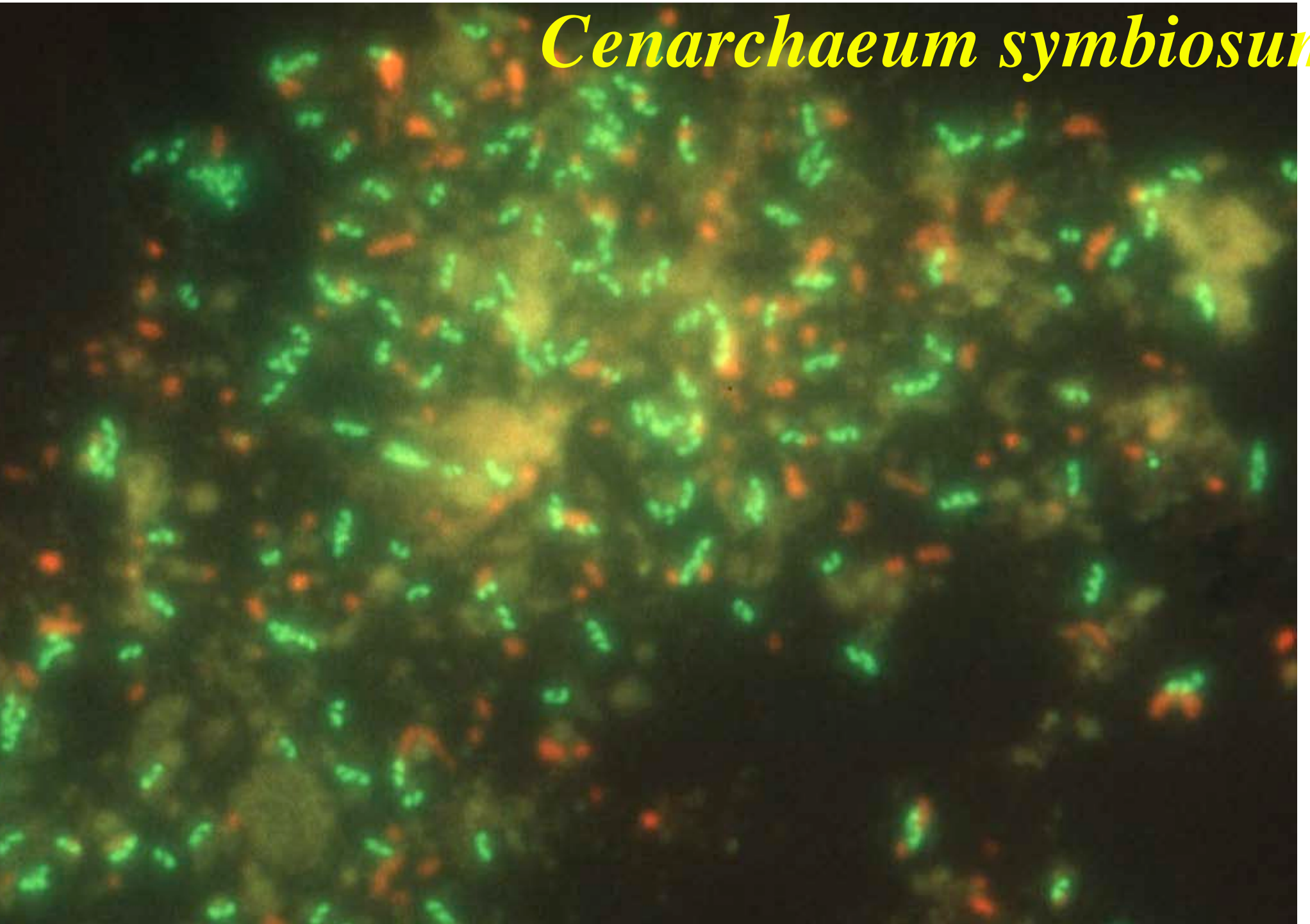
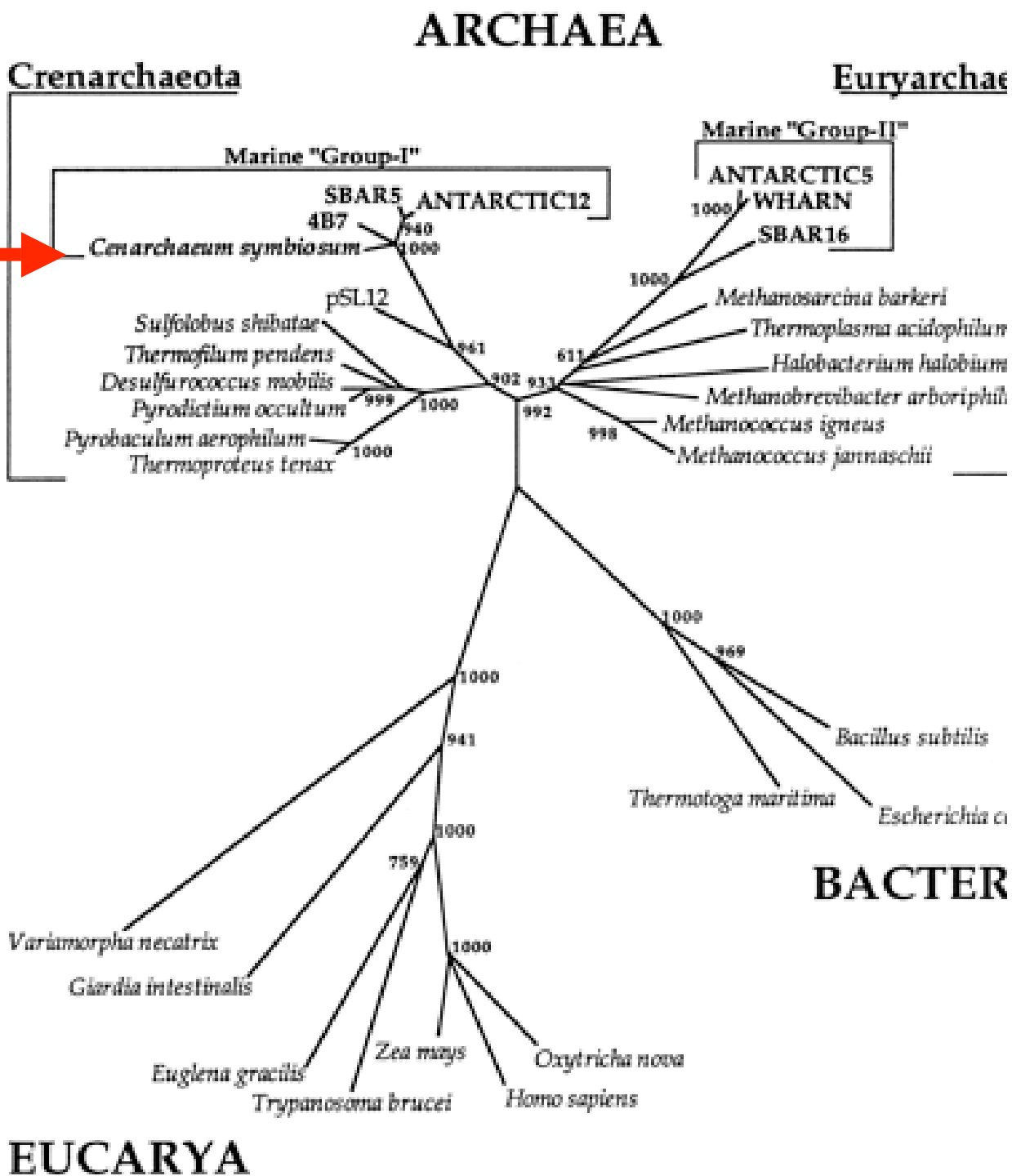
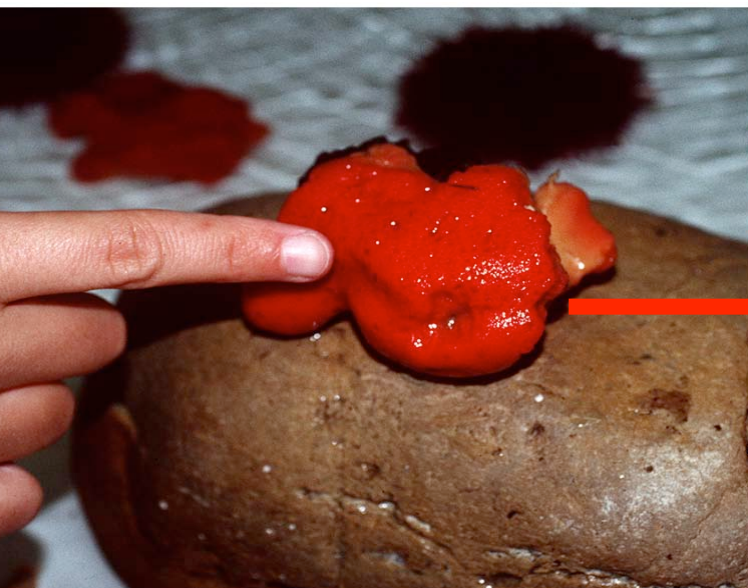


Figure 3 | Near-stoichiometric conversion of ammonia to nitrite by SCM1. Growth of SCM1 in Synthetic Crenarchaeota Media containing ammonium chloride and bicarbonate as sole energy and carbon sources, respectively. DAPI-stained cells were directly counted on filters by fluorescence microscopy. Ammonium consumption and nitrite production were determined in triplicate as described previously²⁷.

as '*N. maritimus*' to inhabit oligotrophic environments where they may function as important primary producers. In environments devoid of organic energy sources and sunlight, the oxidation of

Cenarchaeum symbiosum

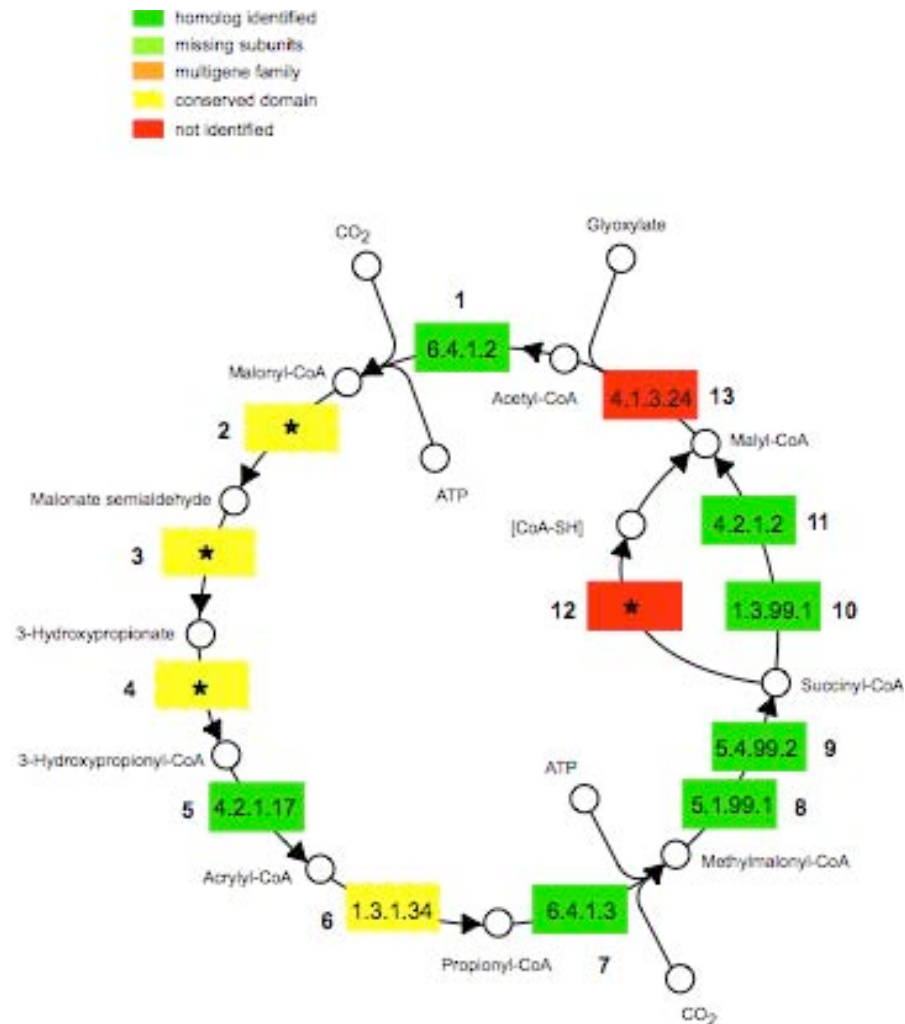




Marine archaeal autotrophy

Hallam et al., PLoS Biol. 4: e95. 2006

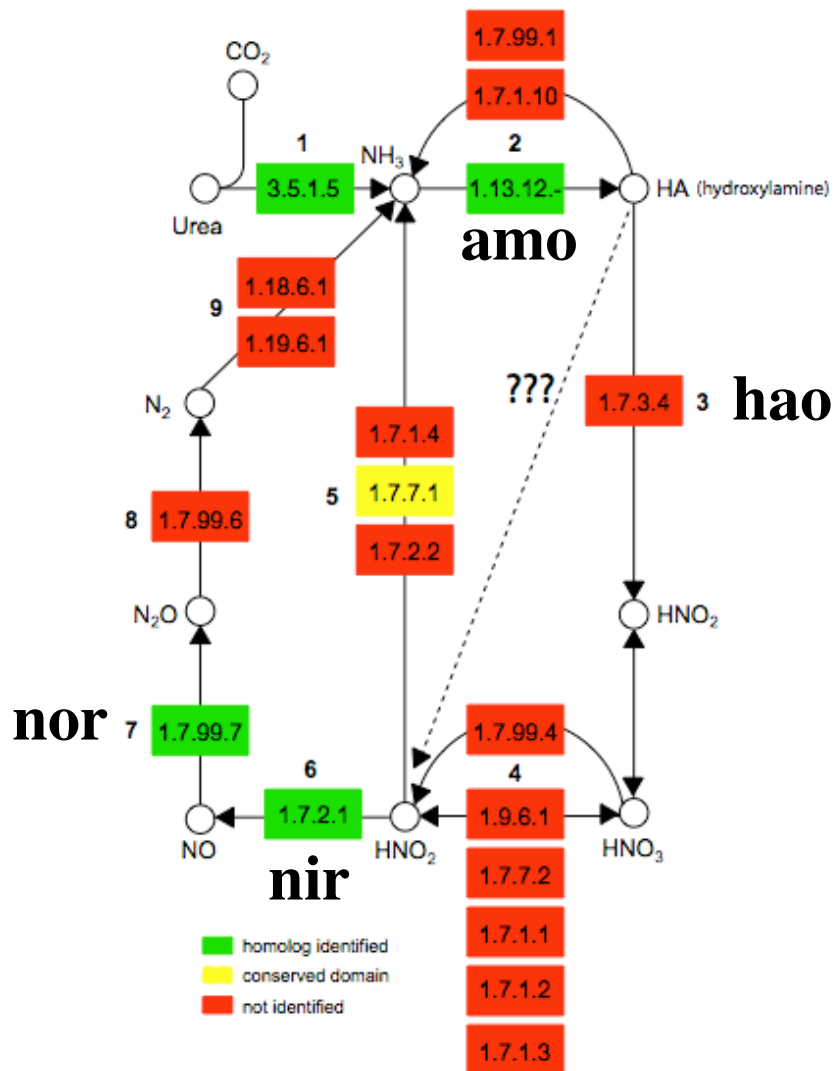
Hydroxypropionate cycle components in *C. symbiosum*



marine archaeal NH_4 oxidation

Ammonia oxidation

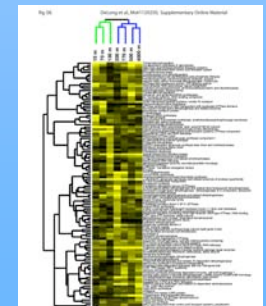
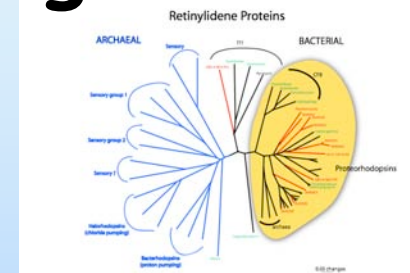
Hallam et al., PLoS Biol. 4: e95. 2006



Gene name	Locus	cenFOS
urea transporter	<i>dur3</i>	+
urease		
α <i>ureC</i>		+
β <i>ureB</i>		+
γ <i>ureA</i>		+
E <i>ureE</i>		+
F <i>ureF</i>		+
G <i>ureG</i>		+
H <i>ureH</i>		+
ammonia monooxygenase		
A <i>amoA</i>		+
B <i>amoB</i>		+
C <i>amoC</i>		+
hydroxylamine oxidoreductase	<i>hao</i>	-
nitrate reductase	<i>nar</i>	-
nitrite reductase	<i>nirK</i>	+
ferredoxin-nitrite reductase	<i>nirA</i>	+

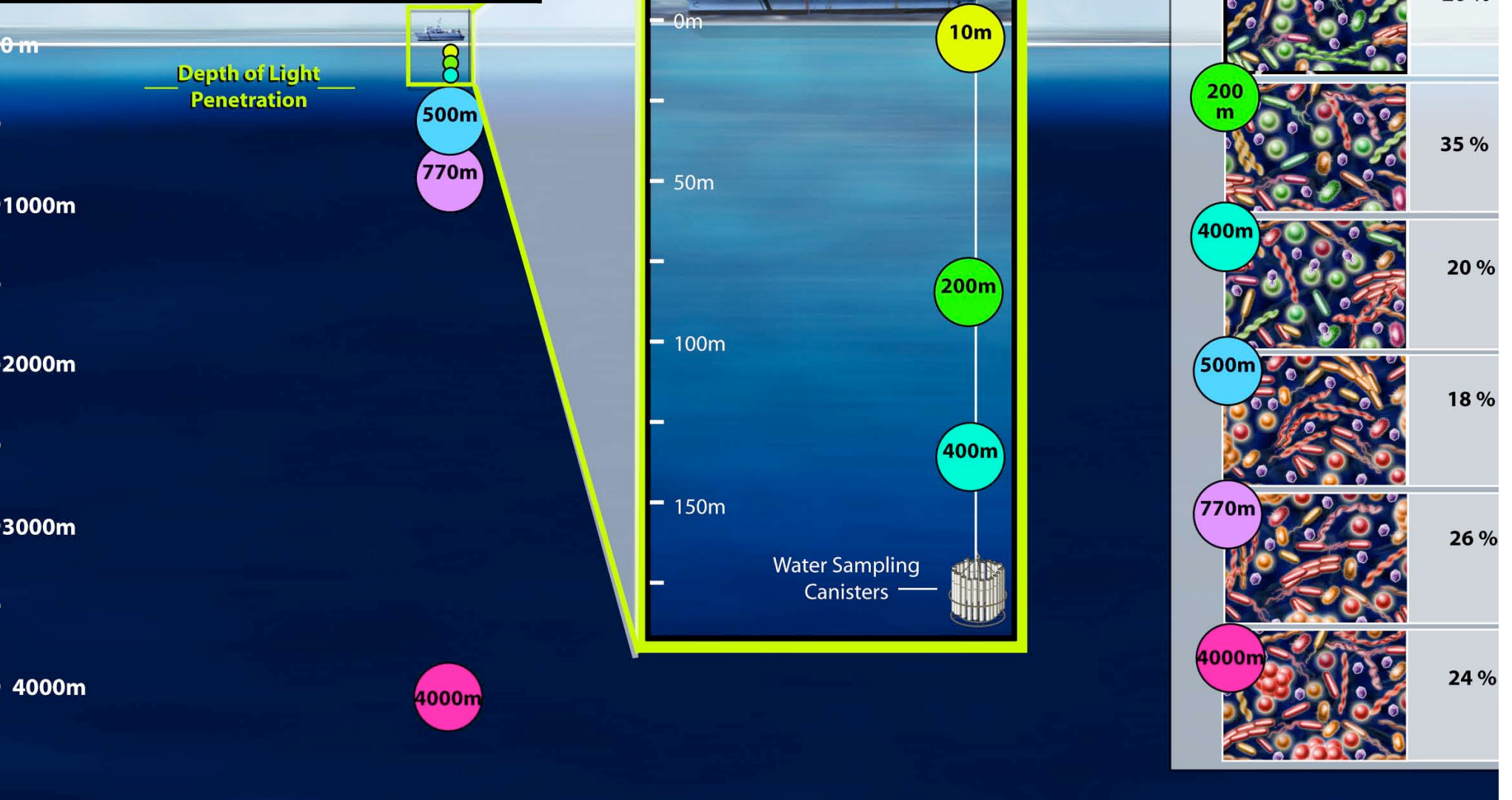
Microbial Community Genomics & Ecology

- Background/Philosophical underpinnings
- Proteorhodopsin ecology/physiology
- Crenarchaeal metagenomics
- Comparative community genomics



GENOMIC PROFILES IN THE PACIFIC OCEAN

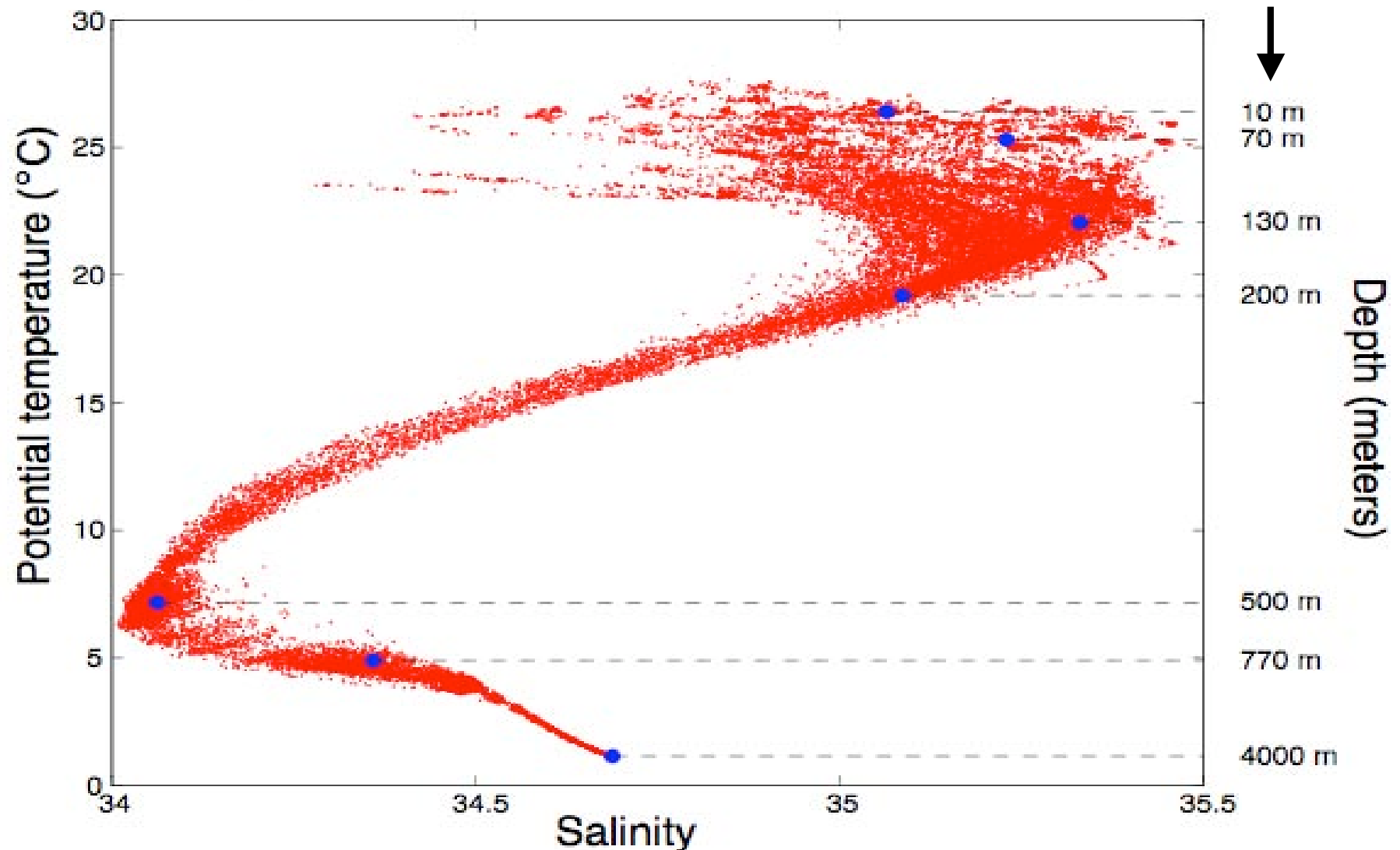
NSF Press Release 06-016
Sequencing Our Seas
http://www.nsf.gov/news/news_summ.jsp?cntn_id=105769

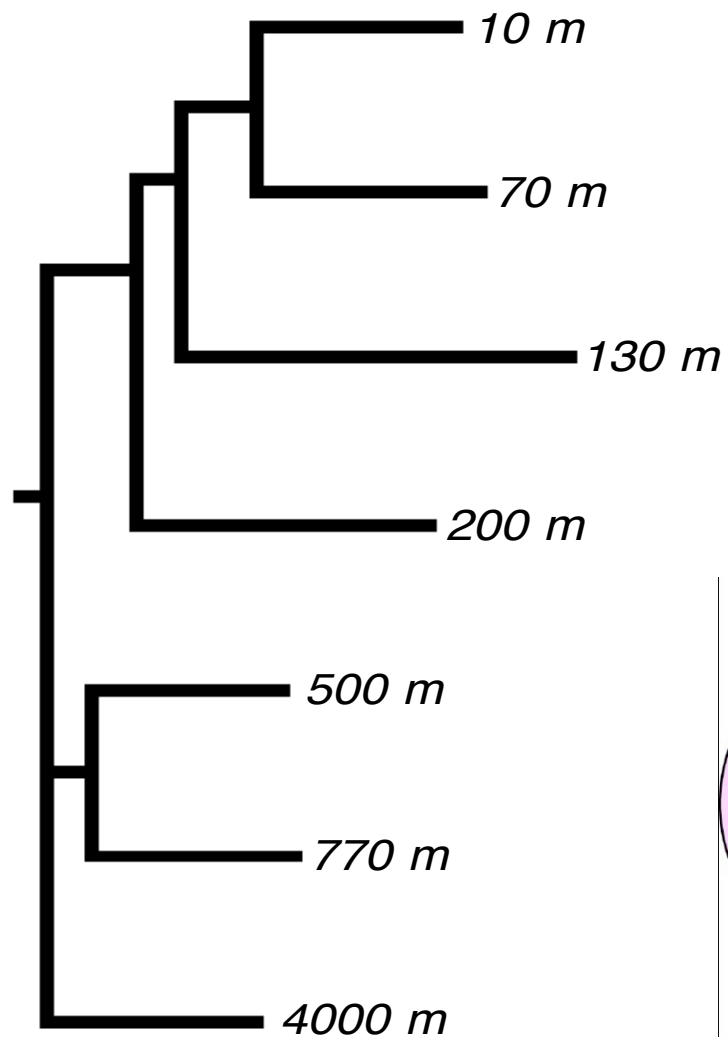


Community Genomics Among Stratified Microbial Assemblages in the Ocean's Interior

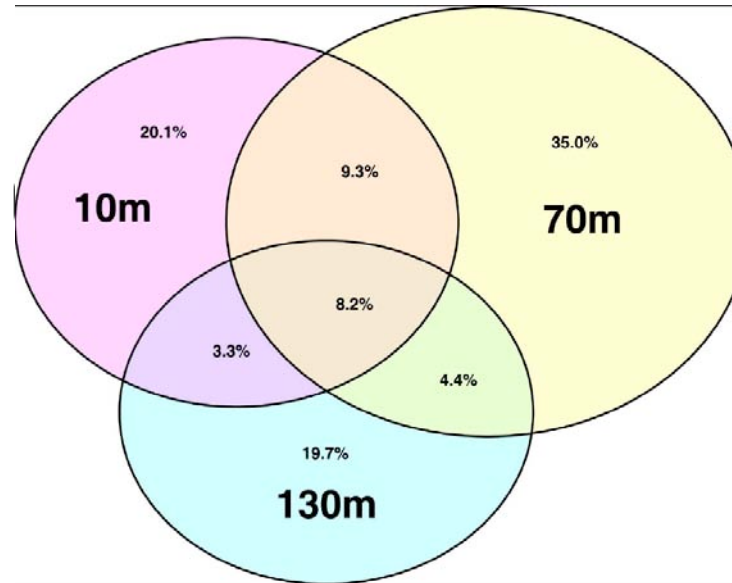
SCIENCE VOL 311 27 JANUARY 2006

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



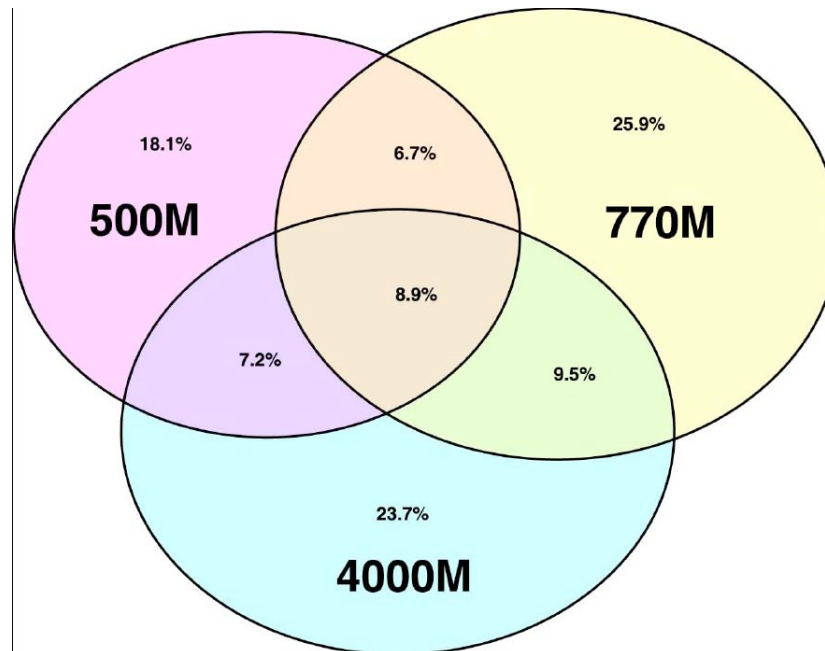


PHOTIC ZONE UNIQUE SEQUENCES



PZ

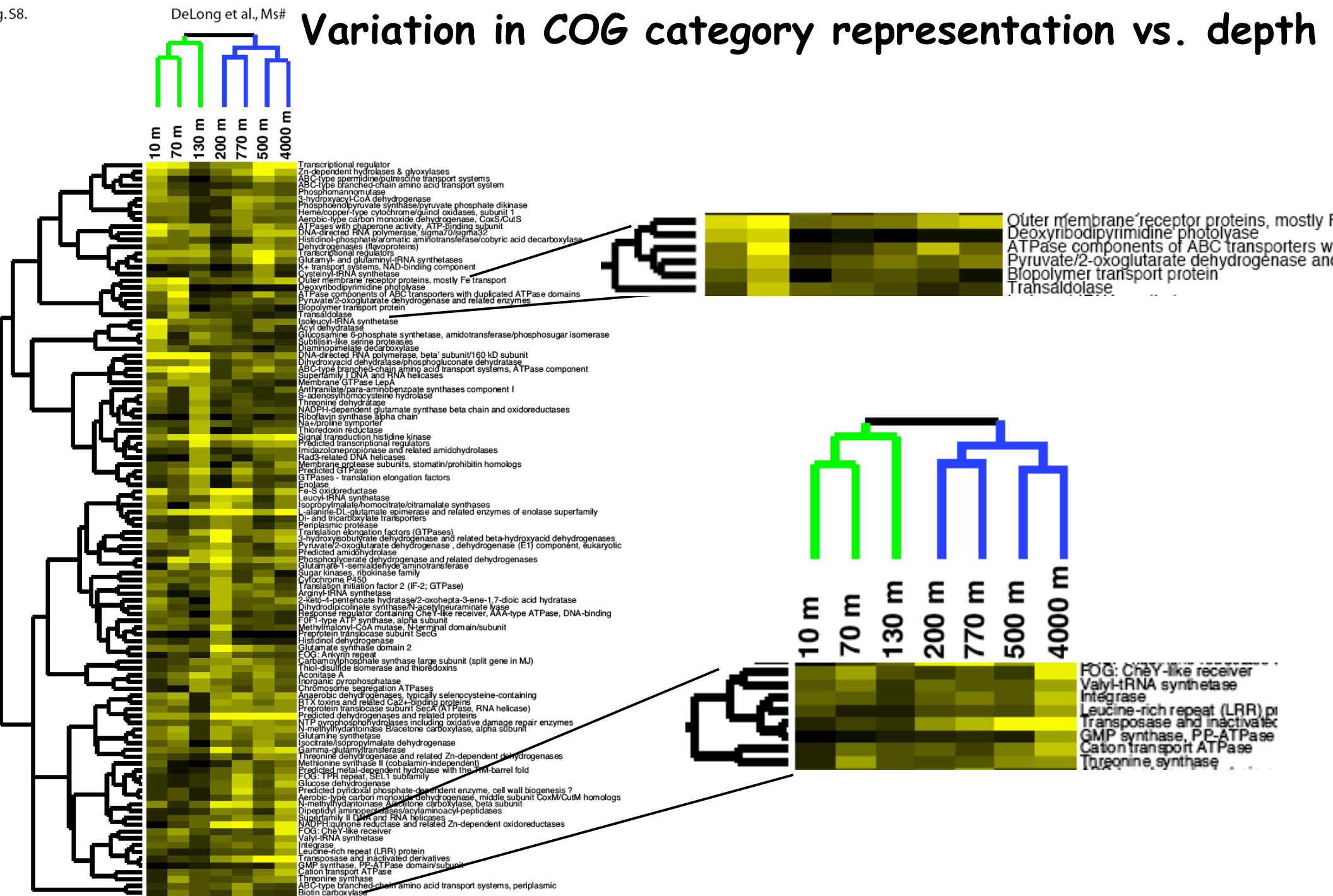
DEEP WATER UNIQUE SEQUENCES

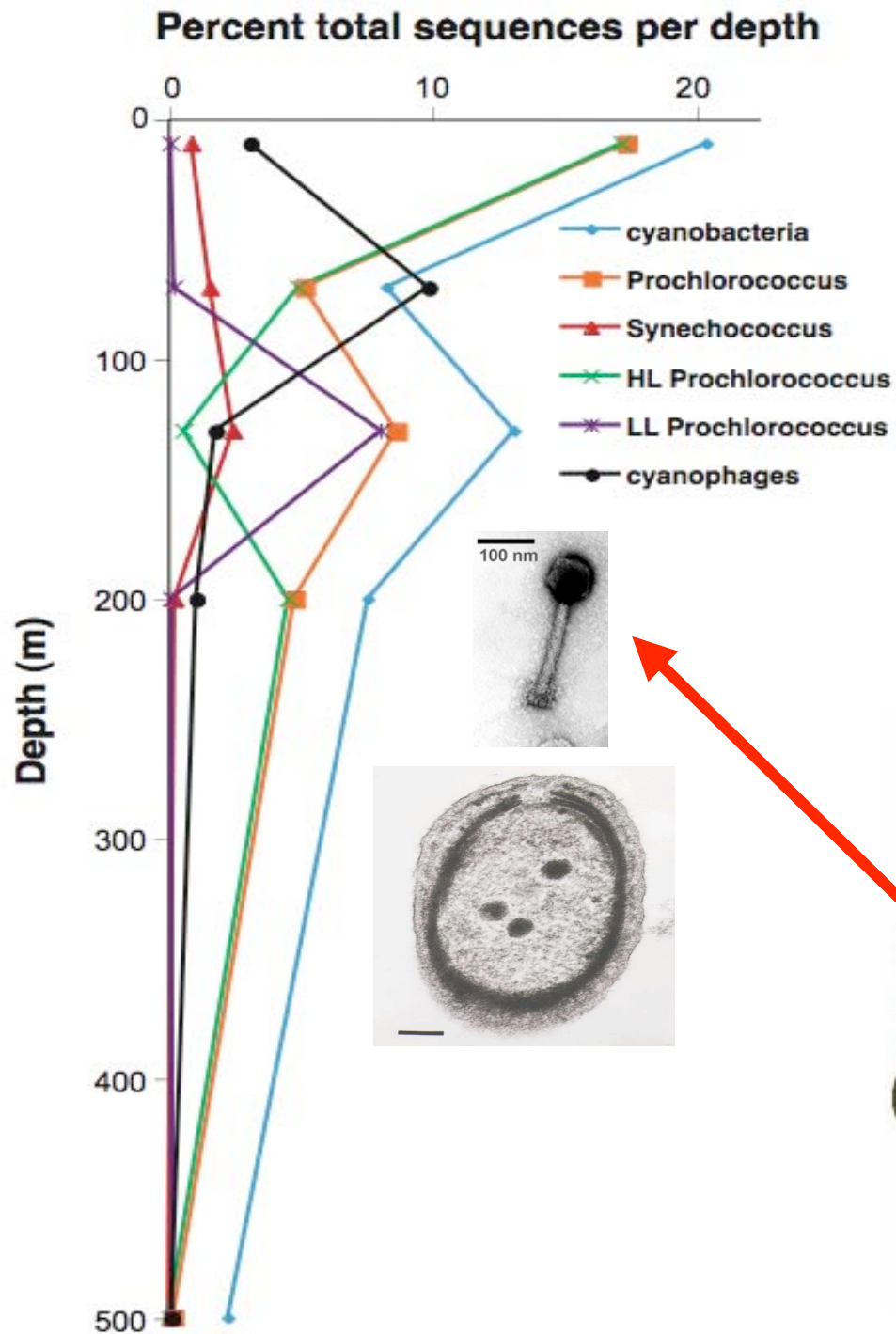


DW

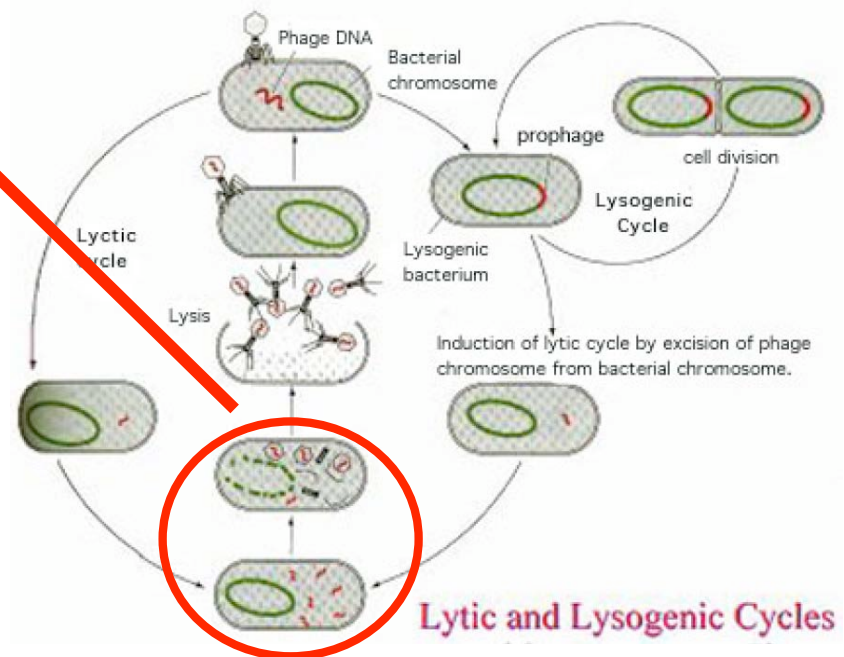
DeLong et al., Ms#

Variation in COG category representation vs. depth



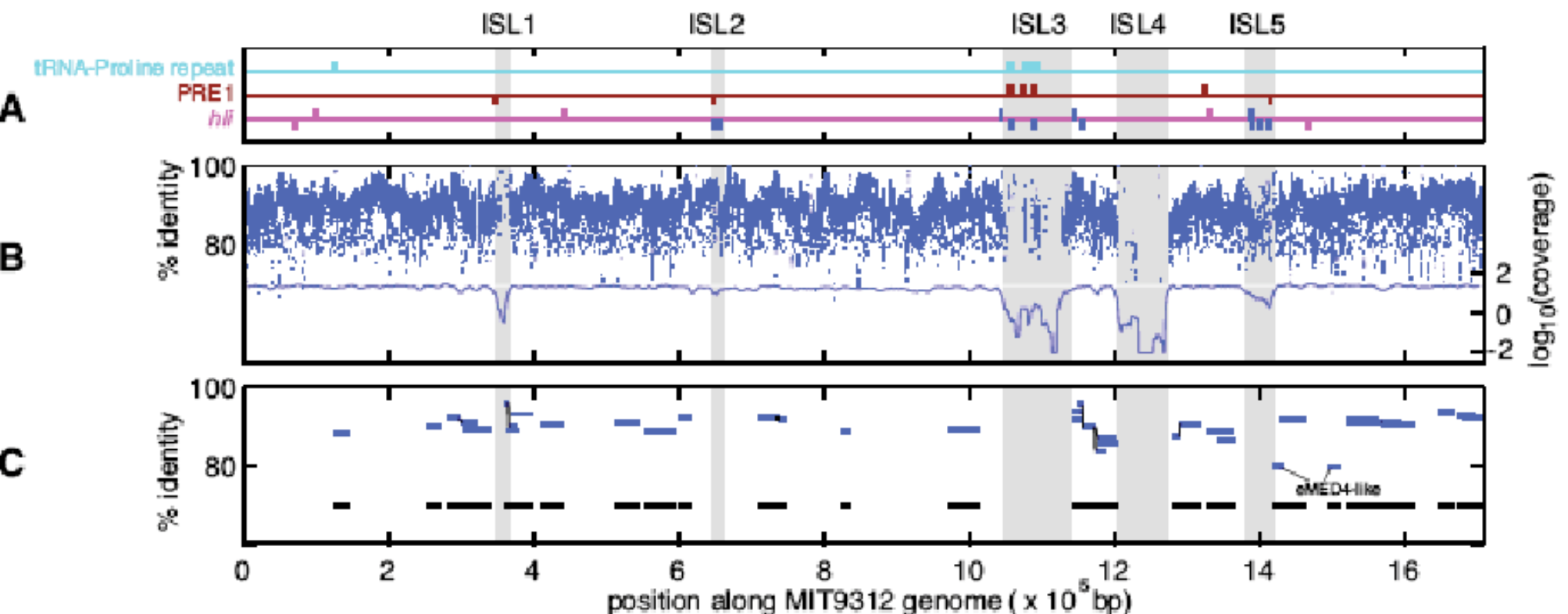


- 1) Prochlorococcus phylotypes evident
- 2) Viral recovery maxima - 70 m
- 3) Viral recovery decrease below PZ

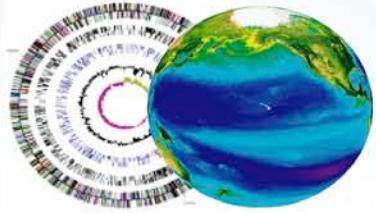


Genomic Islands and the Ecology and Evolution of *Prochlorococcus*

Maureen L. Coleman,¹ Matthew B. Sullivan,¹ Adam C. Martiny,¹ Claudia Steglich,^{1*}
Kerrie Barry,² Edward F. DeLong,¹ Sallie W. Chisholm^{1†} 24 MARCH 2006 VOL 311 SCIEN

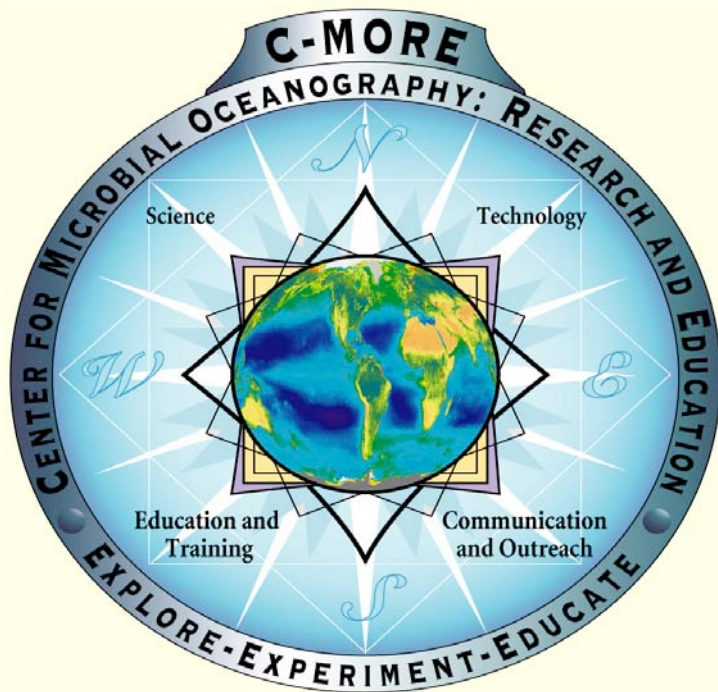


THE FUTURE ???



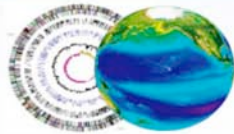
center for microbial oceanography: research and education
c·more *linking genomes to biomes*

Director David Karl, University of Hawaii Manoa



- **Explore**
- **Experiment**
- **Educate**





center for microbial oceanography: research and education

c·more *linking genomes to biomes*

[Home](#)

C-MORE Home

What is Microbial Oceanography, and how do we study marine microbes?

Member Login

Research Themes

I: Microbial Biodiversity

II: Metabolism and C, N, P & Energy Flow

III: Remote and Continuous Sensing; Links to Climate Variability

IV: Ecosystem Modeling, Simulation, and Prediction

Education

Summer Course on Microbial Oceanography

The C-MORE Team

Employment Opportunities

Partner Institutions

School of Ocean and Earth Science and Technology

University of Hawai'i at Manoa

Massachusetts Institute of Technology

Monterey Bay Aquarium Research Institute

University of California at Santa Cruz

Project Summary

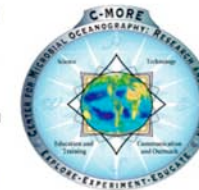
The **Center for Microbial Oceanography: Research and Education (C-MORE)** is a recently established (August 2006) NSF-sponsored Science and Technology Center designed to facilitate a more comprehensive understanding of the diverse assemblages of microorganisms in the sea, ranging from the genetic basis of marine microbial biogeochemistry including the metabolic regulation and environmental controls of gene expression, to the processes that underpin the fluxes of carbon, related bioelements and energy in the marine environment. Stated holistically, C-MORE's primary mission is: *Linking Genomes to Biomes*.

We believe that the time is right to address several major, long-standing questions in microbial oceanography. Recent advances in the application of molecular techniques have provided an unprecedented view of the structure, diversity and possible function of sea microbes. By combining these and other novel approaches with more well-established techniques in microbiology, oceanography and ecology, it may be possible to develop a meaningful predictive understanding of the ocean with respect to energy transduction, carbon sequestration, bioelement cycling and the probable response of marine ecosystems to global environmental variability and climate change. The strength of C-MORE resides in the synergy created by bringing together experts who traditionally have not worked together and this, in turn, will facilitate the creation and dissemination of new knowledge on the role of marine microbes in global habitability.

The new Center will design and conduct novel research, broker partnerships, increase diversity of human resources, implement education and outreach programs, and utilize comprehensive information about microbial life in the sea. The Center will bring together teams of scientists, educators and community members who otherwise do not have an opportunity to communicate, collaborate or design creative solutions to long-term ecosystem scale problems. The Center's research will be organized around four interconnected themes: (1) microbial biodiversity, (2) metabolism and C-N-P-energy flow, (3) remote and continuous sensing and links to climate variability, and (4) ecosystem modeling, simulation and prediction. Each theme will have a leader to help coordinate the research programs and to facilitate interactions among the other related themes. The education programs will focus on pre-college curriculum enhancements, in service teacher training and formal undergraduate/graduate and post-doctoral programs to prepare the next generation of microbial oceanographers. The Center will establish and maintain creative outreach programs to help diffuse the new knowledge gained into society at large including policymakers. The Center's activities will be dispersed among five partner institutions: **Massachusetts Institute of Technology, Woods Hole Oceanographic Institute, Monterey Bay Aquarium Research Institute, University of California at Santa Cruz and Oregon State University** and will be coordinated at the **University of Hawai'i at Manoa**.

Center Opening

On Tuesday 1 August 2006 at 0730 hr Hawaii Standard Time the **Center for Microbial Oceanography: Research and Education (C-MORE)** officially opened its doors on the UH at Manoa campus and across the nation. The formal opening ceremonies were conducted in the format of a 90-minute videoconference on "Opportunities and Challenges" for the discipline as a whole. Team members from all partner institutions and program officials from the National Science Foundation all participated in this benchmark celebration. The videoconference was taped and can be viewed in full below. The opening event was also commemorated with a "first day of issue" cover that was posted at Honolulu and mailed to all of the participants (see below).

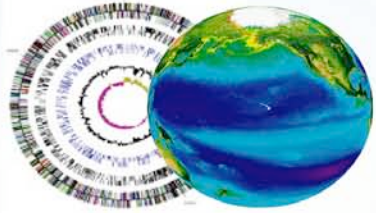


<http://cmore.soest.hawaii.edu>

C-MORE Int. HQ – Univ. Hawaii

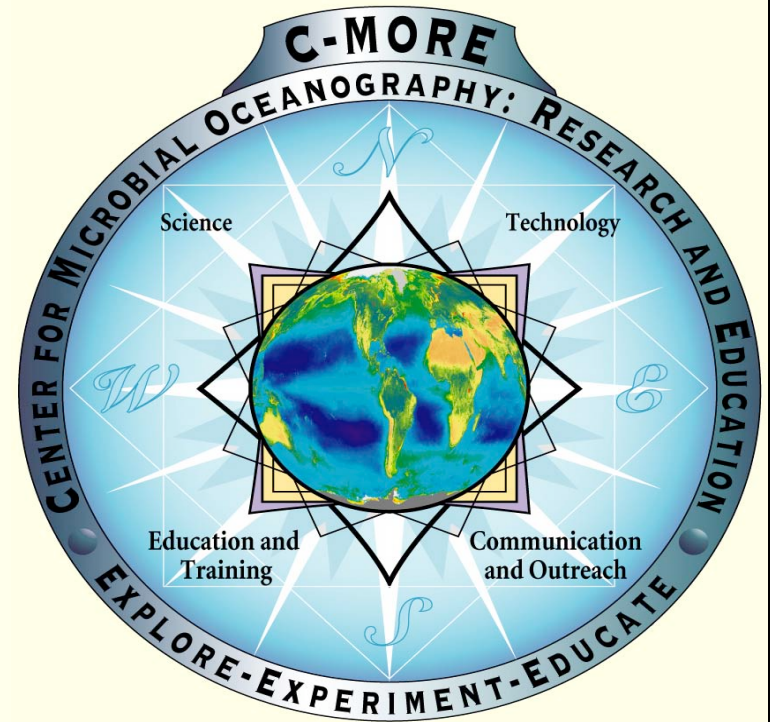
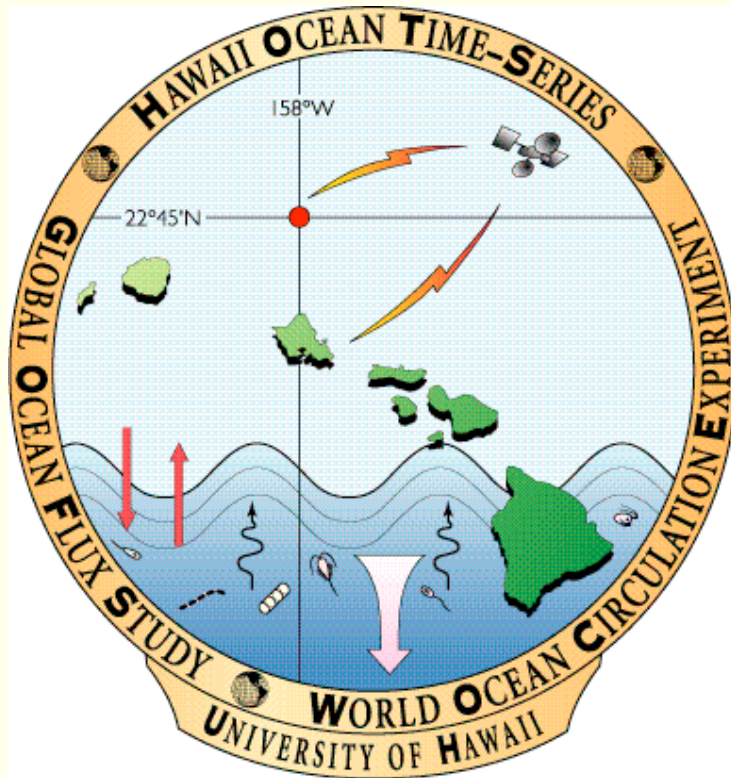


Honolulu, Hawaii, USA



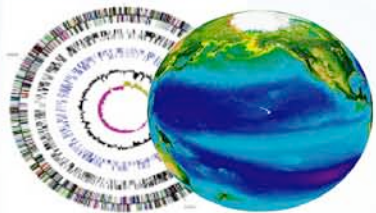
center for microbial oceanography: research and education
c·more *linking genomes to biomes*

Director David Karl, University of Hawaii Manoa



C-MORE GOALS: TO UNDERSTAND

- Mechanisms that drive and sustain diversity & function in oceanic microbes (**systems biology**)
- Mechanisms that link organisms together in robust networks (**ecosystems biology**)



center **for** microbial oceanography: research and education

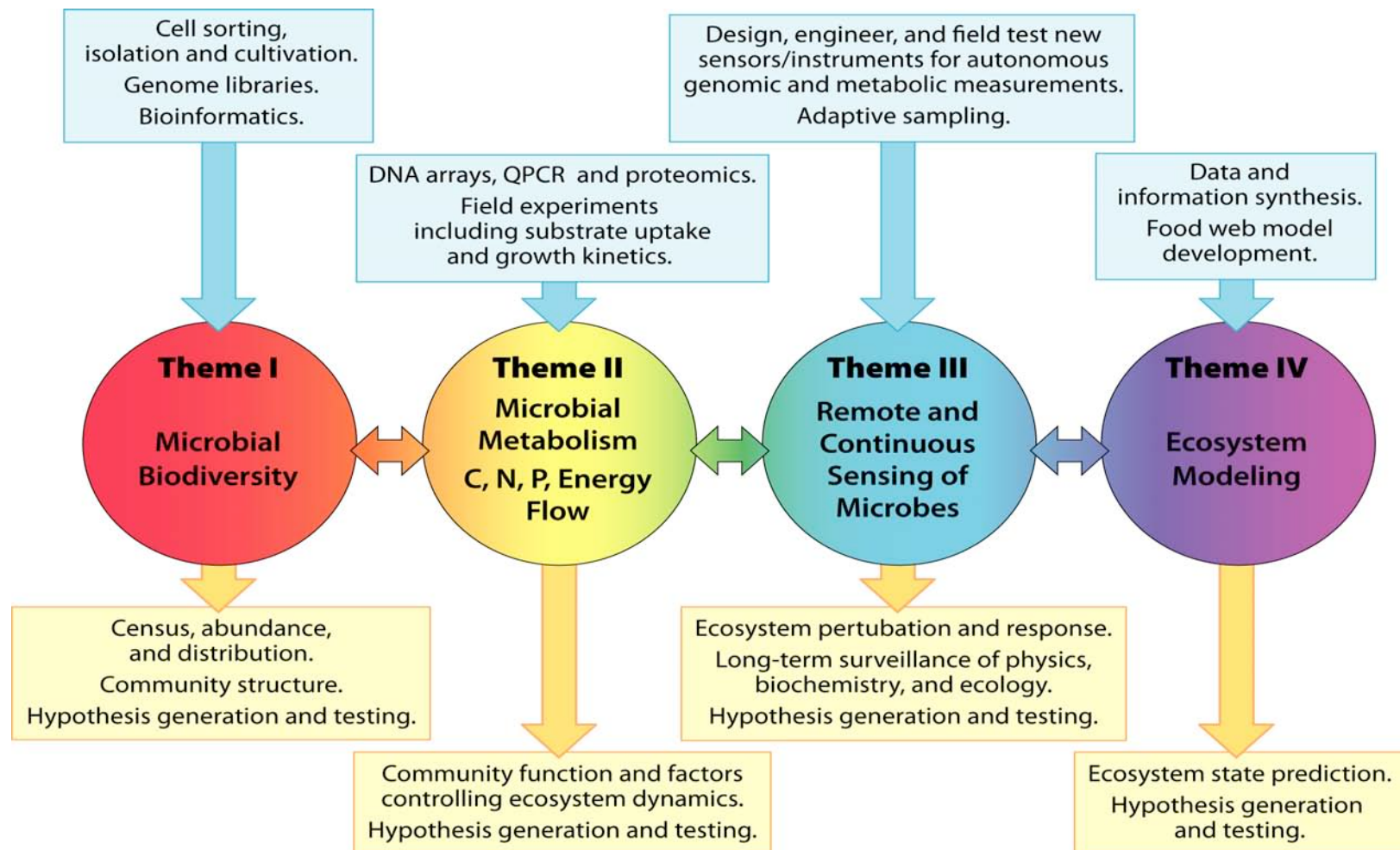
C·more *linking genomes to biomes*

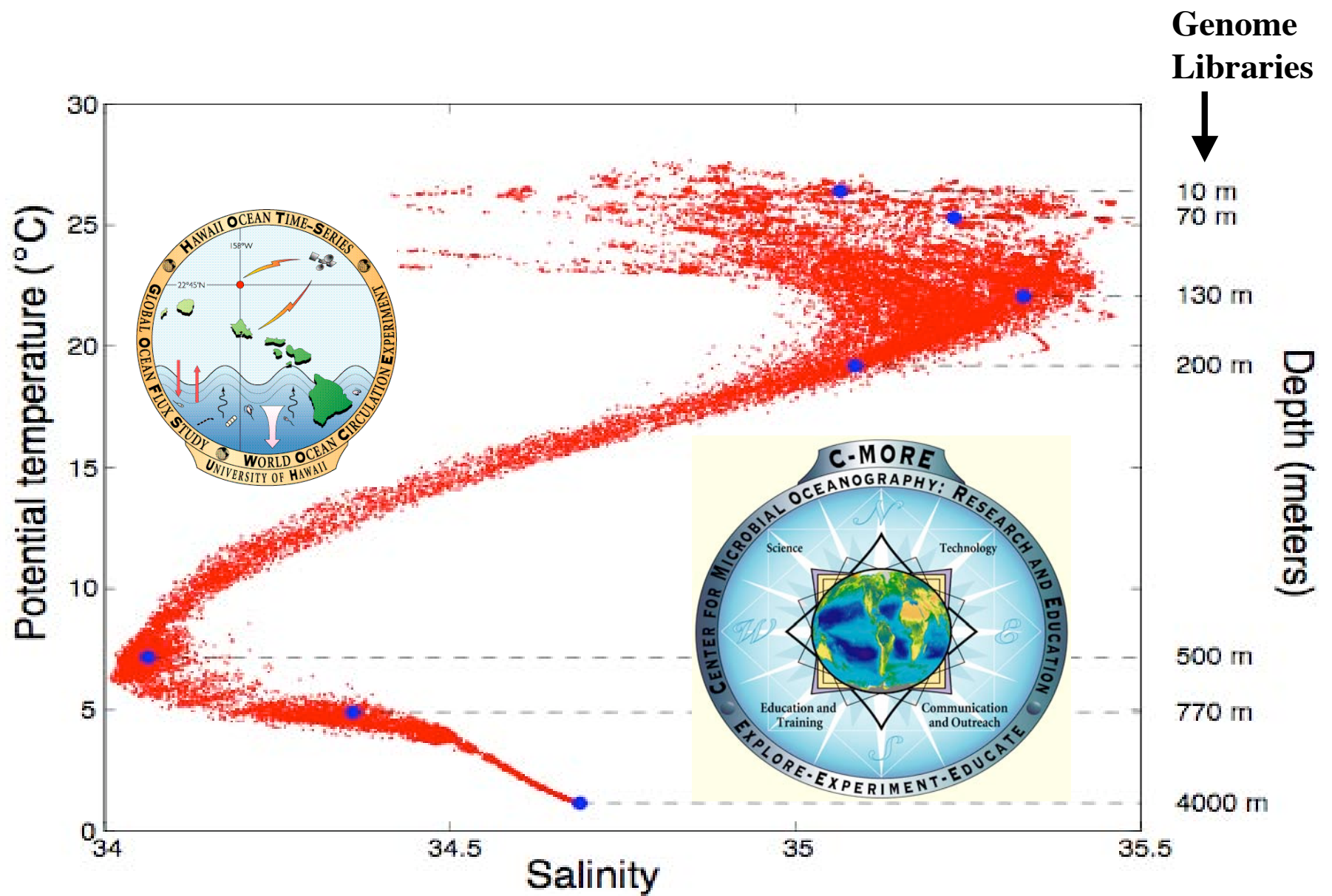
THE GRAND CHALLENGE



- Establish the “parts list” or blueprint: *genomics and phylogenetic, isolate diversity*
- Decode the assembly manual: *gene regulation, physiology and metabolism*
- Integrate across disciplines: *ecogenomics, ecophysiology and systems ecology*

C-MORE RESEARCH

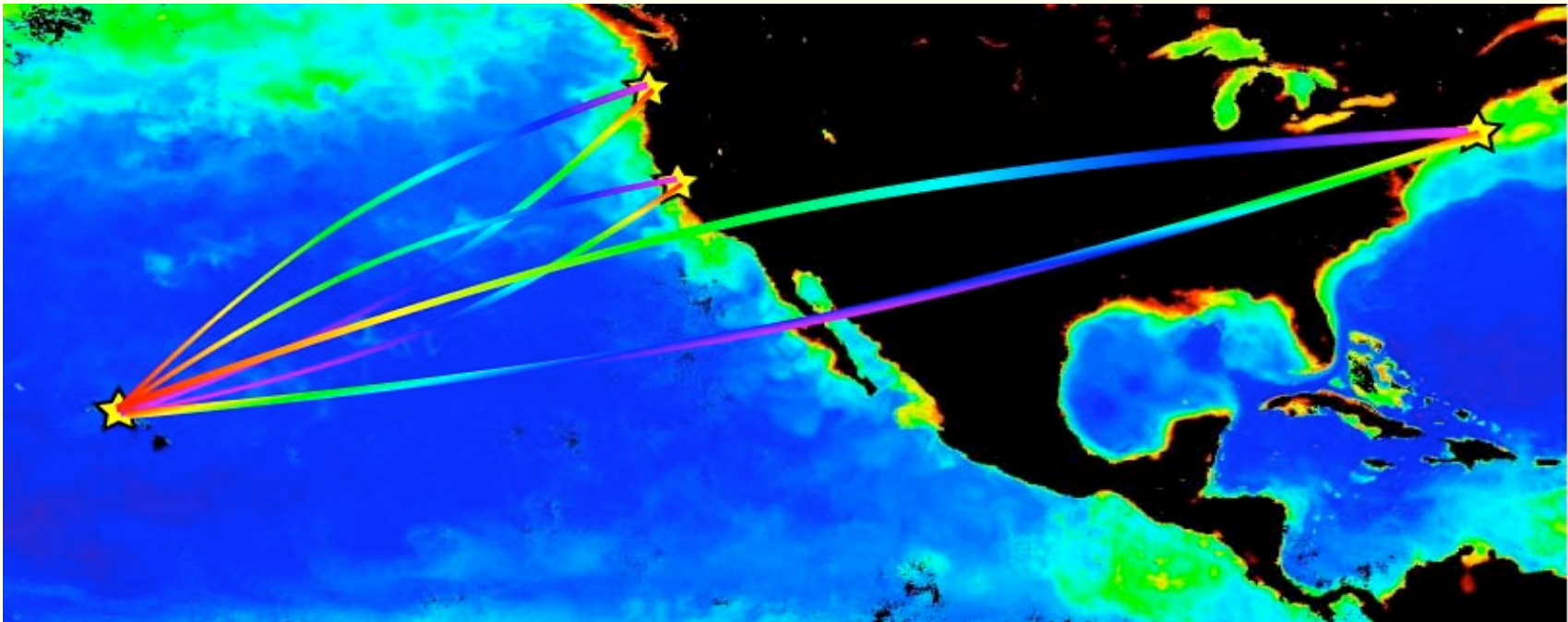




C-MORE CONNECTIVITY

University of Hawaii = Lead Institution

MBARI • WHOI • OSU • UCSC • MIT



FORMAL EDUCATION & TRAINING



curriculum, teacher training, mentoring, outreach

C-MORE “Summer at Sea”

If interested,
join us next summer
for our annual
Agouon Institute-
sponsored summer
training course



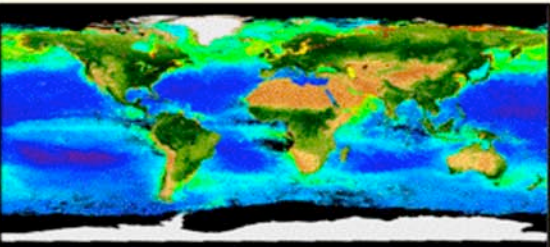
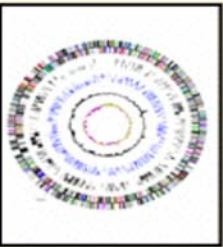


MICROBIOLOGY

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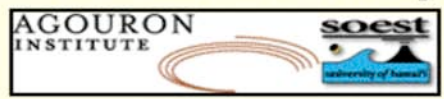


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