

Trichodesmium bloom coincident with higher iron supply in the southwest Pacific



There is much interest in whether iron limitation affects *Trichodesmium* growth. Cruise KM0703 in the southwest Pacific (chief scientists Jon Zehr and Joe Montoya) included measurements of iron in the euphotic zone by Ed Boyle and Ruifeng Zhang at MIT as well as many microbiological properties. For 14 out of 17 stations, Fe in the euphotic zone was relatively low (0.1-0.3 nM, <0.4 μ m). But at one station (24: 15degS, 178degE), a *Trichodesmium* bloom coincided with consistently high Fe in the euphotic zone (0.54 nM in the surface, >0.4 nM in the upper 80m), significantly higher than the non-bloom stations immediately to the east and west (<0.12 nM). According to cruise participant Angelicque White, the adjacent stations had ~105nM soluble reactive P while the high iron bloom station had 40nM SRP, implying that Fe-stimulated N fixation was removing SRP from the surface waters. She also noted that extracted phycoerythrin and ac-s c650 were higher in the upper waters of the *Trichodesmium* bloom station compared to station 25 to the east. Analyses of samples for unfiltered "total dissolvable iron" (which includes Fe in the biological particles as well as truly dissolved) at station 24 were more than twice as high as the <0.4 μ m Fe, indicating that the initial Fe supplied to this site was very high indeed. Interestingly, station 25 (immediately to the east) had a *Crocospheara* bloom (another nitrogen fixer) despite low dissolved Fe (0.08 nM).

Aerobic production of methane by *Trichodesmium* IMS101

Based on the work of Karl et al. (2008)¹ which describes a new pathway for the production of the greenhouse gas methane under aerobic conditions in the marine environments, several laboratory experiments were designed and executed in a collaborative effort between Dave Karl, Angelique White, Lucas Beversdorf and Ricardo Letelier. The goal of these experiments was to assess the utilization of methyl-, ethyl- and 2-aminoethyl-phosphonates as sources of phosphorus by diazotrophs (*Trichodesmium* IMS101 and *Crocospaera* sp.) and to quantify the production of methane and ethane during the uptake of these dissolved organic compounds.

Initial studies carried in late 2007 and a series of further experiments in 2008 confirm that *Trichodesmium* IMS101 is able to utilize and convert into particulate organic phosphorus all the dissolved organic carbon in the form of methyl- and ethyl-phosphonate (Fig. 1), releasing methane and ethane as by-products (Fig. 2). These results further support the hypothesis that nitrogen fixation fueled by DOP can be an important source of methane, explaining the excess concentration of this greenhouse gas observed under aerobic conditions in the upper euphotic zone of some oligotrophic pelagic regions.

¹Karl, D. M., L. Beversdorf, K. M. Bjorkman, M. J. Church, A. Martinez and E. F. DeLong. Aerobic production of methane in the sea. 2008. *Nature Geoscience*, 1: 473-478.

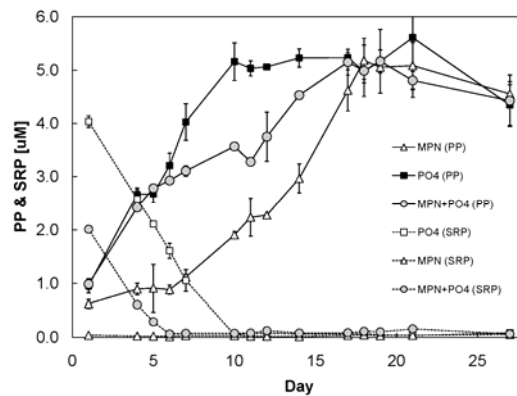


Fig 1. Uptake of soluble reactive phosphorus (SRP) and methyl-phosphonate (MPN) by *Trichodesmium* IMS101 derived from the depletion of SRP and the accumulation of particulate phosphorus (PP). The three different treatments represent incubations with 5 μM PO_4 , 5 μM MPN, and 2.5 μM MPN + 2.5 μM PO_4 .

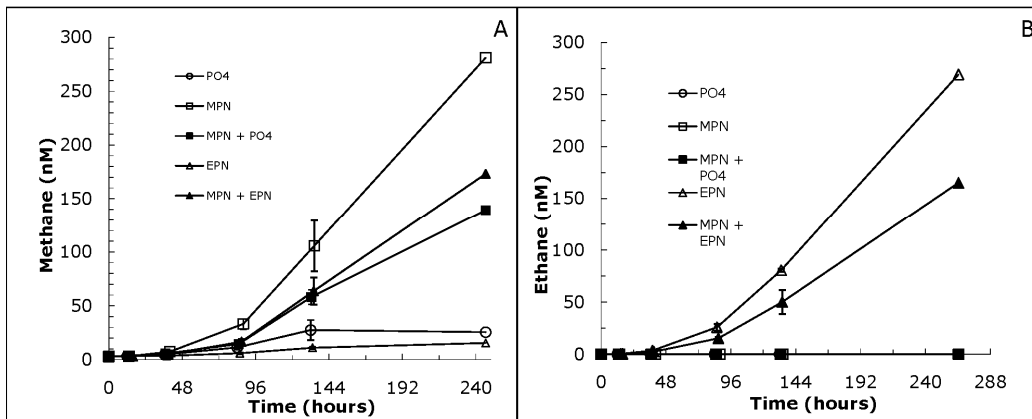


Fig 2. Evolution of methane (A) and ethane (B) in *Trichodesmium* IMS101 cultures grown with inorganic phosphorus (PO_4), methyl-phosphonate (MPN), ethyl-phosphonate (EPN), ethyl-phosphonate plus inorganic phosphorus (EPN+ PO_4) and methyl-phosphonate plus PO_4 (MPN+ PO_4).

Particulate Phosphorus fractionation by *Trichodesmium* spp. during the South Pacific SPEEDO and BULA cruises.

In the spring of 2007, members of the Letelier lab participated in two cruises transiting from the South Pacific to the North Pacific Subtropical Gyre. The primary objective of our research was to determine the phosphorus (P) composition of *Trichodesmium* versus bulk particulate matter (i.e. relative proportions of inorganic [PIP] and organic phosphorus [POP]) relative to environmental conditions. This work was intended to build upon laboratory research defining the underlying physiological mechanisms of variable elemental stoichiometry in *Trichodesmium* spp. Results indicate that *Trichodesmium* P-composition is significantly different from that of bulk particulate material. Notably acid-soluble inorganic phosphorus pools, or particulate inorganic phosphorus (PIP), comprise a much larger proportion of *Trichodesmium* biomass than that of bulk plankton (Figure 1). This difference was observed in samples collected from both SPEEDO and BULA transects. We are currently conducting laboratory experiments to determine the biochemical basis of this unusual P-fractionation pattern.

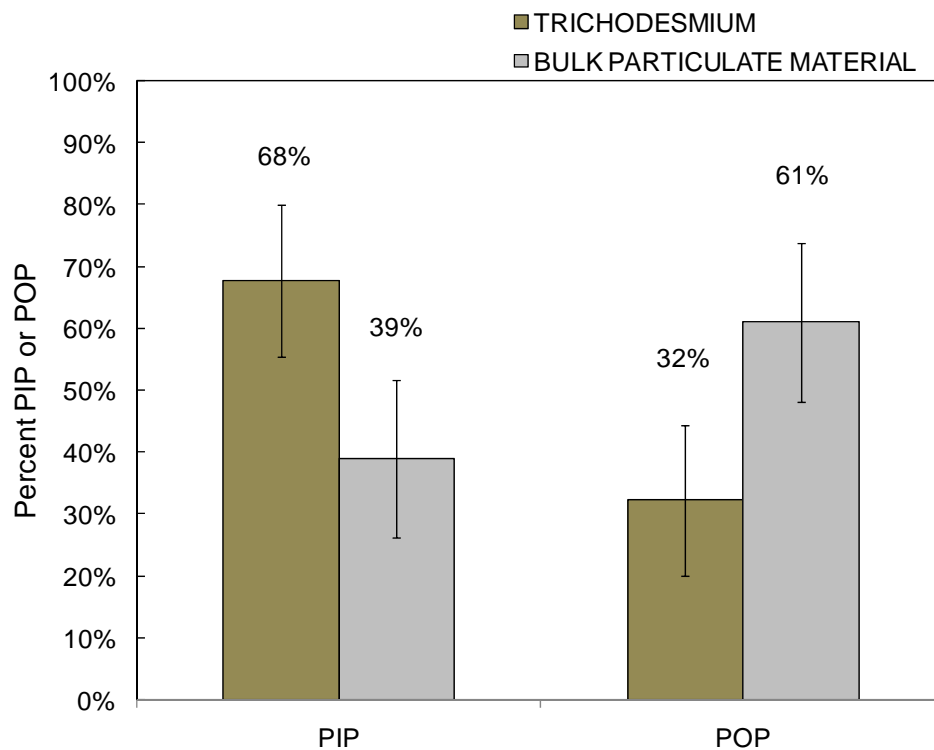


Figure 1. Relative fractionation of *Trichodesmium* particulate material versus bulk particulate material between acid soluble inorganic pools and organic pools. These data indicate that *Trichodesmium* allocate a greater proportion of P to inorganic compounds such as acid-soluble polyphosphate or internal pools of orthophosphate.

While P-acquisition and storage patterns in a P-replete environment can inform our understanding of the competitive capacity of individual diazotrophy genera, we were also engaged in determining the environmental conditions under which *Trichodesmium* and other diazotrophs bloom. In this regard, the most salient gradients encountered along the path of these cruises were that of temperature (as we traveled in and out of the Pacific warm pool) and productivity. Significant accumulations of

Trichodesmium (Station 14, 25) and *Crocosphaera* (Station 24) were observed in the South Pacific transect. Interestingly, each of these blooms was observed within the boundaries of the Pacific warm pool, as defined by the 28.5 degree isotherm (Figure 2). Concentrations of both soluble reactive phosphate and iron (see *Trichodesmium* and iron highlight) also appeared to increase in areas with high sea surface temperature. These observations suggest that the seasonal and decadal changes in the extent of the Pacific warm pool may play a significant role in the regional distribution of diazotrophic blooms.

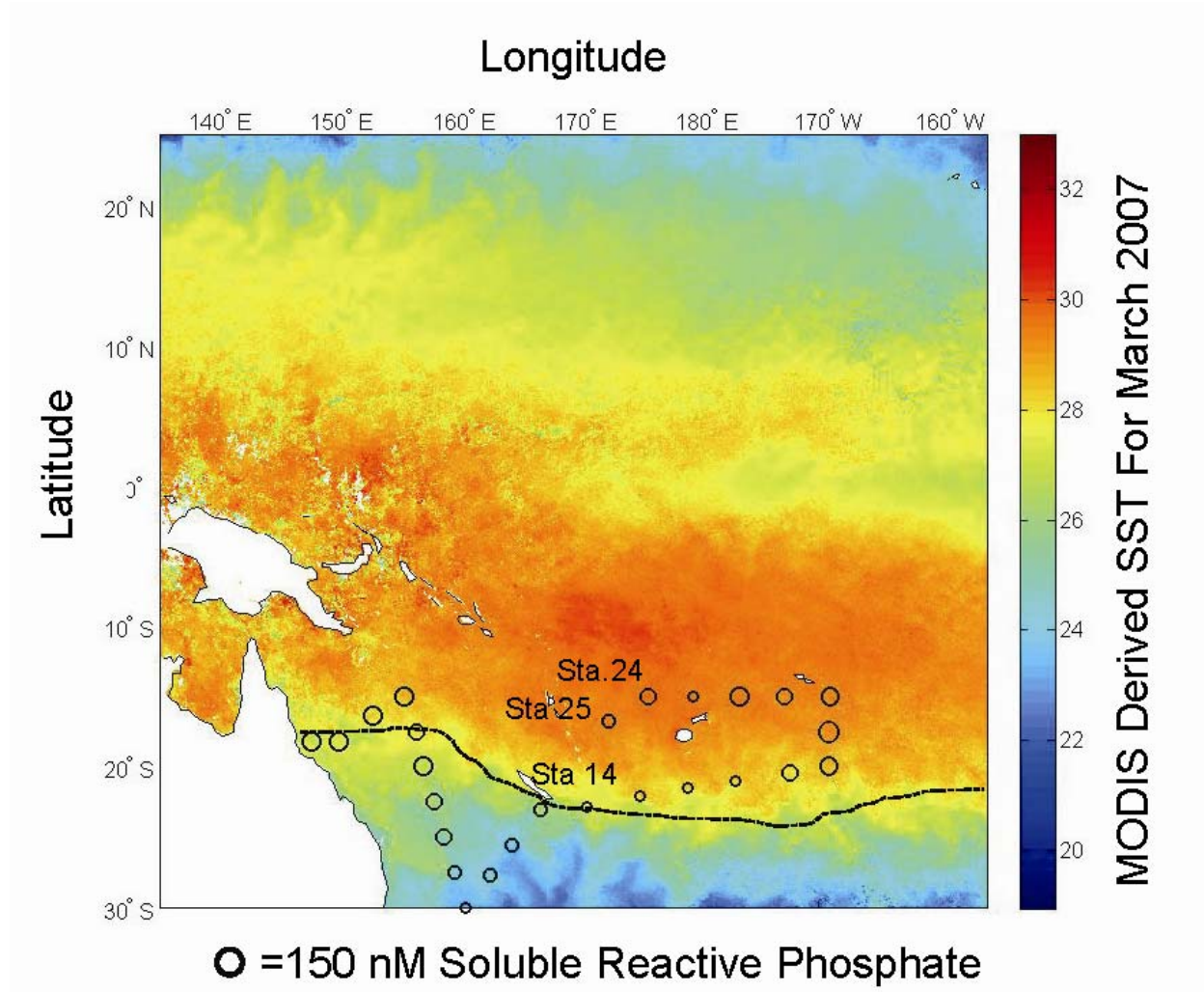


Figure 2. Concentrations of soluble reactive phosphorus (circles) for each station along the track of KM0703 shown relative to means sea surface temperature for the month of March, 2007. The general southern boundary for the Pacific Warm Pool is shown by a dotted line.

Evidence for alternating metalloenzyme production during the diel cycle in *Crocospaera watsonii* by global proteomic analyses

Using global proteomic analyses of the important marine diazotroph *Crocospaera watsonii*, Mak Saito and colleagues have identified more than 750 expressed proteins. Obvious diel patterns are present that demonstrate a mechanism for efficient use of iron by alternating use of the iron between photosynthesis and nitrogenase.

Iron containing nitrogenase proteins are clearly present during the dark photoperiod when nitrogen fixation occurs, and degraded during light photoperiod.

During the light photoperiod, the soluble iron-containing protein cytochrome c is abundant, but is absent during the dark photoperiod.

Crocospaera watsonii Diel Protein Expression

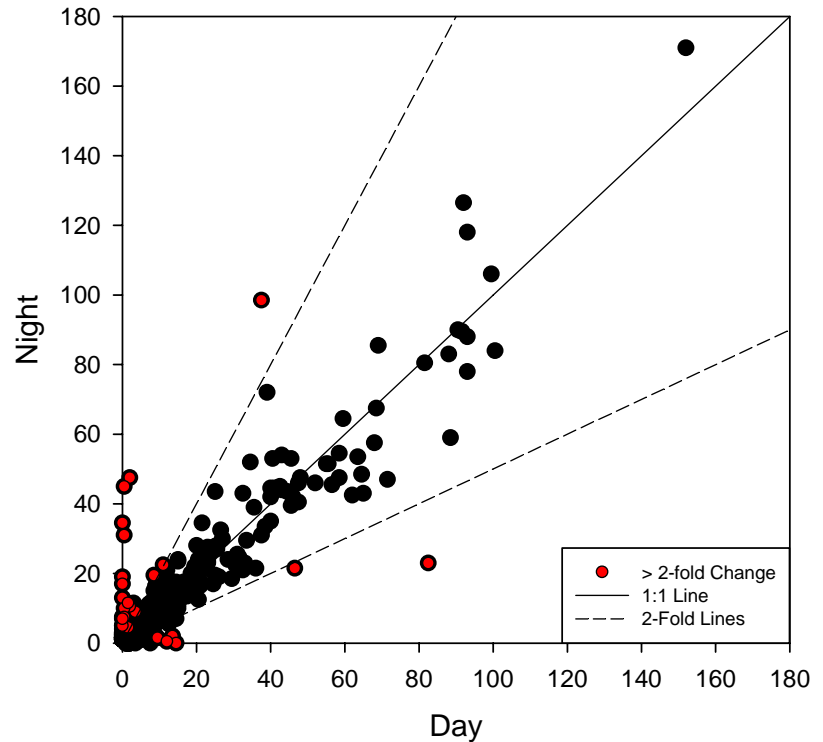
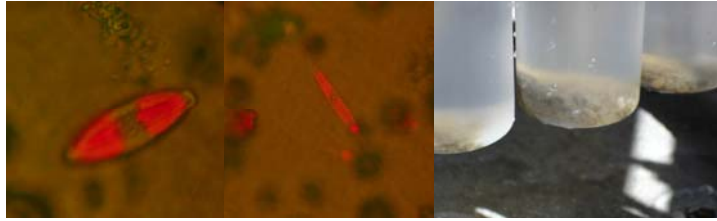


Table 4. <i>Crocospaera</i> proteins with >2 fold changes in expression	Day1	Day2	Night1	Night2	Difference (D-N)
Ferredoxin	29	0	0	0	14.5
Cytochrome c, class I	15	9	1	0	11.5
Phosphoribulokinase/uridine kinase	11	8	2	1	8
Photosystem II 12 kDa extrinsic	16	11	2	2	11.5
Rhodanese-like	1	2	5	4	-3
hypothetical protein	0	0	5	5	-5
NifT/FixU	0	0	8	6	-7
Aminotransferase, class V:Nitrogen-fixing	0	1	8	7	-7
Transcriptional regulator AbrB	3	4	8	10	-5.5
Heme oxygenase (decyclizing)	1	0	8	12	-9.5
Cysteine synthase K/M:Cysteine synthase A	1	3	11	10	-8.5
Nitrogen fixation protein NifW	1	2	8	15	-10
hypothetical protein	0	0	11	15	-13
NAD(P)(+) transhydrogenase (AB-specific)	0	0	17	17	-17
Glyceraldehyde-3-phosphate dehydrogenase,	0	0	20	18	-19
Transcriptional regulator AbrB	8	9	17	22	-11
Ketose-bisphosphate aldolase, class-II:Fru	43	50	22	21	25
Oxidoreductase FAD/NAD(P)-binding:CpcD phy	11	11	23	22	-11.5
S-layer homology region	72	93	26	20	59.5
Nitrogenase molybdenum-iron protein alpha	1	0	28	34	-30.5
Nitrogenase molybdenum-iron protein beta c	0	0	38	31	-34.5
Flavodoxin, long chain	1	0	45	45	-44.5
Nitrogenase iron protein	2	2	50	45	-45.5
6-phosphogluconate dehydrogenase, decarboxylase	35	40	96	101	-61

Bloom or Bust: Oceanic Diatom Dynamics in the North Pacific Ocean



Marine photosynthesis plays a vital role in controlling global carbon dioxide and oxygen inventories. However, unlike in terrestrial ecosystems where multi-cellular organisms (*e.g.* grasses, trees) constitute the largest pools of photosynthetic biomass, in the sea most of the photosynthesis is carried out by microscopic organisms. These crops of tiny plankton, most of which are invisible to the human eye without the aid of microscopes, live short but highly productive lifestyles. These microorganisms grow, reproduce, and die all in less than a few days. Nonetheless, during their short life spans, oceanic plankton produce nearly one-half of all the oxygen in the biosphere, while simultaneously consuming carbon dioxide.

Diatoms are among the most productive and wide spread of these marine photosynthetic organisms. These single-celled, eukaryotic microorganisms are the equivalent of oceanic weeds, capable of exceptionally fast growth under suitable conditions. Unique among these organisms, diatoms assimilate silicon into their cell walls, thereby inherently linking the silicon cycle to the cycles of carbon and other essential nutrients in the sea. As they exhaust nutrients in the sunlit regions of the ocean, they begin a long, gradual descent into the depths of the ocean, thereby transferring material and energy harvested from the upper ocean to the deep sea. As a result, diatoms form particularly intriguing biological linkages between the atmosphere and the deep sea.

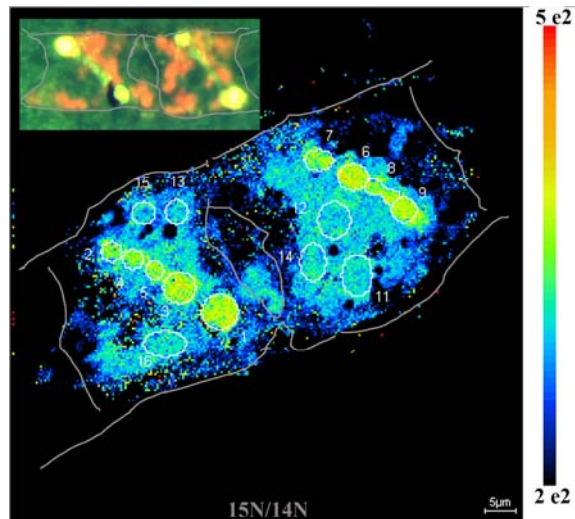
C-MORE graduate student Binglin Li has been working under the mentorship of CMORE researcher Matthew Church to examine the processes controlling the growth, diversity, and carbon sequestration potential of oceanic diatoms in the North Pacific Ocean. By combining classic oceanographic approaches with molecular-based evaluation of diatom diversity, Binglin's work has revealed that despite the near chronic absence of available nutrients in the upper ocean, diatoms flourish throughout vast regions central Pacific Ocean. His research has revealed that this low nutrient ecosystem harbors numerous genera of marine diatoms whose abundances and diversity follow a successional pattern depending on the magnitude and sources of nutrient input to the upper ocean.

This research, made possible by funding from CMORE, is providing important information on the general role of ocean biology in controlling the movement of carbon from the atmosphere to the seabed. Moreover, by studying the conditions that favor the growth of specific groups of diatoms, Binglin's research is elucidating the sensitivity of ocean food webs to environmental perturbations.

A symbiotic advantage: Diatoms and cyanobacteria work together to make the most in a nitrogen depleted ocean

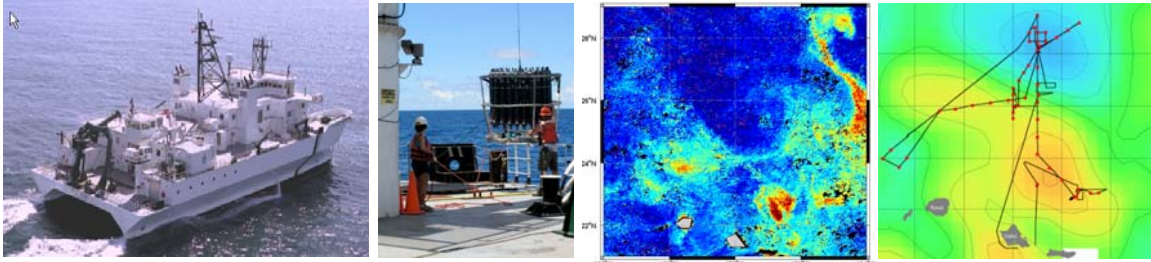
The term “symbioses” was first defined loosely by Anton de Bary (1879)¹ as two or more differently named organisms living together. Although ubiquitous in nature, few of the marine planktonic systems have been well characterized, and comparatively less is known of the functional role of the symbiont for host and vice versa. Some of the earliest reports of planktonic symbiosis describe the associations of heterocystous cyanobacterium *Richelia intracellularis*, with various diatoms, including *Hemiaulus* spp. As most heterocystous cyanobacteria reside in brackish or estuarine habitats, it appears that *Richelia* has made the successful transition to the open ocean by engaging in symbiotic associations with diatoms. Although it seems obvious that the basis of the relationship would be nitrogen, as heterocystous cyanobacteria are capable of diazotrophy and their respective hosts do not, fixation and transfer had not been demonstrated in these unique consortia.

Recently, Rachel A. Foster, a postdoctoral scholar and Jonathan P. Zehr, a professor at UCSC Ocean Sciences, used high-resolution nanometer-scale secondary ion mass spectrometry (nanoSIMS) in collaboration with Marcel Kuypers of the Max-Planck-Institut für Marine Mikrobiologie, to measure the cellular distribution of N uptake by *Richelia* symbionts and in addition, within the host (*Hemiaulus*). All samples were from at-sea incubations and provide the first evidence for the fixation and transfer of N within these planktonic symbioses. This nanoSIMS approach also revealed for the first time the link between a unique microbial consortium and its biogeochemical significance and lends further evidence that certain diatoms have a competitive advantage in the open ocean by taking up *Richelia* symbionts. The next obvious question is what, if anything, does the symbiont receive from the association?



The nanoSIMS results shows $^{15}\text{N}/^{14}\text{N}$ on a color scale in a chain of 2 *Hemiaulus-Richelia* symbioses. Note the “hot spots” of enrichment along the trichomes of *Richelia* (yellow) and in host cell structure. Inset is the epi-fluorescent micrograph of the same cells prior to nanoSIMS analyses.

¹ de Bary, A. (1879). Die Erscheinung der Symbiose. In “Vortrag auf der Versammlung der Naturforscher and Ärzte zu Cassel.” Verlag von K.J. Trubner, Strassburg, Germany. Pp. 1-30.



Ocean Perturbation Experiment (OPEREX)

29 July – 14 August 2008
 Chief Scientist Z. Kolber, MBARI

Science Objective

- Investigate the mechanisms of summer blooms in the North Pacific Subtropical Gyre
- Explore the potentials and limitations of perturbation experiments at sea.

The North Pacific Subtropical Gyre (NPSG) is characterized by vanishingly low nutrient concentration and low biomass standing stocks. Periodically NPSG surface waters bloom forming long meanders of high chlorophyll concentrations extending over large spatial scales. The NPSG blooms in July-August 2008 were extremely dynamic and ephemeral. The bloom features, intensity, and spatial distribution changed on the daily basis. The most intense bloom was observed in the transition zone between a pair of anticyclonic and cyclonic eddies along 157.7°W (Fig. 1, below). Bloom extended along the 24°N line, and was driven by a system of four eddies with the surface chlorophyll distribution clearly following that of the gradients in the sea surface height (Fig. 1B, C).

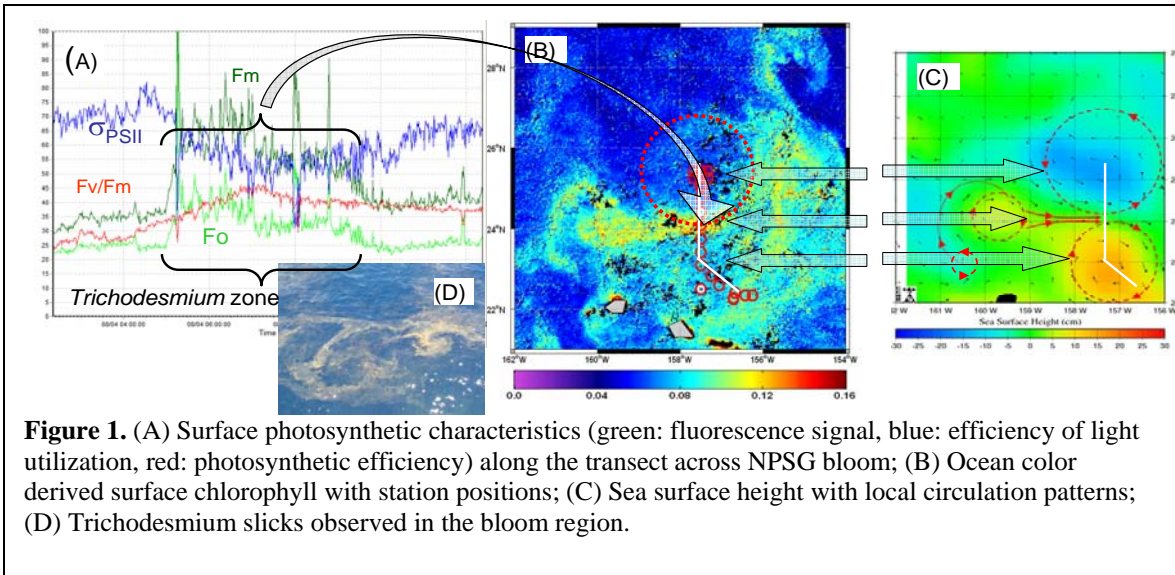


Figure 1. (A) Surface photosynthetic characteristics (green: fluorescence signal, blue: efficiency of light utilization, red: photosynthetic efficiency) along the transect across NPSG bloom; (B) Ocean color derived surface chlorophyll with station positions; (C) Sea surface height with local circulation patterns; (D) *Trichodesmium* slicks observed in the bloom region.

Sections of the photosynthetic properties (Fig. 2, next page) and nutrients (Fig.3, next page) indicate local transport and upwelling of phosphorus to the surface within the bloom region which stimulates growth of *Trichodesmium*, resulting in local nitrogen fixation leading to secondary blooms of eukaryotic phytoplankton and cyanobacteria at the surface.

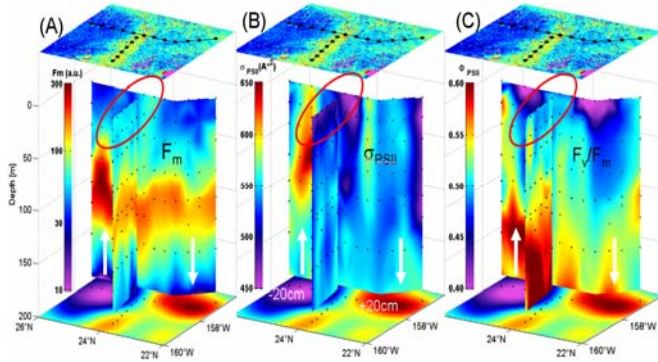


Figure 2. Sections of photosynthetic properties of phytoplankton in the OPEREX bloom area. (A) Increased surface chlorophyll biomass within the bloom; (B) depressed functional absorption cross section; (C) enhancement of the surface photosynthetic yields.

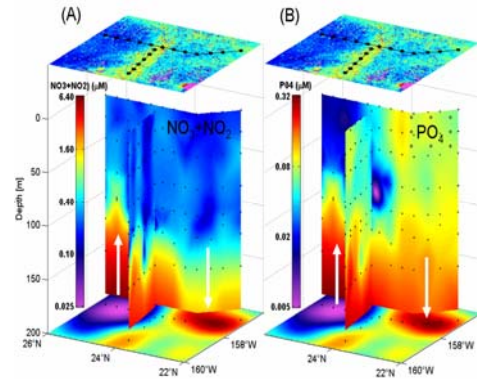


Figure 3. Sections of (A) $\text{NO}_3 + \text{NO}_2$, and (B) PO_4 along the cruise track in the OPEREX study area. Arrows indicate the centers of the upwelling and downwelling eddies.

Enrichment and pH manipulation experiments

To investigate the effects of deep water upwelling on phytoplankton growth three enrichment experiments were performed with 10% of the 200m, 300m, and 500m water (Fig. 4A, B). Up to 15 times increase in the biomass concentration was observed in response to these enrichments, supporting the potential role of the upwelling eddies in stimulating chlorophyll blooms. The effects of the anticipated ocean acidification on NPSG phytoplankton populations were investigated in ship-deck pH experiments. No significant effects of 0.3 units pH shift in “out-bloom” waters were observed. In the “in-bloom” waters, however, negative effects of the 0.3 units pH shift were clearly detectable (Fig. 4C). The effects of pH shift on the enriched populations were less clear. The initial growth under low pH was faster than in the ambient conditions, but reversed by the end of incubation, when nutrients were exhausted (Fig 4D). These results indicate that phytoplankton responses to ocean acidification may vary between nutrient-replete and nutrient-deplete portion of the ocean.

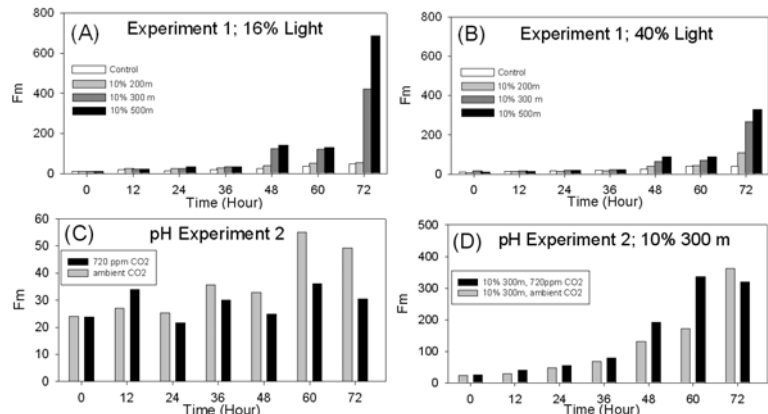


Figure 4. Deep water enrichment experiments at 16% light (A) and 40% light (B). (C) pH shift experiments in mixed layer populations and in (D) 10% 300m enriched populations.



Outreach Activities

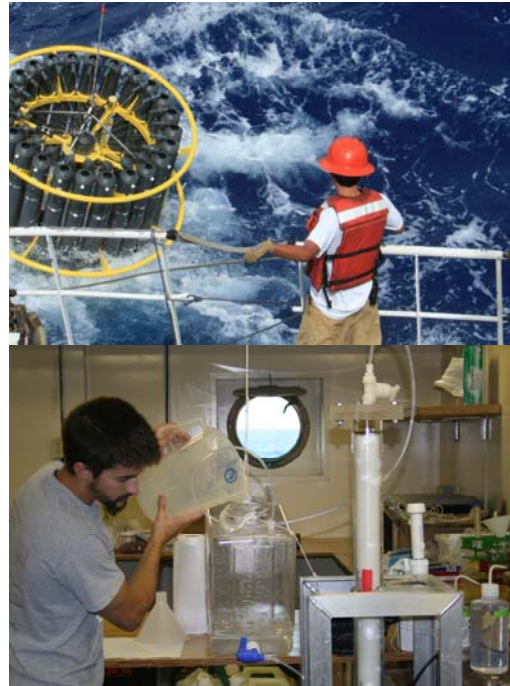
Miriam Sutton, a North Carolina middle school teacher, was participating in the OPEREX research cruise as a Teacher at Sea. During the cruise, she provided communication and developed educational activities that assisted teachers in bringing the research project into the classroom. She has established an online blog to communicate with teachers and students while at sea. In addition, Miriam maintained OPEREX web pages, allowing school children and the general public to participate in our adventure.

A malfunction in the marine microbial loop?

Under CMORE leadership, scientists from The Woods Hole Oceanographic Institution and The University of Hawaii University, Manoa, are working together to solve a half-century-old mystery in the ocean carbon cycle. Marine microbes make up less than 1% of the total organic matter in the ocean. Nearly all the rest, representing some 700 billion tons of carbon, an amount equal to all atmospheric carbon dioxide, is dissolved in the seawater itself. Dissolved organic matter (DOM) is made up of proteins, carbohydrates, and the thousands of compounds produced and consumed during microbial cycling. Radiocarbon measurements show DOM can persist for thousands of years, but even the most refractory organic carbon is not eternal: concentrations of dissolved organic carbon decrease from by 30%, from 48 μM to 34 μM , as deep ocean circulation drives water from the North Atlantic to the North Pacific Ocean.

CMORE investigators are working to understand why the ocean is literally filled with organic carbon. It has long been believed that DOM is structurally complex at the molecular level, and therefore intrinsically resistant to degradation. Microbial regrowth experiments seem to confirm this, even when nutrient enriched seawater is incubated with microbial heterotrophs, little DOM is consumed. However, Fulbright postdoctoral fellow Mar Nieto-Cid and CMORE graduate student Jamie Becker

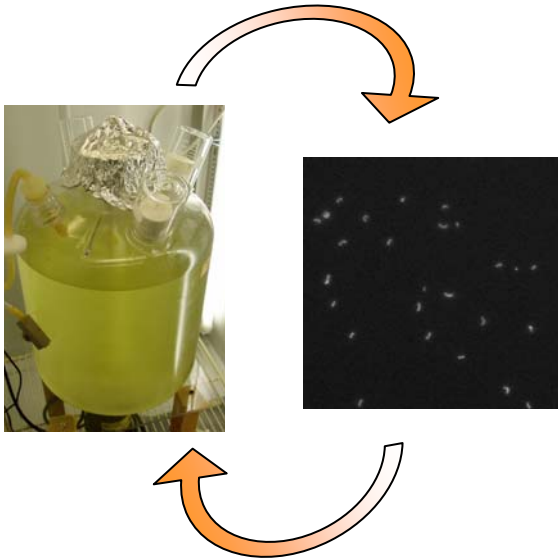
have found that once DOM is separated into different molecular size fractions by nanofiltration, a relatively high percentage of the organic carbon can be consumed by marine microbes. Experimental incubations show more than 20% of DOM in surface waters can be degraded in as little as 10 days. Surface waters contain higher levels of reactive DOM than deep waters, but even waters collected at 3500m lose more than 10% of their organic carbon after nanofiltration and microbial degradation. These results suggest that a large portion of DOM may not be intrinsically resistant to microbial degradation after all, but may be protected by the physical associations within the organic matter. Physical associations between dissolved organic molecules might act to suppress microbial activity, and the large reservoir of organic carbon dissolved in the ocean may arise in part from a malfunction in the microbial loop. Further research, including more interdisciplinary measurements on controlled experiments and genomic analysis of metabolic pathways, are needed to assess the role of physical processes in directing the cycle of marine dissolved organic carbon.



Top: Oceanic seawater sampling for dissolved organic matter.

Below: Jamie Becker, a CMORE graduate student prepares a microbial degradation experiment on board ship.

Microbial cycling of dissolved organic carbon



Linking marine microbial communities through the production and consumption of organic matter. Organic compounds produced by the autotroph *Crocospaera watsonii* (left) fuel the growth of certain marine bacteria, like members of the SAR11 clade (right), the most abundant bacterial group in the ocean.

Every drop of seawater contains more than a million microbial cells, and each one is a veritable microfactory- capable of producing and consuming vast amounts of complex dissolved organic carbon every day. C-MORE investigators Daniel Repeta and graduate student Jamie Becker of Woods Hole Oceanographic Institution and Michael Rappé at the Hawaii Institute of Marine Biology have teamed up to understand how microbes cycle organic carbon between production and respiration, and how diversity in marine autotrophic and heterotrophic communities is linked.

In Woods Hole, the complex mix of organic compounds manufactured by marine autotrophs is separated into its major components using high pressure liquid chromatography. Fractions are then characterized by mass spectrometry and nuclear magnetic resonance spectroscopy. The uptake and metabolism of these fractions are screened for uptake using pure cultures of both heterotrophic and autotrophic microbes isolated at the Hawaii Institute of Marine Biology.

To date, the team has uncovered several new linkages between organic matter production and consumption. For example, it's been found that specific compounds produced by the marine nitrogen-fixing cyanobacterium *Crocospaera watsonii* stimulate the growth of certain bacteria, like members of the highly abundant heterotrophic SAR11 clade, but not others. In collaboration with C-MORE investigator Edward DeLong at MIT, the research team is beginning to use genetic tools to investigate the metabolic pathways involved in the uptake of these organic compounds. These efforts will further our understanding of the role that marine microbes play in carbon cycling and expand our knowledge of the ocean's role in regulating Earth's climate.

Bacterioplankton community composition and dynamics in the oligotrophic North Pacific subtropical gyre

Although planktonic microorganisms dominate biomass and the transformation of inorganic nutrients, organic matter, and energy in the oligotrophic open-ocean, long-term studies of community structure and population dynamics are relatively scarce. As part of C-MORE and the multidisciplinary Hawaii Ocean Time-series program, Michael Rappé and colleagues have assessed the spatiotemporal dynamics of the bacterioplankton community at Station ALOHA, a site representative of the oligotrophic North Pacific subtropical gyre. Terminal restriction fragment length polymorphism and quantitative PCR analyses of 16S ribosomal RNA genes amplified from bacterioplankton collected over a four-year period (2004-2008) revealed clear spatial patterning with depth. The deep chlorophyll maximum appears to form a boundary dividing the epipelagic layer (0-200 m) into two distinct microbial communities, whose compositions were strongly influenced by phytoplankton dynamics. Temporal variability was generally weak, with only moderate seasonal dynamics detected in the upper mixed-layer. Spatial and temporal dynamics in bacterial taxa were examined using null model analyses, which revealed that, in addition to environmental filtering, interspecific bacterial interactions may play an important role in assembling bacterial communities in the oligotrophic ocean.

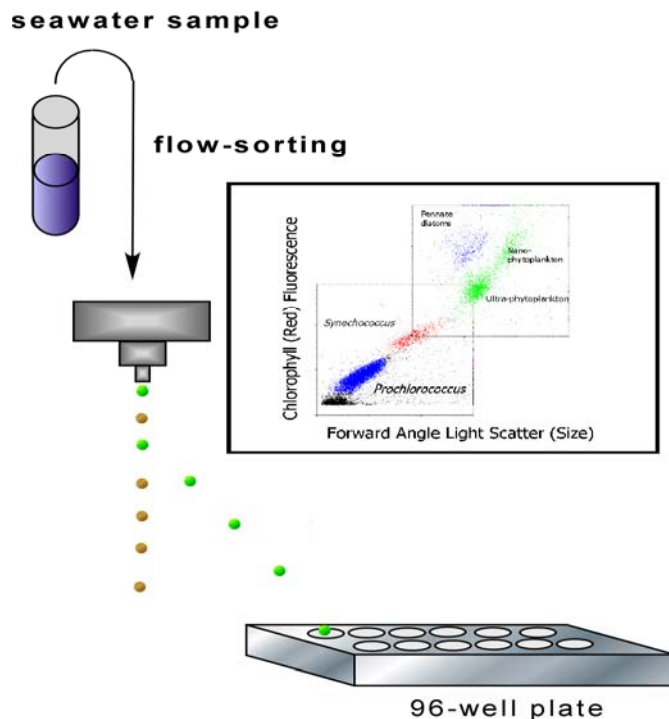
Dynamics of the SAR11 bacterioplankton lineage in relation to environmental conditions in the North Pacific subtropical gyre

A quantitative PCR assay for the SAR11 clade of marine Alphaproteobacteria was applied to nucleic acids extracted from monthly depth profiles sampled over a three-year period (2004-2007) from the open-ocean Station ALOHA in the ultra-oligotrophic North Pacific Ocean gyre. This analysis revealed a high contribution (average 36% of 16S rRNA gene copies) of SAR11 to the total detected 16S rRNA gene copies over depths ranging from the surface layer to 4000 meters, and revealed consistent spatial and temporal variation in the relative abundance of SAR11 16S rRNA gene copies. On average, a higher proportion of SAR11 rRNA gene copies were detected in the photic zone (<175 m depth; mean = 38%) compared to aphotic (>175 m depth; mean = 30%), and in the winter months compared to the summer (mean = 44% vs. 33%, integrated over 175 m depth). Partial least square to latent structure projections identified environmental variables that potentially regulate SAR11 dynamics and provided tools for developing a predictive model to explain time and depth-dependent variations in absolute SAR11 abundances. Moreover, this information was used to hindcast temporal dynamics of the SAR11 clade between 1997 and 2006 using the existing HOT dataset, which suggest that interannual variations in upper ocean SAR11 abundances were related to ocean-climate variability such as the El Niño Southern Oscillation.

Single cells and ecosystems: Unveiling the diversity of microbes in the Sea

The oceans contain millions of micro organisms in each teaspoon of water, and the diversity of different cell types is staggering. These tiny metabolic machines form the base of the food web in the oceans, and contribute half of the photosynthesis — conversion of solar energy to living biomass — on our planet. As such, they play important roles in the regulation of our atmosphere and global temperatures.

One of the barriers to truly understanding the scope and function of marine microbial diversity has been our inability to look at the genetic inventory of the cells, one cell at a time. How different genes are combined in each cell defines the cells' distinct functions in the ecosystem. It describes their heritage. It describes their capabilities. One way to get at this information is to culture the cells and then study them. But most of the cells — an estimated 99% — in marine ecosystems cannot be cultured. Their growth requirements are so unknown to us that we do not know how to give them the type of seawater constituents they need to reproduce. Thus the only way to begin to understand the metabolic capabilities of these cells is to collect them one at a time, and sequence their genomes. Since many are less than 1/100 the width of a human hair, this is an extremely challenging problem.



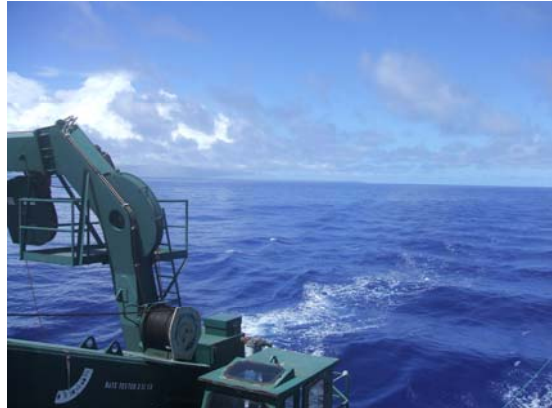
S.W. Chisholm and colleagues have recently cracked this problem by combining a number of cutting edge technologies -- developed for biomedical research -- and applying them to marine microbial systems. They first detect the cells using lasers focused on seawater flowing through a capillary flow cell. As a cell passes through the laser, the cells scatter light, and some of them fluoresce in distinctive colors. Based on these properties the cells can be physically sorted (at a rate of 30,000 cells/second) into individual micro-test-tubes, so that each tube holds *only* a single cell. Then each cell's genome, the DNA that encodes all of the genes that define the cells ecological niche, is amplified in a way that provides enough DNA for genome sequencing. Cutting edge "next generation" sequencing approaches are then applied to obtain the complete genomes of each cell. Sound straightforward? Like most things in science, it seems simple on the surface, but the big challenge here has been

keeping the sample free of extraneous DNA (small pieces of free DNA are everywhere in seawater). Through a series of innovative steps this group has succeeded in keeping the pipeline clean, such that the integrity of each genome is maintained intact. Interestingly enough, this work on single cell sequencing of marine microbes is being followed closely by biomedical researchers, where applications of single cell genomics abound.

The next step is to apply this approach on a large scale, and sequence the genomes of microbes that represent the full diversity of uncultured cells in the oceans. This will give us an unprecedented window into marine microbial diversity, and the metabolic capabilities of biogeochemical provinces in the sea.

Oceans of genes

Microorganisms dominate living carbon in the world's oceans, and just like humans, they contain genes which allow particular types of activities to occur. While genes in humans result in things like blue eyes, in marine microorganisms their genes allow them to take up different types of nutrients, and perform photosynthesis. Because of the enormous diversity of different types of microorganisms in the ocean, and the fact that we cannot isolate many of them, understanding of their gene composition comes from obtaining all the gene sequences of everything in seawater at different locations, a study known as



"metagenomics". Previous metagenomics studies have shown that the diversity of oceanic bacteria is very large, and that microbial communities are much more diverse than previously believed, containing millions of new genes never before observed.

Ian Hewson and Jon Zehr from the University of California Santa Cruz, and David Karl of the University of Hawaii collected and analyzed metagenomic samples from several locations during a C-MORE cruise in the central Pacific Ocean, between American Samoa and Hawaii. This region has several distinct types of oceanic habitats. In the North and South Pacific Ocean water is typically blue and abundance of microorganisms is low, while near the equator spinning of the earth and the resulting upwelling effect on ocean circulation results in much higher concentrations of nutrients at the surface, and, hence, abundances of microorganisms are higher. Over a million fragments of genes were analyzed from these samples using a high throughput DNA sequencing technology.

Because we do not know the sequence of every microorganism on earth, only a small fraction (roughly 1/3) of sequences obtained could be identified. However, the genes that were identified were remarkably similar even from different sampling locations. This was surprising since previous studies have reported great microbial genetic diversity. Interestingly, the composition of microorganisms of the blue waters of the South and North Pacific were similar compared to those from the equator. The frequency of genes that were expected to be found based on the types of nutrients available at the different locations was greatest in waters with high nutrient availability. Thus, the composition of microorganisms at different locations in the oceans appears to be tightly linked to the availability of nutrients, and, consequently the adaptation of microorganisms to utilize them. However, these genes made up a relatively small percentage of all genes. Overall, the results suggest that microorganisms contain genes of similar function in waters of very different character, but rarer genes determine the composition of microorganisms across broad swathes of the ocean.

Taking the pulse of the planet using DNA-based sensors



Researchers at the Monterey Bay Aquarium Research Institute have developed a robotic device that uses DNA and other biomolecules as sensors to detect the presence and abundance of oceanic microbes. The instrument, known as the Environmental Sample Processor or “ESP,” aims to add a new dimension to ocean research and monitoring. Current applications of biomolecular analyses are largely dependent on returning samples to a laboratory. The ESP was designed to reduce that dependency by providing researchers with a “lab in a can” that can be accessed and operated remotely from essentially anywhere in the world where an internet connection is available. This provides a fundamentally different approach for applying molecular sensing technology as a basis for studying and monitoring the oceans. An array of such virtual laboratories also creates new opportunities for effecting water quality measurements and conducting long term environmental assessments. Development of the ESP was made possible through

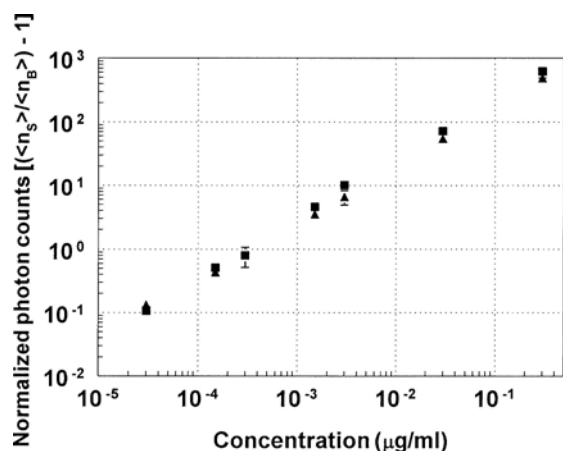
collaborations with workers at Lawrence Livermore National Laboratory, partners constituting the Center for Microbial Oceanography Research and Education, and members of the NOAA/National Ocean Service Marine Biotoxins Laboratory. Funding was provided by NSF, NASA, and the David and Lucille and Gordon and Betty Moore Foundations.

Photo: Divers inspecting the subsurface instrument package during pre-deployment testing.

Integration of the Capillary Waveguide Biosensor with the MBARI Environmental Sample Processor

In recent years, increasing attention has been focused on the pressing need to develop automated, *in situ* methods for the determination of the presence, abundance and activity of marine microbes. The National Oceanographic Partnership Program (NOPP)-sponsored workshop entitled "Monitoring and Measurement of the Ocean Genome" held in Washington, DC on March 7-8, 2005 issued an executive summary noting that "*ocean observatory facilities are a central feature of the future of ocean science, management and monitoring activities and will require associated instrumentation to serve as the necessary sensory organs.*" Workshop participants concluded that "*Arguably the least well developed instrumentation, and the most important from both scientific as well as societal perspectives are biological sensors. For ocean science, few if any robust bio-monitoring devices are currently available.... Development efforts for autonomous biological sampling and sensing instruments are nascent and much more effort will be required to produce readily available and robust biological sensors.*" Given this feedback from the research community, it is not surprising that the National Ocean Research Priorities Plan and Implementation Strategy (1-26-2007) identified sensors for marine ecosystems as one of the four highest-priority areas of research that should be pursued in the next 2-5 years. New prototype biosensors are promising but much research and development work is still needed before they can become a real and trustworthy alternative.

Recognizing the need for automated biological sensors focused on marine microbial organisms and processes, we developed the **Capillary Waveguide Biosensor (CWB)** (Dhadwal et al., 2004, 2007a, b). The CWB is a benchtop instrument capable of measuring picogram quantities (e.g. Fig 1, at right) of specific, targeted nucleic acids derived from marine microbial communities, through repeated cycles over long intervals. Based on its demonstrated capabilities, we will now move on to the logical next step and transform the CWB into an automated, *in situ* monitoring device. The approach will be to couple the bench top instrument to the **Environmental Sample Processor (ESP)** developed by Christopher Scholin and colleagues at the Monterey Bay Aquarium Research Institute (MBARI).



The goal of our research partnership is to develop a rapid-response, quantitative and sensitive optical biosensor for use in moored and deployable instruments, specifically targeted to fundamental questions in microbial oceanography.

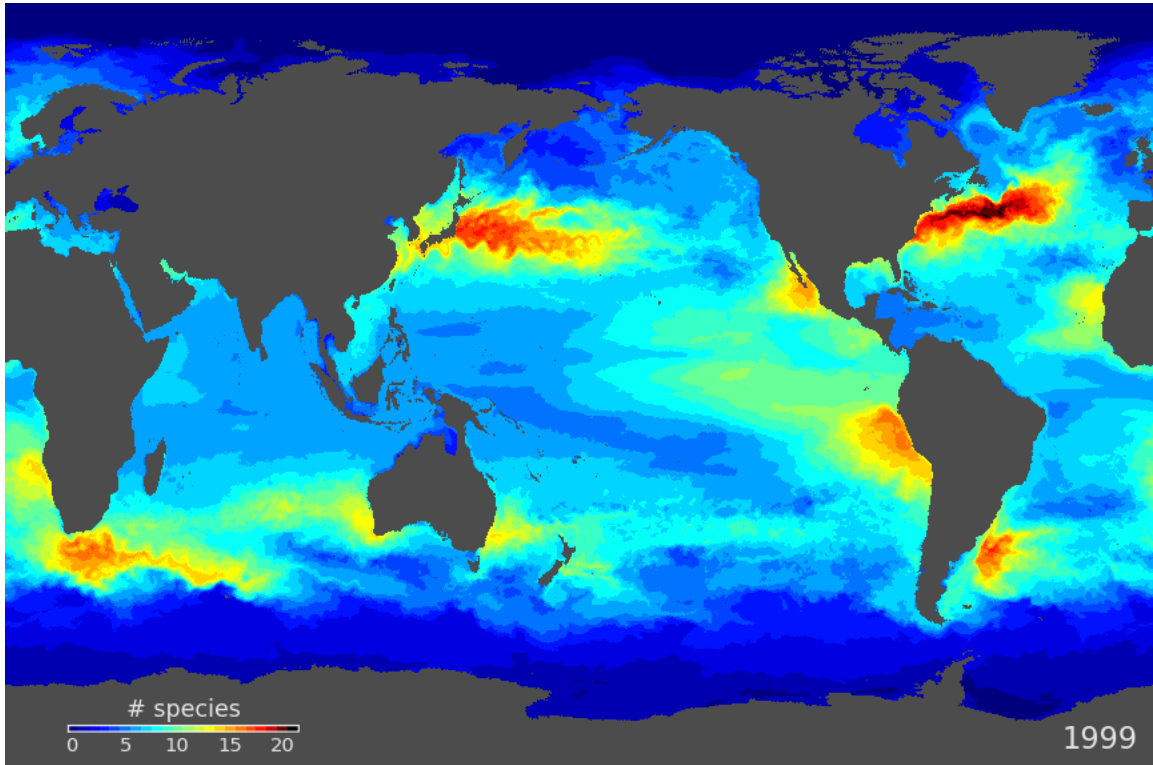
Dhadwal, H.S, P.F. Kemp, J.Y. Aller, and M.M. Dantzler. 2004. Capillary waveguide nucleic acid based biosensor. *Analytica Chimica Acta* 501: 205–217.

Dhadwal, H. S. B. Mukherjee, P. Kemp, J. Aller, Y. Liu, and J. Radway. 2007a. A Dual Detector Capillary Waveguide Sensor for Detection and Quantification of Hybridized Target Species. *Analytica Chimica Acta*. 598: 147-154.

Dhadwal, H. S., J. Y. Aller and P. F. Kemp. 2007b. Method and apparatus for detection and quantification of hybridized target. New Technology Disclosure Technology Transfer Office. The Research Foundation of State University of New York

Modeling ocean microbes

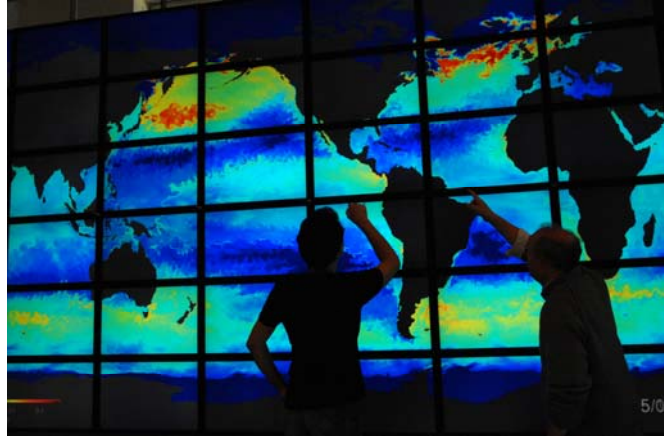
The following results were obtained using an ocean circulation and biogeochemistry model with a self-assembling representation of microbial communities. The model explicitly represents ocean circulation and mixing (at relatively coarse resolution) as well as the cycles of nitrogen, phosphorus, silica and iron, as well as many tens of phenotypes of phytoplankton and two grazers. Phytoplankton types are distinguished by their stoichiometric requirements, their ability to utilize different forms of inorganic nitrogen, and the sensitivity of their growth rate to light, temperature and nutrients. The virtual ecosystem "self-organizes" according to the relative fitness of the initialized organisms. It selects for a subset which persist to populate the virtual environment.



The relatively rich ecosystem of the self-assembling model allows us, for the first time, to examine the emergent patterns of diversity and co-existence in a relatively realistic marine ecosystem model. Though the absolute diversity of phytoplankton types is low compared to real world observations (reflecting the number of limiting factors in such models, Armstrong and McGehee, 1980), the spatial patterns may still be relevant. Two broad features are present in the model (an eddy-resolving version of which is illustrated in Fig. 1, above): (a) "Hot spots" of high diversity associated with the boundary currents and other energetic regimes of circulation, and (b) a background gradient with very low diversity in the polar and sub-polar regimes and higher diversity in the stable subtropical and tropical oceans. The background gradient is consistent with observations from a variety of marine and terrestrial ecosystems. Recently two studies (Pommier et al., 2007; Fuhrman et al., 2008) used genomic approaches to infer consistent meridional gradients in the diversity of bacterioplankton in opportunistic samples from around the globe.

Investigation of our numerical model and idealized theory suggest that this gradient might be governed by the seasonality of the environment in marine microbes (and not by temperature, nutrient concentration, or other hypothesized mechanisms).

MIT researchers Oliver Jahn and Chris Hill look at an animation of a simulation of surface ocean primary production (Figure 2, at right). Primary production is the rate at which new organic matter is created by marine microbes from inorganic resources and energy from the sun. The animation is displayed on a 250 million pixel LCD wall that Hill, Jahn and colleagues designed and brought online in MIT's Stata Center in 2008. The LCD wall contains 60 Samsung panels collectively driven by 30 IBM computers. It was funded by a grant



from the Gordon and Betty Moore foundation as part of the MIT Darwin project, a marine microbiology modeling project led by MIT researcher Mick Follows. Through the efforts of Hill, Jahn and their collaborators the LCD wall provides the MIT community with a 13 x 24 foot programmable canvas that can be used to examine all manner of large images and movies, such as the one shown, that frequently contain more detail than can easily be comprehended on a desktop system. The display surface can also be used to aid comprehension by displaying many related images and movies concurrently. High-resolution information from disciplines as diverse as city planning to astrophysics to systems biology modeling and from instruments as diverse as electron microscopes to the Chandra x-ray telescope can be inspected and visually understood in this way.

R. Armstrong and R. McGehee, Competitive exclusion, *The American Naturalist* 15 (1980), 151-170

Center for Microbial Oceanography: Research and Education New Educational Programs

C-MORE's Education office has three key goals: increase scientific literacy in microbial oceanography among the general public, provide state-of-the-art training to the next generation of microbial oceanographers, and increase the number of under-represented minorities pursuing careers in the geosciences, and related science, technology, engineering, and mathematics (STEM) disciplines. To accomplish these goals, C-MORE has created and implemented a variety of programs over the past year, of which three are highlighted below.

"Key Concepts in Microbial Oceanography" brochure (outreach)

Modeled after the Ocean Literacy Principles, this brochure is designed to establish a benchmark for scientific literacy among the general public in microbial oceanography. It was created by scientists and educators, including C-MORE graduate students and post-docs, to guide C-MORE's education program. The six key concepts identified in the brochure are:

- 1) Microbes were the first life forms on Earth and have been around for billions of years.
- 2) Microbes are everywhere, extremely abundant, and diverse. They represent 98% of the ocean's biomass!
- 3) Life on Earth could not exist without microbes.
- 4) Microbes significantly impact our global climate.
- 5) Most marine microbes are beneficial.
- 6) There are new discoveries everyday in the field of microbial oceanography.

Want to know more? Request a free brochure by emailing cmore@soest.hawaii.edu today! Or download a pdf version from <http://cmore.soest.hawaii.edu/education.htm>

C-MORE Scholars Program (undergraduate)



Currently in its pilot year, the C-MORE Scholars Program provides Native Hawaiians, Pacific Islanders and other students from traditionally underrepresented groups various opportunities to enhance their undergraduate education experience. The program's centerpiece is a closely mentored research experience, offered at three academic levels depending on the student's skills and knowledge level. Students also receive career and academic advising, free tutoring in math and science courses, professional development training, and cohort-

building activities. C-MORE Scholars are expected to give back to their community: they actively participate in C-MORE's outreach activities throughout the academic year. Students may reapply to be a C-MORE Scholar each semester, and there is a required orientation at the start of the Fall and Spring semesters.

C-MORE Summer Course in Microbial Oceanography (graduate & post-doc)

C-MORE is pleased to offer "Microbial Oceanography: Genomes to Biomes", an international summer course for graduate students and post-doctoral researchers. To be held June 08 to July 17, 2009 at the University of Hawaii in Honolulu, this state-of-the-art course will explore the dynamic and fundamental role marine microbes play in shaping ocean ecology and global biogeochemistry. During these six weeks, the students will receive intensive laboratory and computer training, and will work as a team to plan and implement a research cruise. This course is team-taught by a number of the world's most renowned microbial oceanographers, including several C-MORE faculty members from both the University of Hawaii and C-MORE Partner Institutions.

Undergraduate intern research: dinoflagellates and ciguatoxin

C-MORE undergraduate research intern Jan Nakaya worked with scientists from the NSF/NIEHS-funded Oceans and Human Health Center, the Pacific Research Center for Marine Biomedicine (PRCMB) studying the taxonomy, physiology, and ecology of ciguatoxin-producing dinoflagellates, *Gambierdiscus sp.* The particular question she asked was "Is there any correlation between the taxonomic composition of the microbial consortia found in cultures of *Gambierdiscus* and the ability of the dinoflagellates in those cultures to produce ciguatoxin?" She found that, indeed, the consortium associated with a toxin-producing culture of *Gambierdiscus* was qualitatively quite distinct from consortia found associated with cultures that did not produce toxin. With PRCMB sponsorship, she presented her work at the Oceans and Human Health Gordon Conference during the summer of 2008, in the form of a poster entitled **Microbial Consortia Associated with Ciguatoxin-Producing Cultures of the Dinoflagellate *Gambierdiscus*.**

Upon the conclusion of her C-MORE internship and the award of her B.S. degree in Marine Science, Ms. Nakaya took a position as chief technician in an industry-academia partnership focused on the investigation of the potential biofuel value of marine microbes.

Eco-DAS: Ecological Dissertations in the Aquatic Sciences

Ecological Dissertations in the Aquatic Sciences (Eco-DAS) continues the series of symposia formerly known as DIALOG I-VII (Dissertations Initiative for the Advancement of Limnology and Oceanography), but takes that series in new directions. Key elements of the remodeled symposia include:

1. Fostering sustained, cross-disciplinary interactions among the top new researchers in ecological oceanography and limnology, to the benefit of both the science and the researchers.
2. Increasing the success rate of new researchers seeking funding to build their research programs, by familiarizing them with the diversity of available research opportunities, and introducing them to representatives of funding agencies with whom they will interact in future.
3. Increasing the likelihood of professional success for these new researchers by:
 - Highlighting their initial work through high-visibility, open-access publication of a formal symposium proceedings volume, to be published in 2009;
 - Focusing that volume on interdisciplinary and collaborative aspects of their work; and
 - Establishing mentoring relationships between participants and established scientists.

Eco-DAS VIII was held on 11-16 October, 2008, at the East-West Center immediately adjacent to the University of Hawai`i, Manoa campus. Thirty-eight invited participants, 4 mentors and 4 representatives of federal funding agencies met for six days to present and discuss state of the art research in the ecology of aquatic ecosystems, to strengthen existing collaborations and form new partnerships, and to discuss the most challenging issues in aquatic ecology today. *See poster on following page.*

Eco-DAS funding is provided by NSF with contributions from ONR, NASA and NOAA. Eco-DAS is sponsored by the **Center for Microbial Oceanography: Research and Education (C-MORE)**, the University of Hawai`i School of Ocean and Earth Science and Technology (SOEST) and the Department of Oceanography, and the American Society of Limnology and Oceanography (ASLO).

For more information, visit the Eco-DAS website at:
<http://cmore.soest.hawaii.edu/eco-das/index.htm>

Eco-DĀS VIII

Ecological Dissertations in the Aquatic Sciences

East-West Center, University of Hawai'i at Mānoa
11–16 October 2008

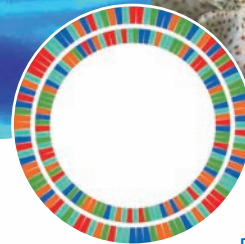
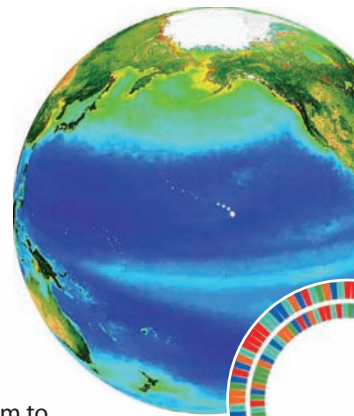
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 - a. Highlighting their initial work through high-visibility, open-access publication of a formal symposium proceedings volume;
 - b. Focusing that volume on interdisciplinary and collaborative aspects of their work; and
 - c. Establishing mentoring relationships between participants and established scientists.

Symposia are currently funded for fall of 2008, 2010, and 2012. The 2008 symposium will be held at the East-West Center, University of Hawai'i at Mānoa campus, 11–16 October. Applicants for the fall 2008 symposium must have received their PhD on or after 30 April 2007, or expect to receive it before 30 April 2009. The dissertation work of the applicant must deal with an important ecological problem in oceanography or limnology. Applications will include: a current resume, a letter of support from the applicant's current (graduate or postdoctoral) advisor, a personal statement regarding the applicant's goals and reasons for applying, and a substantive outline of a proposed chapter to be included in the formal symposium proceedings.

Applications are due by 30 April 2008. For more information regarding the symposium, including application requirements and procedures, see cmore.soest.hawaii.edu/eco-das/.

Funding provided by NSF with contributions from ONR, NASA and NOAA. Eco-DĀS is sponsored by the Center for Microbial Oceanography: Research and Education, the University of Hawai'i School of Ocean and Earth Science and Technology (SOEST) and the Department of Oceanography, and the American Society of Limnology and Oceanography (ASLO).



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Above images by participants in 2007 Hawai'i Summer Session in Microbial Oceanography.

C-MORE sponsored Microscopy Workshop for Phytoplankton and Bacterioplankton Identification Hawai'i Institute for Marine Biology (HIMB), Coconut Island, HI (Sept. 21-26, 2008)

The individuals most and best trained in plankton cell identification by microscopy and basic cell counting techniques are typically in the more senior positions and are reaching the point of retirement. It seemed only necessary to provide a platform for the dissemination of the knowledge and invaluable skill set of our most experienced microscopists to the next generation of scientists.

Co-organizers, Rachel A. Foster, a postdoctoral scholar from UCSC and Michael Rappé, assistant professor at University of Hawaii, led a small workshop of 13 participants at the Hawai'i Institute of Marine Biology on Coconut Island. Two esteemed senior experts, Edward J. Carpenter, a professor of SFSU, and John W. Waterbury, associate scientist of the Woods Hole Oceanographic Institution (WHOI), were invited to tell their "secrets" on collection strategies and cultivation "recipes" for isolating marine microbes. Participants were also trained in fluorescently labeled *in-situ* hybridization (FISH) microscopy techniques, and learned side by side with the experts on how to use different light filters of an epi-fluorescent microscope to identify the local plankton of Kaneohe Bay, Hawai'i.



John B. Waterbury showing participants of the C-MORE funded Microscopy Workshop for Phytoplankton and Bacterioplankton Identification (Sept. 21-26) how to "seed" cultures from seawater concentrates. From right to left: Misty Scevola, Andrew Allen, John Waterbury, Jan Nayaka, and Sheree Watson.

Survey of Underwater Plastic and Ecosystem Response (SUPER)

Plastic trash in the North Pacific Ocean has been dubbed the Great Pacific Garbage Patch and the Pacific Plastic Vortex. Although this area was discovered over ten years ago, there is much that we still don't know about the composition, distribution, fate, and consequences of the refuse.

During the Survey of Underwater Plastic and Ecosystem Response (SUPER), C-MORE researchers took the first steps to understanding how plastic debris in the ocean impacts this essential community of organisms. In September 2008, C-MORE researchers, students, and technicians from the University of Hawaii and Oregon State University conducted a seminal expedition across the North Pacific Subtropical Gyre to research the ecosystem characteristics and impacts of recalcitrant marine debris.



Some of the questions addressed during the 12-day cruise include:

1. Do plastic particles provide a unique habitat for microbes?
2. What kinds of microbes are associated with plastic debris?
3. Does plastic waste affect rates of bacterial production and metabolism?
4. Does plastic waste affect the distribution and cycling of nutrients in the ocean?

During the twelve-day cruise, the crew sampled 15 stations along an oblique course from Honolulu, HI to California. Each of the 14 trawls along the 2215 km-long transect yielded several hundred pieces of plastic fragments. These samples are being used to characterize the diversity and productivity of plastic-associated microbial communities, while water samples that were collected at each station will be analyzed to describe regional biogeochemistry. As samples are analyzed, data are posted at:

<http://hahana.soest.hawaii.edu/cmoresuperhicat/superhicat.html>

The success of this preliminary investigation made the expedition super, indeed! We hope that our study will contribute to understanding the effects of refractory debris on marine ecosystem dynamics and will stimulate further interest in this contemporary issue.



Lucy Marcus, a documentary filmmaker and marine biologist, joined the C-MORE SUPER (Survey of Underwater Plastics: Ecosystem Response) Cruise to record and describe the research activities aboard this cruise, which dealt with the effects of particulate plastic accumulations in the North Pacific gyre on microbial life. Lucy has provided photo/video documentation of the cruise, blogging about the activities at sea, and assisting with sample collection and processing. The blog, photos and video aim to provide students and the public with meaningful, scientific, and occasionally entertaining commentary about the materials, methods, and basic results of the 12-day cruise, as well as an introduction to daily ship life and the personnel involved with the cruise. For more information about the video and

blog, visit the cruise website:

<http://cmore.soest.hawaii.edu/cruises/super/index.htm>

Doney testifies before Congress



Scott Doney testified twice before congressional hearings on issues of climate change, marine ecosystems and ocean acidification.



A quote from one testimony was used as a wall display to frame an exhibit on climate change at the newly opened California Academy of Sciences in San Francisco CA.

C-MORE partners with Discovery Channel for episode of the *Planet Earth* series

Ricardo Letelier and Dave Karl recently published a paper in the journal *Marine Ecology Progress Series* where they presented a novel hypothesis for microbial-based carbon dioxide sequestration in tropical seas. Their paper was part of a special "theme section" in that journal on the legal, ethical and environmental consequences of nutrient fertilization as a means of ameliorating greenhouse gas induced climate degradation of our planet. In their model, Letelier and Karl proposed using artificial upwelling to stimulate phytoplankton growth and carbon dioxide uptake. Based on a quantitative assessment of the vertical distributions of nitrate, phosphate and dissolved inorganic carbon at the Hawaii Ocean Time-series benchmark, Station ALOHA, the authors hypothesized that controlled upwelling of deep water with a low nitrate-to-phosphate ratio (<16:1 by moles) would lead to the selection for nitrogen-fixing microorganisms due to the excess phosphate remaining after complete removal of nitrate by an initial diatom-based bloom. The secondary bloom of nitrogen-fixing microorganisms would remove excess carbon dioxide, a portion of which would be lost through gravitational settling of particulate organic carbon to the deep sea. It was emphasized that the use of natural seascape engineering to enhance the ocean's biological carbon pump may have unintended ecological consequences, but was worthy of further study. Sitting idle or criticizing those who do take a position on geo-engineering are not acceptable options because human-induced climate change is already having measurable and deleterious environmental consequences.

About the same time as this upwelling study was being conducted, the authors were approached by the Discovery Channel with a proposal to include the first ever field test of the open ocean upwelling hypothesis as one of six 1-hour episodes in a new educational television series called *Project Earth*. Each of the episodes would chronicle a novel geo-engineering prospect to address the climate crisis, from theory to conceptual experimental design to field testing. Our episode, *Hungry Oceans* (as in hungry for nutrients) was filmed by Impossible Pictures during research cruises in May and June 2008. More than 150 hours of professional high definition video were recorded, including shore-based scenes in several C-MORE laboratories and interviews with C-MORE personnel. The result was a dramatic and informative science educational film that, to date, has been well received by both the general public and most of our scientific colleagues.

Discovery Communications, the parent corporation of Discovery Channel, is the world's leading nonfiction media company with a focus on science education. Their programs, like *Hungry Oceans / Project Earth*, reach more than 1.5 billion cumulative subscribers in 170 countries. C-MORE is now a part of this science education and outreach legacy.



C-MORE hosts international ocean acidification conference

One of the least-understood consequences of increasing carbon dioxide concentrations in the atmosphere is that the oceans are becoming more acidic.

This is because CO₂ in the air dissolves in seawater to form carbonic acid — a weak acid that makes the oceans slightly more acidic. The rate of change is extremely rapid and it is expected that by the end of this century, the oceans will be more acidic than they have been for more than 20 million years. Indeed, ocean acidification has been termed “the other CO₂ problem” by C-MORE co-PI Scott Doney.

Over geological time scales, the pH of the seas has changed significantly in response to variations in atmospheric CO₂. Indeed, the ocean has in the past been more acidic than we expect it to become over the coming decades. But what is different this time is the speed of change. Ecosystems have proved their ability to accommodate change when it is gradual, usually over hundreds of thousands of years. We do not know how well the marine ecosystem will adapt to changes that will occur over decades.

Microbes are the most important organisms in the sea. In contrast to the land, where plants are large and long-lived, in the seas most of the primary production comes from microscopic algae, or phytoplankton. These have tiny biomass and their generations last only days. The productivity of this phytoplankton depends in turn on bacteria and archaea to regenerate nutrients. So it was a priority to determine how marine microbes would respond to a high-CO₂ world.

Microbes control biogeochemical cycles and keep the planet habitable. This means we need to know how microbial populations will respond to rapid climate change. We need to do experiments to understand how marine microbes will respond to pH change.

Such experiments will be complex because pH varies naturally over the course of a year. When phytoplankton populations begin to grow in the spring they consume CO₂ that is dissolved in seawater. The result is that pH increases for a period of a few weeks. The dissolved CO₂ gradually increases as a result of bacterial activity and the pH declines to a more typical values. In a high CO₂ world, this seasonal variability will still exist but the microbial populations will be exposed to a different range of pH values than in the present day.

From 24-26 February 2009, C-MORE will host an international symposium to discuss and debate the impacts of rising CO₂ and ocean acidification on marine microbes. The first day of the conference will coincide with a symposium of scholarly talks that will be open to the public. On day two, C-MORE will also host a parallel session that will engage a selected group of 15 teachers who will also learn about the important issue of ocean acidification. This lesson will include a review of the components of a new science kit that has been prepared by the C-MORE Education team to provide hands-on classroom exercises geared towards grades 6-12.

One outcome of the workshop will be a report that will review our current understanding and future challenges. Hopefully, this effort will facilitate future research as well as inform policy makers and the public at large.



An International Symposium at the University of Hawai'i at Mānoa

Rising CO₂, Ocean Acidification, and Their Impacts on Marine Microbes

Tuesday 24 February 2009

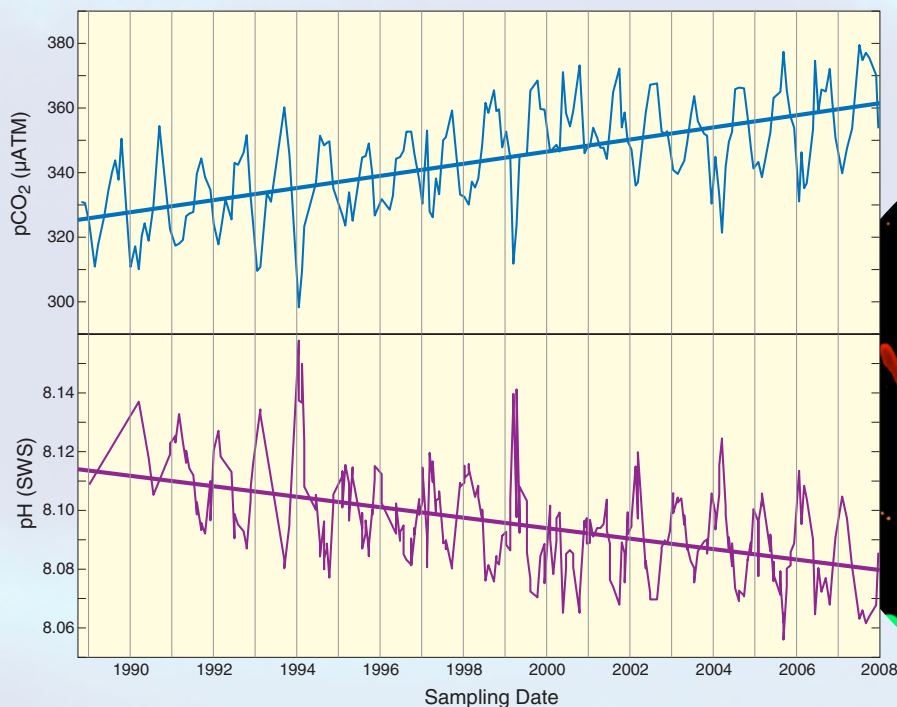
8:30 am – 4:00 pm

Coffee at 8 am

**Keoni Auditorium,
East-West Center,**

University of Hawai'i at Mānoa

The Station ALOHA Curve



Lunch provided

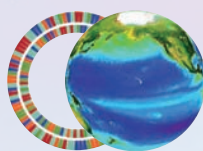
*RSVP by Monday 16 February
to Sharon Sakamoto
(sharons@soest.hawaii.edu)*

**For agenda and background information, visit:
cmore.soest.hawaii.edu/oceanacidification/**

Organized, sponsored and hosted by



Plymouth Marine Laboratory (PML) and
Center for Microbial Oceanography:
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