

the primary food for 4.5 years from hatching to metamorphosis. Larval shell increased in width and length from 0.24 x 0.20 to 3.0 x 3.4 mm (greatest dimensions perpendicular and parallel to shell axis). Mean shell sizes increased slowly during their later years as larvae. The final protoconch width was similar to the 2.7 and 2.8 mm width on shells of field collected snails, indicating that size at metamorphosis was close to that in nature. Larvae had 4 narrow velar lobes. The total transverse spread across the velar lobes was as great as 2 cm. Fouling on shells of old larvae included diatoms and vorticellid and foliulinid ciliates. The larvae spent their last two years mostly on the bottom of the gently stirred glass jars with velar lobes extended. They did not metamorphose until the 11 survivors, out of the 4000 initially cultured, were presented with subtidal rocks and shells as substratum. Five metamorphosed juveniles survived and grew, the two females first reproducing 3.5 years after metamorphosis. This extraordinarily long larval period in culture may not reflect the natural duration but indicates the possibility of larval periods far longer than previously suspected. The larval duration exceeded the time from metamorphosis to first reproduction and greatly exceeded previous estimates of maximum time for larval transport in ocean currents.

## OS21G-141 0830h POSTER

### Response of Anchovy (*Engraulis ringens*) off Northern Chile to the 1997-1999 El Niño - La Niña Sequence

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Anchovy are known to be strongly dependent on environmental condition over their life cycle. The 1997-1999 El Niño-La Niña sequence presented an excellent opportunity to observe their response to large scale changes in oceanographic conditions off northern Chile. Observations from a sequence of cruises sponsored by Chilean Fisheries Institute (IFOP) and other data allowed us to determine that response. The data include spatial and vertical anchovy distribution off northern Chile (18°S - 24°S), sea surface temperature (SST) images, CTD data from seasonal cruises and wind stress from coastal stations. The data on anchovy came from industrial fisheries catch data and anchovy vertical and spatial distributions from seasonal acoustic cruises.

The data was separated into coastal and oceanic and latitudinal zones to create a time series suitable for statistical analysis. The sequence started in March 1997 with warm and salty waters propagating along the South America coast. Maximum temperature and salinity anomalies in surface water were 4°C and 0.6 respectively. The anomaly reached depths of 400 m and was within 50 km of the coast in December 1997. After the maximum in December the anomalies diminished to reach normal values by August 1998. Then the region passed into a cold phase in which the system is highly productive.

At the beginning to the El Niño, the anchovy responded by concentrating along the coast (first 20 km) where they were more vulnerable commercial fisheries. During this time mortality was high because of the effective fishery (high landings) and environmental stress was high because of El Niño conditions. Later the anchovy moved southward along the coast, and deeper in search of the food and colder water that they prefer (14 to 20°C). They were located between 40 m and 80 m depth (20 to 40 m deeper than normal) near the bottom and far out of range of the net of commercial fishing. They remained at the deeper more southern location until the conditions returned to normal in August 1998. When the anchovy reappeared at their normal locations of fisheries, the biomass was relatively high. This suggests that with the onset of upwelling during La Niña period, the stock began their slow recuperation.

## OS21G-142 0830h POSTER

### Prey Selection, Grazing Rates and Egg Production of Calanoid Copepods in the Firth of Forth, Scotland

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In this study we investigated rates of fecundity, feeding, and prey selectivity by the dominant calanoid copepods at a fixed station in the Firth of Forth, an

estuarine system on the east coast of Scotland. At fortnightly intervals over a full annual cycle copepods were collected, and adult females of the dominant species incubated with natural seawater over 24 hours under closely controlled conditions. Species examined included *Acartia biflosa*, *A. discuadata*, *A. clausi*, *Centropages hamatus* and *Temora longicornis*. Egg production rates by these copepods and their grazing rates upon nano- and microplankton were quantified by microscope counts. We describe seasonal feeding rates, and prey selection for each of these species. All species cleared ciliates at the highest rates, with the exception of the highly motile species *Mesodinium rubrum*; while the tintinnids were generally cleared more than the aloricate ciliates. With the exception of *Gyrodinium* spp., all dinoflagellates were grazed at rates lower than other microplanktonic taxa, possibly indicating active avoidance by copepods. Egg production peaked in May for *Acartia discuadata* and *Temora longicornis* with maximum rates of 32 and 33 eggs per female per day respectively, rates peaked in mid-July for *Acartia clausi* and *Centropages hamatus* at 35 and 70 eggs per female per day respectively.

## OS21H HC: 318 A Tuesday 0830h

## Marine Microbial Genomics Session

**Presiding:** G Taroncher-Oldenburg, Princeton University; B Ward, Princeton University

## OS21H-01 0830h INVITED

### The Marine Environment From a Cyanobacterial Perspective

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The genome sequence of the marine cyanobacterium *Synechococcus* strain WH8102 is nearly completed. This microorganism was chosen because cyanobacteria similar to WH8102 are ubiquitous and significant primary producers in oligotrophic marine environments. In addition this strain possesses a unique type of prokaryotic motility and is amenable to genetic manipulation. The genome is estimated to be 2.7 Mb with approximately 2390 ORFs. The transporter complement of *Synechococcus* WH8102 was analyzed by screening its genome against a database of known and putative transporters by BLAST and HMM-based analyses. Approximately eighty transport systems were identified comprising 130+ genes. Comparison with the transporter complement of other complete genomes indicated that WH8102 has an emphasis on transport of inorganic anions, in particular with multiple transporters for nitrate, sulfate and chloride. In terms of organic nutrients it is predicted to transport a variety of amino acids and a limited number of sugars. The transporters and other activities of the cell are coordinated by a surprisingly small number of two component regulatory systems compared to the freshwater cyanobacterium *Synechocystis* PCC6803. Ultimately the WH8102 genome will provide us with a better understanding of how cyanobacteria perceive and respond to the marine environment.

## OS21H-02 0900h

### Defining the Fe Scavenging Mechanism of Marine *Synechococcus* Using Molecular Approaches

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Cyanobacteria of the genus *Synechococcus* are prominent components of the marine biosphere that contribute significantly to primary productivity. Recent field studies have shown that growth by marine *Synechococcus* can be limited by bioavailable Fe. Despite the demonstrated physiological importance of Fe for open ocean *Synechococcus*, we know very little about how they scavenge it from the environment. Recently the Joint Genome Institute and the Department of Energy sequenced the complete genome of *Synechococcus* WH8102. In an effort to understand how these cyanobacteria persist during periods of Fe deprivation, we have performed physiological and genomic experiments to define their Fe scavenging mechanism. By determining how these microorganisms respond to Fe stress, we will gain insight into how and when this important trace element can limit their growth in situ. This knowledge will greatly increase our understanding of how marine Fe cycling impacts oceanic processes.

## OS21H-03 0915h

### A Search for Cobalt Proteins in *Synechococcus*: Overexpression of the Gamma Carbonic Anhydrase Enzyme and a Genome Wide Analysis of Cobalt Limited Cells

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The marine cyanobacteria have an absolute cobalt requirement for which zinc cannot substitute. Cobalt concentrations in seawater are extremely low and may therefore affect primary productivity or phytoplankton species abundance. Yet it is not known what the predominant biochemical function of cobalt is in the surface oceans. We hypothesize that the metal in the active site of the gamma carbonic anhydrase of marine cyanobacteria may be cobalt and this may be a major use of cobalt in the surface oceans. The gamma carbonic anhydrase gene was PCR-amplified from genomic DNA of marine *Synechococcus* WH8102, cloned, and the correct sequence was verified by complete double strand sequencing. The gene was then cloned into an expression vector, overexpressed into *E. coli*, and purified and characterized from inclusion bodies. Strategies for refolding the protein with cobalt and zinc will be presented. Results from a parallel whole genome microarray study of cobalt limited *Synechococcus* WH8102 to identify other potential cobalt dependant proteins and pathways will be discussed in the context of our limited understanding of the biochemical function of cobalt in the cyanobacteria.

## OS21H-04 0930h INVITED

### Chronology of the Transcriptional Response to Environmental Stimuli in Cyanobacteria

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Aquatic microorganisms exhibit a wide range of adaptation mechanisms to a variety of changes in their environment. The response to a new stimulus can occur at different levels, but is most often centered on fine tuned variations in the transcriptional profile of the cell. In this contribution we will illustrate the molecular chronology of such changes as they occur at the whole genome level. Two different examples of response to environmental stimuli in cyanobacteria are presented. First, we will analyze the transcriptional program elicited by the light to dark transition in the freshwater cyanobacterium *Synechocystis* sp. PCC6803. Special attention is given to genes related to light harvesting, energy transformations and central carbon metabolism. In a second example, the whole genome response of the marine cyanobacterium *Synechococcus* sp.

WH8102 to changes in levels of the trace metal cobalt is investigated. Common characteristics to the transcriptional profile dynamics in both cases are coregulation of polycistronic genes and overshoot dynamics that are ubiquitous in most biological systems. Results on specific genes and pathways will also be presented.

#### OS21H-05 1030h INVITED

##### Creating Large and Small Insert Chromosomal Libraries From Naturally Occurring Microbial Populations: Nuts And Bolts

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Secrets of the natural microbial world, including the specific biological properties and function of microbes in Nature, can in part be revealed by directly sequencing the genomes of these organisms. There are a number of different strategies and approaches for archiving and extracting the genomic sequence from microbes present in natural populations. One approach, of course, is simply to cultivate the microbe, and sequence its genome using now standard shotgun sequencing strategies. This approach is not always practical, feasible, or possible. Another approach is to construct large or small insert genomic libraries from mixed microbial assemblages, and either randomly, or systematically, sequence and analyze microbial genomic fragments. The different strategies and vectors include small insert shotgun libraries (insert size around 3 kilobases (kb)), fosmid or cosmid libraries (insert sizes around 40kb), and bacterial artificial chromosome (BAC) libraries (inserts up to 200 kb), and each approach has its strengths and weaknesses. We have had success with preparing libraries from naturally occurring bacterial or viral populations. Libraries currently being analyzed include those from bacterial and viral populations of marine plankton, and microbial communities in anaerobic marine sediments. These are now providing significant new insight into the genomic and functional properties of microbes from diverse ecosystems.

#### OS21H-06 1100h

##### A General Method for Growing Unculturable Microorganisms

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The majority of microorganisms from the environment resist cultivation in the laboratory. Several Bacterial and Archaeal groups at the division level have been identified with no known cultivable representatives. The 16S rRNA approach provided important insights into the spectacular diversity of uncultivated microorganisms. However, it does not provide access to the actual cells and means to grow them. Such access would be highly desirable for both basic and applied environmental sciences. Here we report a new general method for growing previously uncultivated microorganisms. Diffusion growth chambers have been designed that allow the growth of these microorganisms in pure culture by providing a simulated natural environment. We will discuss design of the chambers, provide examples of first uncultivables growing in our laboratory, characterize these novel organisms using 16S rRNA data, and outline the potentials of the new method.

#### OS21H-07 1115h INVITED

##### Nitrogen Assimilation: from Genomes to Gene Expression in the Oceans

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Nitrogen (N) assimilation is intimately linked to controls on primary production in the open ocean. The application of the polymerase chain reaction has provided information on the diversity and distribution of the genetic information for specific N utilization pathways, from transport to assimilation. Amplification of nitrogenase (nif), and assimilatory nitrate reductase (nar and nas) genes indicates that the genetic capability for different N metabolic pathways is dispersed throughout microbial phyla, and that genotypic as well as phenotypic differences among microbial assemblages are likely to be important in determining the pathways of nitrogen use, and the ecological distribution and activities of individual species. Gene expression assays provide ways of identifying important players in nitrogen metabolism.

Assimilatory nitrate reductase genes are less widely distributed among cyanobacteria and heterotrophic bacteria than might be expected. It has recently been shown that *Prochlorococcus* does not contain nitrate reductase genes, which suggests that the genome has eliminated unnecessary genetic information for organisms living in oligotrophic surface ocean waters. Nitrogenase-containing microorganisms are more diverse and abundant in the open ocean than previously believed, but relatively few major clades have been discovered. There is a high diversity of nitrogenase-containing microorganisms in some high fixed N environments such as the Chesapeake Bay and deep waters of Mono Lake. Thus, ecosystem comparisons suggest that nitrogenase diversity is not selected for by N-limiting conditions, and that genes are not necessarily eliminated from the genome in non-N-limiting environments. The data indicate that there are multiple ecological and evolutionary forces selecting for genome composition of individual species or phylotypes, including selection at the organism or community level.

Over 50 microbial genomes have been sequenced or are in the process of being sequenced, as well as genomic fragments from marine environments. Statistics from these prokaryotic genomes indicate that 1) N metabolism genes are not well-represented in these genomes or that the genes have not been annotated correctly, 2) that the genomes that have been sequenced may not be good models for the study of N assimilation in the environment and/or 3) that nitrate might not be used by many prokaryotic microorganisms. Genomic information provides important contextual information, including gene arrangements and new genes to target in environmental studies, yet one of the major limitations of genomic information is that some biochemically-important microorganisms can be relatively low in abundance, making it difficult to obtain biochemically-relevant information directly from genomic fragments obtained from the environment.

#### OS21H-08 1145h

##### A Multisystematic Approach Towards Understanding the Metagenome of the Episymbiotic Community Associated With *Alvinella pompejana*

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A diverse episymbiotic bacterial community is associated with the tube-dwelling polychaete, *Alvinella pompejana*. This association exists in an extreme deep-sea hydrothermal vent biotope characterized by high concentrations of heavy metals and the steepest thermal gradient experienced by any organism yet described. Detailed rRNA analysis of the episymbiotic communities associated with *A. pompejana* demonstrates the dominance of a diverse assemblage of a single subdivision (epsilon *Proteobacteria*). Because of the complex nature of this association, no specific roles have been defined for this unique symbiosis by habitat characterizations, in situ enzyme assays, classical cultivation techniques or molecular analysis. Initial approaches to investigate the symbionts centered on rRNA analysis, where two filamentous epsilon *Proteobacteria* dominate the microbial community. Current work in our laboratories centers on a whole genomics approach. High throughput sequencing efforts allow the creation of a metagenome, where genomes of a diverse ecological unit

are cloned and sequenced. These collective genomes can be thought of as a core genome, containing all the genes necessary to perform the diverse biogeochemical reactions that make up a specific community function. Initial analyses presented here include the sequencing of two large insert fragments (approximately 40kb each) specifically linked to the two dominant symbiont phylotypes. We have also begun to use a metagenome approach in order to understand the symbiont community at a functional ecological level. A cDNA library has been made from ribosomal depleted RNAs isolated from an *A. pompejana* symbiont community from 9°N, East Pacific Rise. Preliminary sequence analysis from this library will also be presented.

#### OS21I HC: 314 Tuesday 0830h

##### Reforming Education in the Ocean Sciences for All Citizens II

Presiding: J Cherrier, Florida A&M University; C

Thoroughgood, University of Delaware; P Coble, University of South Florida

#### OS21I-01 0830h INVITED

##### The Art of the Possible, The Science of the Priorities: Educational Opportunities for the Ocean Sciences

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Graduate education in our field is changing as the focus of research moves to address the questions driven by the concerns and values of the twenty-first century. Undergraduate education is changing with the shift from teaching to learning, especially with the shift to experiential learning and collaborative learning. In ocean sciences we are coming to terms with how to integrate collaborative learning and experiential learning into our mandates for teaching and research on campus. The vast responsibility of public involvement and education still is open. At the K-12 levels four broad terms dominate the agenda, namely standards, assessment, technology and communication. How can ocean sciences help teachers gain the knowledge of the content areas and the skills of science for elementary level teaching? How can ocean sciences help teachers develop among their students problem solving skills? How can ocean sciences help students become adept at using technology in problem solving? And lastly, how can ocean sciences help students select and discuss a problem and its potential solutions and thereby demonstrate problem solving skills? I will discuss the range of possibilities and suggest some ideas that involve not just ourselves at research focused institutions, but also involve agencies, their staff and the chances for a higher level of collaboration.

#### OS21I-02 0900h

##### Inquiry Based Learning and Assessment in General Education Science Courses

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Two major goals of General Education Science Courses are to recruit top students into science and to provide a large number of non-science majors with the critical thinking skills that they may use throughout their adult lives. In this way ocean and/or environmental sciences may become an integral part of the daily lives of the general public. While most educators agree that effective science learning occurs in small groups with hands-on experiential learning and interaction between the teacher and student, many administrators prefer to maximize university resources by increasing class sizes.

In an attempt to provide quality science instruction to a large General Education audience, Introduction to Environmental Sciences was offered to 230 students at UMassBoston in the Fall of 2001. Due to unique circumstances, 50 of the students were required to attend weekly discussions (ES 120; 10-15 students/section) while the other 180 were required to write 4 papers (ES 101). All 230 students attended the same two 75 minute lectures each week. In class peer-instruction, group activities, and a class web site were used to engage students. On a traditional exam of multiple choice and short answer questions, ES 120 students performed