

## OS21F-123 0830h POSTER

## Nutrification levels and Benthic Community Dynamics in Brazilian Coral Reefs

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Coral reefs are undergoing increasing deterioration worldwide, one of the major causes of coral reef demise being nutrification (large increase in nutrient availability changing the center of productivity from the benthos to the plankton). At early stages, nutrification causes phytoplankton blooms, reducing water transparency. Continued nutrient load may cause coral-algal phase shift, with calcification decrease and benthic dominance by deposit and suspension feeders and algae.

To assess nutrification levels in Brazilian reefs, measurements of the distribution patterns of nutrients and chlorophyll concentrations were conducted in three coastal and offshore reefs with distinct nutrient inputs along the south coast of Bahia State. Seawater and porewater samples were analysed for soluble reactive phosphorus, total oxidised nitrogen and reactive silica. Benthic surveys were performed at all sites to investigate the relationships between benthic community composition and nutrient and chlorophyll concentrations. Sampling was undertaken in dry and rainy seasons.

Nutrient profiles for control sites contrasted markedly with those from impacted sites. Results of both seawater and porewater nutrient measurements revealed the occurrence of consistent spatial and temporal patterns. An inshore-offshore gradient reflects the occurrence of land-based point sources, with significant amount of nutrients being delivered by human activities on the coast (untreated sewage and groundwater seepage). Another spatial gradient is related to distance from a localized source of pollution (an urban settlement without sewerage treatment) with two nearshore reefs presenting distinct nutrient and chlorophyll concentrations. Seasonal variations suggest that submarine groundwater discharge (SGD) is the primary source of nutrients for the coastal reefs during rainy season. The data also suggests that the SGD effect is not restricted to nearshore reefs, and may be an important factor controlling the differences between landward and seaward sides on the offshore reef.

Benthic community assessment revealed that turf algae is the dominant group in all studied reefs and that zoanthids are the organisms most adapted to take advantage of nutrient increase in coastal areas. At nearshore reefs, there was a negative correlation between zoanthids and algal abundance and a positive correlation with the amount of available space for settlement. On the offshore reef, correlation of algal cover with both zoanthids and available space were negative, suggesting that hard substrate may be the primary limiting factor for algal settlement and growth in the nearshore reefs. Highly variable physical disturbances (like wave energy and low tide exposure) between landward and seaward reef sides appear to be the factors controlling algal distribution in the offshore reef. Highly spatial variability in coral cover ultimately reflects the patchy distribution of stony corals over the reefs.

## OS21F-124 0830h POSTER

## Effect of Bleaching on Lipid Biomass in two Hawaiian Coral Species

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Bleaching events can result in mass mortality among corals. However, the impact of these events is not consistent throughout the reef: some corals are not affected, while others either recover or die as a result of bleaching. Scleractinian corals acquire photosynthetically derived energy from their endosymbiotic zooxanthellae and store any excess in the form of lipid. Decreases in zooxanthellae and/or chlorophyll a during bleaching could result in decreased photosynthesis and energy acquisition. We hypothesize that bleached corals have lower lipid levels than healthy, unbleached

corals. Lipid levels were measured in 50 *Porites compressa* and *Montipora verrucosa* corals collected from Coconut Island Reef, Kaneohe Bay, Hawaii following a bleaching event. Bleaching severity was quantified by the concentration of the algal chlorophyll a pigment. Results for *P. compressa* were consistent with our hypothesis: lipid levels decreased with bleaching severity. For *M. verrucosa* no change in lipid levels was observed due to bleaching. This suggests that *M. verrucosa* is able to decrease its metabolic rate and its demand for stored lipids during bleaching. Understanding the changes in the lipid biomass of different coral species from bleaching through recovery will enable us to better assess the metabolic effects of bleaching on corals. These results could be useful for identifying bleaching-resistant corals most suitable for conservation.

## OS21F-125 0830h POSTER

## The Impact of Heat-Induced Bleaching on the Fluorescence of a Caribbean Reef-Building Coral

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Seven paired specimens of the Caribbean coral *Montastraea faveolata* were heat stressed in order to evaluate the fluorescent response of green and orange host-based pigments. One sample from each pair was subjected to elevated temperatures for 28 days, followed by a recovery period lasting 53 days. At regular intervals, high resolution (~400  $\mu\text{m}/\text{pixel}$ ) multispectral images of induced fluorescence were recorded at wavelengths corresponding to the target pigments, plus chlorophyll. The imagery revealed that fluorescent signals of both the green and orange pigments were concentrated at polyp centers and declined by 70-90% in regions between polyps. Chlorophyll fluorescence, however, exhibited a rather uniform distribution across the entire coral surface, except around polyp centers, where it decreased by 10-30%. A normalized difference ratio between the green and orange pigments (GO ratio) was developed to facilitate comparison with chlorophyll fluorescence. Subsequent analysis indicated a high correlation between a sustained GO ratio of less than zero and coral death. Furthermore, the GO ratio appears to be a more sensitive bleaching diagnostic than chlorophyll fluorescence and was resistant to contamination from other sources of chlorophyll fluorescence, such as filamentous algae.

## OS21F-126 0830h POSTER

## Oxygen Dynamics in Turf Algae Canopies on Coral Reefs

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Many coral reef systems are dominated by algal turf and macroalgae cover. Because turf algae have high photosynthetic production and respiration rates, this group is particularly important for reef metabolism and may play a central role in controlling the oxygen budget of coral reefs. To better understand turf algae's role, diurnal changes of dissolved oxygen (DO) in the boundary layers over coral reef turf was examined. Small-scale oxygen gradients in turf algae were assessed in a flume using a polarographic oxygen microelectrode. During the daytime, algal photosynthesis enriched the near bottom water with oxygen. Steep gradients from high oxygen concentrations in the bottom boundary layer to lower concentrations in the water column (at saturation) existed during the daylight. Oxygen concentrations within the bottom boundary layer were significantly affected by water velocity and were very dynamic due to altering irradiance levels. At night, algal respiration caused a substantial uptake of oxygen from the seawater, oxygen concentration gradients reversed; and the water within the bottom boundary layer commonly became hypoxic. In situ measurements of dissolved oxygen in the backreef of Discovery Bay, Jamaica also showed diurnal changes and a substratum specific effect. Additionally, a survey was conducted to assess the distribution of algal canopies on the reef of Discovery Bay, Jamaica in winter 1999. The data in conjunction with earlier studies, indicate a slow recovery from an algae-dominated reef system in the 1980's and early 1990's. In particular, a phase shift from macroalgae to turf algae was observed on shallow fore reef sites. A hypoxic bottom boundary layer caused by algal respiration could produce a competitive advantage for algae for substratum and may possibly contribute to the slow recovery of sessile benthic organisms. Together,

the results of this study contribute to a broader understanding of the characteristics of turf algae habitats and their demography. Such information is of particular importance because, for many coral reefs, algal cover is expanding as a result of anthropogenic and natural environmental changes.

## OS21G HC: Hall III Tuesday 0830h

## Zooplankton: Feeding, Growth, and Distribution III

## OS21G-127 0830h POSTER

## Molecular Analyses of Protistan Assemblages From the Sargasso Sea Suggest Radical Community Shifts in Nutrient-Amended Bottle Incubations and Throughout the Water Column

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Studies of protistan growth and grazing routinely involve the containment of natural microbial assemblages in bottles and often include the amendment of seawater samples with nutrients or organic matter (e.g., primary productivity measurements; microbial grazing using the dilution technique). In dilution experiments, protistan grazers are a major source of recycled nutrients. The reduction of grazers by dilution is usually compensated by the addition of inorganic nutrients to promote the same growth-rates of primary producers across the entire range of dilutions. The Sargasso Sea is an oligotrophic region of the Atlantic Ocean characterized by low biomass but high species diversity. Deckboard incubation experiments were conducted in the Sargasso Sea during August of 2000 to determine the effect of bottle incubation, as well as nutrient and organic matter amendment, on the structure of naturally occurring protistan communities. Both nutrient and yeast-extract additions stimulated large blooms of primary producers, measured by the increase of chlorophyll, in experimental treatments. Changes in community composition in the < 200  $\mu\text{m}$  size-class were estimated during 72-hour incubations and throughout the water column using PCR-based techniques including Terminal-Restriction Fragment Length Polymorphism (T-RFLP) and cloning of full-length 18S rRNA genes. Vertical profiles of T-RFLP patterns in the Sargasso Sea suggest dramatic changes in protistan community structure from the surface to the base of the euphotic zone. Analysis of Restriction Fragment Length Polymorphism (RFLP) patterns from the clone libraries suggests that only a small fraction of phylotypes present at the beginning of an experiment survive to the 72-hour time-point. Previous studies have suggested that amendment of seawater with nutrients and organic compounds reduces the diversity of natural populations by encouraging the growth of weed-like microbes. We observed that while amendment caused radical shifts in community composition the overall diversity of the protistan community remained similar to starting conditions.

## OS21G-128 0830h POSTER

## Do Growth Rates of Antarctic Protists Compensate for low Temperature?

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Growth rates of aquatic microorganisms in coastal waters off Antarctica are potentially limited by perennially low temperature, yet the importance of this effect for the growth rates of Antarctic protists (microalgae and protozoa) is not well characterized. The

growth rates of 10 species of phototrophic protists and 6 species of heterotrophic protists from Antarctic waters were measured at 0°C. All were clonal cultures that were established and maintained at temperatures less than 2°C prior to this study. Prey for heterotrophs and nutrients for phototrophs were provided in excess. The organisms examined covered a wide range of taxonomic groups, including diatoms, dinoflagellates, ciliates, heliozoans, choanoflagellates, chrysomonads, prymnesiophytes, prasinophytes, volvocidans and cryptomonads, and included species known to periodically dominate the protistan biomass of Antarctic coastal waters. Maximal growth rates for phototrophs ranged from 0.12 d<sup>-1</sup> for *Polarella* sp. to 0.56 d<sup>-1</sup> for *Phaeocystis* sp., with an average growth rate of 0.26 d<sup>-1</sup> for all 10 species. *Phaeocystis* sp., which forms massive blooms during austral spring and summer, grew significantly faster in continuous light. Maximal growth rates for heterotrophs ranged from 0.12 d<sup>-1</sup> for an unidentified hypotrich ciliate to 0.54 d<sup>-1</sup> for *Paraphysomonas* sp., with an average growth rate of 0.28 d<sup>-1</sup> for all 6 species. These rates were comparable to literature values for growth rates of Antarctic protists measured both *in situ* and in the laboratory. Despite isolation and maintenance at ambient Antarctic temperatures, the growth rates of these protists do not appear to show a dramatic compensation for low temperature. These data have direct implications for protistan microbial processes in high latitude environments.

## OS21G-129 0830h POSTER

### Genetic Structure of Haddock (*Melanogrammus aeglefinus*) Stocks in the Northwest Atlantic Ocean

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This study examines the genetic structuring of spatially discrete spawning aggregations of haddock (*Melanogrammus aeglefinus*) in the Northwest Atlantic and investigates the potential genetic impact of intensive fishing on Georges Bank. We analyzed genetic change at four microsatellite loci for Georges Bank haddock over a 40 year time span in which significant changes in demographics and abundances have occurred in the population. Allelic diversities have changed little indicating that although the commercial fishery has collapsed, stock sizes have remained large enough to insulate against major reductions in genetic variation due to drift. Results indicate significant genetic divergence among decadal separated samples. Potential causes for these differences include admixture from other spawning regions, fluctuations in the effective number of spawners contributing to a single spawning event, drift, or a combination of these. Discrete spawning aggregations from Georges Bank, Browns Bank, the Scotian Shelf, and Nantucket Shoals were examined indicating significant differences among stocks. Genetic distance based measures supported the clustering of Scotian Shelf, Browns Bank, and Georges Bank haddock to the exclusion of Nantucket Shoals haddock. Haddock spawning on Nantucket Shoals may be genetically discrete from other haddock populations in the Northwest Atlantic.

## OS21G-130 0830h POSTER

### Food Sources of Vent Crab Larvae, *Bythograea thermydron*: Implications for Larval Dispersal

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During cruises to the 9 N vent site in 1998 and 2000, we used stable isotopes (carbon and nitrogen) to investigate the diet of the vent crab *Bythograea thermydron*. During those cruises we collected and analyzed the stable isotope composition of postlarvae (megalopae) and juvenile crabs, as well as potential prey items for the crabs. Our preliminary observations showed that the

carbon isotope values of megalopae were closer to non-vent organisms collected at 2600m in sites of the Eastern Pacific Rise (-17 to 21.3 ‰) and are consistent with our previous work that suggested that megalopae larvae develop in the water column external to vent sites. Stage 1 juvenile crabs showed a wider range of isotopic values (-18.6 to -23.2 ‰) compared to the megalopae (-20.4 to -22.4 ‰), but in general resemble the isotope composition of the megalopae. The wider range of isotopic signatures observed in the juveniles suggest that crabs are switching diets after metamorphosing and recruiting into the vent site. In addition, the isotope ratios of juvenile crabs clearly show a change in dietary patterns with crab size. The large isotopic difference between the early crab stages and vent organisms further suggests that megalopae and small juveniles are not preying on vent species.

## OS21G-131 0830h POSTER

### Carbon and Hydrogen Isotopic Compositions of Biomarkers From Deep-sea Mussels Living Three Different Hydrothermal Vent Sites: Implications to Their Ecosystems

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Various faunal activities have been observed around hydrothermal systems on the deep-sea floor. The faunal activities depend primarily on the products of chemoautotrophic bacteria, some fauna harbor bacteria as endosymbionts and others are feeding. In this study, compound-specific carbon and hydrogen isotopic compositions of several fatty acids from the soft tissues of deep-sea mussel *Bathymodiolus* were determined and compared between two species and among three hydrothermal vent sites in order to clarify their bacterial ecosystems, as a part of the "Archean Park" project supported by Special Coordination Fund.

Two species of *Bathymodiolus* were obtained from three different hydrothermal vent sites: *Bathymodiolus platifrons* harboring methanotrophic endosymbionts was collected from the No.4 Yonaguni and Hatoma seamount hydrothermal vent sites in the western Okinawa Trough, and *B. septemdiarium* harboring thiotrophic endosymbionts was collected from Suiyo seamount hydrothermal vent site in the Izu-Ogasawara island arc. A gill part, where endosymbiotic bacteria were active, was dissected from each specimen. The relative abundance of saturated n-fatty acids ranging from C14 to C18 in gill are similar among the three vent sites, those of unsaturated C16-C20 fatty acids are different among the sites. The bulk  $\delta^{13}C$  values (relative to PDB) of gill are quite different among the three vent sites (-45.0 per mil for Yonaguni, -25.3 per mil for Hatoma, and -36.0 per mil for Suiyo). The same specimen of *Bathymodiolus platifrons* harboring methanotrophic bacterial symbiont shows significantly different  $\delta^{13}C$  values between Yonaguni and Hatoma vent sites.

The fatty acids in the specimens from Hatoma and Suiyo vent sites are depleted in  $^{13}C$  up to 7.4 per mil relative to the corresponding bulk gill. However, the fatty acids from the Yonaguni site are enriched in  $^{13}C$  relative to the bulk gill. The  $\delta^{13}C$  values of individual fatty acids from the Hatoma site range from -150 to -85 per mil (relative to SMOW), which are heavier than those from the Suiyo (-226 to -163 per mil). The D-depleted fatty acids of the specimen from Suiyo vent site suggest that the mussel should assimilate isotopically-light magmatic water or hydrogen. These isotopic compositions of bulk gill and fatty acids reflect different metabolic pathways and/or energy sources of endosymbiotic bacteria under various conditions. Compound-specific carbon and hydrogen analyses are useful means to evaluate bacterial ecosystems at hydrothermal vents.

## OS21G-132 0830h POSTER

### Spatial Distribution of Fiddler Crab Larvae: Are Patches Formed at Hatching?

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Results of earlier work in our laboratory indicate that fiddler crab larvae (*Uca pugnax*) are distributed in the coastal ocean in discrete patches on a spatial scale of hundreds to thousands of meters. However, the mechanisms by which these patches are formed and maintained are not well understood. The goal of this study was to determine a) if patches of fiddler crab larvae are formed at the time of hatching and b) if these patches remain cohesive as they are transported through the primary estuary into the coastal ocean. A two-pronged sampling approach was used during the summer spawning season of 2001. The sampling strategy was based on the well-established pattern of nocturnal, spring tide spawning in this species. The first sampling approach entailed high-frequency plankton sampling in a secondary estuary draining an extensive salt marsh near the mouth of Delaware Bay (~38.8°N, 75.2°W). Sampling consisted of two-minute plankton tows every ten minutes for an entire nocturnal tidal cycle; a current meter was deployed at the sampling site during each collection period. This sampling protocol was completed once during each spring-tide period from late June through early August. Data were analyzed by autocorrelation, and the point in the time series at which the correlation coefficient crossed zero was interpreted as the characteristic temporal scale of the patch. Current-meter data were used to convert the temporal series to a spatial series and thus to convert the temporal scale to a spatial scale. The second sampling protocol employed a visually tracked drifter (drogued at a depth of 1 m) that marked a parcel of water as it moved from the secondary estuary into the mouth of Delaware Bay. The drifter was released at maximum ebb flow during a nocturnal spring-tide period. The drifter was then followed until the ensuing slack water when extensive plankton sampling was undertaken around it. This type of sampling consisted of continuous plankton tows along a saw-tooth transect centered on the drifter and was conducted four times during the spawning season. Data from the transect sampling were used to construct isopleths of larval density in the area around the drifter, which provided a visualization of patch structure in the area. Overall, the results of the investigation indicate that patches are formed at the time of hatching and that these initial patches remain cohesive on a scale of at least hours to days.

## OS21G-133 0830h POSTER

### The use of Morphological and Behavioral Data for the Identification of Scyphozoan Polyps and Ephyrae

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The break in the life cycles of most cnidarians, with benthic polyps and the pelagic medusae in different habits and under different constraints, has made understanding this benthic-pelagic coupling difficult. The polyps can act as a seed bank for medusae. When the populations of medusae are not found in the bay, the polyps are still resident. These polyp communities are dynamic and important in their own right, but can also represent the potential biodiversity of the pelagic environment. Understanding the ecology of pelagic jellies is only half of the story. To fully understand the ecology of these organisms we must understand the polyps ecology as well. This lack of understanding of the links between the benthic and pelagic was pointed out to be the single largest problem facing the study of jellyfish bloom ecology at the recent International Conference on Jellyfish Blooms. A significant problem in addressing this issue is the difficulty in identifying both the polyps and the young medusae commonly found in the field. Scyphozoan polyps are morphologically very similar in size and shape, making even genus level identification tenuous at best. The same holds for young ephyrae.

The aim of this research was to examine the morphometrics of both the polyps and the ephyrae to develop a species specific matrix of characteristics which will allow the positive identification of polyps and ephyra, both in aquaria and in the field. A month long experiment was conducted which tracked the movements, morphology, and asexual reproduction rates of five common species of scyphozoans. These data have shown that there were interesting differences between the test species. The maximum rate of polyp movement, the asexual cyst development rate, and the overall growth patterns were found to be different between the five species. The data show that with a few morphological measurements, it may indeed be possible to delineate between these species.

## OS21G-134 0830h POSTER

### Ingestion Rates and Selectivity of Copepods Feeding on Natural Microplankton in a Large, Temperate Estuary (San Francisco Bay, CA)

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Copepods are an important dietary component for many at-risk and harvestable fish species; thus, to improve estimates of fish production, copepod feeding behavior must be better understood. Traditionally, most copepods have been assumed to consume primarily algal cells, thereby serving as a direct trophic link between phytoplankton and fish. However, many estuarine copepods are now recognized as omnivorous on both algal and protozoan (microzooplankton) prey, who are themselves grazers of phytoplankton. Consumption of microzooplankton therefore adds another trophic level to the planktonic food web, potentially reducing energy transfer efficiency upward to fish.

In order to assess copepod feeding preferences and diet composition in San Francisco Bay (SFB), we conducted a series of incubation experiments with *Acartia* spp. feeding upon the natural assemblage of <200-micron prey from two locations: the deep channel in South Bay (SB) and San Pablo Bay (SPB). Seven sets of experiments between February and May 2000 encompassed the spring phytoplankton bloom. Except during a bloom of small, chain-forming diatoms (*Skeletonema*) in SB, *Acartia* never significantly consumed cells <10 microns. In all experiments during the bloom, the distribution of prey types in *Acartia* diet differed significantly from the available prey distribution ( $p < 0.05$ ). In SB, *Acartia* consumed mainly small (15-40 microns) autotrophic prey, while in SPB *Acartia* more often consumed larger (25-75 microns) heterotrophic ciliate prey.

These results confirm that *Acartia* copepods are omnivorous in SFB, and that very often the planktonic system is primarily a web with 4 or more levels, with microzooplankton playing a significant trophic role as prey for copepods. This quantitative information about copepod feeding behavior is important for updating planktonic food web models, and ultimately for managing fisheries in SFB.

## OS21G-135 0830h POSTER

### Effects of Hypoxia on the Survival and Life History Traits of *Acartia tonsa*: Role of Season and Feeding

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Current research in our laboratory suggests that hypoxia may impact the population dynamics of the copepod *Acartia tonsa* through sublethal effects on life history traits e.g. growth, development, and fecundity. This study examines the potential influence of feeding and season on these results. *Acartia tonsa* were collected in the late fall and reared at 15°C at saturating DO (control), and reduced DO concentrations of 1.5 or 0.7 ml/L. Oxygen concentrations were maintained in replicate flasks, by bubbling with air (control), or mixtures of nitrogen and oxygen. Survival, development, growth, and fecundity are being determined and will be compared to the results obtained previously for animals that had been collected in the summer and reared at 25°C (see abstract by Marcus, Sedlacek, and Richmond). In addition, using gut fluorescence as an indicator, we are comparing the ingestion rate of adults reared under the different oxygen regimes to determine if reduced feeding is associated with reduced body size and fecundity observed for animals exposed to hypoxia.

## OS21G-136 0830h POSTER

### Food Limitation of *Acartia* in the San Francisco Estuary due to a Benthic Competitor.

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The copepod genus *Acartia* dominates the zooplankton biomass, and is a key link in food webs, at intermediate salinity in many temperate estuaries. In shallow regions of the San Francisco estuary, *Acartia* abundance declined after 1987, coincidental with the spread of the introduced clam *Potamocorbula amurensis*. Each year since that introduction, abundance of *Acartia* has been low from late spring or early summer through fall, the time period when clams are abundant. This decline may have occurred through either competition for food or predation by clams on nauplii. We examined food limitation of reproduction by *Acartia* (Acartiura sp.) from October 1999 to September 2001, by measuring individual female reproductive rates in 24-hour incubations. Mean reproductive rates remained below 15 eggs female<sup>-1</sup> d<sup>-1</sup> for most of the year. Higher egg production occurred mainly during and after spring blooms of ~1 month duration, dominated by the diatom *Skeletonema costatum*. The highest individual reproductive rate was 103 eggs female<sup>-1</sup> d<sup>-1</sup> and the highest mean for a sample was 52.7 eggs female<sup>-1</sup> d<sup>-1</sup>.

Reduction in phytoplankton biomass due to filtration by *P. amurensis* in shallow water could explain why *Acartia* abundance has declined. Long-term benthic monitoring data from two stations in San Pablo Bay and several spatially-intensive benthic surveys show that this clam has been persistently abundant since at least 1992, with a median abundance from the long-term data of 1300 m<sup>2</sup> at both a channel and a shoal station in San Pablo Bay. Median abundance from a survey in August 2001 was ~900 m<sup>-2</sup>, and we calculate that the community filtration rate was sufficient to suppress phytoplankton biomass in August 2001, and probably for most summers during our study. Phytoplankton blooms, with consequent high egg production, occurred during spring when abundance of *P. amurensis* was low. Still to be determined is the extent to which significant predation by clams on nauplii may have exacerbated the effects of food limitation.

## OS21G-137 0830h POSTER

### Use of Elemental Fingerprinting to Evaluate the Dynamics of Larval Exchange in Southern California Mussel

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Information about larval origins and trajectories is essential for accurate modeling of population dynamics in coastal species with planktonic larvae, and ultimately for effective management of coastal resources. We are generating methods to evaluate sites of larval development for newly settled mussels (*Mytilus* spp. and *Musculista senhousia*) in southern California, with the goal of assessing the extent of self seeding and exchange between populations. Trace-element composition (fingerprints) of larval structures and tissues can reflect the environmental conditions experienced by an organism during development. Concentrations of Al, Ba, Cu, Mn, Al, Cd and Sr in shells of new recruits, determined by solution-based ICP-OES (Inductively Coupled Plasma-Optical Emission Spectrometer), differ among bay and coastal habitats, probably due to variation in pollutants, runoff and temperature. Discriminant function analyses (DFA) of solution-based elemental composition data have indicated our ability to distinguish mussels based on site of collection, species, shell zone, and shell size, indicating the importance of evaluating specific regions of the larval and post-settlement shell. Different bay and coastal locations also have distinct seawater elemental signatures. Solution-based elemental techniques employed to date confer little ability to distinguish and target larval versus newly settled juvenile mussel shell, thus they have been of limited use in establishing population connectivity. We are currently developing protocols to use a 213 nm Laser Ablation unit combined with a double focusing, single collector, magnetic sector ICP MS (Inductively Coupled Plasma-Mass Spectrometer) to conduct elemental analysis of specific regions of the shell (8-20 micron diameter). This methodology should allow us not only to determine the site of origin, but also to construct possible trajectories for individual larvae. Realized larval exchange will be compared to predictions based on a physical connectivity model created for the southern California bays and coastal zone.

## OS21G-138 0830h POSTER

### The Effects of Thin Layers of Prey on the Vertical Distributions of Larval Herring (*Clupea pallasii*)

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Thin layers consisting of vertical prey patches of extreme concentrations are thought to affect zooplankton behavior. The objective of this study was to determine how such thin layers affect the vertical distribution of larval herring (*Clupea pallasii*). In two-meter tall experimental tanks we ran separate experiments to investigate the effects that thin layers of prey have on the vertical distribution of five, ten and fifteen day old herring larvae. In our experimental tanks we created a thin layer of prey (rotifers, *Brachionus plicatilis*) through density stratification achieved with varying salinities. We set up our control tanks to be homogenous with respect to both prey and density. We took water samples from valves distributed over the height of each tank to monitor the location of the thin layer of rotifers and used video cameras that panned the height of the tank to monitor the vertical distribution of herring larvae over the duration of the experiment. We found that the distribution of larval herring is affected by the presence of a thin layer. In tanks containing a thin layer of prey larval herring tended to aggregate around the thin layer, at a depth of approximately 1 meter. In the tanks with a homogenous distribution of food the larval herring tended to aggregate at the surface, nearest the light source. Thus thin layers can affect directly the vertical distribution of larval herring, and perhaps indirectly their horizontal distribution, as herring larvae live in environments (e.g., estuaries) where advective transport is also often vertically heterogeneous.

## OS21G-139 0830h POSTER

### Effects of Saline Tidal Intrusions on the Zooplankton of a Coastal Lake

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In tidal, brackish systems, salinity may influence the abundance and taxonomic composition of crustacean zooplankton communities, whereas water currents may affect the distribution of these communities. Lake Waihoia is a shallow, tidal, coastal lake that receives brackish inflows of 0 - 4.8 ‰. To determine the relative effects of salinity and tidal currents on zooplankton abundance and distribution in this lake, crustacean zooplankton, salinity, chlorophyll *a* and particulate suspended matter were measured monthly over two years. Tidal currents were traced using drogues, and zooplankton was sampled over tidal cycles. Tidal currents reached velocities of 21 m min<sup>-1</sup> closest to the tidal source, and decreased significantly with increasing distance from this source. Tidal inflows significantly affected the distribution of the zooplankton over a tidal cycle. Salinity explained 26% of the variation in the abundance and species composition of the zooplankton assemblage, and accounted for > 60% of the species-environment correlation. Increases in salinity resulted in a change in crustacean dominance from the predominantly freshwater calanoid copepod, *Boeckella hamata*, and cladoceran, *Daphnia carinata*, to the predominantly estuarine copepod, *Gladioferens pectinatus*. Based on our findings, we predict that future increases in salinity and tidal currents associated with reductions in freshwater inflow and/or increased tidal inflows may cause significant changes in the zooplankton community structure, and affect trophic interactions in this lake.

## OS21G-140 0830h POSTER

### Teleplanic Larvae in Culture: 4.5 Years from Hatching to Metamorphosis.

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Larvae of the NE Pacific snail *Fusitriton oregonensis* from field collected egg capsules were reared in 2 liter volumes of water with the alga *Rhodomonas* as

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.