

shoreline-inner mudbank sediment cycling model where downdrift mudbank migration is generated by erosion of trailing edge mangrove shoreline deposits, that, in turn, are recycled back to the leading-edge shoreline by fluid muds and are stabilized by mangroves.

OS12S-06 1505h

### The Eel Canyon, Northern California as a Modern Conduit and Sink of Terrigenous Sediment

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Recent studies have shown that submarine canyons near large fluvial sediment sources and/or adjacent to a narrow shelf may be actively transferring terrigenous sediment offshore during modern, highstands of sea level. The present study addresses the importance of the upper Eel Canyon (<1000m water depth) as a terrigenous sediment sink and conduit to the deep sea over seasonal and decadal time scales.

Radioisotopic and textural data indicate that the Eel Canyon consistently receives fluvial sediment from the Eel River during winter storm/flood seasons. <sup>7</sup>Be and x-radiographic data from box cores show that sediment is preferentially deposited in the upper canyon thalwegs (<400 m water depth) relative to canyon walls and deeper portions of the canyon (400-1000 m water depth). These data are supported by *in situ* ROV sampling, where recent sediment layers were thin on steep canyon walls and thick in channels. Near-bottom tripod data have shown that frequent down-canyon gravity-driven transport events occur in a thalweg, which may account for the observed depositional pattern. In addition, high concentration (up to 20 mg/l) intermediate nepheloid layers (INLs) have been observed at shelf break depths over the entire upper canyon, contributing to the total mass of terrigenous sediment deposited. Results show that >12% of the Eel River sediment discharge is sequestered in Eel Canyon over seasonal time scales.

<sup>210</sup>Pb accumulation rates also indicate that sediment is preferentially accumulating (1.5-4.0 cm/y) in the upper thalwegs over decadal time scales. However, the spatial sedimentation pattern is not as distinct, suggesting a more complicated sedimentation history over longer time scales. Sub-bottom chirp data show that some feeder gullies may be filling with modern sediment, as indicated by thicker sediment packages within the gullies compared to steep side-walls. Core data indicate that large down-canyon transport events have occurred within the main thalwegs over decadal time scales, redistributing terrigenous sediment to deeper water. A sediment budget over decadal time scales indicates that a few percent of the Eel discharge accumulates in the upper canyon. Therefore, the Eel Canyon head appears to be both an important conduit and sink of modern terrigenous sediment.

OS12S-07 1520h

### In Situ ROV Observations of Sedimentation Patterns in the Eel Canyon, Northern California

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Submarine canyons have long been identified as having complicated sedimentation processes due to irregular bathymetry. However, few studies have addressed small-scale variability of sedimentary environments within canyons because of the difficulty of precise shipboard sampling of the seabed. *In situ* sampling by submersible or ROV is necessary to capture the spatially heterogeneous nature of sediment deposition. Previous work has shown that the Eel Canyon seasonally receives fluvial sediment, making this canyon an ideal location to study active sedimentation processes. The MBARI ROV *Ventana* was used to characterize depositional environments over canyon (km), channel (100 m) and sample (10 m) spatial scales. Sub-environments within the canyon were identified by (1) direct video observations of the seabed surface and (2) sedimentological analysis of push-core sediment samples (up to 1 m length).

Preliminary results indicate that the patterns of deposition at the canyon and channel spatial scales agree

with previous analysis of shipboard-collected samples. The northern upper thalwegs (<400 m water depth) appear to be consistently receiving more sediment by rapid, seasonal deposition compared to the southern thalwegs. This conclusion is supported by increased preservation of physical sedimentary structures (layers and laminations) in high deposition areas. In addition, thick sediment layers are preferentially deposited near the channel thalwegs (within 50 m) compared to channel walls. Observations of considerable variability in the benthic community between thalwegs and walls also reflect the different sedimentation environments (i.e., habitat) experienced over channel scales.

Sample-scale variability in seabed characteristics can be directly related to sediment transport processes occurring at the head of the canyon (~130 m water depth). Thick sediment layers are preserved in the seabed at the thalweg axis, however, only 30 m from the axis, a wall of exposed strata ~5 m high was observed. This indicates an erosive process has removed sediment creating an incised channel. Bottom-boundary-layer measurements at this location have shown that gravity driven sediment transport events are common, which suggests this erosive process may be actively altering canyon morphology during the present sea-level conditions (high stand).

OS12S-08 1535h

### The Interplay between a Mountainous River and Nearby Submarine Canyon in Southern Taiwan

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Rivers and submarine canyons are two important sediments transport systems in the continental margin. Rivers deliver fresh water and terrestrial matters, such as sediments and pollutants, from land to the sea. Submarine canyons are also natural conduits for the transfer terrigenous sediments to the deep sea. These two major transport systems are rare in the world to be next to each other. Here in southern Taiwan, the head of the Kao-ping Submarine Canyon (KPCY) is located approximately 1 km seaward from the mouth of the Kao-ping River forming a unique river-sea system. Kao-ping River represents high mountainous rivers in the world. These rivers might be accountable for over 20 % of the sediment flux in the ocean. Meanwhile, the temporal variation of the discharge in Kao-ping River can be divided into flood and dry season due to the influence of the Monsoon. 80 % of the annual discharge concentrates in the flood season. Especially, the daily mean runoff can be one order of magnitude higher than the annual mean runoff during typhoons and thunderstorms. The suspended sediment concentration (SSC) can also increase episodically 4 to 5 times higher after the typhoon passed. The sediment-laden river effluent is dispersed over the head of the KPCY. The KPCY is a statically stable environment due to stratification, which is effected by the tidal regime inside the canyon and by the seasonal variability in the river hydraulic cycle. Previous studies have shown that the KPCY is not only a trap but also a conduit for fined-grained sediment. Our preliminary findings show that clay (near the canyon floor) and very fine to medium-grained silt (in the lower part of the canyon) compose the largest fraction of SSC in the canyon. The sand fraction in the SSC in the canyon came from the shelf floor above and showed highest correlation with the river sediment discharge. On the other hand, finer fraction in the SSC in the canyon is more subject to the tidal frequency variations.

OS12S-09 1550h

### The Efficiency of a Catastrophic Capping Layer Deposited in the Saguenay Fjord During the Flood of 1996, Quebec, Canada.

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In July 1996, an important flood took place in the Saguenay region, in Quebec. This disaster was marked by the catastrophic swelling of some tributary rivers of the Saguenay Fjord, which carried and deposited about 20 million tons of sediment in the upstream section of the fjord. This flood layer, identified as turbidite deposit with a variable thickness ranging from 10 cm to 10 m, not only had bad consequences. In fact, the new sediments have recovered the underlying contaminated sediments with a clean layer of sediments over

a large surface now acting as a capping layer. This event provided a unique opportunity for a group of engineers and scientists to investigate the performance of the flood deposit as a physical and/or biogeochemical barrier to the migration of contaminants associated with the underlying, indigenous sediments up to the new water/sediment interface. Depending on the particular expertise of the investigators involved in the project, this flood layer was distinguished from the indigenous sediments by its geotechnical properties (e.g., weak consistency and low resistance), its high water content, the absence of benthic organisms, or the presence of inherited geochemical components. This paper presents some results of the geological and geotechnical aspects of the performance and integrity of the capping layer. The results indicate that consolidation of the flood and pre-flood sediments was completed in the first 3 months after the deluge, and also, that the consolidation behaviour is influenced by the bioturbation. In addition, it is shown that the multibeam sonar can be a useful tool to monitor the evolution of some properties of capping layers, such as, water content and density. Up to now, the layer is effective to isolate the contaminants, but in long-term, it seems that slope instability related processes might affect the integrity of this flood layer.

OS12T HC: 318 A Monday 1330h

### Viruses and Prokaryotes in Aquatic Systems II

**Presiding:** C Brussaard, Netherlands Institute for Sea Research; C Suttle, Univ. of British Columbia; R Goericke, Scripps Institution of Oceanography Integrative Oceanography; H Grossart, Grossart, H.-P.

OS12T-01 1330h

### The fate of intracellular Fe from marine microbes following viral lysis

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Viruses are pervasive in marine environments and are responsible for a significant proportion of microbial mortality. Estimates from different systems suggest virus-mediated lysis of marine microbes ranges from 15 to 50% of total mortality. Since the chemical speciation of Fe has been demonstrated to be an important factor controlling primary productivity in high nutrient low chlorophyll (HNLC) environments, we hypothesized that viral activity may be an important source of organically complexed Fe. Here we report the results of laboratory studies focusing on the character of Fe in viral lysates of a marine *Synechococcus*, a cyanobacterium that dominates some HNLC environments.

Lab cultures of *Synechococcus* WH 7803 were maintained with <sup>55</sup>Fe to label intracellular pools so that the fate of Fe could be tracked after viral lysis. Cells were subsequently exposed to lytic cyanophages, and a variety of fractionations used to characterize Fe in the lysates. Intracellular Fe released by viral activity was found to partition into different size classes as compared to Fe released from unlysed controls. After viral lysis, 60 to 81% of initial intracellular was found in the dissolved size class compared to only 19 to 45% for unlysed control. And while all the iron released by cells in the absence of viruses was only found in the less than 3kD size class, a significant proportion of virally released dissolved Fe was found in the greater than 30kD size class. At least 50% of the dissolved Fe released from lysed cells bound to XAD-16 resin, suggesting that at least this amount is organically complexed.

To determine if virus-mediated cell lysis of cyanobacteria releases Fe that is available for uptake, we inoculated labeled lysates with cells resistant to the lytic cyanophages. Almost 100% of the Fe released from lysed cyanobacteria can be taken up by a resistant cyanobacterial strain within 48 hours. A portion (ca 33%) of the Fe released by cyanobacteria lysis is also available to heterotrophic bacteria. Characterization of the availability of Fe in lysates to different marine plankton as well as analysis (by electrochemical techniques) of the stability constants of Fe-organics complexes in lysates provides added evidence to the importance of virus-mediated Fe recycling in marine systems.

## OS12T-02 1345h

## Viral Generation of Dissolved Organic-Fe in a Coastal HNLC System

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Viruses are well-characterized agents of microbial mortality, persisting at high abundances in all marine environments examined to date. Here we report that the lytic activity of naturally occurring viral populations liberates sufficient organically-complexed Fe to drive the recycling of total dissolved Fe measured in a recently identified high-nutrient low-chlorophyll (HNLC) coastal upwelling system.

A novel, non-invasive dilution technique was used to determine viral production rates. Rates of viral production were estimated at a station in the Humboldt Current and at three stations in the Peruvian upwelling, where estimated ambient Fe concentrations ranged from 0.04 to 0.10 nM. These estimates, combined with information on burst size and bacterial Fe quotas, suggest that viral activity would result in a flux of organically complexed Fe ranging from 0.02 to 0.08 nM d<sup>-1</sup>. When combined with lab studies on size fractionation, the results imply that Fe-released by viral lysis of bacterioplankton would result in complete turnover of the dissolved iron in ca 2.1 (0.6 to 6.25) days. The results also demonstrate that significant quantities of organic-N and P would be released during this process. The bioavailability of organically complexed Fe has been shown to regulate primary production in pelagic HNLC marine environments and more recently in HNLC coastal marine upwelling zones. However, the character and source of the Fe-organic complexes in seawater has remained a mystery.

Since Fe in cellular components (e.g., cytochromes, porphyrins) is highly available to marine phytoplankton these results suggest that virus-mediated Fe release may be the major mechanism supplying bioavailable Fe in this system. Our data demonstrate that viral activity in this (and potentially other) marine systems is critical to the recycling of the bioavailable Fe that supports primary production, maintains the biological Fe cycle and drives carbon sequestration in marine surface waters.

## OS12T-03 1400h INVITED

## Marine Phytoplankton Viruses - Ecology, Physiology and Host Virus Interactions

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The overall aim of our investigations have been to understand the ecological significance of phytoplankton viruses in marine ecosystems.

We have isolated and characterized viruses infectious to both bloom-forming (e.g. *Emiliana huxleyi*) and non bloom-forming (e.g. *Chrysochromulina ericina*, *Pyramimonas orientalis*) phytoplankton species. Most of them are large dsDNA viruses and have several properties suggesting they belong to the Phycodnaviridae. The various host virus systems have further been used in laboratory experiments designed to increase our understanding of possible factors that may regulate the viral activity. These experiments have demonstrated that that virus production in some host-virus systems depends on the host's cell cycle, and that an algal population under viral attack acquires a virus resistance that prevents host extinction and enables the host to coexist with the virus. Ecological implications of our results will be discussed.

We have applied flow cytometry (FCM) and pulsed field gel electrophoresis (PFGE), which has recently been developed for use in aquatic viral ecology, to study

the abundance and diversity of algal viruses in mesocosms and natural marine ecosystems. We also investigated the effect viral activity exert on the remaining microbial community. Our results suggest a close linkage between algal, viral and bacterial populations and they demonstrate how algal viruses can regulate algal populations by terminating blooms or keep the populations at non-blooming levels.

## OS12T-04 1415h

Virus Induced Mortality of *Phaeocystis globosa* : a Mesocosm Study and Modeling Exercise

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Viruses are present in high number in marine waters and are shown to infect a wide spectrum of hosts, including bloom-forming phytoplankton species. Lytic viruses affect the dynamics of the host directly by lysing the host cells upon release of progeny, but as a result of the released cell content enhance the activity of the microbial food web and thus influence succession and diversity. The present study will show the dynamics of the colony-forming phytoplankton *Phaeocystis globosa*, blooming under 3 different N:P ratio's (N:P of 4, 16 and 44) in indoor mesocosms of 850L. The mesocosms were filled with natural seawater and inoculated (1% v/v) with *P. globosa* (colonies and single cells). The effect of the different N:P ratios on the development and mitigation of the blooms was studied. Results on virus dynamics and the role of virus mediated mortality of *P. globosa* in the control of these blooms (as compared to total phytoplankton mortality) will be shown. Blooms developed in one week, with the P-limited bloom (high N:P) collapsing earliest while producing large aggregates. In general, viral induced mortality of *P. globosa* was significant but could not prevent bloom formation. The novel finding that colonial cells grew faster than the single flagellated cells is likely part of the explanation. The results could be simulated very well using a newly developed mathematical ecosystem model with focus on the microbial food web. A delayed increase in light intensity in another mesocosms (N:P 16) resulted, however, in only a very weak bloom (despite enough nutrients present), enhanced phytoplankton cell lysis rates and strongly enhanced viral abundance. The dynamics of the microbial food web in this mesocosm could not be modeled satisfactory without adding viruses as an important controlling agent. The implications for natural situations will be discussed.

## OS12T-05 1430h INVITED

Novel Algal Viruses and Their Role in the Bloom Dynamics of *Heterosigma akashiwo*

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*Heterosigma akashiwo* is a toxic bloom-forming alga that is responsible for massive mortality to finfish populations around the world. The onset of these blooms is correlated with stratification, although factors controlling the severity and duration of these blooms are poorly understood. Recent discoveries suggest algal viruses may play an important role in the mortality of *H. akashiwo*. The viruses are lytic and cause lysis of laboratory cultures of *H. akashiwo*; however, their impact on blooms is unknown. The objective of this research was to examine host and virus interactions to establish their effect on bloom dynamics and the propagation of infection. Two novel virus-host systems were examined to resolve the roles of the virus and host: a single-stranded RNA (HaRNAV) and a double-stranded DNA virus that infect the same strain of *H. akashiwo*.

*Heterosigma akashiwo* is phototactic and migrates up to 10 m/d to exploit deep nutrient pools during stratified bloom conditions. We used settling columns to determine the effect of viral infection on the motility of *H. akashiwo*. Within 24 hours, uninfected cells were swimming at approximately 7.3 m/d, whereas cells infected with HaRNAV or the DNA virus were sinking at 12.5 and 7.3 m/d, respectively. There were no other signs of infection 24 hours post-infection, however by 48 hours approximately 50% of cells infected with either virus had lysed. As sinking *H. akashiwo* cells would encounter decreasing levels of light in the natural environment, we examined the lytic cycle under light and dark conditions. The lytic cycle of both systems was

the same in the light and dark, with approximately 50% of the population lysed by 48 hours. Fewer infectious viruses were produced in the dark than the light; however, this decrease was more prominent with the DNA virus system than HaRNAV.

The results of this study suggest that natural populations of *H. akashiwo* infected with viruses would rapidly lose their ability to swim and may reach the benthos or drop below the euphotic zone before lysis occurs. If the cells encounter aphotic conditions, the lytic cycle will progress; however, the number of viruses produced by the infection will be dependent upon available energy and the type of virus infecting the host.

## OS12T-06 1445h

*Prochlorococcus* and *Synechococcus* Cyanophages Along a Coastal to Open-Ocean Transect

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Direct observation of viral-like particles (VLPs) using transmission electron microscopy and epifluorescence microscopy has revealed very high abundances (up to 100,000,000 phage per ml) in natural waters. Since the marine cyanobacteria (*Prochlorococcus* and *Synechococcus*) are considered the most abundant photosynthetic organisms on the planet, it is not surprising that culture-based assays (most-probable number and plaque assays) have shown that infectious *Synechococcus* cyanophages are also abundant, with phage:host ratios ranging from 1:10 to 8:1 in coastal ocean ecosystems. In striking contrast to the phage:host ratios for coastal *Synechococcus*, however, *Prochlorococcus* cyanophage numbers in the open oceans are at least 3 orders of magnitude lower than total host cell abundances. Several hypotheses might explain this difference: (1) There may be fundamental differences between open ocean and coastal ocean pressures on cyanophage, (2) *Prochlorococcus* and *Synechococcus* cyanophage titers may not be directly comparable due to the difficulties in interpreting the strain-specific cyanophage titers to obtain a "total cyanophage titer," and (3) Lower growth rates of *Prochlorococcus* relative to *Synechococcus* may result in reduced phage production rates.

We are investigating these hypotheses by examining host and phage dynamics along a N. Atlantic transect from the coast to the W. Sargasso Sea. Cyanophage titers for representative strains of both *Prochlorococcus* and *Synechococcus* are being determined using plaque assays for a side-by-side comparison of these communities. Preliminary screening suggests that the pressures on free cyanophage in open oceans may be fundamentally different from those in coastal waters. Thus far we have observed significantly lower phage:host ratios in open ocean vs. coastal samples, regardless of the host strain used. The completed results will be presented and their ecological relevance discussed.

## OS12T-07 1500h

## Cultivation of the Ubiquitous Marine Bacterium SAR11

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The alpha proteobacterium SAR11 was among the first new organisms discovered when cultivation independent approaches based on ribosomal RNA gene cloning and sequencing were applied to survey microbial diversity in natural ecosystems. It accounts for 26% of all ribosomal RNA genes detected in seawater, and has been found in every pelagic marine bacterioplankton community studied by these methods. SAR11 is representative of a pervasive problem in microbiology: despite its ubiquity, it has defied cultivation efforts. Genetic evidence suggests that diverse uncultivated microbial taxa dominate most natural ecosystems, prompting widespread efforts aimed at elucidating the geochemical activities of these organisms without the benefit of cultures for study. Here we report

the first isolation of SAR11. Eighteen cultures were obtained by means of newly developed high throughput procedures for isolating cell cultures by the dilution of natural microbial communities into very low nutrient media. The volume of these cells, ca.  $0.01 \mu\text{m}^3$ , places them among the smallest free-living cells in culture.

#### OS12T-08 1530h

##### Anoxygenic Photosynthesis in the Open Ocean: Is it important?

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Some groups of marine bacteria within the alpha-Proteobacteria are capable of anoxygenic photosynthesis in oxic environments. Their primary photosynthetic pigment is bacteriochlorophyll a (BacChl a). Recently Kolber et al. (2001, *Science* 292: 2492 - 95) reported that such bacteria are abundant in the upper ocean and that these might contribute significantly to photosynthetically driven electron transport since measured and inferred ratios of BacChl a and Chlorophyll a (Chl a) were about 0.8% in coastal environments and as high as 10% in the Eastern Tropical North Pacific. The authors suggested that the globally averaged BacChl a/Chl a-ratio could be as high as 5 to 10%. To determine if such high values are representative of other marine environments, concentrations of BacChl a were measured in samples collected in eutrophic nearshore and meso- and oligotrophic offshore environments, i.e. off Southern California and Peru, in the Eastern Tropical North Pacific and the Sargasso Sea. Additional samples from the south Pacific will become available soon. Data in hand at the present time suggest that the average BacChl a/Chl a ratios are ~1% in nearshore and 0.5 to 1% in offshore environments, including the Eastern Tropical North Pacific. Assuming that rates of photosynthesis scale with concentrations of photosynthetic pigments, these data suggest that the contribution of BacChl a-driven anoxygenic bacterial photosynthesis to energy production in coastal eutrophic and offshore oligotrophic environments is small, substantially smaller than the suggested global average of 5 to 10%.

#### OS12T-09 1545h

##### Relative Abundance and Biomass Production of Bacterial Groups in the Delaware Bay Estuary

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We used microautoradiography and fluorescent in situ hybridization (Micro-FISH) to test the hypothesis that the relative abundance of bacterial groups determined by FISH reflects their contribution to biomass production, i.e. thymidine and leucine incorporation. Experiments were conducted in the Delaware Bay estuary which has characteristic physical, chemical and biological structure, including a point source of freshwater input from the Delaware River, a turbidity maximum where freshwater and seawater first mix, and a seasonal chlorophyll maximum about 50 km from the mouth of the estuary. FISH indicated that alpha and beta proteobacteria and Cytophaga-related bacteria dominate bacterial communities in different parts of the salinity gradient. It is not clear if dominant groups of bacteria are important consumers of organic matter because total bacterial abundance is thought to be a poor predictor of bacterial biomass production, one measure of organic matter use. Our results indicate that the most abundant groups do comprise the largest fraction of communities assimilating thymidine and leucine. In June beta proteobacteria were most abundant at a freshwater station and at the turbidity maximum, while alpha proteobacteria made up the largest fraction of the community at the chlorophyll maximum and at the mouth of the estuary. These dominant groups also comprised the largest fraction of the communities assimilating thymidine and leucine. The picture was different in March when Cytophaga-related bacteria were abundant at all four stations and equal in abundance to alpha proteobacteria at the chlorophyll maximum and at the mouth of the estuary. Among cells assimilating thymidine and leucine, Cytophaga-related bacteria were outnumbered by alpha proteobacteria by a factor of two or more, suggesting that Cytophaga-related bacteria contributed less to bacterial production than their abundance would imply. Differences in the metabolism of thymidine and leucine by the abundant groups may elucidate variation of thymidine and leucine incorporation at the whole community level.

#### OS12T-10 1600h

##### Combining Lipid Biomarkers and RNA Phylogenetic Analysis to Follow the Response of Bacterial Communities to DOM Sources in Estuaries

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Understanding how specific groups of bacteria contribute to and regulate biogeochemical reservoirs is dependent on the ability to recognize their presence in the environment and those factors which alter their community structure. We used a series of enrichment experiments to examine the impact of dissolved organic matter (DOM) from different sources on bacterial community structure in the Delaware estuary and Chesapeake Bay systems. Amendments of protein and glucose were used to investigate the impact of DOM availability on bacterial abundance, growth and lipid markers in the absence of grazers. Detailed molecular level lipid analysis was compared with fluorescence in situ hybridization (FISH) to link changes in the heterotrophic bacterial community with their chemical signature as seen in lipids. Over the 48 hour incubation times, growth on natural DOM from sites ranging from freshwater to lower Bay showed significant changes in bacterial growth and abundance in protein amended incubations compared to controls. Dramatic changes were observed in bacterial derived fatty acids among all sites by 48 hours, with a four-fold increase in a suite of specific odd chain and branched fatty acids when protein was added. FISH analysis of bacterial community structure shows that the shift in lipid composition is due to an increased abundance of Cytophaga-Flavobacteria and to a lesser extent, the alpha-proteobacteria. These results are consistent with results of separate Micro-FISH experiments which suggest that Cytophaga-Flavobacteria dominate protein use whereas alpha-proteobacteria use free amino acids. By linking geochemical signatures of actively growing bacteria with phylogenetic analysis, this work provides a path to determine which bacteria are active consumers of DOM as well as follow their contribution to organic carbon pool in the water column and sediments.

#### OS12T-11 1615h

##### Single Cell Respiratory (CTC) Activity of Marine Bacteria: Variations Over Seasonal Time Scales and Trophic Gradients

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Bacterial respiration at the single cell level can be measured using the fluorescent probe, CTC, with flow cytometry. We measured the proportion of active cells in the context of the overall plankton community over seasonal time scales in coastal Maine waters, and along trophic gradients from enriched coastal Maine waters and Georges Bank to the oligotrophic Sargasso Sea. CTC-active cells were always less than 15% of the total population, and the proportion generally varied with temperature. Occasionally, the active proportion was unusually higher or lower suggesting other, chemical or biological controls on respiratory activity.

The CTC method was also used in a bioassay to measure stimulation of respiration by simple substrates in short-term experiments. This bioassay shows what compounds the active subpopulation of bacteria is capable of respiring at given time and place. Substrates (monomethylamine, glucose, dimethyl sulfide, and leucine) were added at low concentrations (50 nM to 5  $\mu\text{M}$ ) to the sample and incubated for 30 minutes prior to the CTC incubation. In the Sargasso Sea, low concentrations of glucose and methylamine consistently stimulated respiration over the untreated controls. Dimethyl sulfide had a weaker positive effect and leucine showed little or no stimulation of activity. The CTC bioassay is a very sensitive indicator that can be used to measure bacterial respiratory activity at short temporal and small spatial scales.

#### OS12T-12 1630h

##### Interactions Amongst Particle Ccolonizing Marine Bacteria

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The microenvironment of marine bacteria is heterogeneously structured. Particulate loci of dissolved organic matter, such as live phytoplankton and detritus, create gradients of dissolved organic matter. Bacteria typically occur on marine particles at numbers that are 1-many orders of magnitude higher than in the surrounding water. Their activities cause particle solubilization and remineralization at high rates. Population dynamics of bacteria on particles depend on the rate at which bacteria colonize particles from the ambient water, and the growth and mortality dynamics of particle colonizing bacteria. Thus, it is of great interest to understand the factors that govern their abundance and activity.

We have isolated 50 strains of particle colonizing bacteria on various media and have determined partial sequences of their 16S rRNA gene. Motility and chemotactic behaviour of these strains were studied by using dark-field microscopy and capillary assays. Interactions amongst the isolates were examined by 2 different ways: a) pro- and antibiotic effects were determined in agar diffusion assays and b) colonization and growth dynamics on artificial surfaces (agar beads) were studied in pure and mixed cultures. Of the 50 different strains tested 40 (80%) were motile and 32 (64%) showed chemotactic behaviour in the presence of nutrient point sources (Marine Broth) indicating their ability to behaviourally respond to the organic matter field. Twenty five strains (50%) inhibited one or up to 24 different phylotypes reflecting variable interactions between different strains. Colonization experiments show that the abundance of particle colonizing bacteria differ in the absence or presence of inhibitory bacteria. But even in mixed cultures without any inhibitory strain the abundance of single strains can be highly different as compared to that of the pure culture. Hence interactions amongst marine bacteria influence colonization and growth dynamics of bacteria on particles and may control their solubilization and remineralization rates.

#### OS12T-13 1645h

##### Diversity and Distribution of Coral-Associated Bacteria

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Reef building corals are being decimated to an unprecedented extent by disease. Microbiologists have consequently turned their attention to potential pathogens of corals. However, we know very little about the normal bacterial associates of healthy corals. In particular, the culture-independent techniques that have revolutionized our understanding of planktonic marine bacteria have never been systematically employed to study the bacteria living with corals. To assess the diversity of coral-associated bacteria, we sequenced over 1000 bacterial 16S rDNAs from three coral species (*Montastraea franksi*, *Diploria strigosa*, *Porites asteroides*) in Panama and Bermuda. In this library, we identified a total of 430 ribotypes, a number which represents approximately 10% of all the previously reported marine 16S rDNA sequences in GenBank. Chao2 statistical analysis predicted that the combined libraries may have contained as many as 6,000 distinct bacterial ribotypes. Over 80% of the coral-associated ribotypes represent novel bacterial species (i.e., <97% identity to the nearest GenBank entry). Samples from Panamanian corals were more diverse than those from Bermuda, suggesting that global patterns of relative diversity found in coral reef metazoans may also occur in coral-associated prokaryotes. Some bacterial ribotypes were associated with specific coral species and positions within colonies, suggesting ecological specificity. Thus corals appear to represent a landscape of diverse prokaryotic types. As coral reefs worldwide continue to decline, there is a new urgency to understand the nature of the relationships between healthy corals and their associated prokaryotes. Characterizing these organisms and documenting their patterns of distribution, as we have begun to do here, is an essential first step.