

OS31B-21 0830h POSTER

Allochthonous CDOM is a Low Quality Substrate for Microbial Growth in Coastal Waters.

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Colored dissolved organic matter (CDOM) of terrestrial origin is rapidly removed from waters draining continental margins. The mechanisms (and their rates) necessary to explain this disappearance are not well understood. Generally, rates of bulk DOM biodegradation are low and relatively invariable in estuarine transects. Our current hypothesis is that physicochemical changes in mixing waters through an estuary may change the optical and biogeochemical properties of CDOM, thus altering its microbial utilization. In this study, 100 liter water samples were collected during transects from offshore marine to freshwater stations in the Chesapeake Bay, USA. CDOM was concentrated using tangential flow ultrafiltration (TFF) and natural bacterioplankton were concentrated on 0.2 µm filters from 3-5 watershed locations. Incubations were performed within days of collections wherein each sample's bacteria was incubated at in situ temperatures in "CDOM-free" TFF permeates with the addition of each station's CDOM concentrate. Bacterial production, respiration, DOC concentration, cell numbers, bulk CDOM fluorescence, specific CDOM fluorescence and viral abundance were measured over the course of 2-4 week incubations. Five separate samplings were conducted representing early and mid spring, summer, fall and winter. Allochthonous CDOM was generally degraded at a higher rate than autochthonous CDOM for all stations sampled and marine bacteria degraded more freshwater CDOM than marine CDOM. Similarly, freshwater bacteria often degraded more marine CDOM than freshwater CDOM. Bacterial production rates did not show any predictable trends with source of CDOM added. However, bacterial growth efficiencies (BGE) calculated from bacterial production and respiration measurements, were found to be lower in incubations amended with allochthonous CDOM. This indicates that allochthonous CDOM was preferentially respired rather than incorporated into cellular material, and thus behaved as a low quality food source for natural bacterioplankton. Bacterial conversion of terrestrially-derived organic matter to CO₂ in the coastal margin may help to explain the lack of terrestrial character found in biomass and natural organic matter in oceanic waters and sediments. We are currently using these data to develop a model of organic matter degradation through coastal estuaries in which the allochthonous component is always preferentially biodegraded. This model will be presented as a means to explain how relatively constant rates of DOM degradation through a coastal transect may still account for a significant fraction of allochthonous DOM removal.

OS31B-22 0830h POSTER

Carbon Cycling in Mangrove Ecosystems

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Mangrove forests occupy around 105 km² world-wide, and cover 75 percent of the tropical and subtropical coastlines of the Americas (Field 1995). These highly productive ecosystems are traditionally viewed as large exporters of carbon and other nutrients to adjacent coastal zones. Limited work has been done

to quantify carbon recycling within these systems and to identify the export sources from tropical mangrove ecosystems. There are several potential sources of organic matter that need to be considered: terrestrial sources, the mangrove vegetation, and marine sources including sea grasses and phytoplankton. These sources may be traced using stable isotopic signatures of carbon, nitrogen and sulfur. This study investigates nutrient cycling in mangrove forest sediments by comparing the stable isotopic signatures of organic matter buried in the sediment with those from terrestrial, mangrove and marine plants in a variety of mangrove ecosystems on the Yucatan Peninsula, Mexico (Dittmar, Lara et al. 2001; Kendall, Silva et al. 2001). This work may also elucidate the role of anthropogenic impacts affecting nutrient cycling within the mangrove ecosystem, a growing concern in heavily populated tropical coastal regions.

Dittmar, T., R. J. Lara, et al. (2001). River or mangrove? Tracing major organic matter sources in tropical Brazilian coastal waters. *Marine Chemistry* 73: 253-271.

Field, C. (1995). Impact of expected climate change on mangroves. *Hydrobiologia* 295: 75-81.

Kendall, C., S. R. Silva, et al. (2001). Carbon and Nitrogen isotopic compositions of particulate organic matter in four river systems across the United States. *Hydrological processes* 15: 1301-1346.

OS31B-23 0830h POSTER

Optical Properties of CDOM Derived From Copepod Grazing Processes

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Copepod grazing has been shown in previous studies to be an important fraction of the dissolved organic matter (DOM) pool. Yet their influence on the colored fraction of DOM has not been studied. A better understanding and characterization of chromophoric dissolved organic matter (CDOM) in ocean waters will (1) aid in determining the biological processes involved in its creation, (2) establish its contribution to carbon cycling, and (3) improve estimates of water color by remote sensing. This study aims to identify changes in ocean color attributable to copepods by characterizing optical properties of seawater specific to by-products of copepod grazing activity.

Experiments were conducted in the Gulf of Maine to investigate if copepod grazing influences CDOM composition. The optical analysis of CDOM was conducted by monitoring absorbance of dissolved organic matter (CDOM) as well as a more specific fraction of that pool, fluorescent dissolved organic matter (FDOM). FDOM is a more sensitive measurement capable of resolving smaller changes that may be attributable to biological inputs or removals. Optical absorbance and fluorescence spectra were collected from both treatment and control bottles that were incubated onboard ship for 24 h. Results from this study found that CDOM and FDOM increased throughout the experiment in treatment bottles. These changes in the composition of CDOM and FDOM during the 24 h grazing experiments will be discussed within the context of biological processes occurring during the incubation, including a possible microbial impact.

OS31B-24 0830h POSTER

Cycling of colloidal organic carbon and nitrogen during estuarine phytoplankton blooms

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While dissolved organic matter in the ocean plays a significant role in the global carbon cycle, understanding the dynamics of marine organic pools has been hampered by poor characterization of their composition and lability. To establish the influence of phytoplankton blooms on the cycling of dissolved and particulate organic carbon and nitrogen, we conducted a field study during a series of blooms in a small, shallow, enclosed embayment on Shelter Island, NY, USA. Using cross-flow filtration with a 1 kDa membrane, we collected high and low molecular weight (HMW & LMW) dissolved organic matter (DOM; less than 0.2 µm), along with POM (greater than 0.7 µm). Results demonstrated a significant, and near equivalent enhancement in levels of particulate and dissolved organic carbon during phytoplankton blooms under both high nitrate

and nutrient deplete conditions. Size fractionated results indicated that HMW organic carbon was responsible for most (80 percent) of the DOC enhancement during blooms, as increases in LMW organic carbon were small. In contrast, substantial amounts of organic nitrogen were produced in all size fractions (particulate, HMW and LMW) during blooms. Contrary to hypotheses that C-enriched DOM accumulates only under nitrogen deplete conditions, we observed that the accumulation of C-enriched DOM was more dependent on algal species composition than ambient inorganic nitrogen levels, as DOC:DON ratios were higher during periods of elevated nitrate compared to low nitrate conditions dominated by phytoplankton with heterotrophic capabilities. An excess of HMW organic carbon formation rates (7 µM per day) over decay rates (5 µM per day) suggests that recalcitrant colloidal organic carbon formed during phytoplankton blooms could contribute to the older age of the world's DOC pool.

OS31B-25 0830h POSTER

Variability in the Relationship between Colored and non-Colored Dissolved Organic Matter in the Mississippi River Plume

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We studied the relationship between dissolved organic matter (DOC) concentrations and light absorption coefficient of colored dissolved organic matter (CDOM) in coastal waters of the Gulf of Mexico influenced by the Mississippi River Plume. Two stations within the Mississippi River were sampled twice per month over seven months to determine the temporal variability of the relationship between DOC and CDOM for the end-member. We also collected surface water samples for CDOM and DOC analyses and measured above water reflectance along the Mississippi River Plume. In this paper, we evaluate the variability of the CDOM-DOC relationship and its usefulness in the determination of DOC concentrations using passive optical sensors.

OS31C HC: Hall III Wednesday 0830h**Viruses and Prokaryotes in Aquatic Systems III**

Presiding: S W Wilhelm, University of Tennessee; W H Jeffrey, University of West Florida

OS31C-26 0830h POSTER

The Phage Genomic Tree

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The most abundant biological entities in the ocean are phage, yet little is known about their biodiversity or geographical distribution. The biggest limitation to addressing these issues is our inability to characterize uncultured phage species, primarily because there is not a single genetic element that is conserved in all phage. Based on the overall similarity of 99 completely sequenced phage genomes, we propose a novel taxonomic system for classifying phage. The Phage Genomic Tree groups phage into taxa that predict several aspects of phage biology and correspond well with the current, morphology-based International Committee on Taxonomy of Viruses system. Additionally, each taxa in the Phage Genomic Tree has at least one conserved genetic marker which is shared by all members. We are

calling these markers Signature Genes. The Signature Genes can be used to measure the species richness of uncultured phage and will allow us to monitor phage biodiversity in a manner analogous to using rDNA in organisms.

OS31C-27 0830h POSTER

Genome Sequence of a Novel Marine Phage Infecting *Vibrio parahaemolyticus*

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Despite the high abundance of viruses in marine ecosystems, there is a lack of available sequence information for comparison. We selected a lytic virus (VpV 262) that infects the marine bacterium *Vibrio parahaemolyticus* for sequencing. *Vibrio parahaemolyticus* is a marine bacterium that causes gastroenteritis from the consumption of raw or undercooked shellfish. We are interested in using viruses infecting this bacterium as models for examining the diversity of natural viral communities and the role of viruses in structuring marine microbial diversity. VpV 262 was isolated from the Strait of Georgia, BC, Canada, and sequenced via high-throughput analysis of a shotgun-cloned library. The 50 nm podovirus was found to have a 45,874 bp linear dsDNA genome with 100 bp terminal redundancy. There are 73 open reading frames identified, packed tightly into two long converging transcription units. Based on identification of a few genes by sequence homology, one transcription unit is composed of early and replicative functions and the other of structure and morphogenesis functions. Some non-coding functions for which candidate sites are identified include a tRNA gene, and origins of replication. The most prominent homologies are distant and are to the presumed morphogenic genes of Roseophage S101, with evidence of considerable rearrangement. A T7-like maturase gene links VpV262 to the family Podoviridae. There is also evidence of horizontal gene transfer between VpV 262 and its bacterial host, as evidenced by a recently acquired bacterial type DNA polymerase. However, codon usage is in equilibrium between early and late genes, but not between the virus and *V. parahaemolyticus*, suggesting VpV 262 may have a broader host range (thought to be uncommon in Podoviridae) or has recently changed hosts. These data are consistent with considerable lateral gene transfer and illegitimate recombination within marine bacteriophage communities.

URL: http://biochem.uthscsa.edu/~hs_lab/vpv/vpv.html

OS31C-28 0830h POSTER

Fundamental changes in light scattering associated with infection of marine bacteria by bacteriophage

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Bacteria and phytoplankton are key determinants of the oceans inherent optical properties. Despite their high abundance, marine viruses have generally been thought to play a minor role in ocean optics due to

their small scattering cross-sections. Nevertheless, the role of specific viral infection on the optical properties of bacteria and phytoplankton has remained unknown (i.e. as viruses disrupt micron-sized host cells to produce sub-micron cell debris). Here, we report that the chief optical impact of viruses is associated with infection and lysis of their hosts. We quantitatively describe, for the first time, two optical changes associated with infection and lysis of marine bacteria (heterotrophic and photosynthetic) by bacteriophage: 1) rapid, strong shifts in the magnitude and shape of the optical volume scattering function (VSF) and 2) rapid production of colored dissolved organic matter (cDOM). Qualitatively, these changes result in nearly complete clearing of turbid host bacterial suspensions.

OS31C-29 0830h POSTER

Viriobenthos Abundance and Production in Neritic and Basin Sediments of Southern California

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Despite several reports of high abundance in marine sediments, the origin of benthic viruses is poorly understood. Sediment virus abundance has been argued to result from both autochthonous (attached hosts and hosts living free in porewaters), and from allochthonous (hosts in overlying water) inputs. Virus production and decay were determined using dilution techniques in subtidal Los Angeles Harbor sediments, an artificial eutrophic embayment characterised by large-grained sands (mean grain size ~ 250 micrometers). Virus production rates in these sediments ranged from 1.0 to 1.8 x 10⁷ virus-like particles (VLP) cm⁻³ h⁻¹. Allochthonous inputs of viruses in the region are estimated at approximately 2 x 10⁵ VLP cm⁻² h⁻¹. These results suggest autochthonous hosts produce most of the benthic viruses in this region, however allochthonous viruses may contribute significantly to sediment populations in areas of higher sedimentation. Analysis of San Pedro Basin sediments (> 900 m water depth) and estimates of adsorption to suspended matter in the water column indicate that autochthonous hosts produce the majority of viruses in deep basin sediments since total daily arrival of adsorbed viruses is < 0.2 percent of ambient abundance. The allochthonous input of viruses on settling suspended matter may represent a small but significant carbon transfer into deep basin sediments.

OS31C-30 0830h POSTER

Interactions Between the Parasite *Parvilucifera infectans* and a Natural Plankton Community in Hopavågen Bay, Norway.

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The parasite *Parvilucifera infectans* Norén et Moestrup (Perkinsozoa) commonly infect and kill free-living dinoflagellates, and can be a regulating factor in dinoflagellate blooms. The infective stage of *P. infectans*, the swimmers, are small flagellates and thus susceptible to grazing by microzooplankton. We investigated if *P. infectans* (ex. *Alexandrium andersonii*) could affect the growth of naturally occurring dinoflagellates from Hopavågen Bay, Norway. We also studied if natural assemblages of microzooplankton (e.g. ciliates) could control the parasitic infection of dinoflagellates by preying upon the swimmers. *P. infectans* infected natural assemblages of the dinoflagellate *Scrippsiella trochoidea* in Hopavågen Bay, but with lower success (<10%) compared to the cultured dinoflagellate *A. andersonii* (25% at 14°C, 50% at 20°C) after 60 h incubation. During the experiments, *S. trochoidea* formed cysts, and it is likely that this prevented parasite infection. Ciliates from Hopavågen Bay did not directly prey on swimmers of *P. infectans*, and natural communities of microzooplankton had little/no effect on the infection of *S. trochoidea*. Thus, infection success was mostly dependent on temperature and of host species. Compared to *A. andersonii*, *S. trochoidea* from Hopavågen Bay seems to

have a better protection against parasite infections by *P. infectans*, possibly due to its ability to form cysts.

OS31C-31 0830h POSTER

Phylotype-Specific Growth Rates of Marine Bacterioplankton

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In order to test the hypothesis that bacteria affiliated with different phylogenetic groups grow at different rates and respond differently to substrate addition, we examined the growth rates of four phylogenetically distinct bacterial subpopulations (i.e., α -proteobacteria, β -proteobacteria, γ -proteobacteria and *Cytophaga-Flavobacteria*) in diluted seawater cultures with and without the addition of glucose. The fluorescence *in situ* hybridization technique using 16S rRNA targeted probes was combined with semi-automated image analysis, allowing us to determine changes in cell abundance and size composition of individual bacterial groups. Experiments were conducted in the Delaware Bay Estuary. We found that the growth rates vary greatly depending on bacterial phylogenetic affiliation. Bacteria belonging to the γ - subdivision of proteobacteria were dominant (representing 28% of total bacteria that were detected by the eubacterial probe) in the sample water used for the experiment, and these bacteria grew at the highest rates (0.15 - 0.18 h⁻¹) in both control and glucose amended bottles during the initial phase of experiment (0 - 12 hours). During the same period, the growth rates of α -proteobacteria and *Cytophaga-Flavobacteria* were lower (0.05 - 0.1 h⁻¹), although the growth rates of these bacteria tended to increase with prolonged (24 hours) incubations. The growth of β -proteobacteria was not detected (<0.01 h⁻¹). We suggest that individual bacterial groups contribute quite differently to bacterial production and uptake of dissolved organic matter in the Delaware Bay.

OS31C-32 0830h POSTER

The Contribution of Specific Bacterial Groups to Bacterial Respiration and Production in the Delaware Estuary

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The purpose of this study was to explore using data on single-cell activity and community structure to explain variation in respiration and bacterial biomass production in the Delaware estuary. To accomplish this goal, bacterial community respiration rates, production, and growth efficiency, as well as single-cell bacterial respiratory activity (reduction of CTC), and community structure were examined at four stations along the salinity gradient of the Delaware estuary. During four cruises in 2001, bacterial production and oxygen consumption in the estuary varied 3-fold and 6-fold respectively, while bacterial abundance changed by only a factor two. Bacterial respiration was 17 to > 100% of the total community respiration with total respiration rates ranging from 52 to 676 mmol O₂ m⁻²d⁻¹ and bacterial respiration rates varying from 48 to 497 mmol O₂ m⁻²d⁻¹ in the water column. Bacterial production was more closely correlated with the number of CTC+ cells than it was with bacterial abundance. The percent of CTC+ cells ranged from 55 % to 2 % over the year. Stations with the highest percentages of CTC+ cells, the freshwater site in June and the chlorophyll maximum in August, were dominated by beta-proteobacteria as determined by fluorescent *in situ* hybridization. The freshwater reaches of the Delaware estuary had high bacterial respiration and production, CTC+ cells and beta-proteobacteria. In contrast, the more saline waters of the Delaware Bay had low bacterial respiration, but high bacterial growth efficiency, and were dominated by alpha-proteobacteria and *Cytophaga-Flavobacteria*. These data on the abundance and activity of specific bacterial groups are beginning to help us understand respiration and biomass production of the bacterial assemblage and of the total microbial community.

OS31C-33 0830h POSTER

Phosphate Limitation of Respiration and Uncoupling of Bacteria from P Regenerators in Size-fractionated Samples from the Sargasso Sea

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Respiration was measured in unfiltered seawater collected in the upper 75 m of the water column along a transect in the Sargasso Sea and at the Bermuda Atlantic Time Series Station (BATS, 31°50' 00N; 64°10' 00W) during a cruise in July and August 2001. Respiration rates in the upper 25 m water column were on average $1.36 \pm 1.22 \mu\text{mol O}_2 \text{ L}^{-1} \text{ d}^{-1}$ exhibiting large spatial and short-term (d) variability. Addition of inorganic (PO_4 or NO_3) and organic (glucose) nutrients indicated that plankton respiration was limited by phosphate in the surface mixed layer extending to 10 m depth. Size-fractionation revealed that bacterial abundance in the $< 0.6\text{-}\mu\text{m}$ fraction was $\sim 80\%$ of the bacterial abundance in unfiltered seawater samples, however, respiration rates in the size fraction $< 0.6\text{-}\mu\text{m}$ contributed on average only 23% to planktonic respiration. Addition of phosphate to the $< 0.6\text{-}\mu\text{m}$ -size fraction in both, short (24h), and long (5d)-term experiments increased respiration rates 2-fold and therefore its contribution to planktonic respiration. These results let us conclude that the assessment of bacterioplankton respiration in the phosphate-limited surface mixed layer by size fractionation was severely underestimated due to the separation of bacterioplankton from organisms that are responsible for the regeneration of inorganic nutrients.

OS31C-34 0830h POSTER

Tidal Effects on Coastal Bacterioplankton in Spring and Fall

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We examined whether the abundance and composition of particle-associated and free-living bacterial communities are affected by tidal dynamics in the German Wadden Sea in spring (May) and fall (November). In spring during a phytoplankton bloom, dry weight, POC, and chlorophyll a showed tidal variations, even though maxima and minima of these parameters did not occur simultaneously. Numbers of particle-associated bacteria, retained on 5 μm Nuclepore filters, also exhibited tidal variations, which covaried inversely with chlorophyll a. In contrast to May, all mentioned parameters covaried during the tidal cycle in November with maxima preceding high and low tide by one hour. The composition of the bacterial community, analyzed by denaturing gradient gel electrophoresis of PCR-amplified 16S rDNA fragments, remained stable throughout the tidal cycles, except that in May one band was absent during high tide. The analysis of the bacterial community by fluorescence in situ hybridization with group-specific oligonucleotides exhibited tidal variations in spring but not in November. The variations in May appeared not to be related with any of the other parameters measured. Our results demonstrate that the tidal dynamics in the Wadden Sea have a measurable influence on dry weight, POC, chlorophyll a concentration, and bacterial cell numbers, but which differs in fall and spring. The stable pattern of the particle-associated bacterial community is probably due to the hydrodynamic forces, which break, mix, and redistribute the present particles and aggregates.

OS31C-35 0830h POSTER

African Dust Microbes: An Inoculum for Coral Reef Diseases?

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Attempts have been made to link coral diseases to a variety of anthropogenic effects (e.g. sewage input, nutrients from agricultural runoff). Yet, coral reefs have continued to decline during the last two decades, even in remote areas of the Caribbean where anthropogenic inputs are not occurring. This prompted the hypothesis that dust from North Africa, which seasonally impacts the Caribbean, could be showering harmful microbes into these delicate reef ecosystems, precipitating some of these diseases. Records from Barbados document a continued rise in the amount of dust crossing the Atlantic since 1970, coincident with the worsening drought conditions in the Sahara/Sahel region of Africa. Spikes in the dust record correspond to some of the major coral morbidity/mortality events in the Caribbean. It has been determined that a terrestrial fungus, *Aspergillus sydowii*, is the cause of disease in Caribbean sea fans; and the infectious form of this fungus has been identified in African dust samples taken in the Virgin Islands. Most other coral diseases have unknown etiologies.

It has been established in several studies that Mali, West Africa, is one of the dust sources for the Caribbean. We have used microbiological and molecular techniques to purify and identify over 60 bacterial and 20 fungal isolates from a series of dust storms sampled in Bamako, Mali. 81% of the bacteria belong to genera found in aquatic or marine environments, including halotolerant *Bacillus*, *Paracoccus*, *Planococcus*, and *Staphylococcus xylois* (the causative agent of septicemia in loggerhead turtles in the Canary Islands). Of these, five bacteria are very similar to isolates obtained from African dust storms in the Virgin Islands; and one is 100% identical by 16S rDNA sequencing (> 700 bp) to a Virgin Island isolate. Of the bacteria, 8% are animal pathogens, 7% are plant pathogens, and 12% are opportunistic human pathogens. The fungi are mainly *Cladosporium* sp. and *Aspergillus* sp. These microbes are being spread over great distances by dust in the wind, and some may well be etiological agents for uncharacterized coral diseases.

OS31C-36 0830h POSTER

Combined Molecular and Chemical Tracer Approaches for In Situ Identification of Nitrate Utilization by Marine Bacteria

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Accumulating evidence suggests that bacteria compete with phytoplankton for inorganic nitrate (NO_3^-) and that heterotrophic bacteria may have a profound effect on the flux of NO_3^- via the "biological pump", and therefore carbon (C) in ocean margins. Whether autotrophic or heterotrophic organisms utilize available inorganic nitrogen is critical because sinks for dissolved nitrogen that do not incorporate inorganic C represent mechanisms which reduce the incorporation of C from the ocean/atmosphere into the biosphere. However, the processes that regulate the assimilation of NO_3^- by bacteria are not well understood because it is difficult to differentiate between bacterial and phytoplankton N uptake using conventional chemical tracer techniques. Under the auspices of the US Department of Energy program Biotechnology Investigations Ocean Margins Program (BI-OMP) we have developed molecular PCR based tools including PCR, RT-PCR, qPCR, and TR-FLP that target the functional assimilatory nitrate reductase gene (*nasA*) in heterotrophic bacteria and coupled the investigation of the presence, abundance, and diversity of *nasA* containing bacteria with estimates of uptake of NO_3^- by the bacteria size class ($> 0.2 \mu\text{m}$; $< 0.8 \mu\text{m}$) in diverse coastal and continental-shelf environments. Accumulating evidence using this dual molecular and chemical approach indicates that *nasA* containing bacteria are ubiquitous and that heterotrophic bacteria are responsible for a significant fraction of NO_3^- uptake in coastal and continental-shelf environments.

OS31C-37 0830h POSTER

Isotope Signatures for N_2O Production by Marine Nitrifying Bacteria

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Nitrous oxide (N_2O) is a potent greenhouse gas and is also involved in stratospheric ozone destruction. The ocean is a large source of N_2O , releasing an estimated 7-11 Tg N_2O -N to the atmosphere annually. Despite efforts to understand the biogeochemistry of N_2O , there is still debate regarding the relative importance of nitrification and denitrification in the production of N_2O in the ocean. Several lines of evidence indicate that nitrification by ammonia-oxidizing bacteria is the dominant source of marine N_2O . However, the published isotope values for N_2O produced by the terrestrial ammonia-oxidizer *Nitrosomonas europaea* imply that nitrification would produce N_2O that is too low in ^{15}N to fit available isotope data from the ocean. Here we show that this discrepancy, which overshadows interpretation of N_2O isotope measurements, may be resolved by focusing specifically on N_2O produced by marine nitrifiers at substrate concentrations closer to ambient levels in the ocean. We report that the isotope ratio ($^{15}\text{N}/^{14}\text{N}$) of N_2O produced by the marine ammonia-oxidizer *Nitrosomonas marina* is higher than the N_2O produced by *N. europaea* and thus better fits the model of N_2O produced by nitrification in the upper ocean. We also show that the isotope effect for nitrite reduction ($\epsilon_{\text{N}_2\text{O}}$), a key factor in the isotopic offset of N_2O from ammonia, is lower in *N. marina* than in *N. europaea*, supporting the N_2O isotope difference between the two nitrifiers. Furthermore, the $\epsilon_{\text{N}_2\text{O}}$ for *N. marina* decreases with substrate concentration, indicating that even less isotope fractionation should occur in the ocean than in culture studies. Our results suggest that the isotope values of N_2O in many regions of the ocean are completely consistent with a nitrification origin for this gas.

OS31C-38 0830h POSTER

Picocyanobacteria of the Hudson River Estuary, NY

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Picocyanobacteria are photoautotrophic bacteria which contain phycocyanin and may contain phycoerythrin, and are less than two micrometers in size. Picocyanobacteria and their role in the Hudson River estuary, until recently, have been poorly characterized, although much of the rest of the Hudson ecosystem has been studied in detail. For one date in mid summer in 1999, two in 2000, and monthly from May through October 2001 samples were taken from 9 locations along the length of the river. These sites were spaced over an approximately 100 mile length of the Hudson River with the first site located in Nyack, NY, approximately 20 miles from the mouth of the Hudson, and the last site 105 miles to the north in Troy, NY. This spatial and temporal sampling scheme allowed for the characterization of the picocyanobacteria and their habitats over the length of the river for 3 consecutive growing seasons. The river was characterized by a salinity gradient along its length, but temperature remained constant (less than one degree C difference from north to south). There were 2 distinct types of picocyanobacteria with similar phycocyanin contents, but different chlorophyll a contents (10 to 500 relative fluorescence units). The low fluorescence group underwent cell division in the afternoon. For a specific site, this group ranged two to three orders of magnitude in concentrations from 1,000 cells/mL in the spring to 100,000 cells/mL or 1,000,000 cells/mL in mid summer. For a specific date, concentrations were two orders of magnitude larger in the southern most sites (200,000 cells/mL) than in the northern sites (3,000 cells/mL). The high fluorescence group underwent cell division in the early evening, ranged in cell concentration for a specific site from 6,000 cells/mL in the spring to 28,000 cells/mL in mid summer, and ranged for a specific date from 20,000 cells/mL in the south to 4,000 cells/mL in the north. Additionally, the scatter of the two groups differed by an order of magnitude with the low fluorescence group having the lower scatter.

OS31C-39 0830h POSTER

Short-term variability of bacterial production and consumption of dimethylsulfide (DMS)

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Biological transformation rates of dimethylsulfide (DMS) and dimethylsulfoniopropionate (DMSP) were determined during 48 hours in the St. Lawrence estuary in July 2000. A drifting buoy was used to follow a water mass in which concentrations of DMS, dissolved DMSP (DMSPd) and particulate DMSP (DMSPp) were measured every 2 hours at the surface and at the depth of fluorescence maximum (2-6 m). DMS production and consumption rates were determined every 4 hours during onboard incubations. Dinoflagellates, mostly *Alexandrium tamarense* and *Scrippsiella* sp., dominated the phytoplankton community. During the course of the experiment, DMSPp and DMSPd concentrations varied from 20 to 120 nM and from 2 to 22 nM, respectively, and DMS concentrations increased from 0.2 nM to 6.0 nM. The DMS accumulation can be explained by an excess of DMS production over DMS consumption. Gross DMS production rates ranged from 0 to 2.0 nM h⁻¹, with the highest rate observed following a pulse of DMSPd. In general, DMS production rates exhibited large short-term variability in phase with the semi-diurnal tidal cycle. DMS consumption rates varied between 0 and 0.6 nM h⁻¹, with highest rates (> 0.3 nM h⁻¹) measured when DMS concentrations exceeded 3.0 nM. Elevated levels of DMSPd and DMS seem to rapidly trigger bacterial DMSPd cleavage and DMS consumption. During this experiment, processes of the DMS cycle show significant short-term variability and respond very rapidly to changes in the physical environment. This needs to be taken into consideration in the development of DMS production models.

OS31C-40 0830h POSTER

Fluid Flow as a Controller of Methane Oxidation Rates in Marine Sediments

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Methane oxidation activity within marine sediments associated with cold seeps of the San Clemente Escarpment during an Alvin cruise in 2000 was measured at various locations. The Navy Fan, a 100 to 200 m section that overlies older San Clemente strata, is characterized by the presence of distinct sand layers ranging from 3 to 5 cm in thickness that provide discrete pathways for migration of fluids at high lateral advective rates. The San Clemente fault cuts through the Navy Fan deposits and exposes migration pathways on a 60 m high scarp wall with fluid discharge sites along the escarpment zone demarcated by chemosynthetic communities and barite deposits. Sediments collected at seep sites on the scarp exhibited elevated methane turnover times ranging from 2 to 45 days within the upper 10 cm. Methane oxidation rate maxima within the sediment were observed at depths corresponding to pore-water anomalies of dissolved metabolites indicative of lateral flow of methane-rich fluids within the sediment. Seep sites located at the base of the scarp are characterized by vertical fluid flow along high permeability conduits of the San Clemente fault. Sediments collected at these sites exhibited methane turnover times of 8 days to 27 years in the upper 10 cm with the majority of oxidative activity confined to the upper 0.5 cm. Nearby

background (non-seep) sediments had relatively longer methane turnover times of 42 days in surface sediments and greater than 300 years below 2 cm depth. Methane turnover times for San Clemente seep sediments supplied by lateral flow of methane-enriched fluids were significantly higher than those observed elsewhere in methane-saturated sediments characterized by disruptive gas bubble flows driven by decomposing methane hydrates. Fluid flow characteristics appeared to be a more important controlling parameter of methane turnover times in marine sediments than methane pore-water concentrations except in surficial sediments directly in contact with bottom seawater.

OS31D HC: Hall III Wednesday 0830h

Coupled Biophysical Processes, Fisheries Resources, and Climate Variability in Coastal Ecosystems of the Northeast Pacific Ocean V

Presiding: H P Batchelder, College of Oceanic and Atmospheric Administration; P T Strub, College of Oceanic and Atmospheric Sciences; W T Peterson, National Marine Fisheries Service

OS31D-41 0830h POSTER

Ocean Climate Variability off Oregon?

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A line of stations along 44.6 N extending 150 km from the Oregon coast is being sampled 5 times per year for 6 years beginning in July 1997. Temperature and salinity along this line were also measured regularly from 1961 to 1971; averages and standard deviations from the 1961-71 data provide a standard of comparison for the present sampling program.

We calculate temperature anomalies between recent observations and the corresponding seasonal average values from 1961-71, and normalize the anomalies by the seasonal standard deviation to indicate statistical significance (a value >2 corresponds to a probability >0.95). El Niño strongly affected the temperature of Oregon coastal waters between July 1997 and Sept 1998: upper ocean waters were significantly warmer than the corresponding 1961-71 averages. The positive anomalies off Oregon lingered several months past the end of El Niño in the equatorial Pacific Ocean. El Niño also affected the currents: the northward geostrophic flow observed in Nov 1997 and Feb 1998 was stronger than the 1961-71 fall and winter averages. Since Nov 1998, water temperatures off Oregon have not been significantly different from the corresponding 1961-71 seasonal averages. Sections usually show both positive and negative anomalies that are small (<2) in most locations. The main exception is a slight midsummer warming of a zone centered at a depth of about 150 m over the outer continental slope, about 100 km west of Newport. The location and distribution of this slight summer warming suggests that poleward advection by the California Undercurrent may be stronger or more persistent now than it was during the 1961-71 reference period. The recent summer sections of geostrophic velocity do not show an obvious increase in the strength of the Undercurrent, but do indicate that a larger portion of the cross-section is subject to northward flow. The higher resolution ADCP data indicates the core of the Undercurrent is flowing about 10 cm/s northward in summer.

Our present sampling program resumed at onset of El Niño 1997-98 during a warm phase of Pacific Decadal Oscillation. A cold phase of PDO began in 1998 and has persisted since. The equatorial Pacific has been in a cold (La Niña) regime for the last three years but waters off Oregon are not significantly cooler than during the 1961-71 period, which was also a cool phase of PDO. Will this cool phase of PDO and near-normal temperatures off Oregon persist through the next El Niño?

OS31D-42 0830h POSTER

Altimeter SSH and Alongshore Transport Anomalies in the NE Pacific During 1999-2000

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Along the U.S. west coast and British Columbia, there have been reports of zooplankton species changes following the 1997-1998 El Niño. Cooler coastal water and more abundant zooplankton and baitfish have also been reported. Replacement of warm-water species with species associated with colder water (as reported off southern California, Oregon and Vancouver Island) could be explained by either advection from farther north or by stronger upwelling, leading to cooler water that favors the growth of cool-water species.

Using over 8 years of TOPEX/POSEIDON and ERS altimeter data, we investigate changes in Sea Surface Height (SSH) and alongshore geostrophic transport along the margin of the NE Pacific Ocean, from 20°N to Kodiak Island. Comparisons are made to Coastal Upwelling Index time series and NCEP winds. The period prior to the El Niño is represented by data from October 1992 through September 1996. Data from October 1998 through September 2000 represent the period following the El Niño. SSH values show a decrease of 5-10 cm during 1999-2000 in the 100 km next to the coast from Baja California to Southern Alaska. Initial calculations of alongshore transport are not as conclusive. After an initial period of equatorward transport along much of the coast during spring of 1998, alongshore transport anomalies during 1999-2000 are only consistently equatorward off California, but not at other latitudes. A more thorough analysis of SSH, transports and winds will be presented in the poster.

OS31D-43 0830h POSTER

Satellite Data Analysis of the Influence of El Niño 1997/1998 on the Pelagic Ecosystem off California

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The influence of El Niño event 1997/1998 was evaluated off central and southern California via multidisciplinary analysis of remote-sensed data. The EOF statistical method was applied to sea surface temperature anomalies (SSTA) measured by AVHRR radiometers, anomalies of water circulation derived from sea surface height anomalies (SSHA) measured by TOPEX/Poseidon radar altimeter, and meteorological information. EOF statistics demonstrated that an El Niño event occurred during the second half of 1997 and the first half of 1998, with sea level elevated along the coast and with SSHA gradients indicating retarding of both the equatorward California Current and the alongshore poleward Southern California Counter-current. The positive SST anomaly developed first in the Southern California Bight and then in the zone of upwelling to the north of Point Conception. The anomalies of upwelling index and the wind stress curl pattern also changed during the El Niño event, but these changes were observed later than hydrological variations and were too weak to explain the observed changes in SSTA and SSHA. Seasonal summer minima of remote-sensed (CZCS and SeaWiFS) chlorophyll concentration were observed in all zones of the region under study during the entire period of observations (1978/1986 and 1997/2000), suggesting that nutrient limitation is regulated by strength and depth of seasonal pycnocline. Seasonal maxima were observed during summer in zones of upwelling, during spring in the regions adjacent to upwelling zones, and during winter in the southern area, far from upwelling zones due to winter cooling. The main factors stimulating the growth of phytoplankton biomass were the intensity of coastal upwelling and wind stress. In 1997/1998 the remote-sensed phytoplankton biomass significantly decreased during the summer chlorophyll minimum. SSTA increased first in the Southern California Bight and then in the more northern upwelling zones without significant changes of wind pattern. All these variations during the El Niño event were consistent with deepening of pycnocline resulting from Kelvin waves propagating northward along the coast. We conclude that oceanic teleconnection,

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