

toxic dinoflagellate species responsible for harmful algal blooms (HABs) in the Gulf of Maine (GOM) are examined. Daily images coincident with five ECOHAB survey cruises in 1998 and 2000 are composited over each cruise period to create mean patterns for each sample period. Contours of surface *Alexandrium* concentrations superimposed on images of SST and SST frontal zones show that high concentrations of *Alexandrium* are located primarily in the eastern Maine coastal current (EMCC) and that frontal zones in this region generally act as boundaries to their surface distributions. The most consistent results of a series of linear regressions are a linear relationship between satellite SST and *Alexandrium* that was used in a simple model to extrapolate/interpolate the distribution of *Alexandrium* based on satellite data. The regression results also suggest a seasonally shifting optimal temperature range for maximum *Alexandrium* concentrations. No qualitative or quantitative relationships between the SeaWiFS chlorophyll data and GOM *Alexandrium* distributions were found. Relationships between satellite-measured SST patterns and toxicity events in the western GOM were examined during a paralytic shellfish poisoning (PSP) closure in May 2000 to test the hypothesis that toxicity events in the western GOM require a transport mechanism linking *Alexandrium* cells in the EMCC to shellfish beds in western GOM. Thermal patterns evident in the satellite SST data at the time of the May 2000 closure were consistent with enhanced connectivity and advection between the two regions. Ten years (1990-1999) of retrospective toxicity data from five sites along the coast of Maine and coincident AVHRR SST data are used to test the temporal stability of this relationship. Results show that the occurrence of strong thermal gradients between eastern and western GOM, indicative of reduced alongshore connectivity, play a role in the occurrence and timing of toxicity event in the western GOM.

## OS12F-189 1330h POSTER

### Growth and Grazing Rates of the Prostomatid Ciliate *Tiarina fusus* on Red Tide and Toxic Algae

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We investigated growth and grazing rates of the prostomatid ciliate *Tiarina fusus* when feeding on several species of red-tide and/or toxic algae (RTA). *T. fusus* ingested the dinoflagellates *Lingulodinium polyedrum*, *Scrippsiella trochoidea*, *Heterocapsa triquetra*, *Prorocentrum minimum*, *Amphidinium carterae*, and the raphidophyte *Heterosigma akashiwo*, but rarely consumed the dinoflagellate *Ceratium fusus*, and did feed on the dinoflagellate *Prorocentrum micans*. *T. fusus* exhibited positive growth on *L. polyedrum*, *S. trochoidea*, and *H. akashiwo*. Specific growth rates of *T. fusus* increased rapidly with increasing density of *L. polyedrum*, *S. trochoidea*, and *H. akashiwo* before saturating between 500-1,000 ng C ml<sup>-1</sup>. Maximum specific growth rate of *T. fusus* feeding on *L. polyedrum* (0.47 d<sup>-1</sup>) was much higher than when feeding on *S. trochoidea* (0.13 d<sup>-1</sup>) or *H. akashiwo* (0.10 d<sup>-1</sup>). Threshold prey concentrations (where net growth = 0) for *L. polyedrum*, *S. trochoidea*, and *H. akashiwo* were 34-160 ng C ml<sup>-1</sup>. Maximum ingestion rates of *T. fusus* on *L. polyedrum*, *S. trochoidea*, and *H. akashiwo* were 23.4, 10.2, and 6.5 ng C predator<sup>-1</sup> d<sup>-1</sup>, respectively, while maximum clearance rates were 4.5, 0.2, and 0.6 l predator<sup>-1</sup> h<sup>-1</sup>, respectively. *T. fusus* exhibited comparable or higher maximum growth, ingestion, and clearance rates than previously reported for the mixotrophic dinoflagellate *Fragilidium cf. mexicanum* or the heterotrophic dinoflagellates *Protoperdinium cf. divergens* and *P. crassipes*, when grown on the same prey species. Grazing coefficients calculated by combining field data on abundances of *T. fusus* and co-occurring RTA with laboratory data on ingestion rates obtained in the present study suggest that *T. fusus* sometimes has a considerable grazing impact on the populations of *H. akashiwo*.

## OS12G HC: 319 B Monday 1330h

### Novel Techniques for Chemical Characterization in Marine Systems I

**Presiding: H E Hartnett, Rutgers University; L Minor, Old Dominion University**

## OS12G-01 1330h INVITED

### Comprehensive Two-Dimensional Gas Chromatography: A New Tool for Geochemical Research

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Recent analytical and conceptual advances in chromatography have led to the development of comprehensive two-dimensional gas chromatography (GCxGC), which has a tremendous capability to separate, identify, and quantify trace organic compounds in complex geochemical samples. GCxGC uses two different chromatography columns coupled serially by a thermal modulator to produce a volatility by polarity separation and distribute compound peaks across a two-dimensional retention time plane. This is in contrast to "heart-cutting" two-dimensional GC, which only allows select components in the first column to be re-chromatographed on a second column. The GCxGC two-dimensional separation produces an order of magnitude more resolved peaks than traditional GC methods, and the grouping or ordering of the peaks in the GCxGC chromatogram facilitates the identification of unknown compounds. Furthermore, spatial band compression during modulation has the additional advantage of more than an order of magnitude increase in signal-to-noise ratio, thus improving the detection and quantification of minor components. For example, we have used GCxGC to investigate the composition and distribution of alkenones (35 to 39 carbons) in Black Sea sediments. These compounds differ in chain length, degree of unsaturation, and position of the ketone group (either methyl or ethyl). In this case, GCxGC analysis resolved and helped tentatively identify more of these compounds than was previously thought to exist. New alkenones include C35:2Me, C37:4Et, C37:1Me, C38:4Me, C38:1Et, and C39:4Et. (Alkenone nomenclature is as follows: Cx:y Me or Et, where x is the total number of carbons in the compound, y is the number of double bonds, and Me or Et designates methyl or ethyl ketones, respectively). It is especially worth noting that the placement of the ketone group by one carbon unit (methyl or ethyl) allowed for discrete bands of these compounds to be resolved. We have also found that GCxGC may be equally adept in determining the alkenone unsaturation index in total sediment extracts and hence avoiding time-consuming "clean-up" steps when using these compounds for paleothermometry. Another application of GCxGC that we are exploring is resolving the unresolved complex mixture (UCM) of petroleum hydrocarbons. These compounds are the most abundant, ubiquitous, and understudied class of organic contaminants in estuarine and coastal sediments. The term UCM is derived from traditional GC and refers to a hump of unresolved and, hence, unidentified hydrocarbons in gas chromatograms. Initial efforts have been able to separate and identify discrete bands of normal, branched, one-ring, and two-ring alkanes and one-, two-, and three-ring aromatics. Additional applications focused on natural and anthropogenic organic compounds as well as future efforts will be discussed.

## OS12G-02 1345h INVITED

### A Molecular Multi-Isotopic Approach for the Study of Organic Matter Cycling in the Oceans

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Over the past several years it has become feasible to measure the isotopic characteristics of individual organic compounds in complex natural matrices such as marine sediments. In addition to the stable isotopes of carbon, techniques have been developed for examining natural abundance variations in other stable isotopes (D/H,  $\delta^{15}\text{N}$  and  $\delta^{18}\text{O}$ ), as well as for radiocarbon at the molecular-level. Here, we illustrate how multi-isotopic measurements on individual compounds can improve our understanding of organic carbon cycling in the ocean.

Coupled measurements of  $\delta^{13}\text{C}$  and  $\Delta^{14}\text{C}$  better define organic carbon inputs, both in terms of quantity and mode of transport:  $\delta^{13}\text{C}$  measurements on molecular markers (biomarkers) of marine primary productivity (e.g., algal sterols, fatty acids, alkenones) may help to define environmental conditions and the physiological status of by the precursor organisms;  $\Delta^{14}\text{C}$  measurements on these same compounds provide a temporal context for the processes that act upon phytoplanktonic organic matter, from its synthesis in the surface ocean to its burial in marine sediments. We have observed, for example, that sediment redistribution processes such as resuspension and lateral advection can significantly "pre-age" organic matter that is preserved in some sedimentary regimes. When paired with similar measurements on vascular land plant biomarkers (e.g., epicuticular waxes, lignin phenols), constraints can be placed on the terrestrial residence time of the latter and on the importance of terrigenous organic carbon in marine sediments. Recently, we have expanded this multi-isotopic approach to include compound-specific D/H measurements, and found this can provide complementary information to that available from carbon isotopes.

In addition to describing this multi-isotopic approach, this paper will describe methods and existing challenges associated with molecular-level radiocarbon measurements, and discuss future analytical developments.

## OS12G-03 1400h

### A Compound-Specific Isotopic Tracer for Organic Nitrogen Source: Amino Acid $^{13}\text{C}$ Fractionation Patterns

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Most of the organic nitrogen which can be identified at the molecular level in organisms, sinking particles, and dissolved matter is present as amino acids. Unfortunately, in the geochemical realm, molecular-level amino acid analysis has had limited ability to provide source information because overall amino acid compositions from different sources are too similar. On the isotopic level, however, distinct biochemical pathways associated with differing metabolic processes result in characteristic stable isotopic fractionation patterns. In

proteinaceous materials such shifts are large, in the range of 5-20 among individual amino acids. Photosynthetic metabolism results in a highly reproducible pattern, while in comparison material from heterotrophic sources produce distinct and repeatable offsets in several amino acids. Thus the overall distribution of amino acid fractionation in the main protein amino acids offers a powerful potential tool to discriminate metabolic and organism-level source of organic nitrogen. We examine this technique using oceanic samples of dissolved and particulate material from the central Pacific, focusing on the potential to distinguish nitrogenous materials from prokaryotic vs. eukaryotic, and autotrophic vs. heterotrophic sources.

## OS12G-04 1415h

### Combining Molecular Level Analyses and Nuclear Magnetic Resonance Spectroscopy (NMR) to Characterize Dissolved Organic Nitrogen (DON) in the Marine Environment

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The use of ultrafiltration to isolate milligram quantities of marine dissolved organic matter (DOM) has greatly advanced our understanding of the chemical components dominating this reservoir. We are now able to combine sophisticated analytical techniques such as NMR, and mass spectrometry (MS), with more traditional molecular level analyses, to elucidate the chemical structure and, as a consequence, the cycling of different components of DOM in the ocean. Here we describe the use of these techniques to identify the chemical species that dominate the dissolved organic nitrogen (DON) reservoir in both the surface and deep ocean. Dissolved organic nitrogen is the largest reservoir of fixed nitrogen in the surface ocean. Based on the depth profiles of DON concentration in the open ocean, it appears that approximately half of this reservoir is reactive on relatively short timescales. Using a combination of <sup>1</sup>H, <sup>13</sup>C and <sup>15</sup>N NMR, coupled with selective chemical degradation techniques and molecular level analyses of monosaccharides, amino acids and acetate, we are able to show that the reactive high molecular weight DON is present within surface derived polysaccharides that are up to 50 % N-acetyl amino sugars. The non-reactive DON appears to be a complex mixture of compounds dominated by proteins that are resistant to chemical hydrolysis. We are also in the process of isolating and further characterizing the individual components of the DON reservoir using a combination of biochemical techniques such as electrophoresis and selective enzymatic degradation.

## OS12G-05 1430h

### Phosphorus Cycling and Regeneration in the Ocean: An Evaluation Using 31P-NMR

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Phosphorus (P) is an essential nutrient utilized by all living organisms. It has been recognized as a limiting nutrient in some oceanic systems and is possibly the ultimate limiting macronutrient for marine productivity over long time scales. Phosphate availability to phytoplankton growth, and thus the effectiveness of the biological pump depends on input of P to the euphotic zone via upwelling of deeper water and from river sources in coastal environments. Despite the recognition of the important role P plays in controlling marine productivity, relatively little is known about P cycling and regeneration within the ocean (Benitez-Nelson, 2000). Basic questions still remain unanswered such as: What phosphatic compounds are preferentially regenerated? How does P regeneration vary spatially and temporally? and, What determines the depth

and rate of P regeneration? Identification of the P compounds in the ocean is necessary to determine the origin, transformation, and potential bioavailability P, and to understand the structure of P compounds that ultimately are incorporated in the geological record.

We have assessed changes in the molecular composition of the particulate phosphorus pool in various water depths and oceanic settings using 31P-NMR spectroscopy. Particulate matter was analyzed from sediment traps from 3 different oceanic regimes: a coastal environment, an open ocean environment, and a polar environment. These different oceanic regimes represent areas spanning a wide range of productivity, soluble reactive phosphate concentrations in the euphotic zone, sea-surface temperatures, and planktonic communities. Preliminary results indicate that the oceanic particulate P pool is composed of: orthophosphate, phosphomonoesters, phosphodiester, pyrophosphate and phosphonates. Variability in the relative contribution of these components to the total P pool has been observed both spatially and with depth/age. Results will be interpreted in terms of preferential formation and/or degradation of specific organic compounds. The information gained with respect to the distribution and change of bond structure in these samples is valuable for assessing the potential reactivity of different P compounds.

## OS12G-06 1445h

### Characterization and Preliminary Field Trials of a Bioluminescent Reporter of Iron Bioavailability

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The role of Fe in the control of productivity and community structure of planktonic assemblages is well established in oceanic HNLC areas and several large lakes. Dissolved iron concentrations can be very low in the surface layer and dependent on both the presence of dissolved organic ligands and light penetration. The limitation of heterotrophic bacterial production by Fe availability in these systems is still debated due to conflicting field results showing either a primarily organic carbon stress or Fe stress. Therefore, the development of an approach to distinguish between organic carbon and iron bioavailability represents one of the significant challenges for the Fe field research. We have developed a biomolecular tool to track the response of heterotrophic bacteria to ambient Fe concentrations. Bioluminescent reporters, constructed by fusing the *fepA-fes* promoter of *Escherichia coli* (a siderophore biosynthesis gene) to a *luxCDABE* transposon, were integrated into the chromosome of a halotolerant *Pseudomonas putida* as well as marine heterotrophic prokaryotes. Light production from the *lux* cassette is thus linked to the activation of the report bacterium high-affinity Fe transport systems (an indication of Fe-limitation), making it a useful indicator of Fe availability. The *P. putida* bioreporter has been successfully tested both in lab and field studies. Laboratory cultures were grown under degrees of Fe limitation generated by the addition of concentrations (0 to 150 nM) of well-characterized chelators (desferrioxamine B [DFB], ferrichrome) as well enrichment with inorganic Fe (5 to 20 nM). Preliminary characterizations suggest the growth rate of the bioreporter decreased significantly by a factor 2 and 3 for DFB and ferrichrome additions relative to iron-replete treatments. However, a relative light increase of 25% and 40% was observed for the same chelators between iron-limited and iron-rich media. These results confirm the hypothesis that these bioreporters can be used to monitor Fe availability. Field studies in a low Fe system (the central basin of Lake Erie) were performed with DFB added to trace metal clean collections of water at concentrations of 0, 12, 20, 30, 40 and 50 nM. Bioreporters expressed Fe-stress (ca a 200% light increase) at concentrations of DFB > 30 nM, (but not < 20 nM DFB) indicative of the removal of bioavailable Fe, with increasing light produced at both 40 and 50 nM DFB. In a similar experiment with 0.2 - μm prefiltered water a dramatic increase in light production (ca 600% relative to 0 nM DFB controls) was observed at the lowest (12 nM) concentration of chelators, more than 2-fold higher than the unfiltered water sample. These results suggest that removal of the particulate size class forced cells into Fe-stress more rapidly when DFB was added, suggesting that a significant component of the bioavailable Fe flux is particulate in nature.

## OS12G-07 1520h INVITED

### Identification of Metal-Complexing Ligands in Sea Water using Electro Spray Mass Spectrometry

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Organic complexation affects the bioavailability and distribution of trace metals in seawater. Electrochemical methods have shown that Cu<sup>2+</sup> forms strong complexes with organic ligands in the surface ocean, and several laboratory studies have shown that copper-specific ligands are released by photosynthetic marine organisms in response to elevated copper concentrations. These compounds need to be isolated and identified before their role in the biogeochemical cycling of trace metals can be fully understood. Electro spray mass spectrometry (ESI-MS) provides information about the structure of dissolved organic ligands and their metal-ion complexes that cannot be obtained using electrochemical methods. Using 8-hydroxyquinoline and tannins as model ligands, we'll show that ligands can be characterized by ESI-MS and that the location of the copper binding site can be determined in complex molecules. We'll also present results on copper binding ligands from coastal waters of British Columbia, extracted using immobilized Cu<sup>2+</sup>-ion affinity chromatography (IMAC), monitoring the UV absorbance at 255 nm during elution. Salts and residual metal ions were removed on line using a custom made XAD-16 column. Ligand concentrations were higher at low salinity and in surface waters, suggesting that these ligands are produced in surface waters and/or delivered to the region via the Fraser River. Analysis of the extract with highest UV absorbance identified a Cu<sup>2+</sup> ligand of molecular weight 259. The mass and isotopic distributions are consistent with a dipeptide containing two metal-binding amino groups. This result is consistent with the findings of other studies attempting to characterize Cu<sup>2+</sup> ligands in seawater. The structure of the identified ligand is similar to that of rhodotorulic acid (a microbial siderophore), indicating that small peptides and related compounds can act as strong, specific metal chelators in natural waters.

## OS12G-08 1535h INVITED

### Characterization of Thiols in Seawater by Electro Spray Mass Spectrometry of Monobromobimane Derivatives

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Recent studies suggest that certain thiols, such as glutathione, are present in appreciable quantities in surface waters where they may be important metal chelators. Much of this data was obtained by cathodic stripping voltammetry. Here we show that while this is a useful method that can provide additional information about metal complexation, it is not selective for specific thiols, and indeed the species detected in general do not behave like glutathione, the compound frequently inferred to be the major thiol present.

HPLC of derivatized thiols is a more powerful approach, provided that standards are available for all the thiols in the sample, to enable identification based on retention times alone. However, some peaks in real samples do not correspond to common standard compounds. Here we report the use of electro spray mass spectrometry coupled with HPLC for thiols derivatized with monobromobimane, and we show how this approach provides useful structural information for a variety of thiols found in natural waters.

OS12G-09 1550h

### Chemical Characterization and Bioavailability of Dissolved Organic Matter using Atmospheric Pressure Electro Spray Ionization Mass Spectrometry

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Dissolved organic matter (DOM) is a complex mixture of organic compounds and is an important source of C and N to rivers and estuaries. As such, DOM can fuel bacterial metabolism, but the reactivity of DOM varies by source and season. Until recently, our understanding of DOM reactivity and bioavailability has been limited to bulk-level analyses or to some specific fraction of the DOM pool. We present new results using Atmospheric Pressure Electro Spray Ionization Mass spectrometry to characterize the bioavailability of DOM from various sources. This analytical technique provides information on molecular weight, abundance and acid/base properties. We demonstrate differences in the reactivity of individual compounds and chemically characterize the bioavailable and refractory pools of DOM before and after microbial degradation. Samples from a variety of aquatic sources (forested, agricultural and urban) had different molecular weight distributions or 'fingerprints', as well as different degrees of bioavailability. In an experiment with urban stormwater, approximately 40% of the DOM compounds were bioavailable, and almost all of the available compounds exhibited similar chemical characteristics. This approach has extended our understanding of DOM processing in aquatic systems by providing molecular-level information on the previously uncharacterized complex mixture of DOM compounds.

OS12G-10 1605h

### Techniques for the Analysis of Intact Protein in Marine Sediments

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Proteins represent the largest biochemical class of compounds identified in marine sediments. Traditional thought suggested that proteins were very labile, and therefore unable to withstand diagenetic transport and alterations. The majority of studies to date on sedimentary protein concentrations and dynamics have relied on the analysis of protein subunits, i.e. amino acids or peptide bonds. This has limited, or eliminated, all information on the size, type and source of the protein or peptide along with any sequence information. The primary focus of our research has been to develop techniques to look at intact proteins and peptides in seawater, sediments, and pore water. Recent advances in proteometrics now allow for a higher tolerance for salts and impurities from biological matrices and also permit greater sensitivity for protein analysis. With the development and use of LC-ESI-MS-MS and MALDI-TOF-MS systems we are able to observe cleavage patterns of known proteins by natural bacterial assemblages. Most recently, we have also extracted and analyzed naturally occurring proteins from sediments and seawater from the Washington coast. Results to date indicate a predominance of extractable protein in the mid-size range of 30kDa.

OS12G-11 1620h

### The Application of Electrospray Ionization FT-ICR Mass Spectrometry to the Study of Natural Organic Matter

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Molecular level characterization of natural organic matter has been elusive due to the inherent complexity of natural organic mixtures and the fact that individual components are polar and macromolecular. Electro spray ionization (ESI) is a "soft" ionization technique that ionizes polar compounds from aqueous solutions prior to acceleration into a mass spectrometer. In this study, we have combined ESI with an ultra-high-resolution mass spectrometer, the Fourier transform ion cyclotron resonance mass spectrometer (FT-ICR MS), to examine individual molecules within a variety of natural organic mixtures. With the high resolution of the FT-ICR MS (<1 ppm error in mass accuracy), we have been able to resolve >9,000 compounds within the 300-1000 Da mass range. At low m/z, the resolution is high enough to assign exact molecular formulas allowing specific components of these mixtures to be identified. In addition to molecular identification, we can now use ESI FT-ICR MS to examine molecular-level changes in different organic mixtures as a function of relevant geo-processes, such as microbial alterations and photochemistry. In this presentation, we will highlight the capabilities of the instrument by showing molecular-level resolution mass spectra of different organic mixtures such as humic substances, riverine DOM and bacterial exudates. In addition, we will present an example of the potential of this technique for molecular-level comparisons as a function of photochemical alteration of riverine DOM.

OS12G-12 1635h

### Development of a High Specificity ELISA Assay to Trace the Source and Fate of Biopolymers in the DOC Pool.

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Dissolved organic carbon (DOC) is the largest pool of active organic carbon on earth. Understanding the cycling of DOC is crucial to predict ocean processes ranging from food web dynamics to climate change. To investigate the complex degradation dynamics taking place in the water column it is critical to develop probes of high sensitivity and specificity that can identify the source and trace the fate of specific moieties found in DOC. The unicellular alga *Phaeocystis* (Prymnesiophyte) is a leading contributor of biopolymers to the dissolved organic carbon pool (DOC). During spring, subpolar and polar oceans blooms of *Phaeocystis* release huge masses of polymer gels. Most of this material is partially processed by bacteria and other microbial species. However, the final fate of the bulk of *Phaeocystis* primary production remains uncertain, and the contribution of *Phaeocystis* polymeric material to the global DOM pool is unknown. We developed an ELISA assay (enzyme linked immunosorbent assay) to quantify the concentration and contribution of *Phaeocystis* extracellular polymers to the global DOC pool. The concentration of *Phaeocystis* polymer found in field samples of DOM taken from the Ross Sea, the North Water Polynia and the Gulf of Alaska can range from 0.33  $\mu$ M to 20  $\mu$ M carbon. Our results indicate that ELISA provides a powerful highly specific method with nanomolar sensitivity to identify and measure the complex moieties found in DOM. (Supported by grants from the US DOE-BIOM Program and NSF Division of Bioengineering Biocomplexity Program)

OS12H HC: 314 Monday 1330h

### Interactions Between Macro- and Microorganisms in Aquatic Sediments II

Presiding: R Haese, Utrecht

University; J Kostka, Florida State University

OS12H-01 1330h

### Interactions Between the Cold Seep Tubeworm, *Lamellibrachia cf. luymesii*, and Interstitial Sulfate Reducing Bacteria: A Perpetual Motion Machine?

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*Lamellibrachia cf. luymesii* is similar to its hydrothermal vent relatives in that it has no mouth, gut or anus and obtains its nutrition from symbiotic chemoautotrophic sulfide-oxidizing bacteria. Also like its vent relatives, *L. luymesii* supplies sulfide to its symbionts using special hemoglobins in its vascular and coelomic fluids that have a very high affinity and capacity to bind and carry sulfide. However, unlike the well-studied East Pacific Rise hydrothermal-vent tubeworms, adult *L. luymesii* live in an environment where sulfide is normally not detectable around its gas exchange organ, the obturator plume. We have recently demonstrated that under some conditions a posterior extension of the worms, nicknamed a root, is capable of taking up sulfide at rates sufficient to fuel net inorganic carbon uptake, or in other words, autotrophy. We have also found that very high (millimolar) levels of sulfide are often present deep in the sediment, around the buried posterior ends of the worms.

Where does this sulfide come from and how is it replenished? It is unlikely to come from deep sources as the oil reserves in this region of the Gulf do not contain sulfide. Furthermore, these pools are present at greater depths than can be explained by diffusion and reduction of seawater sulfate. We will present a hypothesis for a mechanism to deliver the high sulfide flux necessary to supply the roots of the tubeworm aggregations in the Gulf of Mexico, current evidence supporting this hypothesis, and the results of models that constrain the flux of sulfide required by the aggregations and the volume of sediment that supplies this sulfide.

OS12H-02 1345h

### Comparison of Clambed and Microbial Mat Habitats at Eel River Methane Seeps, Northern California Margin: Microbiological, Geochemical and Biological Interactions

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During 2 cruises (2000 and 2001) we investigated the methane seeps in the Eel River Basin on the northern California margin (500 m). The study area was characterized by 2-m to 10-m patches of bacterial mats and clambeds occurring in close proximity to each other. Our combined studies focused on the microbial processes and resulting geochemical gradients and their role in structuring the different benthic assemblages. We measured concentration profiles using microelectrodes (oxygen, sulfide), applied conventional chemical methods (sulfate, methane), and carried out in-situ