salinity front, the velocity structure, and other aspects of the Meddy structure. The outward flux associated with this detrainment is used to calculate the total rate of microstructure dissipation demanded by the model.

Partway through the year, the microstructure dissipation was surveyed. This was found to be most intense in the intrusive frontal zone, and to a lesser degree, just above and below the Meddy core. The volume integrated thermal dissipation rate was estimated from these observations, and agreed with that demanded by the model to better than 10%. We conclude that this method and model can be used in other less well-constrained situations to estimate the cross-frontal intrusive heat flux.

OS41T-07 1020h

Critical Internal Wave Reflection, High-Frequency Internal Waves, and Turbulence in Mono Lake and Lake Tahoe, California

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The internal wave field was measured with an array of temperature moorings located over varying topographic slope angles in Mono Lake, CA and Lake Tahoe, CA. We present observations of the spectral distribution, and spatial and temporal variability of high-frequency internal waves. In particular we focus on waves in the frequency band critical for local bottom slopes, and on waves at higher frequencies, approaching N. Internal wave breaking near the critical frequency for sloping topography is hypothesized to be one of the important mechanisms by which energy is lost from the internal wave field to turbulent dissipation near boundaries. Because high-frequency internal waves can be a signature of shear instabilities, the energy at the near-N frequencies also may be related to turbulent dissipation. The low-frequency, basin-scale internal waves in Mono Lake appear to be directly forced by the wind. The spectral energy density from the total time series in each lake falls off as ω^{-2}, however over smaller time blocks, occasional anomalies from the G-M spectrum appear at intermediate and high frequencies. These peaks occur on specific density surfaces and are not distributed throughout the water column. We investigate the relationship between such events and phase of the basin-scale waves and wind strength. Spectra at varying depths are examined for evidence of critical-frequency energy enhancement over four sites with different bottom slope angles. Preliminary results suggest that critical reflection may not be a dominant mechanism for turbulent dissipation in Mono Lake. Microstructure profiles concurrent with some of our temperature measurements are used to ascertain whether a direct relationship can be made between turbulent dissipation and internal wave energy in the near-critical or near-N frequency bands.

OS41T-08 1035h

Flow Structure and Turbulence Distributions in the Coastal Ocean from PIV Data

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Particle Image Velocimetry (PIV) allows measurements of the instantaneous distribution of two velocity components within a sample plane. This technique overcomes the inability to separate the unsteady flows associated with turbulence from those induced by surface waves in the coastal ocean, which adversely affects the data obtained using point measurement techniques. The availability of instantaneous spatial distributions of velocity enable us to calculate spatial turbulence spectra and structure functions. To estimate the Reynolds shear stress, we calculate the covariance of velocity components, cov(Δu,Δw), as a function of separation between measurement points, r. Trowbridge (JAOT, **15**, 290) shows that, provided the separation is larger than the characteristic turbulence scale and smaller than the surface wavelength, cov(Δu,Δw) is equal to twice the Reynolds shear stress and insensitive to slight misalignments of the velocity components. In our system the sample area varies between 0.3x0.3 - 0.5x0.5m, each containing 63x63, 2-D velocity vectors, spaced 0.5-0.8cm apart, respectively. Two such sample areas positioned on the same vertical plane and separated horizontally by 1m have been used for calculating the distribution of cov(Δu,Δw) up to r=1.5 m. The data shows, as expected, that cov(Δu,Δw) increases with r at small separations and then reaches asymptotically a constant value at scales of about 1m. The spacing required to reach a plateau increases with distance from the bottom. When the covariance reaches this plateau and the length scale is still substantially smaller than the wavelength of surface waves ($\sim$100m in our measurements), we cover the relevant turbulent length scales and the data is still free of wave contamination. We have used this method for measuring the distributions of shear stresses in the bottom boundary layer of the coastal ocean.

To obtain the data, a submersible PIV system was deployed at two locations close to the LEO-15 site in regions with depths of 12 and 20m. The PIV and auxiliary instruments were mounted on adjustable seabed platforms, which enabled us to orient the sample areas with the flow and perform measurements at any desired elevation, from very close to the bottom up to 10m above the bed. Specific details of the system are presented in another abstract (Katz et al.). Data were collected at different elevations and under different mean flow and wave conditions for periods in excess of 20min each, and at rates of up to 3.3Hz. The PIV data are augmented and compared to simultaneous measurements of turbulence using an airfoil probe and of surface waves using a pressure transducer. CTD and ADCP are used for profiling the entire water column.

The results include vertical distributions of mean velocity, dissipation rate and shear stress under different mean current and wave conditions. The dissipation rates are estimated from the turbulence spectra. There is clear evidence that a log layer exists only when the amplitude of the wave induced motion is significantly smaller than the mean flow. Distributions of vorticity enable us to identify and follow the transport and development of large scale eddy structures within the sample areas. Conditional sampling enables us to correlate between the characteristics of the turbulence and the phase of the wave induced flows. The analysis is performed at different ratios of mean flow to amplitude of wave induced motion, including cases with zero mean flow.

Funded in part by NSF and in part by ONR.

OS41T-09 1050h

Anisotropy and Reynolds Number Effects in Turbulent Stratified Shear Flow

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Shear and stratification are ubiquitous features of turbulent flow in the ocean. A prototypical example of this flow with uniform shear and stratification has been studied extensively in the past decade using direct numerical simulations. The numerical simulations provide great detail of the flow. For example, all components of the viscous dissipation rate can be computed from the numerical data. Due to the presence of shear and stratification, the overall dissipation is distributed unevenly over its components. It was found that the contribution of the vertical gradient of the downstream velocity component increases from about 20% for unstratified flow with $Ri = 0$ to about 30% for weakly stratified flow with $Ri = 0.1$ and to about 50% for strongly stratified flow with $Ri = 1$.

In field experiments, generally only a limited number of these components can be measured. Therefore, numerical simulations can help to estimate the overall value of the dissipation rate from the measured components. However, the Reynolds number of the direct numerical simulations is relatively low compared to oceanic flow and great care has to be taken in an application of the numerical results to oceanic flow. This contribution discusses Reynolds number effects on the Reynolds stress anisotropy, buoyancy flux, and dissipation rate components. It was found that Reynolds number effects on Reynolds stress anisotropy and buoyancy flux are limited to very low values of the Reynolds number but that they persist to larger values of the Reynolds number for dissipation rate components.

The direct numerical simulations are performed on a parallel computer and the computational domain has up to $512 \times 256 \times 256$ grid points. The spatial discretization is accomplished by a spectral collocation method and the time advance uses a fourth-order Runge-Kutta scheme.

This study is supported with computer time by the National Partnership for Advanced Computational Infrastructure (NPACI).

OS42A HC: Hall III Thursday 1330h

Molecular Ecology of Carbon and Nitrogen Cycles in Ocean Margins II

Presiding: **F Wilkerson,** San Francisco State University**; J Paul,** University of South Florida

OS42A-92 1330h POSTER

Bacterial life strategies in an oligotrophic riverine environment: Microcolony formation versus living 'single'.

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The activity and the different life strategies of heterotrophic riverine bacteria as well as their major bacterial groups had been investigated in the highly pristine and oligotrophic River Tagliamento (Italy). Attached bacteria showed low abundance but very high biomass production. An opposite activity was observed for free-living cells from the water column. Temperature and low nutrient and DOC concentrations seem to overall control the activity pattern. From our samples eubacteria generally dominated the bacterial community living in the water column (70%) as well as attached on the substrate (100%). Eubacteria were comprised by >67% of alpha-, beta-proteobacteria and cytophaga. Mostly alpha-proteobacteria appeared to form microcolonies in the oxygenated hyporheic zone. Additionally, Atomic Force Microscopy of bacteria in water under controlled pH clearly demonstrated that coccoid-shaped cells develop large exopolymers to randomly colonize the surface of the carbonaceous substrate. Patches of biofilms could also be observed. According to our results, we propose that in competition for scarce resources, cells exhibit an active exchange between free-living and attached phases.

OS42A-93 1330h POSTER

Uptake of Selected DOM Components by Bacterial Groups in the Delaware Estuary

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Assemblages of aquatic heterotrophic bacteria display a high degree of phylogenetic and metabolic diversity, though the link between phylogeny and metabolic activity remains unclear. This link can be investigated using a combination of microautoradiography and fluorescence in situ hybridization (Micro-FISH). Previous investigations using Micro-FISH observed certain phylogenetic groups dominate the uptake of specific components of the DOM pool. The dominance of a phylogenetic group, however, may vary in an environment such as the Delaware estuary where large shifts in the abundance of certain phylogenetic groups occur. In an investigation of the Delaware estuary with both FISH and Micro-FISH, large changes in the bacterial community composition were observed along the salinity gradient. Beta Proteobacteria and Cytophaga-Flavobacteria were the most abundant groups in the fresh waters, while the alpha Proteobacteria and Cytophaga-Flavobacteria were the most abundant in the saline waters. Similar to previous studies, preliminary Micro-FISH data suggest that Cytophaga-Flavobacteria dominated the degradation of protein in saline waters. Acetate was utilized primarily by the alpha Proteobacteria in saline waters, while the beta Proteobacteria and Cytophaga-Flavobacteria were the main acetate degraders in fresh waters. These data indicate that as the community composition changes along the salinity gradient, different phylogenetic groups dominate the degradation of the same compound.

THU

OS42A-94 1330h POSTER

Is there a relationship between microbial diversity and microbial activity: a comparative analysis of microbial communities in two marine sediment types.

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Sandy sediments are less well-studied than silty sediments in benthic microbial studies. In this study, we were interested in the relationship between microbial diversity and activity in these two common sediment types. Therefore, eleven microbial-biogeochemical [abundances, CTC-activity, CO_2 production (CO_2R), and denitrification (Dn P), nitrogen fixation (NF P) rates] and molecular measures (16S, nirS, nirK, nifH T-RFs, Sorensen's Index, 16S clone sequence analysis) were employed to compare microbial communities in a sandy vs a silty sediment type. Site DB is a >86% silty/clayey sediment w/ 0.78-0.92 porosity, 6-11 uM $PW_{NO3+NO2}$, 11-13% organic carbon, 0.5-2.6 ug/g chla. Site NH is a >90% sandy sediment w/ 0.45-0.47 porosity, 7-28 uM $PW_{NO3+NO2}$, <1% organic carbon, 1.2-4.5 ug/g chla. Total bacteria were more numerous in DB than NH (9-18 vs. 0.5-3 x 10^9/g dws), with more CTC-active cells (10-37 vs. 2-6 x 10^8/g dws). All measures of metabolic activity were higher in DB than NH: [(CO_2 R: 0.07-0.60 vs. 0.03-0.44 mmol CO_2/m^2/hr), (Dn P: 16-38 vs. 1-12 umol N/m^2/hr), (NF P: 0.13-0.31 vs. 0.00-0.02 pmol C_2H_4/m^2/hr)]. However, both structural (13-19 vs. 17-20 T-RFs) and functional gene diversity (15-91 vs. 9-33 T-RFs) was higher in NH vs. DB. Though functional genes showed larger differences between sediment types, all measures of microbial diversity were consistently higher in sandy vs silty sediments. From 40-68% of the populations were unique to each sediment type. This study of marine benthic communities suggests there is an inverse relationship between microbial diversity and microbial activity.

OS42A-95 1330h POSTER

Picoeukaryote Abundance, Diversity, Growth and Grazing Mortality at a California Current Monitoring Site.

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Picoeukaryotes are ubiquitous in the marine environment and often form a significant portion of the biomass in the less than 2 micron size fraction. However, the degree to which they contribute to carbon fixation and trophic transfer in marine systems has not been explored, most attention having been focused on their prokaryotic counterparts. We have measured abundance of Prochlorococcus, Synechococcus, and photosynthetic picoeukaryotes on a weekly basis at a coastal California monitoring site at the Scripps Institution of Oceanography (La Jolla, CA USA). In addition, growth and grazing mortality rates of these organisms have been estimated on a seasonal basis using a dilution based approach. Estimated picoeukaryote growth rates ranged between 0.76 - 1.30 day-1. These growth rates were often 3 times that of Prochlorococcus (range 0.20 - 0.46 day-1), and twice that of Synechococcus (range 0.51 - 0.85 day-1). While the variation in growth rates of each group was relatively small over the seasons, grazing rates varied considerably and often corresponded to changes in abundance. These data suggest a relatively strong grazer mediated control of the observed picoplankton population dynamics. Furthermore, photosynthetic picoeukaryotes and Prochlorococcus were grazed at higher rates than Synechococcus. Picoeukatyote diversity, based on full-length 18S rRNA gene sequence (approx. 1800 bases) from seasonally generated clone libraries, was high at this location and also varied between sampling periods. Green algae, including Ostreococcus, were commonly found, as were unidentified Stramenopiles and Alveolates. The implications of this work suggest more important ecosystem roles for these tiny eukaryotes than has previously been recognized.

OS42A-96 1330h POSTER

Development of a molecular marker for monitoring bacterial utilization of phytoplankton released glycolate

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Phytoplankton production and release of organics are tightly coupled to bacterial uptake and growth. Traditionally it has been difficult to quantify these interactions as the rates of phytoplankton release and bacterial uptake are rapid. We have identified a system, diatom photorespiration, that allows us to focus on a phytoplankton-specific compound and the corresponding bacterial enzyme required for its utilization. Phytoplankton release various dissolved carbon and nitrogen organics into seawater, especially during photorespiration when they are stressed by high light and/or high oxygen concentration. The photorespiration-specific compound glycolate has been found to exhibit a diel variability in concentrations in many different marine waters. Both lab and field studies have shown that bacterial uptake is significant enough to deplete glycolate concentrations at night. Marine bacteria may utilize glycolate either as an energy source for uptake of other substrates or for biosynthesis and growth. In bacteria, glycolate is metabolized by the enzyme glycolate oxidase. We have developed degenerate CODEHOP PCR primers to the gene encoding the D-subunit of bacterial glycolate oxidase (glcD). Using these primers, we PCR-amplified and sequenced the first glcD sequences from laboratory cultures of two marine heterotrophic bacteria, *Oceanomonas doudoroffii* and *Pseudomonas stutzeri*, and from environmental samples. The amino acid sequences of glcD from the lab cultures and environmental samples were novel sequences most closely related to other known bacterial glcD sequences. We are currently using these primers to study the transcription of glycolate oxidase in laboratory cultures under different growth media to determine whether we can use this marker to monitor bacterial utilization of glycolate in the field. With such a marker, this system will also represent a good model for investigating phytoplankton-bacterial interactions without requiring the two groups of organisms to be physically associated.

OS42A-97 1330h POSTER

Photorespiratory Gene Expression Under Changing Light Conditions in the Centric Diatom Thalassiosira weissflogii

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Diatoms are significant contributors to oceanic primary productivity and play important roles in global carbon and nitrogen cycles. Although commonly associated with export production and the biological pump, diatom cells can also excrete fixed carbon as dissolved organics. One possible mechanism behind the excretion of dissolved organic carbon (DOC) and dissolved organic nitrogen (DON) from diatom cells is photorespiration. Photorespiration is a consequence of the light-dependent fixation of O2 by the enzyme Rubisco, the central enzyme of photosynthetic carbon fixation. Conditions observed to promote photorespiration include high irradiance and high O2/CO2. A key enzyme of the photorespiratory pathway is glycine decarboxylase (GDC). We have sequenced the cDNA for the T-protein subunit of GDC (GdcT) from Thalassiosira weissflogii. This is the first sequence of a photorespiratory gene from any marine alga. Using competitive RT-PCR, we have demonstrated the regulation of this gene by light. Transfer of cells acclimated to irradiances below and above growth-saturation to the dark for 24 hr decreases GdcT mRNA. When these cells are then transferred to high light, the cells acclimated to irradiances below growth-saturation rapidly accumulate (within hours) much higher levels of GdcT mRNA than cells acclimated to growth-saturating irradiances. These results suggest that recent light history may dictate the extent of photorespiration in a changing light environment. Furthermore, cells acclimated to constant light conditions transcribe GdcT, even at very low irradiances, suggesting photorespiration may be ubiquitous to diatom cells in all light environments. We are currently examining transcription of genes for other enzymes closely tied to the photorespiratory pathway such as carbonic anhydrase (CA). Our goal is to understand the environmental regulation of genes encoding key enzymes involved in photorespiration. We will ultimately use GdcT to develop a robust probe for detecting photorespiration in field samples.

OS42A-98 1330h POSTER

Effects of Diatom Photorespiration on Surface-Ocean DOC

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Under normal light conditions, sinking diatomatious aggregates act as a pump by facilitating the transfer of fixed carbon from the euphotic zone to deeper waters. In periods of high light and/or high oxygen, this pump can short-circuit, producing metabolites which can "leak" out of diatom cells and be remineralized by heterotrophs. Our preliminary research has identified a correlation between leaking of dissolved organic carbon (DOC) and expression of a light-inducible gene for the T-protein of glycine decarboxylase, a key enzyme in the photorespiratory pathway. The goal of this research is to quantify bulk DOC leakage resulting from exposure to high light levels.

Axenic cultures of T. weissflogii were adapted to 12/12 light/dark cycles at a light level of 110 $\mu E/m^2 s$. Following this adaptation period, cultures in early exponential growth phase were subjected to increased light levels of approximately 330μE/ m^2s for 12 hours to induce photorespiration. Control flasks consisted of cultures not subjected to the high- light regime. All cultures for both the experimental and control treatments were run in triplicate. Subsamples were collected for subsequent DOC analysis over a twelve-hour period for experimental flasks and for a nine-day period for control flasks. The purpose of extending the incubation period for the experimental controls was to assess the total contribution of bulk DOC by diatoms during steady-state growth.

The net DOC concentrations were significantly greater for those cultures exposed to high light (ΔDOC =190 $\pm$ 17μM) for twelve hours vs. that observed in the experimental controls (ΔDOC=35$\pm$ 22μM) over the same time period. Net DOC concentrations were also significantly greater in cultures exposed to high-light over a twelve-hour period (ΔDOC =190 $\pm$ 17μM) vs. what was observed in the experimental control over the entire course of the nine-day growth cycle (ΔDOC=105 $\pm$ 35μM). The peak of DOC concentration was observed six hours following initial exposure to high light. The rate of DOC increase was 0.35 mg/L per hour for the first six hours following light shock. For the interval between four and six hours, specifically, the rate of DOC increase rises to 0.80 mg/L per hour. These results correlate well with the results of Parker *et al.*, which found that peak concentrations of mRNA for the T-protein of GDC occurred at five hours following light-shock. Further research will be needed to completely elucidate the role of photorespiration and the GDC enzyme in bulk DOC loss by diatoms to the upper ocean. The net change in DOC concentration in the experimental controls over the entire growth cycle is most likely the result of normal diatom metabolic processes rather than nutrient limitation, as increases in DOC concentrations occurred gradually over the course of 9 days rather than as a large peak at the end of the cycle. Given that changes in light can occur many times over the course of the growth cycle, these changes have the potential of significantly affecting bulk DOC concentrations in the upper oceans, and therefore heterotrophic bacterial activity, over short time scales.