water were within the triangle defined by the upstream thermocline and temperature maximum waters and the colder deep waters of the EGC. Entrainment of ambient water is thus not required for explaining the evolution of the characteristics of the overflow plume at the first part of its decent. Less saline overflow water was observed on the upper part of the slope and identified as Polar Intermediate Water (PIW). The PIW properties were similar to those of the thermocline present in EGC already in Fram Strait, and it is conceivable that the PIW source is the upper (Θ>0) part of the thermocline in the Arctic Ocean.

OS11H-09 1050h

Interannual Variations in Wintertime Mixed Layer Depth, Inorganic Carbon and Nutrients in the Irminger and Iceland Seas

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The Irminger and Iceland Seas undergo strong seasonal variations. Relatively warm and saline Atlantic Water prevails west of Iceland in the Irminger Sea but northeast of Iceland in the Iceland Sea, Arctic Water usually predominates but but some Polar Water influence in the surface layers is common. Convective mixing is induced in both regions in winter by winds and heat loss to the atmosphere. The nutrient concentrations in the surface layer that result from the winter vertical mixing processes may vary interannually. The nutrients from vertical mixing and those carried by eddy diffusion into the euphotic zone have strong influence on the regional scope for new production and uptake of CO2 from the atmosphere.

The winter mixed layer depth is found to be variable in the Irminger and Iceland Seas, but it reaches much deeper in the Irminger Sea as a halocline limits the vertical convection in the Iceland Sea. The ranges of the related variations in salinity, density and nutrient concentrations are similar in both regions but the nutrient variations are proportionately greater in the Iceland Sea. The Iceland Sea surface stays undersaturated with respect to carbon dioxide throughout the year whereas the Irminger Sea may become supersaturated in winter on account of vertical mixing. Statistical relationships between mixed layer depth and surface water properties are examined and the effects of interannual variations in advection.

OS11H-10 1105h

The role of convection and seasonal to interannual variability on carbon uptake in the Nordic seas

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Johannessen, T., Anderson, L.G., Bellerby, R.J.J., Messias, M.J., Olsen, A., Olsson, A., Omar, A.M., Skjelvan, I. and Watson, A.

During the EU projects ESOP and TRACTOR new information is obtained regarding the air/sea exchange of CO2 in temperate to polar region. The Greenland Sea is believed to be one of the most important areas on the globe in production of deep water. One of the main issues is to understand whether the thermohaline circulation is stable in its present mode of operation. Despite many years of extensive research, only a crude and qualitative understanding is at hand today, and many fundamental questions related to the basic nature of convective overturning in high latitudes are not resolved: what are the mechanisms, what are the driving forces, what are the quantities and ventilation rates, and what are the quantities of the associated fluxes of carbon? Specifically, we will focus on the carbon cycle the way it express itself during an intensive study of the Greenland/Nordic Seas. The general antropogenic CO2 uptake seems to follow the global uptake of 2 mmol/kg carbon pr. year. The physical carbon pump is stronger in the Greenland Sea than in other regions due to the low temperature in the surface water and the high wind speeds. During the summer a very low fCO2 as low as 200 matm are recorded. In the late spring/early summer a very low fCO2 exist in the surface waters and d13C seems to be decoupled from nutrient. We call upon partial thermal equilibration with the atmosphere to explain the pattern we observe in the Greenland Sea.

OS11H-11 1120h

What Causes the Recent Freshwater Storage and Export Anomaly in the Arctic Ocean?

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In recent ten years, the Arctic atmosphere, sea-ice and ocean changes significantly. The positive phase of Arctic Oscillation or North Atlantic Oscillation persists, causing anomalous atmospheric low pressure and cyclonic circulation over the Arctic Ocean and accompanying the amplification of anthropogenic effects with anomalous higher air temperature extending to the Arctic Ocean from the Eurasian continent. All of these changes may affect freshwater storage in the Arctic Ocean and freshwater export from the Arctic Ocean to the North Atlantic, which may influence the North Atlantic Thermohaline Circulation. We employed a coupled Arctic ocean/sea-ice model and carried out simulations forced by the climate monthly mean and monthly anomaly corresponding to the leading mode of sea level pressure, which is derived from NCEP/NCAR reanalysis data. Results show that the overall freshwater storage are decreased by about 2% between the positive and negative phases of the leading mode. The recent phase shift of atmospheric leading mode gives rise to the piling up of liquid freshwater in the Beaufort Sea and the Canada Basin off the Canadian Archipelago. Correspondingly, the liquid freshwater export through Fram Strait in the upper ocean layer increases by 12.2%.

OS11I HC: 318 A Monday 0830h

Viruses and Prokaryotes in Aquatic Systems I

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

OS11I-01 0830h INVITED

Assessing Viral Diversity in the Sea

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Viruses are believed to be the smallest and most numerous form of life in the oceans and many other aquatic environments. As ubiquitous and obligate intracellular parasites, viruses are persistently and intimately commingling with the genetic material of their hosts. Knowledge of the information content of viral genomes as well as how this information is transmitted and expressed is thus essential if we are to fully understand the physiology, ecology, and evolution of complex plankton communities.

One challenge when analyzing natural viral communities can be obtaining sufficient material of adequate purity. This is especially difficult for deep ocean where viral concentrations can be low. To facilitate collection from such environments, we developed an in situ ultrafiltration system which concentrates bacteria and viruses from 1000 liters of seawater in about 5 hours. The concentrates are useful for studying physical and genetic diversity of natural viral assemblages. We have recently constructed a shotgun library from marine viral DNA that is providing a glimpse of some of the natural genetic diversity of viruses the ocean. With shotgun libraries of very diverse mixed communities it is exceedingly difficult to piece together individual clones into larger contiguous fragments. Two means to improve the information content are to clone larger pieces or to reduce the sample complexity before library construction. In a complementary study related to the latter strategy, we have used the physical variations of viruses as means to fractionate complex assemblages. Pulsed field gel electrophoresis (PFGE) can resolve about 35 to 40 distinct viral genome sizes in a single sample. To further improve resolution we have used multi-dimensional fractionation. In this case, intact viruses are first fractionated based on combinations of size, mass, or surface charge characteristics prior to separation of their genomes. The results indicate that viral diversity in seawater can be grossly underestimated by single-dimension separation using only PFGE. Multi-dimensional fractionation of intact viruses should prove useful for library construction targeting specific groups of viruses. This approach will help establish links between genetic and morphological diversity and is a further step towards culture-independent approaches in viral ecology.

OS11I-02 0845h

Genomic analysis of an uncultured marine viral community

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The worlds oceans contain up to 10 billion viruses per liter, making them the most common biological entities by an order of magnitude. Marine viruses, the majority of which are bacteriophage, have enormous influences on global biogeochemical cycles and are major conduits of genetic exchange. Despite their importance, virtually nothing is known about the diversity of marine viruses or their evolutionary relationships to non-marine viruses. Here we report the first culture-independent analysis of a marine viral community using a genomics approach. Over 70% of the sequences obtained in this analysis were not significantly homologous to previously reported sequences in GenBank. The majority of the significant hits from the uncultured phage library encode genes from phage (32%) and mobile elements within bacterial genomes (30%). Genes from all major families of dsDNA tailed phage, as well as some representatives of algal viruses, were found among the significant hits to previously reported sequences. In addition, we observed sequences related to groups that have never before been reported in the marine environment, such as coliphage lambda. Of the sequences with significant homologies to phage, an overwhelming proportion (44%) were most closely related to the Podoviridae. These hits were almost evenly distributed between marine (Roseophage SIO1) and non-marine (coliphage T7, coliphage T3, and Yersinia pestis phiYe03-12) phage. In contrast, GenBank is biased towards the Siphoviridae, which only comprise a small fraction of our phage hits. Even the Myoviridae, the phage family least represented in GenBank, was more highly represented (20%) in the uncultured library than the Siphoviridae (14%). Therefore, it appears that the Siphoviridae may not be as common in the marine environment as the other groups of dsDNA tailed phage. In addition, we also observed a number of contigs within the library, demonstrating that viral diversity within the near-shore sample was relatively low, and that it is possible to shotgun sequence uncultured organisms from total communities.

OS11I-03 0900h INVITED

Marine Viromics: A Genomic Analysis of Vibriophage 16

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The phage16-like vibriophages are a group of viruses infective for Vibrio parahaemolyticus strain 16, originally isolated from Tampa Bay, FL. These phage were found in coastal, subtropical estuarine environments, including the Gulf of Mexico, the Florida Keys, and Oahu, Hawaii. One phage lysate yielded two phages with differing plaque morphologies, VP16T (turbid plaque) and VP16C (clear plaque), which we have chosen for genomic sequencing. The VP16T sequence has been closed (49,717 bp) while the VP16C is nearing completion (45 kbp in 18 contigs). The VP16T sequence contains 87 ORFs, 69 of which are longer than 70 AAs. The presence of a cos site was inferred by the presence of a terminase-like gene and restriction digest patterns at 37°C versus 65°C. Annealing and ligation studies verified the existence of a cos site, the sticky-end genomic recirularization strategy employed by coliphage lambda. The genome of VP16T seems to be organized into structural genes in the "left" arm of the genome and replicative/regulatory genes in the "right" arm, consistent with the modular theory of phage evolution. Several head, tail, and tail fiber-like ORFs appear in the left side of the genome, while DNA polymerase, split into three ORFs, appear in the right side. Although genes for integration and other lysogeny functions are not apparent, a virulence associated protein (vap), similar to vapE of a prophage-like sequence found in Dichelobacter nodosus, an ovine pathogen, was found. Vibrio parahaemolyticus is a known pathogen (although pathogenicity of V. parahaemolyticus st. 16 has not been investigated) and many Vibrios are known to contain pathogenicity islands of prophage origin.

OS11I-04 0915h

Genomic analysis of a novel marine virus associated with lysis of the toxic bloom former, *Heterosigma akashiwo*

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We have isolated and sequenced a virus, (designated 296), tightly associated with lysis of *Heterosigma akashiwo*, a unicellular eukaryotic phytoplankton species that forms harmful, fish-killing blooms. The virus was purified as a band on a sucrose gradient that contained *H. akashiwo* lytic activity. The particle has an icosahedral structure, is 50 nm in diameter and contains approximately 41-kb of double-stranded DNA. We identified 62 putative open reading frames (orfs) in the genome sequence. Most of the protein sequences predicted to be encoded by these orfs show no sequence similarity to known proteins, but five orfs are predicted to encode proteins with significant sequence similarities to known bacteriophage (phage) proteins. These include phage terminase, lysozyme and recombination proteins. The overall 296 genome architecture resembles sequenced phages. We performed phylogenetic analyses with selected predicted protein sequences for which we were able to propose a possible function on the basis of sequence database homologies in order to explore the evolutionary relationships of 296 to known viruses. These analyses show evolutionary relationships between inferred amino acid sequences in 296 and those from a diverse array of phage (and prophages) representing 3 different families (Myoviridae, Podoviridae and Siphoviridae). Based on morphological and other evidence 296 does not appear to fit into any recognized or described family of viruses and provides further evidence of the extensive virus diversity that remains to be discovered in the marine environment.

OS11I-05 0930h

The Marine Viriome and Evolution

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During the development of large-scale vaccine purification centrifuges at Oak Ridge, it was discovered that the ocean contains a high concentration of viruses (Anderson, N.G., et al, Isolation of viral particles from large fluid volumes in Transmission of Viruses by the Water Route, Gerald Berg, ed., Interscience Publishers, NY. pp 75-88, 1967.) Given an estimated oceanic viral load of 10exp29-10exp30 virions (C.A.Suttle, personal communication), and a turnover rate of a day or so, simple calculations show that the marine viriome is the major mutation producing engine of the planet.

The NCI program supporting these developments assumed vertical viral transmission of oncogenic viruses and I extended this idea by proposing that viral infection was universal, crossed species and phylum barriers, and persisted because it was essential for evolution (Anderson, N.G., Nature 227, 1346-1347, 1970). Perusal of genetic sequence data reveals many relics of this process.

In contrast, current interpretations of evolution usually assume a linear process with all mutations occurring inside a germ line, a process supported by observed sequence conservation. Since proteins having the same function may be made in many different ways, sequence conservation in the presence of continued input of new sequence information appears to require a new explanation. Since proteins are covered with a variety of potentially interactive sites to which antibodies and other paratactic surfaces may be made, one may postulate a large virtual set of paratactic pairs, and that when member of a pair is selected in an organism, its opposite number may be excluded, unless a useful structure is formed (Anderson, N.G., J. Theor. Biol. 60: 401-412, 1976). This would constitute an internal molecular selection mechanism for conserving existing sequences and structures in the face of an onslaught of virally transmitted new information, some of which may have originated in the oceans of the world. Some implications of these ideas to the complexity of living system will be discussed.

OS11I-06 0945h

Genomic evolution of lytic and lysogenic phages

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Currently, the genomes from 91 bacteriophages have been completely sequenced and deposited in the GenBank. It contained 7 genomes in Myoviridae, 9 genomes in Podoviridae, and 37 genomes in Siphoviridae. Although there is only one marine phage genome available in the GenBank up to date, most of phage isolates from marine environments belonged to these three families. Genomic comparison of these phage genomes together with marine cyanophage P60 genome whose sequencing was completed in our lab, we found: 1) podo-phages contained conserved DNA replication machinery (i.e. DNA polymerase gene or primase gene) that likely diverged from the same ancestor with little genetic exchange with host DNA replication system; 2) in contrast, most of sipho- and myo-phage genomes (except for the T4 types) did not contain DNA replication machinery, and occasionally found DNA replication proteins in these phages were most closely related to the DNA replication enzymes in bacteria; 3) the integrase gene was commonly found in the sipho- and myo-phage genomes, but the gene was not conserved among these phages. According to these phage genomes, lytic or virulent infection is prevalent in Podoviridae (except for P22, a temperate phage acting like lambda) while temperate or lysogenic infection is common in Sipho- and Myo-viridae. Mutation rate of lysogenic phages should be much higher than that of lytic phages due to higher frequency of lateral genetic exchange between lysogenic phages and their hosts. Genomic analysis also confirmed that no single genetic marker was conserved across these three phage families. However, phylogenetic diversity of viruses in natural environments can be explored within defined groups on the basis of their infection mechanism, morphology, genome size and their host linkage.

OS11I-07 1000h INVITED

An Ecological Perspective of Viruses Infecting Prokaryotes

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Prokaryotic viruses are typically considered as parasites infecting unicellular organisms. However, lytic viruses might be better described as predators and some lysogenic phage-hosts systems may even show mutualistic interactions, whereas chronic infection might be true parasitism. The phage-host dynamcis may modify every kind of interaction such as the response of the host to competitors and mutualists and its reaction to environmental conditions. Since predators such as lytic phages and grazers (flagellates) should compete for prey, we investigated the effect of grazing on viral infection of bacteria as well as the effect of enhanced nutrient availability (mainly phosphorus) on this interactions. In all three performed experiments, viral abundance, proliferation and infection frequencies of bacteria were higher in the presence of grazers suggesting a synergy of virus-induced and grazer-induced mortality of bacteria. Higher nutrient availability did not influence this type of interaction, however, viral abundance, proliferation and infection of bacteria was enhanced. One of the reasons for this synergy might be that grazing enhances cell specific production and by that viral infection. This synergy suggests that -at least at the community level- competition with grazers is less important for prokaryotic viruses than 'beneficial' interactions.

OS11I-08 1030h

Temporal Dynamics of Viral Infection of Bacterioplankton in the North Sea.

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We used a previously described virus-dilution approach to monitor the impact of viruses on bacterioplankton at 49 stations in the southern part of the North Sea. During 4 cruises between July and December 2000 and an additional cruise in June 2001 we recorded bacterial and viral abundance, turbidity of the water column, bacterial production, burst size, viral production, frequency of infected bacterial cells, and the frequency of virus-mediated bacterial mortality. Viral numbers were highest in June and July averaging 25 x 10^6 ml^{-1} and lowest in December averaging 4 x 10^6 ml^{-1} whereas bacterial abundance averaged 1.2 x 10^6 ml^{-1} in June/July and 0.5 x 10^6 ml^{-1} in December. The average frequency of infected cells per cruise varied between 0.25 and 0.09, viral production rates between 70 and 15 x 10^4 particles ml^{-1} h^{-1}, and the frequency of virus-mediated mortality between 0.6 and 0.1. The viral impact on bacterioplankton appeared to be closely linked to bacterial activity, since viral parameters such as viral abundance and viral infection were correlated best with bacterial production. Furthermore, virus-mediated bacterial mortality peaked around noon and mid-night, whereas the frequency of infected cells appeared to be highest around sunrise and sunset suggesting a tight regulation of viral infection and production on a diel scale. The results of this study confirm 1) that viruses can play a significant role as predators of bacterioplankton and 2) that viral mortality and infection and thus its significance on bacteria-mediated carbon cycling varies considerably on the scale of months and displays a pronounced diel periodicity in surface waters.

OS11I-09 1045h

Viral and Bacterial Community Shifts at an Ocean Time Series Station

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Viruses are thought to be important members of marine communities, with potential influence on mortality, nutrient cycling, and community composition. We examined naturally occurring viral and bacterial communities over time at an offshore time series station located midway between Los Angeles and Santa Catalina Island, California. Measurements included direct counts of prokaryotes and viruses (SYBR Green epifluorescence), bacterial heterotrophic production, frequency of visually infected bacteria (by TEM), bacterial community composition by terminal restriction fragment length polymorphism (TRFLP) of 16S rRNA gene amplicons, viral genome length diversity by pulsed field gel electrophoresis (PFGE), chlorophyll, nutrients, and hydrography, approximately monthly since August 2000. Four depths were examined: 5m, the chlorophyll maximum layer, 150m and 500m. The most dramatic changes occurred during a phytoplankton bloom in April, which was reflected simultaneously by increases in bacterial abundance and production, and virus abundance. The following month, viral abundance remained high despite lower bacterial abundance and production, and there was a peak that month in frequency of infected bacteria. Preliminary TRFLP results with one restriction enzyme showed only modest changes in bacterial community composition over this time. PFGE showed some consistently-occurring viral community components, but also some larger genomes (90 -200 kb) that change over time. It is still too early to determine cause-effect relationships among these microbial communities.

OS11I-10 1100h

Ultraviolet Radiation Induced DNA Damage in Marine Viruses Along a Latitudinal Gradient

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Ultraviolet radiation induced DNA damage (cyclobutane pyrimidine dimers, CPDs) in natural marine virus communities was examined along a latitudinal transect from 41 S to 3 N in the southeastern Pacific ocean. Surface waters were collected prior to sunrise each day and placed in UV transparent incubators kept at in situ seawater temperatures. A replicate treatment was prefiltered through a 0.2 um filter to remove microbial host cells. Both treatments were exposed to ambient solar radiation until approximately one hour before sunset. At the end of the day, the virus fraction was collected from each sample by filtration and concentration. DNA damage was determined in each fraction and compared to DNA damage in sunrise samples and DNA dosimeters. The experimental design allowed us to examine DNA damage induction in viruses with and without their host cells and to infer the role of host mediated repair (e.g. photoreactivation). CPDs in dosimeters and integrated solar irradiance are very highly correlated. There was no relationship between latitude (i.e. increasing solar irradiance) and net dimer production in viruses, suggesting that viruses may be relatively insensitive to damage. The presence of host cells resulted in no consistent pattern or change in the CPD induction of virus particles indicating minimal host mediated repair in the natural virus community. The sunrise residual CPD values in the viruses increased latitudinally with increasing irradiance. Low daily induction of damage in virus incubations but a high residual damage indicates that the sunrise damage levels were the result of DNA damage accumulation over numerous days indicating a long residence time for virus particles in surface waters.

OS11I-11 1115h

Viral and Protistian Control of Bacterioplankton Production Over an Oxic to Anoxic Gradient in Chesapeake Bay Water Column

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Over the past decade a number of approaches for estimating virioplankton production and the impact of viral lysis on bacterial mortality have been developed. However, outside of methods development efforts, few studies have examined changes in virioplankton production over environmental gradients. During summer months the mesohaline portion of Chesapeake Bay is highly stratified with cooler, anoxic, and more saline bottom water separated from warmer, oxic, and fresher surface waters. Virioplankton production and nanoflagellate grazing were estimated in water samples from three depths (surface, mid-water, and bottom). Each sample represented a unique portion of the stratified water column. Protists (ciliates and heterotrophic nanoflagellates) were present throughout the water column and numbers of these organisms were only 2.5 fold lower in anoxic bottom water. Interestingly, grazing estimates based on assumed clearance rates were lower than viral-mediated bacterioplankton mortality. Two methods were used to estimate virioplankton production namely, tritated thymidine (TdR) incorporation and fluorescently labeled virus (FLV) tracer approaches. Each method indicated lower viral production in anoxic bottom waters than in surface water. Dark viral decay rates were lower for deep water (ca. 1% h^{-1}) than for surface waters (ca. 4% h^{-1}). Estimates of viral-mediated bacterial mortality from each of the two methods disagreed widely. Using a burst size conversion of 50, the TdR method indicated that between 4 and 8 % h^{-1} of bacterial production was lost to viral lysis, whereas the FLV tracer approach indicated that ca. 160 % h^{-1} of bacterial production was lost to viral lysis in all incubations. The discrepancy between the methods could be due to increased lysogenic viral production during bottle incubations and an inability of the TdR method to detect that portion of viral production which relies on de novo synthesis of nucleic acid. These initial results indicate that viral lysis exceeds grazing as an agent of bacterioplankton mortality in eutrophic, estuarine waters and that controls of bacterial production in estuaries are similar over dramatic environmental gradients.

OS11I-12 1130h

Viral Dynamics in the Permanently Anoxic Cariaco Basin

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Free viral-like particles (VLP) were enumerated in water column (7-1310 m) and sediment trap samples collected during the CARIACO Time Series Program. Vertical distributions of VLP corresponded to those of bacterial abundance and bacterial net production (BNP), with primary maxima consistently in surface waters and secondary maxima near the O_2/H_2S interface. Temporal variations in VLP (0.81 - 631 x 10^8 VLP L^{-1}) correlated with variations in chlorophyll a, primary production, bacterial abundance and BNP in the upper 250 m. In the suboxic zone (250-450 m), VLP abundance covaried with BNP but not bacterial abundance nor chemoautotrophic production. In anoxic waters (> 450 m), temporal variations in VLP abundance were not significantly correlated with any measured variable. Relationships between viruses, hosts and environment appear to vary between these layers.

Vertical fluxes of VLP associated with sedimenting debris varied between 0.39 and 515 x 10^9 VLP m^{-2} d^{-1}, a range similar to bacteria (0.88-331 x 10^9 bac m^{-2} d^{-1}). VLP-to-bacteria ratios (VBR) in sinking pools were very low, varying from 0.01 to 1.21 and averaging 0.60, demonstrating that VLP were not as numerically important in sinking particles as they were in suspended communities where mean VBR were 16 (oxic), 3 (suboxic) and 31 (anoxic). Comparisons of sinking fluxes with suspended VLP pools demonstrate that vertical transport is relatively unimportant in redistributing viruses in the water column. Removal rates by sinking from the oxic, suboxic and anoxic layers averaged 0.11 % mo^{-1}.

OS11I-13 1145h INVITED

Influence of viral lysates on bacterial carbon cycling

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Organic matter released by viral lysis is potentially an important nutrient source for pelagic marine bacteria. Consequently, part of the dissolved organic carbon taken up by bacteria may be used several times in the microbial community before it is respired or transferred to higher trophic levels. A significant fraction of the bacterioplankton production may be based on such recycling of organic matter within the microbial community, and the liberation of viral lysates may, therefore, have a significant impact on the overall carbon cycling in the marine food web. Input of viral lysates may also affect the bacterial population dynamics since the release of cell contents (cytoplasmic and structural material) from viral lysis may influence the substrate conditions, thereby favouring growth of specific bacterial populations. We have studied effects of viral lysis of marine bacteria on bacterial carbon cycling and population dynamics of in two types of experiments: 1)In culture experiments with individual virus-host systems it was verified that viral lysates were potentially very important as substrates for the bacterial populations, and that release of viral lysates may affect bacterial growth and community composition. We also found indications for a close coupling between release and subsequent uptake of lysates. Non-infected bacteria were apparently colonizing infected cells during the latest stage of infection, suggesting that cell contents were leaking out of the cells before the total disruption of the cell. 2) In culture experiments with natural assemblages of bacteria we examined how a removal of most of the natural viral assemblage affected bacterial growth and respiration. The distribution of 3H-thymidine into different size fractions (dissolved fraction, viral fraction, bacterial fraction and respired fraction) was followed over time in batch cultures. The results indicated that bacterial net growth and bacterial growth efficiency were significantly higher in cultures with a reduced abundance of viruses than in control cultures with the natural viral abundance. The data indicated that viral lysis in natural assemblages of bacteria and viruses significantly affected the bacterial carbon cycling by liberating a fraction of the organic matter already taken up by the bacteria, thus stimulating recycling of bacterial carbon and reducing net bacterial production.

OS11J HC: 323 B Monday 0830h

Nutrient Dynamics in Coastal Ecosystems: Linking Physical and Biological Processes I

Presiding: **J Runcie,** Hawaii Institute of Marine Biology**; J Smith,** University of Hawaii Manoa

MON

OS11J-01 0830h INVITED

Evolutionary Perspectives on Nutrient and Water Movement Effects on Estuarine Macroalgae

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Macroalgae of marine origin form 'nuisance' blooms in certain estuaries which are subject to anthropogenic nutrient enrichment. Most of these algae are ephemeral/ruderal strategists with high specific growth rates at resource saturation and relatively short lifespans.Fossils of an alga which is closely related to some extant 'nuisance' bloom algae have been found in 1.2 billion year old rocks. Since there were no terrestrial ecosystems producing major geochemical effects until 0.5 billion years ago, there would have been no biological enhancement of fluxes of algal nutrients into estuaries during this 0.7 billion years. Over the last 0.5 billion years there have been such biologically enhanced fluxes.During the last 0.1 billion years there have also been local inputs of marine-derived nutrients to coastal sites in the form of the faeces and excreta of secondarily marine vertebrates which return to land to breed (pterosaurs, marine birds, pinnipeds). However, 'ornithocoprophilous' algae are not major components of 'nuisance' blooms. At present the flux of nutrients such as N and P through anthropogenically influenced estuaries can greatly exceed the nutrient use by the 'nuisance' algae. Water movements are also important in moving estuarine algae out to sea, and in removing algae which are overwintering in estuarine sediements and which could otherwise initiate blooms at that site in the following spring.

OS11J-02 0850h INVITED

Hydrodynamics and Nutrient Acquisition by Seaweeds

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The productivity of subtidal seaweeds is often considered to be restricted under slow mainstream flows because the development of a thick diffusion boundary layer (DBL) at the thallus surface reduces rates of inorganic nitrogen and carbon uptake compared to fast mainstream flows. Here I review evidence for reduced fluxes of essential nutrients (nitrogen and carbon) to seaweed thalli under slow flows, and discuss the physiological mechanisms by which seaweeds acquire nutrients from sources other than the mainstream flow. Recent work indicates that the time scales of DBL formation for bladed and branched seaweeds in stagnant flows is seconds, measured using O2 microoptodes. For branched seaweed species, properties of the thallus such as morphology and elasticity influence seawater velocities within the thalli, and the scale of turbulence generated. The time scales of DBL formation around seaweeds and their ability to acquire nutrients from a range of sources indicate that the production rates of seaweeds are unlikely to be restricted under natural situations.