OS22H-14 1710h

Water Column Processes in Mangrove Creeks Receiving Aquaculture Effluent.

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Water column processes in undisturbed mangrove creeks and in creeks receiving effluent from prawn farms in North Queensland, Australia were studied. Small scale discharges into tidal creeks did not elevate dissolved nutrient concentrations compared with non-impacted creeks, but did elevate concentrations of particulate nutrients, chlorophyll and suspended solids proximal to the site of the effluent discharge. Turbulent mixing caused rates of primary and bacterial production downstream from the discharge to exceed rates in the prawn ponds. In the lower reaches of the mangrove creeks and immediately offshore, standing stocks of particulate material and rates of primary and bacterial production were within the range of values found in non-discharge areas. During discharge periods microzooplankton grazing removed >120% of primary production and 117-266% of bacterioplankton production in the mixed lower reaches of the creeks and immediately offshore. Grazing by bacterivores was saturated in the upper reaches of the creeks, but was very high near the mouth of the creeks (5.2-11.8 d^{-1}). Baitfish juveniles were abundant in the creek systems, and fed either directly on macro-particulates by indiscriminate filter feeding, or by selective feeding on microfauna. We suggest that trophic processes and their concomitant respiratory losses are instrumental in the assimilation and dissipation of effluent materials within the creek system, and are responsible for returning concentrations of bio-available materials to ambient levels.

URL: http://www.aims.gov.au/pages/research/pipe/pipe-01.html

OS22H-15 1725h

Are Commercial Fish Farms and Scleractinian Corals Mutually Exclusive?

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It is a widely accepted dogma that scleractinian corals require clear, oligotrophic waters for their survival. Moreover, several field and laboratory studies have found a negative correlation between high levels of nutrients and/or turbidity (such as found in the waters adjacent to fish farms) and coral health and growth rates. Commercial fish farms that employ intensive net cage aquaculture technology release large fluxes of dissolved nutrients and particulate matter to the surrounding waters. Therefore, we would not expect to find stony corals in the waters immediately adjacent to fish cages. During summer and autumn 2000, we carried out a SCUBA-diver census of the corals found within a radius of 45 - 60m around the Ardag fish farm situated at the northern tip of the Gulf of Aqaba (Red Sea) in order to establish the abundance and diversity of coral colonies and their distribution with respect to the fish farm. It is noteworthy that although the Gulf of Aqaba supports some of the richest and most diverse coral reef communities worldwide, there have never been coral reefs in the near-shore region where the Ardag farm was established; presumably because this environment is impacted at least once annually by very heavy siltation following seasonal flash floods. The census revealed that corals generally did not live directly below the cages, however we found more than 470 coral colonies in the zone adjacent to the cages (0 - 50m). We identified 230 corals to 21 genera yet 240 of the corals were not identified and some of these probably belong to additional genera and species, i.e. the coral community adjacent to the fish farm is quite diverse. The largest numbers of corals were found in the shallower parts of the study area, presumably due to higher light levels. However, one of our more surprising observations was that the largest branching colonies found (mostly *Pocillopora* sp.) were situated on some of the fish cage anchor lines, only meters away from the fish cages, at depths of 3 - 4m, i.e. at sites that probably experience the highest fluxes of dissolved nutrients. It is noteworthy that fluxes of ammonia from a typical fish cage may exceed 14 kg per day and each of the 3 Ardag pontoons supports 15 cages or more. These and other observations highlight how poorly we understand the environmental impacts of fish farms.

OS22I HC: 318 A Tuesday 1330h

Bridging the Gap: From Molecular Biology to Marine Ecology I

Presiding: **G F Steward,** University of California, Santa Cruz**; E J Gaidos,** University of Hawaii Manoa**; M G Weinbauer,** Netherlands Institute for Sea Research (NIOZ)

OS22I-01 1330h

Detection of *Pfiesteria piscicida* Using Genetic Markers and Antibodies

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Mitochondrial cytochrome b (mt *cob*), a commonly used genetic marker whose utility in dinoflagellates remains unexplored, and its 5' flanking region were cloned and sequenced for the potentially toxic dinoflagellate *Pfiesteria piscicida* (*Ppcob*). Species-specific PCR primers were designed from unique domains in the *Ppcob* coding and the 5' flanking regions and PCR with these primers showed high species-specificity and sensitivity. In the meantime, antisera against the cell surface antigens of *P. piscicida* (Ppab) were developed using two immunization methods. The subset produced using purified cell wall/membrane fraction displayed high titer and specificity in immunofluorescence staining (IF). Tested against 20 different algal cultures and field samples, the PCR primers and the antisera both consistently recognized *P. piscicida* and gave negative results for other species including *P. shumwayae*. Based on the two methods, some unnamed *Pfiesteria*-like cultures were identified as it P. piscicida and some as non-*P. piscicida*. A quantification protocol was also developed for both the PCR (Time-Step PCR) and immunofluorescence (filter-based IF) to measure *P. piscicida* cell concentration. The protocol provided a lower detection limit of 0.2 and 0.3 cells/mL for the Time-Step PCR and the filter-based IF, respectively. The two methods were used to detect *P. piscicida* in *P. piscicida*-spiked and natural water samples collected from Chesapeake tributaries, eastern Long Island Sound, and Boston Harbor. Results from both methods agreed well. The tests and limited field surveys demonstrate that the combined use of *Ppcob* and Ppab is highly promising in accurate identification and enumeration of *P. piscicida*.

OS22I-02 1345h INVITED

Diversity in the nitrogen cycle: Characterization of functional guilds in the environment

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Complex biogeochemical cycles, such as the microbially mediated nitrogen cycle, are deceptively simple when viewed in terms of the net chemical transformations they include. For example, the oxidation of ammonium to nitrite or the denitrification of nitrate to N2, can be determined from the net nitrogen fluxes measured using geochemical methods during incubations. Every biologically mediated process in a particular environment can be ascribed to the activity of an enzyme, encoded by a functional gene (e.g., ammonia monooxygenase or nitrite reductase). Sequence analysis of such genes from the environment reveals a vast diversity within functional guilds; many different variants or alleles of the same functional genes are seen to be associated with each biogeochemical transformation. We are investigating the extent to which this genetic diversity is important in determining or regulating the overall rates of biogeochemical processes. Gene chips carrying multiple versions of genes involved in the nitrogen cycle are being developed to interrogate the microbial assemblage along a gradient of measured biogeochemical transformation rates from Chesapeake Bay to the Sargasso Sea. Preliminary results on the resolution of gene microarrays, transformation rates and diversity of functional groups in this environment will be presented.

OS22I-03 1400h

Whos blooming? Genetic Diversity of a Centric Diatom During a Spring Bloom

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A characteristic feature of diatoms is their ability to form large blooms. Diatom blooms dramatically impact coastal ecosystems and yet, despite considerable effort, the factors dictating the timing, magnitude or composition of a bloom remain elusive. Bloom dynamics may be difficult to unravel, in part, because of the complex interaction between the environment and the genetic and physiological diversity present within individual species. Dramatic evidence of the interaction between a species and its environment can be observed during blooms, as rapid asexual reproduction leads to an exponential increase in abundance. However, the consequence of a massive increase in cell number on the dynamics of individual cell lines is unknown. We have developed sensitive DNA fingerprinting techniques to examine how the extent of genetic diversity within a diatom species may influence bloom dynamics. Using these techniques, we recently identified an enormous amount of genetic and physiological diversity in a fall bloom population of the centric diatom *Ditylum brightwellii*. In this study, we not only sampled a single population but actually monitored the progression of a *D. brightwellii* spring bloom. Over the course of 11 days, we isolated more than 1000 individual cells from Dabob Bay, a temperate fjord. Analysis of cells isolated during the initial 2 days of sampling reveal lower levels of genetic diversity than we observed in a fall bloom population suggesting that spring and fall blooms may have very different genetic and physiological characteristics. Analysis of subsequent isolates will reveal whether one or many genetically distinct clones dominate at the height of the bloom. Furthermore, our results will provide insight into how environmental conditions shape the genetic composition of a diatom species.

OS22I-04 1415h INVITED

From mRNA to Satellites: A View of the Mississippi River Plume in the Gulf of Mexico

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Coastal plumes can often influence carbon cycling and sequestration many miles into the open ocean. The Mississippi River plume forms a low salinity feature that is constrained by the Loop Current and often can be detected from Louisiana to the Straits of Florida by SeaWiFS ocean color imagery. We have investigated the transcriptional activity and diversity of rbcL, the gene encoding the large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase, the major carbon fixation enzyme, in natural populations of this plume. In 1999, we focused on the genetic diversity of the actively fixing phytoplankton population by sequence analysis of mRNA-derived clones in a profile of the plume. These studies indicated that the low salinity surface water (top 10 m) of the plume was dominated by rbcL sequences consistent with PE-containing Synechococcus. Below the surface waters, a high-light clade of Prochlorococcus rbcL was found, and below that, a low-light clade of Prochlorococcus rbcL clones were recovered. Throughout the water column, a diversity of chromophytic rbcL sequences were found, including those of prymnesiophytes, pelagophytes, diatoms, and others. In 2001, we returned to the plume to study the nitrogen nutrition and diversity of the low salinity, surface plume populations along the axis of the plume. Additionally, the expression of the nitrogen controlling

gene of cyanobacteria, ntcA, was measured. Finally, a method for quantitating diatom rbcL gene expression based upon Real Time, RT-PCR was developed. These results will be discussed in terms of new and recycled production occurring in such plumes.

OS22I-05 1430h

Mitogen-associated protein kinase (MAPK) in *Pfiesteria piscicida* associated with osmotic stress

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Mitogen-associated protein kinase (MAPK) has been identified in a wide range of organisms in which this protein was found to be a molecule involved in cell cycle regulation and signal transduction. In particular, MAPK has been shown to be a component of an extracellular stress signal transduction pathway. This gene has not been identified in marine plankton, especially the unicellular protists, in which such signal transduction pathway would link environmental stresses or fluctuating conditions to cellular responses. Recently, this gene was isolated from the potentially toxic, heterotrophic dinoflagellate *Pfiesteria piscicida*. Using RT-PCR, expression of this gene was determined for physiological conditions including well-fed, recently-starved, severely-starved, and osmotic shocked to low (5 PSU) and high (35 PSU) salinities. Results showed that MAPK in this species was expressed constantly at very low levels under all the feeding conditions (and hence growth status). Exposure of the 15 PSU-grown *Pfiesteria piscicida* culture to the low salinity (5 PSU) did not appear to have significant effect on *Pfiesteria piscicida* cell mobility and MAPK expression. However, when the 15 PSU-grown *Pfiesteria piscicida* culture was exposed to the high salinity (35 PSU), MAPK expression was increased by over 5-fold, suggesting an osmotic shock signal. The results suggest that 1) MAPK in *Pfiesteria piscicida* may serve as an osmotic stress signaling molecule and 2) that *Pfiesteria piscicida* is probably not of oceanic origin.

OS22I-06 1445h

Growth Response of Bacterioplankton Communities in the Southern Ocean to Various Substrate Regimes

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We carried out mesocosm experiments in the Southern Ocean in fall in which we examined the response of the bacterioplankton community to added substrates such as peptone, starch, agar, an extract of a green algae (Scenedesmus), and of the diatom-dominated phytoplankton. One experiment was carried out at the polar front (Exp-1) and one in the coastal pack ice zone (Exp-2). The growth response, measured by leucine incorporation and increase in cell numbers, was most pronounced to additions of the diatom and Scenedesmus extracts and to peptone, and more pronounced in Exp-2 than in Exp-1. Starch stimulated bacterial growth to a lesser extent whereas agar additions did not show any stimulations as compared to a control. Turnover rates of glucose and dissolved proteins showed distinct differences among the various treatments whereas that of free amino acids exhibited only little variations. The analysis of the bacterioplankton community by denaturing gradient gel electrophoresis (DGGE) of PCR-amplified 16S rDNA-fragments at the end of the experiments exhibited pronounced differences and resulted in distinct clusters of substrate-specific communities. The composition of the community in the diatom-extract amended flask was most similar to that of the unamended control. Fluorescence in situ hybridization with group specific oligonucleotide probes also exhibited distinct responses by specific populations among the various treatments.

OS22I-07 1500h

In-Situ Abundance of the SAR11 Bacterioplankton Clade in the North Atlantic Ocean

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SAR11 16S rRNA genes have been recovered from nearly every marine environment, suggesting that this group is ubiquitous in bacterioplankton communities. To obtain information about the actual numbers of SAR11 cells in oceanic ecosystems, we used fluorescent *in-situ* hybridization (FISH). In August 2001, pelagic and mesopelagic samples (1 to 3000 meters) were collected at four stations on a transect in the North Atlantic (32° to 25° North, 64° West). Samples were analyzed by *in-situ* hybridization with a suite of four fluorescently labeled 16S rRNA oligonucleotide probes specific for the SAR11 clade. Results from all profiles indicated that SAR11 accounted for an average of 35% (standard deviation of 5%) of the marine DNA-containing picoplankton community in surface waters from 1 to 150 meters. In some samples above 150 meters, SAR11 counts exceeded 40% and in one sample reached 51% of the total DAPI count. At 250 meters and below, the abundance of SAR11 averaged 18% (standard deviation of 4%). Additional results obtained by hybridizing the same oligonucleotide probes to dot blots of RNA taken from the same stations showed a similar trend in the vertical distribution of SAR11 ribosomal RNA, with SAR11 RNA accounting for 10.5% to 1.5% of total SSU rRNA. The metabolic and biogeochemical functions of SAR11 are unknown, but the quantitatively measured abundance of SAR11 cells in these samples suggests that this organism may play an important role in planktonic communities.

OS22I-08 1515h

Molecular Demonstration of a Dynamic Relationship Between Iron and Phosphorus Bioavailability in the Western North Atlantic

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Recent advances for quantifying phosphorus (P) and iron (Fe) have led to hypotheses that marine nitrogen fixation and primary production may be limited by one or both elements. However, the degree to which the elemental composition of seawater reflects bioavailability is poorly understood. To better examine how P and Fe may constrain primary production and nitrogen fixation we have developed molecular diagnostics of nutritional status in the model diazotroph *Trichodesmium* and applied them to field populations. *Trichodesmium* plays a critical ecological role in the dynamics of many oceanic ecosystems because of its ability to fix atmospheric nitrogen. In culture controls P-stressed *Trichodesmium* colonies induce the P-regulated enzyme PhoA and Fe-stressed colonies express the Fe-regulated protein IdiA. During a study of the Western North Atlantic, cell-specific PhoA activity varied with the dissolved inorganic phosphate concentration, and IdiA expression corresponded to documented changes in atmospheric inputs of Fe-rich dust to the region. Using these specific molecular diagnostics we determined that populations of *Trichodesmium* experienced Fe stress in August and P stress, but not Fe stress, in November of 2000. We propose that Fe and P bioavailability are both important factors controlling *Trichodesmium* productivity, and that a dynamic interplay between these two essential elements may exist in this and other systems.

OS22I-09 1550h

A Comparison of Winter and Summer Distributions of Planktonic Archaea and Bacteria in the West Antarctic Peninsula

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Use of polynucleotide fluorescently labeled rRNA probes allowed a comparison of abundances and distributions of marine Archaea and Bacteria during the austral summer and winter in the Long Term Ecological Research (LTER) study area in the West Antarctic Peninsula. Vertical distributions of Archaea and Bacteria were determined at both inshore and offshore stations on two research cruises in January-February 1999 and June-July 1999. Abundance of prokaryotic plankton including Group 1 (G1) and Group 2 (G2) Archaea, and Bacteria were determined relative to total DAPI stained cells. Together, the G1, G2, and Bacterial probes accounted for >75% of the microbial community indicating prokaryote dominance. The overall abundance of Bacteria was approximately an order of magnitude greater than G1 Archaea, while G2 archaeal abundance was half as great as G1 abundance. Distributions of Archaea and Bacteria varied seasonally and with depth. In the summer, Bacteria dominated the surface waters with the relative contributions of G1 and G2 Archaea accounting for <5% of the total prokaryote community. The relative contribution of G1 Archaea increased with depth, accounting for upwards of 25% of the DAPI stained cells in the deep, aphotic waters. During the winter, the relative contribution of surface water G1 Archaea increased to 5-15% of the total prokaryote community. Despite the increased relative importance of G1 Archaea to winter surface waters, seasonal differences in the absolute abundance of Bacteria were more dramatic than corresponding seasonal shifts in G1 Archaea abundance. For example, bacterial abundance in the surface waters increased nearly an order of magnitude between winter and summer seasons, while G1 Archaea abundance doubled. The dynamic range in bacterial and archaeal abundance suggests that these prokaryotes may be coupled to seasonally variable processes in Southern Ocean habitats.

OS22I-10 1605h INVITED

Bridging the (microbial) gap, from genomes to biomes

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A number of new and evolving technologies are lending increasing credibility to investigations of microbial species, distributions, interactions and activities in natural ecosystems . Currently, one of the biggest challenges is to integrate the many currently available technical capabilities that operate on different scales, into singular, but comprehensive studies of natural ecosystems. There are a number of current examples of disparate obervational capabilities that beginning to be integrated. Currently, three dimensional chemical and redox fields can now be mapped by microelectrodes, and overlain on microbial species distributions revealed by fluorescently labeled ribosomal RNA probes. Additionally, stable isotopic techniques have reached sufficient resolution and sensitivity, so that isotopic composition and phylogenetic identity can be simultaneously determined for individual microbial cell aggregations, in a powerful culture-independent approach. Microbial genomics is now being applied outside the laboratory and applied towards asking "real world" questions, and are already providing some unexpected surprises. Real-time, autonomous remote sensing of a harmful algal bloom in ocean surface waters has also recently been achieved, via molecular probe arrays deployed on moorings fitted with advanced instrumentation. A big challenge presently, and for some time to come, will be to continue to integrate and coordinate diverse observing capabilities, at a variety of spatial and temporal scales.

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This is critical since it is well known that microbial interactions occurring on a scale of microns can influence global biogeochemical cycles on planetary-wide scales.

OS22I-11 1620h

Enumeration of Prochlorococcus Ecotypes in the Red Sea Using Real-time Quantitative PCR

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The marine cyanobacterium Prochlorococcus is a dominant contributor to primary production in oligotrophic ocean systems. Strains of Prochlorococcus can be classified into at least six genetic types, many of which exhibit distinct physiological differences in their responses to light, nitrogen and copper. The recently completed genome sequences of two Prochlorococcus strains which are dramatically different in size, %G+C content and protein coding capacity have provided some clues to the genetic underpinnings of these physiological differences and are an example of the magnitude of the "microdiversity" that can be present in a single functional group. Although all Prochlorococcus strains isolated to date share more than 96% identity in their 16S rDNA sequences, a much larger degree of variation exists in the 16S-23S internal transcribed spacer (ITS) region. We have designed primer sets in the ITS specific for each of the six ecotypes of Prochlorococcus and developed protocols using syber green detection during real time quantitative PCR. Currently the limit of specific detection in field ranges from 50-500 cells/ml for the six primer sets. This method was employed to examine the distribution of Prochlorococcus ecotypes in the Gulf of Aqaba, Red Sea which has a well characterized seasonal cycle of picoplankton dynamics. In the stratified waters of September, 2000 four of the six Prochlorococcus ecotypes were detected, and the populations partitioned the water column with depth. The ecotype distributions will be discussed in relation to measured environmental parameters (light and nitrogen concentrations), the known physiological properties of the ecotypes and their genetic potential as seen from whole genome sequences. The ability to rapidly and specifically enumerate ecologically distinct members of the same functional group (guild) is crucial to understanding the influence the guild as a whole may have on biogeochemical cycling.

OS22I-12 1635h

Seafloor mineral oxidation: A role for Fe-oxidizers

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Seafloor hydrothermal vent environments are of widespread interest in terms of the unique biological communities that are based on chemoautotrophy that is supported by hydrothermal vent fluids. However, much of potential energy available in these systems is held within the solid mineral phases that precipitate during cooling of vent fluids. Calculations have shown that the potential energy available from oxidation of minerals exceeds that which is available from vent fluids exclusively. Previous work has shown that mineral precipitates are potential long-term sources of energy for non-thermophilic chemoautotrophic populations at the seafloor. I will discuss current studies we are undertaking to that address the population size, diversity, and activity of mineral oxidizing microorganisms at hydrothermal vent environments, and discuss the implications these findings have for mineral transformations involving Fe-metabolism for C-fixation generally at the seafloor.

OS22I-13 1650h INVITED

A new Avenue to Link Prokaryotic Diversity and Function: the Live Separation of Complex Marine Prokaryotic Communities by Capillary Electrophoresis - Potential and Limitations.

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Despite the rapidly growing literature on prokaryotic diversity in the sea there is still limited information available on the number, nature and dynamics of the main prokaryotic players in the biogeochemical cycling of elements in the ocean. We developed a method which allows us to fractionate the most abundant members of a complex prokaryotic community according to their electrophoretic mobility, determine their abundance and perform metabolic activity measurements in the same way as done with the bulk community. This method is based on the specific differences in surface charge of prokaryotes. The bacterioplankton community is transferred into a buffer solution, separated in a capillary electrophoresis (CE) and the different fractions collected. Thereafter, the separated bacteria are back-transferred into the original seawater and the abundance and activity measured. In this presentation the principals of the method are outlined and the potential and limitations of this method for linking bacterioplankton diversity and function are discussed. Examples are given from a cruise in the (sub)tropical Atlantic, where the CE-based method has been used to determine the abundance and the metabolic activity of the dominant bacterioplankton groups and their potential for utilizing high versus low molecular weight dissolved organic matter.

OS22I-14 1705h

Chemical and Molecular Characterization of Ontogenetic Shifts in the Chemical Defense in *Bugula neritina* (Bryozoa)

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Bugula neritina is an arborescent bryozoan found in temperate marine habitats throughout the world. Previous research has established that the physically vulnerable larvae of *B. neritina* are chemically distasteful to both vertebrate and invertebrate predators. Adults, however, do not possess this chemical defense. Bioassay-guided fractionation of larval extracts has resulted in the isolation of 3 active compounds. NMR and mass spectral data of the deterrent compounds, as well as other related but non-deterrent compounds indicate that they are bryostatins, which are highly cytotoxic polyketide macrolides. This is the first report of an ecological role for the bryostatins. The volumetric concentrations of 2 of the bryostatins, quantified by analytical HPLC, were found to be around 0.4 mg/mL of larvae. Bryostatin levels fell sharply following larval metamorphoses so that 2-3 d old juveniles had undetectable levels of these compounds. HPLC analyses also failed to detect bryostatins in adults. This precipitous decline in bryostatin levels following larval settlement and metamorphosis was not due to the increase in structural material per unit volume of juveniles or adults. It has been hypothesized that the bacterial symbiont, Canditatus *Endobugula sertula*, which resides in larval and adult tissue, produces the bryostatins. There are several possibilities to account for the ontogenetic changes in the concentrations of the unpalatable bryostatins. These compounds could be constitutively produced throughout the life of the organism and accumulated in the larva; once the larva settles, they could be diluted by the growing tissue. Alternatively, they could be synthesized either in the larva while being brooded by the adult, or in the adult only when it is reproductive. A molecular probe based on the ketosynthase module of the polyketide synthase was developed to determine when the gene is being expressed throughout the different stages. This probe, when applied in RT-PCR and quantitative RNA techniques, allows us to distinguish how the differential production of these defensive compounds is regulated in *B. neritina* as it transitions through these vulnerable juvenile stages, and may lend insight into how *E. sertula* is involved in the biosynthesis of the bryostatins.

OS22I-15 1720h

Identification of Differentially Expressed Genes in Toxic and Nontoxic Life Stages of *Pfiesteria piscicida* Using Serial Analysis of Gene Expression (SAGE)

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Pfiesteria piscicida is a toxic dinoflagellate that inhabits estuaries along the eastern coast of the United States. This organism has a complex life cycle with over 20 distinct stages, several of which are capable of producing a potent neurotoxin. The factors that contribute to toxic *Pfiesteria* outbreaks are unclear, but most likely are regulated by biological, physical and chemical characteristics of the environment. An analysis of these factors and their relationships to *Pfiesteria* life stage composition in situ is essential to the prediction and prevention of toxic blooms. Molecular probes have been developed that target unique sequences in the 18S rDNA gene. These probes are both accurate and sensitive, but provide no information about the abundance of different life stages within the population. We used a modified Serial Analysis of Gene Expression (SAGE) protocol to identify differentially expressed genes for toxic and nontoxic forms of *P. piscicida* flagellated zoospore life stages. SAGE is a powerful technique for constructing comprehensive gene expression profiles of specific tissue or cell types. Although SAGE was developed primarily for biomedical research, the modified protocol presented here is readily applicable to the analysis of differential gene expression in marine organisms. Molecular probes that target uniquely expressed genes identified by SAGE can be used to rapidly assess the presence and relative abundance of specific life stages in environmental samples. Integration of these molecular techniques with the physical, chemical and biological characterization of the environment will provide information crucial to the development of monitoring and long-term management strategies for high-risk areas.

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Recruitment Dynamics of the Three-Spot Damselfish, Dascyllus Trimaculatus, in Moorea, French Polynesia, Using Molecular Markers

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The three-spot damselfish, Dascyllus trimaculatus, recruits to anemones after 21-26 days in the plankton. Once large enough to escape predators, it leaves the anemone and lives as an adult in the nearby reefs.

We placed rows of anemones in the northwestern shore of Moorea, French Polynesia, where anemones are naturally absent, and collected everyday new reruits that had settled during the previous night.

Molecular markers, designed during previous experiments allowed us to study the recruitment dynamics of the species. Further investigation of the same markers on the adult populations allowed us to find relationships linking adult populations to recruitment events.