

**AIMS@JCU**  
**2008 Student Seminar Day**

7th November, 2008

Endeavour Room,  
Halls of Residence,  
James Cook University

**TIMETABLE**

## Timetable

- 9.00am**    **Registration and tea/coffee**
- 9.15am**    **Opening address—AIMS@JCU  
Research Director Dr. Michelle Heupel**
- 9.25am**    **Yui Sato; Stress in Tropical Marine Systems**  
How do corals get the black band? - Transition of bacterial communities in the development of black band disease
- 9.45am**    **Thomas Bridge; Coastal Processes & Modelling**  
Substrates and Benthic Taxa on the Unexplored Great Barrier Reef Shelf-edge
- 10.05am**    **Emily Howells; Stress in Tropical Marine Systems**  
Genetic differentiation and cross-shelf patterns of diversity among Great Barrier Reef populations of *Symbiodinium* (zooxanthellae)
- 10.25am**    **Morning Tea**
- 10.45am**    **Patricia Warner; Stress in Tropical Marine Systems**  
The Missing Link to Population Genetic Structure in Brooding Corals: How far do sperm swim?
- 11.05am**    **Marie Magnusson; Coastal Processes & Modelling**  
Effects of herbicide contamination on tropical microalgae and biofilms
- 11.25am**    **Jean-Baptiste Raina; Stress in Tropical Marine Systems**  
Coral-associated bacteria and their role in the biogeochemical cycling of sulfur
- 11.45pm**    **Jasmine Jaffrés; Coastal Processes & Modelling**  
Changes in heat content and mixed layer depth in the Coral Sea based on Argo observations
- 12.05pm**    **Lunch**

## The seasonal and long-term variation of the mixed layer depth in the Coral Sea and its impact on the Great Barrier Reef

Jasmine B.D. Jaffrés<sup>1</sup>

<sup>1</sup> *AIMS@JCU, Australian Institute of Marine Science, School of Earth and Environmental Sciences, James Cook University, Townsville, QLD 4811, Australia (jasmine.jaffres@jcu.edu.au)*

### Coastal Processes & Modelling Program

Global warming is predicted to result in a significant shallowing of the mixed layer depth (MLD) in many ocean regions, which could have dire consequences for coral reef ecosystems and the ocean's capability for CO<sub>2</sub> uptake. To determine the seasonal variability of the mixed layer depth (MLD) within the Coral Sea, conductivity-temperature-depth (CTD) profiles from Argo float profiles and the World Ocean Database were used. Two different techniques, the threshold and the gradient method, have been used to obtain and compare the MLDs. A distinct seasonality in the mixed layer depth was found throughout the Coral Sea, but was generally more pronounced in higher latitudes as a result of greater seasonality in sea surface temperature (SST) and wind stress. Austral winter MLDs tend to be much deeper than summer MLDs throughout the Coral Sea. A trend towards a shallower MLD could have dire consequences for the GBR as SST is expected to increase more rapidly within a shallow mixed layer, thus likely resulting in more severe and more frequent coral bleaching events. Further CTD profiling in the Coral Sea region is required to monitor long-term changes in mixed layer thickness.

## **Some rare Indo-Pacific *Acropora* species are hybrids, and some common species are polyploids.**

Zoe Richards, Madeleine van Oppen, Carden Wallace, Bette Willis and David Miller.

*ARC Centre of Excellence for coral reef studies, Department of Marine and Tropical Biology, JCU. AIMS at JCU. Museum of Tropical Queensland.*

### **Stress In Tropical Marine Systems Program**

Coral reefs worldwide face a variety of threats and many coral species are increasingly endangered. It is often assumed that rare coral species face higher risks of extinction than common species because they have very small effective population sizes, a predicted consequence of which is decreased genetic diversity and adaptive potential. Here we show that some rare Indo-Pacific corals from the genus *Acropora* have higher genetic diversity than expected and that other common species are polyploids (duplicated chromosomes). Whether these patterns reflect hybrid origins or secondary hybridization following speciation is unclear. The complex genetic patterns and inter-specific gene flow demonstrated here implies increased genetic diversity and adaptive potential in these coral species. Rare *Acropora* species may therefore be less vulnerable to extinction than has often been assumed because of their propensity for hybridization and introgression, which may increase their adaptive potential.

- 1.00pm **Jessica Haapkylä; Stress in Tropical Marine Systems**  
Drivers of coral disease on an inshore reef of the Great Barrier Reef (GBR)
- 1.20pm **Lachlan McKinna; Coastal Processes & Modelling**  
Hyperspectral Monitoring of *Trichodesmium* spp. within the Great Barrier Reef
- 1.40pm **Eneour Puill-Stephan; Stress in Tropical Marine Systems**  
High levels of chimerism in adult populations of the broadcast spawning coral *Acropora millepora* on the Great Barrier Reef
- 2.00pm **Francois Seneca; Stress in Tropical Marine Systems**  
An Ecological Microarray Study of Coral Bleaching
- 2.20pm Afternoon Tea**
- 2.40pm **Severine Choukroun; Coastal Processes & Modelling**  
Variability of the East Australian Current (EAC) flow in the Southern Great Barrier Reef region
- 3.00pm **David Abrego; Stress in Tropical Marine Systems**  
Algal endosymbiont specificity varies among populations and closely related coral species of *Acropora*
- 3.20pm **Paulina Cetina Heredia; Coastal Processes & Modelling**  
Modelling Larval Retention around Reefs by Local Scale Circulation Features
- 3.40pm **Raechel Littman; Stress in Tropical Marine Systems**  
Comparison of Bacterial Communities on Juvenile Corals Infected with Different *Symbiodinium* (Zooxanthellae) Clades
- 4.00pm Poster Presentation & Photo Contest/ Discussion & Judging**  
with Social Drinks & Food Platters
- 4.45pm Award Prize Presentations**
- 7.00pm Close**

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**ABSTRACTS**

**Understanding sex in the white-striped cleaner shrimp -  
Implications for captive breeding**

Vasiliki Tziouveli<sup>1</sup>, Mike Hall<sup>2</sup>, Greg Smith<sup>2</sup>

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**Tropical Aquaculture Program**

*Lysmata amboinensis*, the white-striped cleaner shrimp, is a popular and high-valued marine ornamental species. Reliance on wild collection, combined with limited information on the status of natural populations, has raised concerns about overexploitation of wild stocks, ecological imbalances and reef-damaging fishing techniques. Commercial production of cultured *L. amboinensis* would alleviate the pressure on the populations in sensitive reef ecosystems and present the aquarium trade with year-round availability of domesticated animals. The objectives of this study were to establish a breeding population of captive *L. amboinensis* and to optimise fecundity, as a first step in closing the life cycle of the species in captivity.

The reproductive strategy of *L. amboinensis* has for long been an enigma to aquarists. It exhibits Protandrous Simultaneous Hermaphroditism, an unusual sexual system, unique to this genus among carideans. Accordingly, individuals develop first as males (MP), then change to out-crossing hermaphrodites (SH) and function as both sexes during the reproductive cycle. Knowledge of the minimum size at which males reach sexual maturity and can successfully copulate with hermaphrodites is essential in the initial establishment of hatchery-based reproductive pairs. Equally, knowledge of the minimum size at which males change sex can prove beneficial, since hermaphrodite pairs have a higher reproductive output than male-hermaphrodite pairs.

Male-phase *L. amboinensis* as small as 32.6 mm total length could fertilize their hermaphrodite partner regardless of SH size. The most fecund group was the SH of an average 52.4 mm, with brood size positively correlated to SH body size. However, there was significant egg mass loss during incubation across all groups. The “default” size at sex change was 37.0 mm. There were significant indications of environmental sex determination, with MP reared with similar-sized MP changing sex at a smaller than the default size. The observed pattern is discussed in terms of reproductive opportunities.

## How do corals get the black band? - Transition of bacterial communities in the development of black band disease

Yui Sato<sup>1,2</sup>, Bette L. Willis<sup>2</sup> and David G. Bourne<sup>1</sup>

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### POSTERS

Black band disease (BBD) is challenging the health of reef building corals worldwide. BBD consists of a bacterial consortium forming a microbial mat which migrates across coral colonies causing rapid tissue loss. Although microbial communities associated with BBD have been well studied, little is known about how these complex pathogenic bacterial communities develop. In a 3 year monitoring program, we have found annual summer outbreaks of BBD on corals in the genus *Montipora* around Pelorus Island in the central Great Barrier Reef. Green cyanobacterium infected lesions, which were distinct from the characteristic BBD mat, were consistently identified at the onset of disease. The green cyanobacterial lesions were followed *in situ* and sampled periodically to investigate successional changes in microbial communities as the lesion developed into the characteristic BBD. Terminal restriction fragment length polymorphism (T-RFLP) profiles and clone libraries of sequenced PCR amplified 16S rRNA genes using cyanobacteria- and bacteria-specific primers demonstrated a shift in bacterial ribotype compositions during the transition from cyanobacterial patches (CP) to BBD. Dominant cyanobacteria in CP were closely related to *Trichodesmium* sp. and were replaced by morphologically and phylogenetically distinct cyanobacteria, which were 99% similar to cyanobacteria previously found from BBD in the Caribbean and Red Sea. *Alpha-proteobacteria* ribotypes were dominant in CP libraries whereas cyanobacterial ribotypes dominated BBD clone libraries. Furthermore, disappearance of aerobic *Silicibacter* species and occurrence of sulfate reducing *Desulphovibrio* species coincided with darkening of the edge of cyanobacterial patches. Results suggest that the formation of the characteristic band of BBD may be facilitated by early successional microbial communities associated with CP, which may alter micro environmental conditions and induce the settlement of key pathogenic microbes. This is the first study to document the dynamics of bacterial communities during development of the complex BBD associated microbial consortium.

## Substrates and Benthic Taxa on the Unexplored Great Barrier Reef Shelf-edge

Thomas Bridge

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Drowned Reefs have been identified on continental shelves and around oceanic islands in many parts of the world, including Barbados, Papua New Guinea, Hawaii and Tahiti. In 2007, an expedition on board the *RV Southern Surveyor* explored shelf-edge reef and terrace features at 4 different sites along the GBR margin in depths of 40-160m. Multibeam swath mapping and dredge sampling was combined with high-resolution images obtained by Autonomous Underwater Vehicle (AUV) to provide the most complete study ever undertaken of the GBR Shelf edge.

Data from these virtually unstudied ecosystems reveals a diverse range of habitats and communities. Limestone reef and terrace features provide hard substrates for a diverse range of hard coral, soft coral and gorgonian communities. 24 dredges across the 4 sites yielded a large number of specimens which are currently being studied for taxonomic identification. Initial examinations show many specimens to be different from those found on the modern, shallow water reef, and probably new to science. Detailed multibeam bathymetry and acoustic backscatter combined with AUV data has identified several discrete habitats and taxonomic on the GBR shelf edge. Macrobenthic communities are dominated by calcareous algae, sponges, and a diverse range of both hard and soft corals. Live Scleractinian corals representing 7 families (Acroporidae, Pocilloporidae, Agariciidae, Fungiidae, Poritidae, Faviidae and Oculinidae) have been identified so far at depths to 103m. Commonly the hard substrates also exhibit lush growth of octocorals, including many gorgonians which bear little similarity to those recovered from the shallow-water reef.

## Comparison of Bacterial Communities on Juvenile Corals Infected with Different *Symbiodinium* (Zooxanthellae) Clades

Littman, R.A.<sup>1,2,3</sup>, Bourne, D.<sup>2</sup> and Willis, B.<sup>1,3</sup>

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Reef-building corals host a variety of micro-organisms, including symbiotic dinoflagellates, *Symbiodinium* (zooxanthellae) and an array of bacteria. While *Symbiodinium* is well known for supplying many of the coral's nutritional needs, previous studies have suggested that bacteria can provide many benefits to corals through fixation and passage of nitrogen and production of secondary metabolites such as antibiotics. Infection of coral with genetically different *Symbiodinium* has been shown to differentially affect the physiology of the coral host. However, the effects to the entire holobiont are unknown. This study compares bacterial community profiles of nine-month-old *Acropora millepora* and *A. tenuis* and one-year-old juvenile *A. tenuis* experimentally infected with two different clades of *Symbiodinium*, C1 and D to aid in our understanding of possible interactions between bacterial and *Symbiodinium* communities. Through culture-independent techniques, bacterial communities were profiled using the 16S rDNA gene. Clone library construction, terminal restriction length polymorphism (tRFLP) and denaturing gradient gel electrophoresis (DGGE) fingerprints revealed no discernible pattern in bacterial communities on 9-month juvenile corals containing different clades of zooxanthellae. Of the 12 replicate samples analyzed for each species of coral, none had similar bacterial profiles, suggesting that coral associated bacteria do not appear to be affected by the type of *Symbiodinium* in hospite. However, juvenile samples collected after one year showed differences in bacterial community structure through DGGE analysis and clone library construction. *A. tenuis* containing clade D *Symbiodinium* had bacterial profiles dominated by sequences aligning with *Vibrio* sp. indicating that corals harbouring this symbiont may be more susceptible to potentially pathogenic bacteria.

## Modelling Larval Retention around Reefs by Local Scale Circulation Features

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Larval transport is mediated by circulation patterns. Low frequency, large scale currents can advect larvae for long distances, connecting populations over 100 km. However, local scale circulation features, such as lee reef eddies, can retain larvae near reefs and enhance self-recruitment. To accurately estimate larval dispersal, it is necessary to consider these local scale circulation processes. This study aims to approximate larval retention around reefs as a consequence of recirculation and stagnant flows provoked by the interaction of currents with the complex reef bathymetry that reefs normally display. To characterize eddies formed in the lee of reefs (different shapes) under different circulation regimes (low and/or high frequency dominant) and quantify the retention of larvae we simulate larval transport with a 3D finite difference hydrodynamic model (Sparse Ocean Hydrodynamic Code). The life span, strength and size of eddies is quantified, using vorticity as diagnostic variable. Finally, an approximation of larval retention as a function of reef geometry and prevalent circulation regime is developed, providing a novel tractable approach accounting for local scale circulation features on larval dispersal in regional scale metapopulation models.

## Genetic differentiation and cross-shelf patterns of diversity among Great Barrier Reef populations of *Symbiodinium* (zooxanthellae)

EJ Howells<sup>1,2,3</sup>, MJH van Oppen<sup>1,2,3</sup> and BL Willis<sup>1,2</sup>

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The resilience of *Symbiodinium* (zooxanthellae) harboured by corals is dependent on the genetic diversity and extent of connectivity among reef populations. This study presents genetic analyses of Great Barrier Reef (GBR) populations of clade C *Symbiodinium* hosted by the alcyonacean coral, *Sinularia flexibilis*. Allelic variation at 4 newly developed microsatellite loci demonstrated that *Symbiodinium* populations were genetically differentiated at all spatial scales from 16 to 1,360 km (pairwise  $\Phi_{ST}$  = 0.01 to 0.47, mean = 0.22); the only exception was two neighbouring populations in the Cairns region that were separated by 17 km. This indicates that gene flow is restricted for *Symbiodinium* C hosted by *S. flexibilis* on the GBR. Patterns of population structure reflect longshore circulation patterns and limited cross-shelf mixing, suggesting that passive transport by currents is the primary mechanism by which dispersal occurs in *Symbiodinium* types that are acquired horizontally. There was no correlation between the genetic structure of *Symbiodinium* populations and their host *S. flexibilis* likely due to different factors that affect the dispersal and recruitment of each partner in the symbiosis. The genetic diversity of these *Symbiodinium* reef populations was on average 1.5 times lower on inner-shelf reefs than on mid to outer-shelf reefs. Lower inner-shelf diversity may reflect the impact of recent bleaching events on *Sinularia* assemblages, which have been more widespread and severe on inshore reefs, but may also have been shaped by historical sea level fluctuations or recent migration patterns.

## The Missing Link to Population Genetic Structure in Brooding Corals: How far do sperm swim?

Patricia Warner<sup>1,2</sup>, Bette Willis<sup>2</sup>, Madeleine van Oppen<sup>3</sup>

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Processes that govern the population genetic structure of brooding corals are likely to be different to those that govern population structure in broadcast spawning species, because of differences in the frequency and scale of dispersal associated with internal versus external fertilisation. Limited sperm dispersal in brooding species is predicted to amplify signals of geographic subdivision, but current knowledge of the frequency and scale of dispersal of spermatozoa in brooding corals is scant. To determine the spatial extent of spermatozoa dispersal in the brooding coral, *Seriatopora hystrix*, a paternity analysis was conducted with a 12 m x 12 m mapped study population in Cattle Bay (Orpheus Island) in the central Great Barrier Reef (GBR). Eight polymorphic microsatellite loci were used to compare the genotypes of all *S. hystrix* colonies within the mapped area to those of the brooded larvae of adults collected from the mapped population. This type of genetic parental analysis has never been conducted on a coral species. Our analysis revealed exclusively sexually produced larvae, multiple paternity broods, and 3 instances of apparent self-fertilisation. Paternity assignments indicated limited sperm dispersal and no dominant direction of dispersal within the mapped area. We also assessed the gametogenic state of 20 tagged colonies in the field over three months of biweekly histological monitoring (Sept – Dec 2007) to compare the frequency and periodicity of reproductive events with those reported for southern GBR populations of *S. hystrix*. We found overlapping cycles of gametogenesis, which is consistent with multiple larval release events per year. Knowledge of the distance over which sperm successfully disperse between colonies and the frequency and duration of larval dispersal events provides novel insights into the patterns of genetic exchange within populations of brooding corals. Direct examination of these processes at small, localised scales reveals the fundamental events that underpin broad-scale patterns of connectivity along the GBR.

## Algal endosymbiont specificity varies among populations and closely related coral species of *Acropora*

David Abrego<sup>1</sup>

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Documenting the uptake and early establishment of symbionts in corals with horizontal transmission has important implications to understand how these relationships are regulated. The present study monitored the symbiont community in several cohorts of coral juveniles for a period of up to 3.5 years. Juveniles were sourced from adult colonies from three sites on the Great Barrier Reef and kept at Magnetic Island. The symbiosis in *A. tenuis* juveniles was very dynamic, changing from early D-dominance in most juveniles, to a decrease in D-dominated corals and in the case of the local juveniles, the eventual dominance of type C1 symbionts, the same type found in the local adult population. These results support the existence of specificity in the *A. tenuis*-*Symbiodinium* symbiosis. In contrast, *A. millepora* juveniles did not show significant changes in their symbiont communities. These juveniles were quickly dominated by type D symbionts and remained so for the duration of the study regardless of where the juveniles were sourced from, which suggests a lack of specificity for certain symbiont types. Additionally, we examined if the changes in the symbiont community of *A. tenuis* juveniles were linked to the onset of reproductive maturity but did not find this to be the case. Taken together, the results from this study show that closely related corals exhibit different specificity for their algal symbiont and that the initial establishment of the symbiosis in juveniles can be a very dynamic process affected by environmental and most likely host factors but not by changes in the host associated with reproductive maturity.



## Variability of the East Australian Current (EAC) flow in the Southern Great Barrier Reef region

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Variability of the East Australian Current (EAC) flow in the Southern Great Barrier Reef region is investigated using satellite imagery and oceanographic data along with satellite tracked drifting buoys. The South Great Barrier Reef is known to be a highly productive region, understanding the processes driving it are important for the health of the reef. Latest study of the EAC and its separating point by Mata et al (2005), from a mooring transect deployed along the 30 deg S Latitude, has shown that the EAC sheds an eddy at a periodicity of ~100 days, following this event, the separation point moves to the north.

This disturbance influences the EAC flow upstream. From 21 degrees south, the flow becomes unstable, forming eddies, especially the formation of a cold core eddy over the Marion Plateau which facilitates intrusions of oceanic waters over the shelf which can be observed in the satellite imagery. Satellite tracked drifting buoy trajectories were analysed in the region. From the results, three circulation patterns can be identified:

1 – A strong and narrow current flow from the Tip of Fraser Island to 30 / 36 degrees S (corresponding to the EAC flow and the separation point to the shelf),

2 – Further off the shelf, the surface circulation is directed to the north and seems mainly driven by mesoscale eddies,

3 – And a westerly flow can be identified originating from South of New Caledonia.

Another finding is a surface northerly flow inside the GBR lagoon, from the Capricorn channel up to the Palm Islands, which is consistent with the long term current profiler deployed east of One Tree Island.

Results from the current profiler array shows a highly variable circulation along the Capricorn Bunker shelf, with a mean low current directed North West throughout the year and becomes stronger during the summer months. A wavelet analysis of the alongshore and cross-shelf record shows strong periodicities at 70 to 170 days (eddy band) and annually in both alongshore and cross-shelf currents along the Capricorn Bunker shelf.

## Effects of herbicide contamination on tropical microalgae and biofilms

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PSII inhibiting herbicides have repeatedly been detected in the water and sediments along the Queensland coast in Australia. To predict flow-on effects to marine communities it is important to evaluate effects on microphytobenthic organisms. Here we report on the effects of PSII inhibiting herbicides on microphytobenthos at increasing levels of biological organisation and complexity. A 96-well plate assay measuring inhibition of effective quantum yield [ $Y(II)$ ] using a maxi-imaging PAM was utilized in acute dose-response experiments with the diatom *Navicula* sp. (NQAIF [North Queensland Algal Culturing and Identification Facility] 110) and the prasinophyte *Nephroselmis pyriformis* (NQAIF 117). The herbicides diuron, tebuthiuron, atrazine, simazine and hexazinone, as well as herbicide mixtures and breakdown products were tested. 3-day static batch culture experiments exposing the same species to diuron, atrazine and hexazinone linked the effect of PSII inhibitors at a molecular level ( $[Y(II)]$ ) with higher organisational level impacts (growth rate ( $\mu$ ) and biomass increase). Relationships between all three parameters for both species were consistent ( $r^2 \geq 0.90$ ) and linear (1:1). This validates the utility of PAM fluorometry as a suitable toxicological endpoint clearly related to algal growth, and therefore an excellent predictor of population-scale effects, particularly in habitats predominantly affected by PSII herbicides such as the Great Barrier Reef (GBR). Whole community level effects and recovery after chronic exposure to environmentally relevant concentrations of diuron were then investigated using naturally seeded biofilms. Interestingly, these multispecies fouling communities were less sensitive to diuron than monoclonal cultures were, as measured by inhibition of  $Y(II)$  using a phyto-PAM. There was a clear development of community tolerance to diuron during the four week exposure, and after a subsequent 24-h recovery period, communities pre-exposed to high concentrations of diuron for four weeks were more than four times less sensitive compared to control communities.

## Coral-associated bacteria and their role in the biogeochemical cycling of sulfur

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Marine bacteria play a central role in the degradation of dimethylsulfoniopropionate (DMSP) to dimethylsulfide (DMS) and acrylic acid (AA), with DMS critical in cloud formation leading to cooling effects on climate. High concentrations of DMSP have been reported in scleractinian coral tissues, although to date, there have been no investigations into the influence of these organic sulfur compounds on coral-associated bacteria. Two coral species, *Montipora aequituberculata* and *Acropora millepora*, were sampled and their bacterial communities characterized by both culture-dependent and molecular techniques. Four genera, *Roseobacter*, *Spongiobacter*, *Vibrio* and *Alteromonas*, which were isolated on media with either DMSP or DMS as the sole carbon source, also represented the majority of the clones retrieved from coral mucus and tissue 16S rRNA gene clone libraries. Clones affiliated with *Roseobacter sp.* constituted 28% of the *M. aequituberculata* tissue libraries while 59% of clones from the *A. millepora* libraries were affiliated to sequences related to the *Spongiobacter* genus. *Vibrio sp.* were commonly isolated from DMS and acrylic acid enrichments and were also present in 16S rRNA gene coral mucus libraries, suggesting that under “normal” environmental conditions, they are a natural component of coral-associated communities. Genes homologous to dddD and dddR, previously implicated in DMSP-degradation, were also characterized from isolated strains, confirming that bacteria associated with corals have the potential to metabolise this sulfur compound present in coral tissues. Acrylic acid constituted 18% of the crude coral extracts of *A. millepora*, suggesting that this previously unknown coral component may play an important role in the coral holobiont. DMSP, DMS and AA potentially act as nutrient sources for coral-associated bacteria and results from this study support the hypothesis that these sulfur compounds may be involved in structuring bacterial communities in corals, which may have important consequences for the health of both corals and coral reef ecosystems.

## An Ecological Microarray Study of Coral Bleaching

Seneca, F.<sup>1,5</sup>, Foret, S.<sup>3</sup>, Goffard, N.<sup>4</sup>, Smith, C.<sup>2</sup>, Grasso, L.<sup>3</sup>, Hayward, D.<sup>3</sup>, Saint, R.<sup>3</sup>, van Oppen, M.<sup>2</sup>, Ball, E.<sup>3</sup> and Miller, D.<sup>1,3</sup>

<sup>1</sup>ARC Centre of Excellence for Coral Reef Studies, James Cook University;  
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Reef building corals live close to their upper thermal tolerance limit and prolonged exposure to temperatures 1-2°C above average summer temperatures induces coral bleaching. Current projections suggest that average tropical ocean temperatures could warm by as much as 3°C by the end of this century. Unless corals have the capacity to adapt to the expected climate change, species are likely to undergo dramatic shifts in distribution patterns. To investigate coral stress responses at the molecular level we used microarrays of approximately 17,000 expressed sequence tags (ESTs) from the hermatypic coral *Acropora millepora* to identify genes responsible for an individual's capacity to withstand and recover from bleaching stress. Bleaching responses have typically been investigated largely by subjecting corals to acute thermal stress under laboratory conditions. Our study focuses on 30 colonies within a single bay that have been periodically sampled in situ during a natural bleaching episode and the subsequent recovery phase. During the sampling period, water temperature was continuously monitored and observed to plateau at 32°C for ten days. Individual colonies differed dramatically in their overall responses to similar environmental conditions. Quantitative reductions in symbiont density varied considerably (approximate range 0.7 – 2 million cells per cm<sup>2</sup> of coral tissue), and while some colonies fully recovered after the period of increased temperatures, others died. Our microarray experiments on 8 of these colonies, showing comparable patterns of symbiont loss, identified a large number of genes with expression significantly correlated to decreases in symbiont density. The differentially expressed genes detected have been associated with cellular processes such as oxidative stress response, apoptosis, and calcium homeostasis. The results of this study support the findings of a recent laboratory coral bleaching microarray experiment on *Montastrea faveolata* (Desalvo *et al.*, 2008) where similar cellular processes were identified. The identification of these processes facilitates our understanding of the mechanisms by which corals respond during bleaching episodes, and the implications of these cellular stress responses are discussed.

# High levels of chimerism in adult populations of the broadcast spawning coral *Acropora millepora* on the Great Barrier Reef

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Chimeras are organisms containing tissues or cells of two or more genetically distinct individuals, and are known to exist in at least nine phyla of protists, plants, and animals. Although widespread, and common in marine invertebrates, it is unknown to what extent chimerism is present in wild populations of corals.

The extent of genetic chimeras (i.e. the cohabitation of different genotypes with a single coral colony) was explored within two populations of a common coral, *Acropora millepora*, on the Great Barrier Reef, in Australia, using 8 polymorphic microsatellites.

We found remarkably high proportions of chimerism in the studied populations, which represented 6% overall. Indeed, 10% and 3% of chimerism were found in Magnetic Island and Pelorus Island respectively, when genotypes were differing by at least two alleles. However, the proportion of chimerism in *Acropora millepora* populations presented here are likely to be an underestimate, as our sampling protocol was restricted to a maximum of 8 branches per colony, and a maximum of 2 genotypes were observed per colony. Another finding was the very high relatedness of individuals within chimeras, suggesting they were associations of closely related individuals.

The study found high levels (6%) of chimeras in wild populations of corals and demonstrated that chimerism was a common feature of *Acropora millepora*'s life cycle. Although, brooding corals are known to have the potential to form genetic chimeras in their early life stages under experimental conditions, this study represents the first genetic proof of the occurrence of corals chimeras in the wild. Consequently, chimerism might be much widespread than previously thought and could represent a common life history strategy for colonial marine invertebrates.

# Changes in heat content and mixed layer depth in the Coral Sea based on Argo observations

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The mixed layer plays a crucial role in air-sea interactions through the flux and storage of heat, CO<sub>2</sub> and momentum. The seasonal and long-term variability of the mixed layer depth (MLD) and the ocean heat content (OHC) within the Coral Sea is investigated using Argo conductivity-temperature-depth (CTD) profiles. A distinct seasonality in the mixed layer depth was found throughout the Coral Sea, with much deeper MLDs occurring in austral winter throughout the Coral Sea. This MLD variability was generally more pronounced in higher latitudes as a result of greater seasonality in sea surface temperature (SST) and wind stress. A trend towards a shallower MLD, due to global warming, could have dire consequences for the Great Barrier Reef as SST is expected to increase more rapidly within a shallow mixed layer, thus likely resulting in more severe and more frequent coral bleaching events. However, a general trend towards cooler SSTs and lower OHC has been noted over the last few years. Further CTD profiling is required throughout the entire Coral Sea in order to accurately determine the long-term trends in ocean heat content and the mixed layer depth.

## Drivers of coral disease on an inshore reef of the Great Barrier Reef (GBR)

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Coral diseases have contributed to the worldwide decline of coral reefs and there is concern that they may change the very framework of reefs by impacting key reef-building corals. Few studies have investigated environmental drivers of coral disease on the Great Barrier Reef (GBR), thus there is little understanding of how changing environmental conditions might enhance or diminish coral disease on the Great Barrier Reef (GBR). The relationship between the abundance of the coral disease, atramentous necrosis, and seasonal patterns in both annual seawater temperature and environmental parameters associated with water quality (i.e. particulate nitrogen, phosphorous and carbon, chl-a, dissolved organic carbon, sedimentation and temperature) was investigated in populations of the plate coral *Montipora* in Nelly and Geoffrey Bays at Magnetic Island. Atramentous necrosis mainly affects the genus *Montipora*, a key reef-building coral on inshore reefs. A clear peak in the incidence of atramentous necrosis correlated with a peak in all of the environmental parameters measured after heavy rainfall in the Austral summer of 2008. Further aquarium-based experiments are aimed at elucidating the main environmental parameters and potentially synergistic interactions driving the dynamics of seasonal outbreaks of atramentous necrosis in Magnetic Island populations.

## Hyperspectral Monitoring of *Trichodesmium* spp. within the Great Barrier Reef

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For effective management and monitoring of water quality within the Great Barrier Reef Marine Park, an accurate and complete understanding of nutrient budgets is required. Many nutrient input mechanisms such as coastal runoff, rainfall, reefal fixation and upwelling are well understood or directly measurable, allowing for accurate estimates nutrient contribution. However, the nutrient input from marine phytoplankton is difficult to measure due to temporal and spatial fluctuations in population density. *Trichodesmium*, a genus of nitrogen-fixing cyanobacteria common within the Great Barrier Reef is known to contribute new nitrogen via atmospheric fixation. However, due to the limited understanding of *Trichodesmium* distribution within the Great Barrier Reef (GBR), there is an order of magnitude uncertainty regarding the quantity of Nitrogen fixed by the cyanobacteria.

The ability to monitor and quantify the distribution of *Trichodesmium* within the Great Barrier Reef would allow for a greater understanding of nutrient fluxes. However, surveying *Trichodesmium* using traditional methods such as sea surface observations and phytoplankton netting only allows for localised estimates of population on a finite time scale. In order to address the issues of abundance uncertainty, observations of *Trichodesmium* have been performed within the GBR using an above-water hyperspectral spectrometer on several research cruises. During field observations coinciding with the presence of *Trichodesmium*, the remote-sensing reflectance exhibits behaviour consistent with the bio-optical properties of the species. Data will be presented of hyperspectral remote sensing reflectance for varying surface concentrations of *Trichodesmium* ranging from nil to complete surface coverage.