

# A comparative study of the nutritional composition of soft and hard shell blue swimmer crab, *Portunus pelagicus*

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The blue swimmer crab, *Portunus pelagicus*, is an important species consumed locally in the Indo-Pacific, and exported extensively to US and European markets as pasteurized crabmeat products. There is a increasing market demand for both hard shell crab and soft shell crab of blue swimmer crab. However, their nutritional composition and quality are largely unquantified. To evaluate its nutritional value, the present study measured the meat yield and biochemical composition of hard shell crabmeat and soft shell crab and compared their differences. The results showed that soft shell crab (100%) had a higher meat yield than hard shell crab (30.10%) ( $P < 0.05$ ). Although higher protein content was detected in the hard shell crabmeat, the soft shell crab contained higher moisture level ( $P < 0.05$ ). Therefore, the hard shell crabmeat had high essential amino acids (EAA) and non-essential amino acids (NEAA) contents except for Tryptophan, Histidine and Proline. Based on the FAO/WHO reference amino acid requirement of preschool children, Leucine and Tryptophan are limited amino acids for soft shell crab while only Tryptophan is limited amino acid for hard shell crabmeat. Although soft shell crab contained significantly higher saturated fatty acids, the hard shell crabmeat contained higher PUFA and HUFA. It is interesting that both hard shell crabmeat and soft shell crab have similar levels of C20:5n3 and C22:6n3. Those results indicated that both soft shell crab and hard shell crab are highly nutritious crab products.

## AIMS@JCU 2010 Student Seminar Day

16th April, 2010

Endeavour Room,  
Halls of Residence,  
James Cook University

### TIMETABLE

## TIMETABLE

- 10.00am** **Michelle Heupel; AIMS@JCU Research Director**  
*Opening Address*
- 10.15am **Jessica Haapkyla**  
Season and coral community structure drive coral disease prevalence on Heron Island, Great Barrier Reef, Australia
- 10.30am **Nicola Browne**  
How do the muddy waters surrounding inshore reefs influence coral assemblages?
- 10.45am **Sarah Castine**  
Do aquaculture settlement ponds improve discharge water quality?
- 11.00am **Emily Howells**  
Genetic resilience of *Symbiodinium* populations: The role of coral endosymbionts in adaptation to climate change
- 11.15am **Thomas Bridge**  
Relationships between environmental variables and community structure on Mesophotic Coral Ecosystems along the Great Barrier Reef outer shelf
- 11.30am **Darren Coker**  
Coral-dwelling fishes vacate host coral following bleaching
- 11.45am **Marnie Freckleton**  
Quorum Sensing – Are the Soft Corals Talking?
- 12.00pm **Ana Cano-Gomez**  
*Vibrio owensii* sp. nov., isolated from cultured crustaceans in Australia
- 12.15pm **Kimberley Lema**  
Nitrogen fixing bacteria associated with corals of the Great Barrier Reef
- 12.30pm** **Lunch**
- 1.15pm **Jasmine Jaffres**  
Observed seasonal and long-term MLD and  $fCO_2$  characteristics of the Coral Sea
- 1.30pm **Raechel Littman**  
Responses of the coral holobiont to heat stress

## Changes of lipid class and fatty acid composition during the embryonic development of blue swimmer crab, *Portunus pelagicus* and ornate rock lobster, *Panulirus ornatus*

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Blue swimmer crab (*Portunus pelagicus*) and Ornate rock lobster (*Panulirus ornatus*) are two tropical commercially crustaceans. Because of their large size, high meat yield and delicate flavour, there is an increasing demand for both *P. pelagicus* and *P. ornatus* supply worldwide. Although previous studies have shown lipid nutrition are very important to crustaceans, particularly for Penaeid prawns, no available information could be found on blue swimmer crab and ornate rock lobster. Studies on the changes of lipid composition during early life history stages are indicative of the use of energy substrates during ontogeny, which allow the estimation of nutritional requirements for embryos and exogenous feeding larvae. Therefore, the current experiments were conducted to investigate the changes of lipid class and fatty acid composition during the embryonic development of *P. pelagicus* and *P. ornatus*. For both species, there are significant increases of egg volume and moisture content while the total lipid decreased dramatically. However, the different changing trends could be found on the lipid class profiles between *P. pelagicus* and *P. ornatus*, i.e. the significant increase of the percentage of triacylglycerol (%total lipid) could be found for *P. pelagicus* while there was a trend of “high-low-high” for *P. ornatus*. For the fatty acids, the principal fatty acids are 16:0, 16:1n7, 18:1n9, 18:1n7, 20:4n6 (ARA), 20:5n3 (EPA) and 22:6n3 (DHA) for the eggs of both species. Despite of embryonic stages, the significantly higher DHA and DHA/EPA ratios could be found on the eggs of *P. ornatus* than *P. pelagicus*. However the eggs of *P. pelagicus* contained higher ARA level compared to the eggs of *P. ornatus*. These differences may indicate the two crustacean species have different lipid requirements.

Oral  
Presentation

## Small-scale connectivity in the brooding coral *Seriatopora hystrix*: How far do sperm swim?

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Processes that govern the connectivity of brooding coral populations are likely to be different to those that govern connectivity 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. 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.

Poster  
Presentation

- 1.45pm **Heidi Luter**  
Microorganisms are not responsible for the disease-like syndrome affecting the marine sponge *Ianthella basta*
- 2.00pm **Patricia Warner**  
Connectivity of *Seriatopora hystrix* within the Great Barrier Reef: A work in progress
- 2.15pm **Lachlan McKinna**  
Detection of *Trichodesmium* spp. surface aggregations within the Great Barrier Reef using MODIS imagery
- 2.30pm **Allison Paley**  
Reef-building corals with photoprotective pigments resist thermal bleaching
- 2.45pm **Jean-Baptiste Raina**  
Do organic sulfur compounds DMSP and DMS drive coral microbial associations?
- 3.00pm Tea**
- 3.20pm **Charlotte Johansson**  
Functional groups and coral reef health
- 3.35pm **Scott Seymour**  
Feeding preferences of the urchin *Tripneustes gratilla* inform seaweed selection for integrated aquaculture
- 3.50pm **Xugan Wu**  
Changes of lipid class and fatty acid composition during the embryonic development of blue swimmer crab, *Portunus pelagicus* and ornate rock lobster, *Panulirus ornatus*
- 4.05pm **Adrian Lutz**  
Coenzyme Q and plastoquinone redox balance as a physiological determinant of oxidative stress in coral-algal symbiosis
- 4.20pm **Gergely Torda**  
Spatial and temporal recruiting patterns of the brooding coral species *Pocillopora damicornis* at two locations on the Great Barrier Reef
- 4.35pm Award Prize Presentations**

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**ABSTRACTS**

**Connectivity of *Seriatopora hystrix* within the Great Barrier Reef: A work in progress**

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Recent studies have documented the genetic structure of populations of the brooding coral, *Seriatopora hystrix*, along the length of the GBR. However, the patterns evident from these large-scale surveys should be interpreted within the context of smaller-scale processes that operate within and between local reefs and habitats. With this in mind, we suggest that the connectivity of a particular coral species begins with and is dependent upon its mode of reproduction. However, it is also likely that even within the same reproductive mode population genetic structures reflect strong differences between species. In the case of *S. hystrix*, sperm-casting and internal fertilization suggest that colonies within a population will be connected to others depending upon the extent of synchrony and frequency of reproductive events, as well as the distance and direction in which sperm can disperse from the donor colony. Expected limited dispersal of sperm may result in an extremely reduced area, and thus genetic neighbourhood, in which random mating occurs. Moreover, evidence suggesting limited dispersal of larvae indicates that philopatric settlement of recruits exacerbate levels of inbreeding. All of these processes, in turn, affect the genetic connectivity of a species between populations, as well as within and between reefs and habitats, ultimately leading to the broad-scale patterns observed along the entire reef system. In this study, we investigate the above-mentioned phenomena with respect to *S. hystrix* and its algal symbiont. Preliminary results and progress to date will be presented.

## Sexual maturity and environmental sex determination in the white-striped cleaner shrimp, *Lysmata amboinensis*

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Attempts to close the life-cycle of the white-striped cleaner shrimp *Lysmata amboinensis* (De Man, 1888), a high-value marine ornamental species, in captivity, have heightened in recent years. As a protandric simultaneous hermaphrodite (PSH), individuals develop as males (MPs), then change to hermaphrodites (SHs) and function as both sexes during the reproductive cycle. Knowledge of male size at sexual maturity and of sex change timing would benefit the establishment of hatchery-based pairs and contribute to future captive production of the species.

*Lysmata amboinensis* MPs used in this study were sexually mature at an average 34.0 mm. Regarding the SH size groups, the medium and small SHs produced a similar number of larvae, whereas viable fecundity for the large SH group was approximately 3 times higher, indicating fecundity increases with body size in *L. amboinensis*. Brood loss was noted as having a severe impact on larval production, with potential causes discussed.

The timing of sex change could be manipulated by exposing the shrimp to different social conditions, indicating “environmental sex determination”. Male-phase shrimp reared on their own changed at an average 37.1 mm, which was considered the “default” size at sex change. The “focal MPs” paired with “similar-sized MPs” changed sex at a smaller size than the “default”, while the “non-focals” changed sex at a slightly larger size than the “default”. “Focal MPs” paired with a “larger MP” changed at a larger size than the “default”, and it was the “larger MPs” in the treatment that changed first to SHs. The “non-focal MPs” in the treatment of “similar-sized MPs” changed sex faster than the “non-focals” in the “different-sized” pairs. Finally, the “MPs” paired with “SHs” changed at a smaller size than the “default”. The observed patterns are discussed in terms of reproductive opportunities for “low density” species.

Poster  
Presentation

## Relationships between environmental variables and community structure on Mesophotic Coral Ecosystems along the Great Barrier Reef outer shelf

Tom Bridge<sup>a</sup>, Terry Done<sup>b</sup>, Rob Beaman<sup>c</sup>, Ariell Friedman<sup>d</sup>, Jody Webster<sup>a,e</sup>, Stefan Williams<sup>d</sup> & Oscar Pizarro<sup>d</sup>

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Mesophotic Coral Ecosystems (MCEs) are light-dependent coral reef communities extending from 30-40 m depth to the bottom of the photic zone. They support diverse communities of taxa including Scleractinian corals, octocorals and sponges, and may play a vital role in providing refugia for many shallow-water coral reef taxa from environmental stress. Because MCEs occur below the depths accessible by traditional survey methods such as scuba, they remain one of the most understudied of reef habitats. Increased awareness from both science and management of the importance of MCEs to coral reef ecology coupled with recent technological advances has resulted in studies from MCEs in many parts of the world, including Hawaii, the Marshall Islands, the Red Sea, and the Caribbean. The extensive shelf-edge reef system of the Great Barrier Reef provides an ideal habitat for MCEs. Despite the inferred importance of MCEs to coral reef ecology, no studies on the ecology or community structure of these systems have been conducted. This study presents data from three different MCEs along the GBR outer shelf. Variation in the physical environments and shelf morphology with latitude causes significant differences in community structure along the GBR. This has important implications for management of MCEs within the GBRMP.

Oral  
Presentation

## How do the muddy waters surrounding inshore reefs influence coral assemblages?

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Inshore reefs on the Great Barrier Reef (GBR) are regularly exposed to highly turbid conditions and levels of sedimentation considered harmful to clear-water reef biota. Yet, despite this deleterious pressure, many inshore reefs have high coral cover (>30%) and diversity (>50 sp.). To date, few field studies have been conducted on inshore reefs compared to those growing in clearer offshore waters and consequently, sedimentary processes and their influence on inshore reef ecology, growth and development remains poorly understood. A field intensive survey using hydrodynamic data loggers and a new sediment trap design was implemented. Data was collected from different ecological zones in order to correlate variations in water flow to sediment movements and coral assemblages.

Middle Reef, an inshore turbid reef situated on the central GBR, Australia, is regularly exposed to high turbidity conditions (<50 mg.l-1), yet is characterised by a spatially heterogeneous benthic community and mean live coral cover of >39%. Coral cover and diversity was correlated to spatial variations in the local hydrodynamic and sedimentary regimes. The windward reef edge exposed to high wave activity and characterised by gravelly sands were subjected to low and stable turbidity levels (<2 NTU). Coral cover was high (~70%), but dominated by branching and plate corals. Semi-sheltered regions exposed to limited wave activity and characterised by slightly gravelly muddy sands experienced low but fluctuating turbidity levels (<10 NTU). Coral diversity increased and coral cover remained high (~50%). The most sheltered regions of the reef were characterised by the deposition of muddy sands, and turbidity levels were observed to increase rapidly during elevated wave activity (<40 NTU). Consequently, coral cover was low (~15%) and dominated by sediment resistant species. This research demonstrates that spatial variations in the hydrodynamic and sedimentary regime can lead to small-scale differences in turbidity on inshore turbid reefs. As such, corals are exposed to range of conditions which influence coral growth and subsequent reef development.

Oral  
Presentation

## Spatial and temporal recruiting patterns of the brooding coral species *Pocillopora damicornis* at two location on the Great Barrier Reef

Gergely Torda<sup>a,b,c</sup>, Petra Souter<sup>b</sup>, Bette Willis<sup>c</sup> and Madeleine van Oppen<sup>b</sup>

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Understanding genetic connectivity among and between coral reefs is essential for developing science-based management decisions. Exchange of larvae (hence genes) among populations maintains their genetic diversity, which in turn ensures reef resilience and the ability of populations to adapt to changing environmental conditions. Furthermore, it increases the ability of reef ecosystems to recover from major perturbations by the import of recruits. Here we present the first results of a study on the assessment of ecological connectivity of the model brooding coral species, *Pocillopora damicornis*, on the Great Barrier Reef (GBR). Coral settlement tiles have been deployed at 8 sites around Lizard and the Palm Islands and newly settled Pocilloporid coral recruits sampled every 2 to 3 months. In the course of one year, more than 200 recruits were found on tiles at Lizard Island sites and more than 500 at Palm Island sites. Recruiting patterns show high spatial and temporal variability, ranging between 0 and 97 recruits per site per sampling time, but is continuous throughout the year at all sites. It is hypothesised that coral recruits are largely retained locally, and hence the observed spatial patterns are the consequence of differing habitat types and coral densities between study sites. The observed temporal patterns in recruitment may be related to an optimisation mechanism (e.g. temperature-triggered gametogenesis), similar to, but less pronounced than that of broadcast spawning corals, where corals release gametes when environmental conditions (e.g. water temperature, water movements) ensure successful reproduction. To test this hypothesis and reveal the origin of recruits collected at each sampling point, the genetic characteristics of recruits are compared to those of adult populations from throughout the GBR, and associations between settlement patterns and seasonal patterns in water temperature and salinity are tested.

Oral  
Presentation

## Feeding preferences of the urchin *Tripneustes gratilla* inform seaweed selection for integrated aquaculture

Scott Seymour<sup>a,b</sup>, Nicholas Paul<sup>b</sup>, Symon Dworjanyn<sup>c</sup>, David McKinnon<sup>d</sup> and Rocky de Nys<sup>b</sup>

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*Tripneustes gratilla* is a tropical sea urchin with fast growth rates and high gonad yield, making it an important commodity and a prime candidate for aquaculture in tropical Australia. A series of choice and no-choice feeding assays were conducted throughout the year using algae collected from Rowes Bay, Townsville and Nelly Bay, Magnetic Island. This allowed us i) to determine the preferences of *T. gratilla* for seasonally available seaweeds, and ii) assess a wide diversity of red, green and brown algae. Multiple-choice feeding assays demonstrate that *T. gratilla* strongly prefer select algal species. These preferences were consistent in multiple assays throughout the year, with the most commonly preferred algae species being *Turbinaria ornata*, *Sargassum* spp. *Cystoseira trinodis*, *Dictyosphaeria versluysii* and *Hypnea pannosa*. When presented with a single algal species in no-choice feeding assays, the consumption rates by *T. gratilla* were greater for the preferred algae species than less favoured specimens. The results of these experiments demonstrate that *T. gratilla* has a clear preference for specific algal species, most commonly reds and browns, and that consumption increases when the urchins are offered those species they prefer. This result is important in developing seaweed based diets for tropical sea urchin aquaculture and to encourage sustainable integrated aquaculture practices in tropical Australia.

Oral and Poster  
Presentation

## *Vibrio owensii* sp. nov., isolated from cultured crustaceans in Australia

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*Vibrio harveyi* and related bacterial species are relevant pathogens in Australia, causing high mortalities of larvae and juveniles of fish and shellfish in aquaculture farms. Usually, *Vibrio* isolates from clinical sources are characterized by biochemical tests or 16S ribosomal RNA gene analysis but very often identification is not precise for *V. harveyi*-related species. It is suspected that isolates belonging to this species group might have ended up been misidentified as *V. harveyi* or *V. harveyi*-like in culture collections in Australia. We performed a Multilocus Sequence Analysis (MLSA) based on analysis of 5 protein-coding genes and 16S rRNA gene analysis for the precise identification and phylogenetic analysis of *V. harveyi*-related strains from diverse clinical and environmental sources in Australia. Two bacterial strains (DY05T and 47666-1), isolated in Queensland from diseased cultured crustaceans were shown to belong to a novel *Vibrio* species. The two strains formed a monophyletic group with 94.4% concatenated sequence identity to the closest species *V. harveyi*, *V. campbellii* and *V. rotiferianus*. DNA-DNA hybridization experiments showed that strains DY05T and 47666-1 had 76% DNA similarity with each other but <70% with their closest neighbours *V. harveyi*, *V. campbellii* and *V. rotiferianus*. Strains DY05T and 47666-1 could be also differentiated from their relatives on the basis of several phenotypic characters and fatty acid profiles. Based on the polyphasic evidences presented here, it can be concluded that strains DY05T and 47666-1 belong to the same novel species of the genus *Vibrio*, for which the name *Vibrio owensii* sp. nov. is proposed.

Oral  
Presentation

## Do aquaculture settlement ponds improve discharge water quality?

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The majority of Australia's prawn farms (70%) utilise settlement ponds for the treatment of effluent water from land based aquaculture. However, the mechanisms of nitrogen removal from settlement ponds are poorly understood, despite their prevalence and legislative requirement. This limits the ability to improve treatment techniques and minimise adverse downstream environmental impacts. In our study, the efficacy of settlement ponds in changing water quality at 4 settlement ponds across 3 farms was assessed at peak and off-peak (post-harvest) production. Biological characteristics of these ponds were similar in that there were large diurnal variations in dissolved oxygen over a 24 hr period (between 0-10 mg L<sup>-1</sup> during the night and day, respectively) but relatively constant pH, temperature and salinity. In general the concentration of total suspended solids, chlorophyll a, dissolved nitrogen and particulate nitrogen and carbon in the water leaving the settlement pond was not different to that entering the settlement pond, irrespective of peak or off-peak production stage. These results suggest that new strategies are required to ensure that settlement ponds have the desired effect for treating aquaculture discharge waters. One focus for research is the microbial influence on the nitrogen cycle, which is fundamental to the modification of nitrogen in all aquaculture systems. For example, bacterial processes convert fixed nitrogen from toxic species (such as NH<sub>4</sub><sup>+</sup>) to less toxic species (such as NO<sub>3</sub><sup>-</sup>) and subsequently to nitrogen gas (N<sub>2</sub>) which is lost to the atmosphere (preferred to releasing nitrogen in the effluent). Denitrification (dissimilatory nitrate reduction) was thought to be the major process responsible for production of N<sub>2</sub> in these systems. However, an alternate anaerobic bacterial process, anammox, has been discovered in terrestrial water treatment systems but has not previously been identified or quantified within settlement ponds. This process could present a significant sink for nitrogen due to the highly anoxic conditions found both in the water column (as seen in the diurnal DO fluctuations above) and within the sediments. Preliminary trials have detected anammox and denitrification within the anoxic sediment layer of settlement ponds. These results could provide a new focus to improve settlement pond design to maximise nitrogen remediation and environmental compliance.

Oral and Poster  
Presentation

## Do organic sulfur compounds DMSP and DMS drive coral microbial associations?

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Dimethylsulfoniopropionate (DMSP) and dimethylsulfide (DMS) are key compounds in the global sulfur cycle. Moreover, DMS is particularly important in climate regulation owing to its role in cloud formation. Reef building corals are major contributors to the production of these two compounds and also form diverse and complex associations with bacteria, which are known to play a crucial role in the degradation of DMSP and DMS. Here, we highlight an extensive overlap between bacterial species implicated in DMSP/DMS degradation and those associated with corals, leading to the hypothesis that these two compounds play a major role in structuring coral-associated bacterial communities, with important consequences for coral health and the resilience of coral reefs. We also explore the publicly available metagenome databases and show that genes implicated in DMSP metabolism are abundant in the viral component of coral-reef-derived metagenomes, indicating that viruses can act as a reservoir for such genes.

Oral  
Presentation

## Reef-building corals with photoprotective pigments resist thermal bleaching

Paley AS<sup>a,b\*</sup>, Palmer CV<sup>a,c</sup>, Bay LK<sup>a,c</sup>, van Oppen MJH<sup>c</sup> and Willis BL<sup>a,c</sup>

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Coral green fluorescent protein (GFP)-homologs are largely responsible for the striking colouration observed on coral reefs, and although the role of these fluorescent proteins (FPs) in coral-host tissues remains unresolved photoprotection of algal symbionts is becoming widely accepted. However, polymorphic coral species have been shown to have both highly and weakly fluorescent colour variants, or morphs, suggesting the potential for varied capabilities in photoprotection. Previous studies have found inconsistencies in the susceptibility among these morphs to both light and thermal stress with findings of a down-regulation of and decline in FP production as a result of heat stress. To date, no studies have systematically documented the variation in relative abundances of FPs between intraspecific coral colour morphs or their variation in response to thermal stress. The reef coral *Acropora millepora* has three common colour varieties: red, yellow and green where population dominance by red colour morphs has been observed. This study is the first to document FP variation between intraspecific colour morphs and investigate their response to environmental change. Firstly, the abundance of the 3 FPs found in the three colour morphs of *A. millepora* were compared to document the variability between morphs and their impact on visual appearance. Secondly, the susceptibility to, and recovery potential from thermal stress of these morphs were tested in a heat shock experiment where coral branch condition and FP content were compared between morphs throughout a laboratory controlled thermal bleaching event. Coral colour morphs differ in the relative abundances of the 3 FPs found in *A. millepora* which corresponds to their visual appearance, but each colour variant contains some amount of all 3 FPs. The highly fluorescent green morph which contains the highest concentration FPs had a higher tolerance to thermal stress than its weakly fluorescent red counterpart with lowest overall FP abundance, resulting in substantially less bleaching (64% compared to 100%, respectively) and greater indication of recovery potential of this morph. FP content declined following field collection and transfer into aquaria, remaining low for all colour morphs throughout the experiment except for green and (to a lesser extent) yellow branches exposed to severe temperature stress, where FP content returned to in-situ observed levels following nearly four weeks of recovery at ambient temperature. This study argues that highly fluorescent morphs with greater abundance of photoprotective FPs are more likely to withstand prolonged temperature stress than weakly fluorescent morphs as was previously suggested.

Oral  
Presentation

## Coral-dwelling fishes vacate host coral following bleaching

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Climate-induced coral bleaching often causes rapid and pronounced declines in the abundance of coral-dwelling fishes, but the proximal cause(s) of these declines remain unknown. Declines may be attributed to either movement of fishes to alternate habitats of colonies, or *in situ* mortality, which probably results from predation. It is also unknown whether fishes are affected by bleaching *per se* or only respond to ultimate declines in the live coral cover and physical structure of host corals. This study examined the specific timing of declines in the abundance of coral-dwelling fishes (*Dascyllus aruanus*) following experimental bleaching of host corals (*Seriatopora hystrix*). Furthermore, the role of competition between fishes was investigated to see if this can moderate the success of individuals to relocate to new habitats and what impact they have on the existing social community of fishes. Healthy coral colonies were placed in replicate pairs with associated *D. aruanus* on a sand flat in a shallow sheltered lagoon. One colony from each pair was randomly selected and subjected to osmotic stress to induce bleaching. All fishes were individually tagged to test for movement versus *in situ* mortality. To test if competition regulates the success of fishes to relocate from degraded habitats to alternative healthy habitats, manipulative aquarium experiments were conducted. Fishes of varying sizes were introduced to existing social communities to explore if size or sex influences the success of individuals to join, and what resident fishes displayed aggression towards the intruder. Following host colony bleaching there was a 67% decline in the abundance of fishes on experimentally bleached colonies, alternatively there was no decline in the abundance of fishes associated with healthy or control colonies. Of the fishes that vacated the degraded host colony, approximately half relocated to nearby healthy colonies, but the remainder could not be accounted for and may have either died or migrated over 20m to contiguous reef habitats. Furthermore, the abundance of fishes on the nearby healthy colonies did not increase even though one third of the fishes relocated there. This suggests that the introduction of new fishes influenced some of the resident fishes to vacate the healthy colony. Manipulative experiments in aquaria showed that many of these fishes associated with the healthy colonies might have been forcibly evicted by fishes that had recently joined the community and that competition for this resource reduces the capability of many of the fishes from entering a new habitat with a pre-existing colony. This study shows that coral-dwelling fishes respond rapidly to host coral bleaching, suggesting that coral-dwelling fishes rely on their coral hosts for more than just physical structure and that competition for this limited resource following habitat degradation could reduce the ability of fishes to relocate to alternative healthy habitats.

Oral and Poster  
Presentation

## Quorum sensing – are the soft corals talking?

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Quorum Sensing is the means by which a population of bacteria coordinates its gene expression and has been implicated as a potentially significant process in the establishment of symbioses between bacteria and macro-organisms. The objective of this study was to identify the presence of quorum sensing within the soft coral holobiont. A bacterial biosensor was used to successfully detect the presence of quorum sensing agent/s within thirteen species soft coral. A novel coupling of bacterial biosensors with chemical separation techniques will enable the identity of these quorum sensing agents to be discovered. This is the first time that the presence of quorum sensing inductive activity has been identified within soft coral, previous studies have indicated the presence of quorum sensing inhibitors, suggesting that quorum sensing may be consequential in the development of the soft coral holobiont.

Oral  
Presentation

**TBA**

Jerome Genodepa

TBA

Poster  
Presentation

## Detection of *Trichodesmium* spp. surface aggregations within the Great Barrier Reef using MODIS imagery

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A simple, binary classification algorithm to detect the presence of high surface concentrations of the nitrogen fixing cyanobacterium *Trichodesmium* spp. was developed for 250m spatial resolution imagery of the Moderate-resolution Imaging Spectroradiometer (MODIS). Above-water hyperspectral radiometric measurements of dense *Trichodesmium* surface aggregations ( $>10\mu\text{g/L}$  chlorophyll-a) were made within the Great Barrier Reef (GBR), Australia and used to identify spectral features appropriate for discriminating the cyanobacteria. The magnitude of the hyperspectral water-leaving radiance  $L_w$  at wavelengths longer than 700nm were found to be much larger ( $>0.05 \text{ W m}^{-2}\text{sr}^{-1}$ ) than the visible wavelength range 400-700nm ( $<0.03 \text{ W m}^{-2}\text{sr}^{-1}$ ). Absorption troughs/dips corresponding to chlorophyll-a, carotenoids and phycobilipigments were also evident in the hyperspectral  $L_w$ . The MODIS classification algorithm was based primarily on the “red-edge” affect whereby the magnitude of the MODIS normalised water-leaving radiance ( $nL_w$ ) at the 859nm waveband was much greater than the 678nm waveband. The magnitude of the MODIS  $nL_w$  at the 555nm and 645nm wavebands provided additional information for the classification algorithm.

The classification algorithm yielded an 85% accuracy when tested on a small subset of 13 MODIS images with corresponding *Trichodesmium* sea-truths. Fine scale features consistent with dense *Trichodesmium* surface aggregations such as eddy swirls and windrows appear to be well represented with the algorithm results (see Figures 1 and 2). The algorithm was also found to be robust in the presence of highly reflective, potential confounding affects such as coral reefs, high suspended sediments, and shallow bathymetry.

Oral and Poster  
Presentation

## Coenzyme Q and plastoquinone redox balance as a physiological determinant of oxidative stress in coral-algal symbiosis

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The symbiosis between scleractinian corals and photosynthetic dinoflagellates (zooxanthellae) of the genus *Symbiodinium* produces hyperoxic conditions within coral tissues during daylight exposure that may accelerate the formation of reactive oxygen species (ROS). Increased ROS production under elevated water temperatures is regarded as a leading cause of oxidative stress affecting disruption to the symbiotic partnership, which results in coral bleaching. ROS formation in vivo is usually associated with the electron transport chains of photosynthesis and aerobic respiration. Electron transfer in these metabolic processes is mediated by specific quinone electron carriers: ubiquinone (coenzyme Q = CoQ) in mitochondria and plastoquinone (PQ) in chloroplasts. Maintaining a regulated reduction/oxidation balance in the pools of these quinone electron carriers is critical to efficient energy metabolism. Additionally, the reduced forms of CoQ and PQ are highly effective antioxidants having an important function to scavenge damaging ROS in cellular membranes. Accordingly, the redox states of these electron carriers may indicate the physiological health of coral symbioses. We have developed a liquid-chromatography – mass spectrometry (LC-MS) technique for simultaneous measurements of these quinone pools by modification of protocols used for the analysis of CoQ in human plasma and the analysis of PQ in terrestrial plants. The combined technique thus provides direct assessment of the electron carrier redox states and potentially a measure of oxidative stress in the energy metabolism of both partners. Furthermore, this measure may also be used to elucidate the role of branched electron flow due to chlororespiration in zooxanthellae, as hypothesized by evidence based on pulse amplitude modulated (PAM) fluorometry. We examined the application of this technique on the scleractinian coral *Acropora millepora*. Herein we report changes to the quinone electron carrier redox states of coral respiration and algal photosynthesis under different light conditions and in response to short term heat stress.

Oral  
Presentation

## Season and coral community structure drive coral disease prevalence on Heron Island, Great Barrier Reef, Australia

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This is the first study to investigate the temporal patterns of coral disease prevalence and potential drivers of coral disease around Heron Island, in the Capricorn Bunker sector of the Great Barrier Reef (GBR), Australia. Disease surveys were conducted twice in the austral summer and three times in the winter between November 2007 and August 2009 on six sites around the island. Six disease states were detected: brown band syndrome (BrB), growth anomalies (GA), ulcerative white spots (UWS), white syndrome (WS), skeletal eroding band disease (SEB) and black band disease (BBD). The lowest overall mean disease prevalence was  $1.87 \pm 0.75\%$  (mean  $\pm$  SE) in November 2007 and the highest  $4.22 \pm 1.72\%$  in August 2008. There was evidence of seasonality for two diseases, BrB and UWS. This is the first study to report a higher prevalence of BrB in the winter. BrB had a prevalence of  $3.29 \pm 0.58\%$  in August 2008 and  $1.53 \pm 0.28\%$  in August 2009 while UWS was the most common syndrome in the summer with a prevalence of  $1.12 \pm 0.31\%$  in November 2007 and  $2.67 \pm 0.52\%$  prevalence in January 2008. The prevalence of GA and SEB did not depend on the season, although GA prevalence increased throughout the study period. WS had a slightly higher prevalence in the summer but its overall prevalence was consistently low ( $<0.5\%$ ). Sites with high abundance of staghorn *Acropora* and *Montipora* were characterised by the highest disease prevalence (12% of *Acropora* and 3.3% of *Montipora* were diseased respectively). The results emphasise the importance of seasonality and coral community composition as drivers of coral disease. Given that diseases are known to decrease the resilience of reef-building corals to other stressors and disturbances, potential future changes in seasonal disease prevalence deserve further research effort.

Oral  
Presentation

## Coral disease prevalence and dynamics in the Wakatobi Marine National Park, South-East Sulawesi, Indonesia

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Coral diseases were surveyed in the Wakatobi Marine National Park (WMNP), South-East Sulawesi for the first time in 2005 and 2007. We aimed to investigate disease prevalence and dynamics in this remote area situated in the Coral Triangle. In 2005, only 2 known syndromes were recorded within the sampling area: white syndrome (WS; 0.42% prevalence) and growth anomalies (GA; 0.15% prevalence), whilst 4 diseases were recorded in 2007: WS (0.14%), *Porites* ulcerative white spot disease (PUWS; 0.06%), GA (0.03%) and black band disease (BBD; 0.01%). Total disease prevalence decreased from 0.57% in 2005 to 0.24% in 2007. In addition to prevalence surveys, *in situ* progression rates of 4 diseases were investigated in 2007: BBD on *Pachyseris foliosa*, *P. rugosa* and *Diploastrea heliopora*, WS on *Acropora clathrata*, and brown band (BrB) and skeletal eroding band (SEB) diseases on *Acropora pulchra*. BrB and WS had the highest progression rates,  $1.27 \pm 0.32$  and  $1.09 \pm 0.14$  cm d<sup>-1</sup>, respectively, indicating that diseases may have a significant impact on local *Acropora* populations. BBD had the lowest progression rate ( $0.43 \pm 0.17$  cm d<sup>-1</sup>). Despite low total disease prevalence, progression rates comparable to the ones observed in the Caribbean and Australia indicate that diseases may threaten the reef framework in some locations and add to the degradation of coral reefs in a region already at high risk from anthropogenic impacts.

Poster  
Presentation

## Prevalence of disease in *Ianthella basta* populations from the Palm Islands and Torres Strait

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Sponges form a highly diverse and significant component of benthic communities, often aiding in important functional roles such as bioerosion, consolidation and benthic-pelagic processes. Therefore, the loss of sponge communities can have significant impacts on the surrounding environment. Previous disease epidemics throughout the Caribbean and the Mediterranean caused widespread sponge mortalities. To date, the GBR and Torres Strait have not experienced the catastrophic mortalities observed in other places; however, anecdotal reports suggest an increasing prevalence of sponge disease in these regions. Based on these reports, *Ianthella basta* was selected as a model species to investigate sponge disease on the GBR and Torres Strait. Disease prevalence surveys were conducted at sites around Masig Island (8 sites) and the Palm Islands (12 sites). Surveys from both locations revealed relatively healthy communities, with between 50 to 75% of the sponges showing no signs of disease. However, sponges displaying some signs of disease were recorded at every site, with a higher percentage of sponges showing more advanced stages of disease found in Torres Strait. Initial signs of disease in *I. basta* include discolored, necrotic spots in which sponge skeletal fibers are just becoming apparent. Sponges in advanced stages of disease exhibit tissue degradation with completely exposed skeletal fibers and, in some cases, increased fouling. With the proposed additions of commercial sponge farms in Torres Strait and the GBR, the need to understand disease processes in sponge populations is vital. Outputs from this study will be beneficial to marine managers in constructing risk assessments for sponge disease onset and transmission.

Poster  
Presentation

## Microorganisms are not responsible for the disease-like syndrome affecting the marine sponge *Ianthella basta*

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A disease-like syndrome is currently affecting a large percentage of *Ianthella basta* over a large geographical area, with 43% and 66% of surveyed sponges displaying symptoms in the Palm Islands and Torres Strait, respectively. Symptoms of the syndrome include discolored, necrotic spots leading to tissue degradation, exposure of the skeletal fibers and disruption of the choanocyte chambers. To ascertain the role of microbes in the disease process, a comprehensive comparison of bacteria, viruses, fungi and other eukaryotes was performed in healthy and diseased sponges. All techniques indicated a very low diversity of microbes with both healthy and diseased sponge communities dominated by three strains: an *Alphaproteobacteria*, a *Gammaproteobacteria* and a Group I Crenarchaea. Bacterial cultivation, community analysis by DGGE (bacteria and eukarya), sequencing of 16S rRNA clone libraries (bacteria and archaea) and direct visual assessment by electron microscopy failed to reveal any putative pathogens. In addition, infection assays could not establish the disease in healthy sponges even after direct physical contact with affected tissue. These results provide substantial evidence that microbes are not responsible for the formation of brown spot lesions and necrosis in *I. basta*. Future research will investigate the role of environmental factors and auto-immune dysfunction in the onset of brown spot lesions and necrosis. Preliminary findings suggest that elevated sea water temperatures have little effect on *I. basta*, with similar microbial community compositions between treatments.

Oral  
Presentation

## Sea-level rise, flooding, flushing, and wave heights at a coral atoll

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Coral Atolls abound in the tropical waters of the Pacific and Indian Oceans. Global mean sea-level rise will lead to more frequent episodic flooding of populated atolls and is of great concern to its residents. Flushing time of atolls' lagoons is another concern, since lagoons are a crucial socio-economic resource for residents, and may be impacted by pollution larval recruitment and other factors related to water exchange. Atolls tend to be oceanic, and thus experience relatively high surface gravity wave energy on their encircling fore-reefs. This forces flow into the lagoon and raises water levels. This process is investigated by comparing ~60 years of sea-level data at Midway Atoll, in the Northwestern Hawaiian Islands, with a numerical climate reanalysis. Wave heights clearly dominant changes in sea level anomaly (SLA) in the lagoon: there is a strong positive correlation. SLA is up to 90 cm during large wave events. This process is further investigated by numerical simulation of SLA distribution and residual flows during statistically significant wave conditions; estimated overall lagoon flushing times are found to vary by an order of magnitude depending on wave height.

Poster  
Presentation

## Genetic resilience of *Symbiodinium* populations: The role of coral endosymbionts in adaptation to climate change

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The frequency of coral bleaching episodes is expected to increase with rises in sea surface temperature linked to global warming. While differences in bleaching susceptibility have been linked to different types of algal endosymbionts (genus: *Symbiodinium*) hosted by some corals, we do not yet understand the underlying mechanisms in *Symbiodinium* that contribute to variation in thermal tolerance. Our research addresses the following questions:

*Which Symbiodinium genes are involved in the heat stress response?*

Identification of genes involved in heat stress response will enable functional genetic variation relevant to thermal tolerance to be studied. Candidate genes will be identified under experimental heat stress using gene expression techniques.

*What patterns of genetic variation at heat stress response genes exist among reef populations of Symbiodinium strains?*

Genetic (i.e. allelic) variation at target genes identified under (i) in *Symbiodinium* populations from distinct thermal environments will be assessed. A correlation between allele distribution and thermal environment will confirm a role for these genes in thermal tolerance.

*How much neutral genetic diversity exists within reef populations of Symbiodinium strains and to what extent are recruits exchanged among reefs?*

Sufficient exchange among populations is central to the capacity of damaged reefs to be reseeded from healthy surrounding reefs and for beneficial alleles (potentially involved in increased thermal tolerance) to be spread among reefs. Neutral genetic variation will be quantified using microsatellite markers.

Oral  
Presentation

## Bacterial communities of juvenile corals infected with different *Symbiodinium* (dinoflagellate) clades

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The coral holobiont consists of the host and its microbial partners including the dinoflagellate endosymbiont, *Symbiodinium*, and bacteria. Although genetically different *Symbiodinium* types have been shown to differentially affect the physiology of the coral host, their effects on bacterial partners in the association are unknown. This study compares profiles of bacterial communities associated with juvenile corals of *Acropora millepora* and *A. tenuis* that had been experimentally infected with two different clades of *Symbiodinium*, C1 and D, to investigate possible interactions between bacterial and *Symbiodinium* communities. Three culture-independent 16S rRNA gene profiling methods revealed no discernible pattern in bacterial communities on 9-month old juvenile corals containing different clades of zooxanthellae, suggesting that coral-associated bacteria do not appear to be linked to *Symbiodinium* type *in hospite* in early ontogeny. In contrast to bacterial profiles of adult corals, bacterial communities associated with juvenile corals were highly variable, indicating that bacterial associates are not conserved in these early stages. When juveniles were sampled in summer, bacterial communities associated with *A. tenuis* hosting clade D *Symbiodinium* were dominated by sequences affiliating with *Vibrio* species, indicating that corals harbouring this symbiont may be more susceptible to temperature stress allowing growth of opportunistic microbial community members.

Poster  
Presentation

## Responses of the coral holobiont to heat stress

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The effects of heat stress on the bacterial community associated with coral was investigated to understand how bleaching impacts the stability and health of the coral holobiont (the term used to describe the coral and the diverse array of associated microbes, including the algal symbiont, *Symbiodinium*, bacteria, *Archaea*, viruses, fungi and endolithic algae). Juvenile *Acropora tenuis* corals hosting different *Symbiodinium* types (ITS 1 type C1 or D) were subjected to heat stress in a controlled experiment and the bacterial community shifts assessed through molecular profiling of the bacterial 16S rRNA genes (clone libraries and DGGE). Distinct shifts in bacterial associates on juveniles harboring type D *Symbiodinium* occurred when placed above the coral thermal threshold at 32°C in contrast to control temperature treatments (28°C). *Vibrio* affiliated sequences dominated the bacterial profiles and retrieved sequences affiliated most closely with the coral pathogen, *Vibrio coralliilyticus*, previously implicated in coral disease outbreaks. Coral hosting type C1 *Symbiodinium* did not exhibit major bacterial shifts in the elevated temperature treatment, indicating a more stable bacterial community during thermal stress. A metagenomic approach was further used to determine the metabolic and taxonomic shifts in microbial communities of coral subjected to a natural bleaching event. A direct comparison of the healthy vs bleached coral metagenomic datasets similarly indicated major shifts in microbial associates during heat stress, including bacteria, *Archaea*, viruses, Fungi and micro-algae. The microbial community shifted from a photosynthesis driven metabolism to heterotrophic modes of metabolism including increases in fatty acid, protein, simple carbohydrate and sulfur metabolism along with the increase in virulence and stress genes on bleached coral. In combination, these results demonstrate that thermal stress can result in shifts in coral-associated bacterial communities, which may lead to deteriorating coral health and highlight the importance of inter-kingdom interactions among the coral host, dinoflagellate endosymbiont and bacterial associates for coral health and resilience.

Oral  
Presentation

## Observed seasonal and long-term MLD and $f\text{CO}_2$ characteristics of the Coral Sea

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The seasonal variability of the MLD within the Coral Sea was examined using the conductivity-temperature-depth (CTD) profiles of Argo floats. The Argo program represents a significant advancement for marine studies, with the first Argo floats being introduced into the Coral Sea in mid-2001. A distinct seasonality in the MLD is evident throughout the Coral Sea, but is generally more pronounced in higher latitudes as a result of greater seasonality in sea surface temperature and wind stress. While summer mixed layers are relatively homogeneously shallow throughout the Coral Sea, winter mixed layers in higher latitudes tend to be significantly deeper compared to tropical regions.

Since pre-industrial time, oceanic geochemistry has already significantly changed due to increased atmospheric  $f\text{CO}_2$ . Within the Coral Sea, the first direct measurements of oceanic  $f\text{CO}_2$  ( $f\text{CO}_{2,\text{sea}}$ ) were gathered in the early 1980s. Due to the highly sporadic nature of the  $f\text{CO}_2$  dataset, seasonal and long-term  $f\text{CO}_{2,\text{sea}}$  variability are difficult to discern. Although the seasonal signal of  $f\text{CO}_{2,\text{sea}}$  is not entirely consistent, it exhibits quite a strong seasonality, with the higher summer  $f\text{CO}_{2,\text{sea}}$  values signalling increased outgassing of  $\text{CO}_2$  into the atmosphere during the warmer months. The average rate of increase (1.37  $\mu\text{atm}/\text{year}$ ) of  $f\text{CO}_{2,\text{sea}}$  for the 1983-2001 period is comparable to the global trend of mean atmospheric  $f\text{CO}_2$  over the same time frame. An investigation into the capability of  $f\text{CO}_{2,\text{sea}}$  estimation in the absence of any chemistry data indicates that non-chemical predictors (including sea surface temperature and salinity) provide a reasonably good first order approximation for  $f\text{CO}_{2,\text{sea}}$ .

Oral  
Presentation

## Functional groups and coral reef health

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Coral reefs around the globe experience various levels of degradation. Although some are considered to be healthy and well managed, other coral reefs show strong signs in the reduction of functions and processes. Human induced impacts on critical functional groups, weakens and reduces the links and processes within the system. Over-fishing of herbivores can consequently increase macroalgae populations beyond a beneficial threshold to a state where increased biomass is negative to the system. The composition of functional groups shows great diversity between reefs and between habitats within one single reef. The question is if the composition of functional groups changes in a system less exposed to human disturbance. Ningaloo reef on the west Australian coast is a unique reef ecosystem due to its west-continental location and relative low human impact. Ningaloo has limited documented history of commercial fin-fishing, minimal fresh water run-off and low human development hence is dominated by natural disturbances like high wave energy and cyclones. It was therefore of interest to map the distribution of herbivorous functional groups within this coral reef ecosystem.

Oral and Poster  
Presentation

## Nitrogen fixing bacteria associated with corals of the Great Barrier Reef

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One important proposed functional role for coral associated bacteria is nitrogen fixation. Nitrogen fixation can only be accomplished by diazotrophic bacteria and is fundamentally important because it makes gaseous dinitrogen (N<sub>2</sub>) available for nitrogen limited ecosystems such as coral reefs. Diazotrophic bacteria therefore contribute to an important additional source of nitrogen to corals and particularly to the zooxanthellae whose growth and abundance is nitrogen limited. Diazotrophic bacterial communities associated with three coral species (*Acropora millepora*, *Acropora muricata* and *Pocillopora damicornis*) were investigated among 4 locations (Magnetic Island, Orpheus Island, Davies Reef and Kelso Reef) on the Great Barrier Reef to better understand the nature and specificity of this coral–diazotrophs symbiosis. A diversity profiling technique (clone libraries) targeting the nitrogenase *nifH* gene was used to assess diazotroph diversity among coral species and location. Although diverse diazotrophic bacterial communities were observed between the coral species studied, the same dominant diazotrophic communities were maintained by each coral species among locations. Therefore diazotrophic bacteria associated to corals appeared to be species specific. Moreover, the phylogeny of the coral associated diazotrophic bacteria, revealed a relatedness to plant symbionts, further supporting the hypothesis of a close relationship between diazotrophs and the zooxanthellae.

Oral  
Presentation