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Marine and Tropical Sciences Research Facility Milestone Report, February 2008

Program 5(i): Climate Change: Great Barrier Reef

Project 2.5i.3: Resilience to climate change

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1. Summary of milestone report

The resilience to climate change project is on track.

Milestones for the resilience of coral assemblages project area have been delivered with good progress. A publication on the genetic connectivity of algal endosymbionts of corals (*Symbiodinium*) on the Great Barrier Reef (GBR) has been submitted to the journal *Coral Reefs* and reviewers' reports have been received. An extension for the submission of the revised manuscript has been granted, as the first author of the manuscripts is currently overseas and revision requires some re-analysis.

Population genetic data have been obtained for five *Acropora* species from the Palm Islands. Only small sample sizes were available for *A. aspera*, and extensive data analysis on this species was therefore not conducted.

Specific primers have been developed for population-level markers targeting additional strains of *Symbiodinium* commonly hosted by corals on the GBR. Over thirty potential loci work well across *Symbiodinium* strains and are currently being tested for levels of polymorphism.

A modelling framework for understanding the potential for corals to evolve greater resistance to bleaching under temperature stress was developed and published in *The American Naturalist* in early 2008.

Annual surveys of coral disease have been completed in the northern and southern sectors and are underway in the central sector for the summer 2008 period. A framework for modelling disease abundance is currently being modified to include anomalously low and high winter temperatures.

Preliminary results were obtained to quantify the response of critical functional groups of herbivorous fish to macroalgal increase.

Intensive field sampling of fish and coral assemblages was undertaken in January 2008 and data are now being analysed to assess recovery of coral communities and butterflyfish assemblages since the 2001-02 bleaching event.

Reef & Rainforest RESEARCH CENTRE

2. Summary of project objectives

2.1. Resilience of coral assemblages to climate change

(a) Estimate genetic connectivity among GBR populations of coral and their algal endosymbionts to determine their potential for replenishment following disturbances associated with climate change.

Connectivity within and between coral populations is an important component of coral reef resilience. Exchange of larvae creates and maintains high levels of genetic diversity and buffers populations against disturbance. Migrants may carry new alleles that may be integrated into populations through reproduction, creating new gene combinations on which selection can potentially act. The spread of selectively advantageous alleles at DNA loci involved in physiological responses such as bleaching resistance is a potentially important consequence of migration. Furthermore, gene flow increases local effective population sizes, thereby enhancing the ability of populations to resist rapid random changes in allele frequencies from one generation to the next through drift. Larval-exporting or source reefs with diverse populations of healthy adult corals are essential to maintain the genetic diversity and resilience of larval-importing or sink reefs.

Therefore, an assessment of larval transport in and out of reefs, i.e. the extent to which reefs are self-seeding or accumulate recruits from surrounding areas, as well as the direction of larval dispersal will improve our ability to forecast how reef corals are likely to respond to environmental change. Successful migrants leave a genetic signature of their movements and allow inference of connectivity using population genetic methods. We will estimate genetic connectivity among GBR populations of coral and their algal endosymbionts using analysis of DNA microsatellite loci, and link this information to hydrodynamic models to provide improved estimates of reef connectivity.

(b) Identify mechanisms of adaptation available to local coral populations to understand their potential for adaptation to climate change.

Observed differences in bleaching sensitivity between geographically distinct, conspecific coral populations may be caused by differential expression of genes involved in the bleaching response (as a consequence of either local adaptation or acclimatisation), and/or by the presence of distinct alleles at these loci (due to selection and local adaptation). We will identify fast diverging genes (that are therefore likely to be under selection) in a GBR coral species that is known to show a latitudinal gradient in thermal tolerance using DNA microarray technologies.

Common garden experiments and microarray/quantitative real time PCR analyses will subsequently be used to examine whether or not genetically determined (i.e. a consequence of selection and hence reflecting adaptation) differences in gene expression levels exist between these latitudinal populations.

Theoretical models of the potential for corals to evolve greater bleaching resistance in response to climate change will be developed as part of this objective. Results from the empirical studies described above will be used to parameterise these models and model outputs will be used in turn to guide the design of further experiments.

(c) Identify links between thermal anomalies and coral disease dynamics to predict the response of coral assemblages to ocean warming associated with climate change.

Increases in the severity and frequency of wildlife disease epidemics over the past three decades are thought to be linked, in part, to increasing thermal stress associated with climate change. Understanding the implications of increasing ocean temperatures for the spread of coral pathogens and for disease resistance of corals will significantly enhance current understanding of the resilience of GBR coral assemblages in relation to climate change. We will determine the linkages between seasonal thermal anomalies and the prevalence of coral disease. A modelling approach will be used to evaluate metrics of thermal anomalies based on NOAA satellite data that best explain spatial and temporal patterns in the prevalence of coral disease on the GBR.

The relationship between peaks in disease prevalence and thermal anomalies will be analysed to determine thermal thresholds associated with outbreaks of coral disease. We will also identify interactions between bleaching and disease. We aim to produce algorithms to (a) relate temperature to past disease outbreaks, and (b) develop a product that provides predictive outlooks for outbreaks of key coral diseases, similar to the NOAA hotspot algorithm that predicts bleaching events.

2.2. Resilience of reef fish assemblages to climate change

(d) Quantify current levels of herbivory by reef fishes on the GBR and evaluate the extent to which reefs across the GBR shelf are vulnerable to ecosystem phase-shifts and domination by macroalgae as a result of climate change.

Herbivory has long been considered as one of the primary determinants of coral reef community benthic structure. It was not until recently however, that research efforts began to focus on understanding the role of herbivory in maintaining ecosystem function, and thus quantify the importance of herbivores on coral reefs. The primary goal for this objective in 2007 is to prepare a status and trend report on herbivory by reef fishes on the GBR and to evaluate the extent to which reefs across the GBR shelf are vulnerable to ecosystem phase-shifts and domination by macroalgae as a result of climate change.

This review address issues such as global and local trends in reef herbivory studies, the number of publications based on herbivory, the nature of herbivory on the GBR, and the scale and distribution of such studies. These data will be reviewed in order to produce a status and trend report on herbivory patterns.

(e) Identify critical thresholds in macro-algal phase shifts and evaluate alternate management strategies in order to limit the impacts of climate change on the ability of fish assemblages to prevent ecosystem phase-shifts on coral reefs.

Climate change will influence the community structure of reef fish assemblages, however, it is unknown if these changes will affect ecosystem processes, and subsequently lead to a phase shift from coral to algal dominated reefs. Here, we will utilise and build on existing databases of the distribution and abundance of herbivorous fishes across the GBR to quantify current rates of herbivory. These data will be combined with direct experimental analyses of fish-algal interactions that will enable us to estimate the current capacity of GBR reef fish populations to maintain low macroalgal cover on mid and outer reefs. The second part of this objective will use a modelling approach to permit direct estimation of critical thresholds in the coral – macroalgal phase shift and to evaluate alternative management strategies to respond to changes in macro-algal distributions.

We will combine the results from part one with existing algal distribution data and algal growth trajectories to model fish-algal interactions and outcomes under a range of climate change scenarios. Furthermore, it will provide us with an indication of the relative resilience of different components of the GBR ecosystem. In particular, it will indicate to what extent the current stands of macroalgae on inshore reefs reflect a state of heightened vulnerability to climate change.

(f) Evaluate the long term recovery and resilience of reef fish communities to climate change induced habitat degradation.

The most immediate and substantial effects of climate change on coral reefs are severe episodes of climate-induced coral bleaching, which cause widespread mortality of reef corals. Extensive mortality of reef corals results in the loss of essential habitat for coral reef fishes, leading to reduced abundance and localised extinction of coral reef fishes. While many studies have documented sudden declines in the abundance of fishes immediately following extensive coral depletion, the degree to which fish communities are resilient and may eventually recover is currently unknown.

We will conduct a detailed analysis of the recovery and resilience of fish assemblages at Trunk Reef, central GBR, which were severely impacted by climate induced coral bleaching in 2001-2002. Recovery of reef fish assemblages is likely to be contingent upon increases in coral cover and a return to pre-disturbance structure of benthic communities. Changes in the structure and dynamics of fish communities will be monitored annually and directly compared to temporal changes in the physical and biological structure of benthic habitats.

3. Project Results

Objective	Targeted Activity	Completion Date
(a)	Assessment of small scale population structure and genetic connectivity among populations in the *Acropora aspera* group	June 2008
(b)	Assessment of expression levels of genes involved in the bleaching response in coral populations from different thermal environments	June 2009
(b)	Understanding of the role of selection on expression levels of genes involved in the bleaching response	June 2010
(c)	No activity Year 1	
(c)	Complete surveys of coral disease prevalence at key sites missing from JCU / AIMS LTMP coral disease surveys.	Mar 2008
(c)	Analyse patterns in coral disease prevalence on the GBR in relation to seawater temperature patterns.	June 2008
(c)	Develop a model to predict the likelihood of coral disease outbreaks in response to ocean warming.	Dec 2008
(c)	Present report on the vulnerability of GBR corals to disease in relation to ocean warming.	June 2009
(d), (e)	Collate available data on herbivory patterns on GBR	Dec 2006
(d), (e)	Develop a protocol for quantifying the capacity of inshore reef fish communities to respond to local macroalgal growth; directly identifying the critical functional groups responsible for macroalgal browsing.	Dec 2007

Objective	Targeted Activity	Completion Date
(d), (e)	Complete experimental evaluation of relative susceptibility of dominant inshore macroalgal species to browsing by mobile reef herbivores.	June 2008
(d), (e)	Evaluate Island-scale variation in herbivory on macroalgae using a hierarchical design to explore site and local variation in browsing rates.	June 2008
(d), (e)	Report on Island-scale variation in herbivory and estimated capacity of inshore reefs to respond to increased increased macroalgae.	June 2008
(d), (e)	Complete regional scale evaluation of inshore reef susceptibility to coral-algal phase-shifts and ecosystem collapse. Initiate compilation of herbivore abundance data and preliminary evaluation of ecosystem thresholds.	June 2009
(d), (e)	Complete field and experimental evaluation of algal ecosystem thresholds, modeling of coral algal phase shifts under different climate change scenarios.	June 2010
(d), (e)	Present report on vulnerability of GBR to climate change induced shifts in macroalgae distribution and abundance in relation to fish herbivory and present options for alternate management options.	Dec 2010
(f)	No activity Year 1	
(f)	2007-08 surveys of fish assemblages on Trunk Reef. Report on trajectories for coral cover and fish populations 5-yr post-disturbance.	Mar 2008
(f)	Publish scientific paper based on 2002-2008 results.	Dec 2008
(f)	2008 surveys of fish assemblages on Trunk Reef. Compare fish and coral communities at Trunk Reef to pre-disturbance structure, as well as against other reefs with contrasting disturbance histories	June 2009
(f)	2009 surveys of fish assemblages on Trunk Reef Establish key factors and limitations to recovery in highly disturbed fish communities. Briefing to end-users GBRMPA, DEWHA, DPI&F.	Dec 2009
all	Final end-user briefings, seminars or workshops to communicate results and contribute to management strategies. Publish and disseminate peer-reviewed scientific publications	June 2010

- **Preliminary findings of microsatellite genotyping of populations of the corals *Acropora millepora, A. spathulata, A. pulchra, A. aspera, A. papillare* from the Palm Islands [(a) JCU] and Contribute to JCU report on preliminary findings of microsatellite genotyping of populations of the corals *Acropora millepora, A.spathulata, A. pulchra, A. aspera, A. papillare* from the Palm Islands [(a) AIMS]**

In total, 583 specimens from three locations in the Palm Island group (Pelorus SE, Orpheus NE and N Fantome) were available for this study (Table 1). The 1997 samples were collected by Bette Willis, the 2004 samples by Bette Willis, Madeleine van Oppen and Julian Caley. Genotyping was carried out at AIMS. The sample sizes for some of the species and/or collection points are too small to warrant inclusion in extensive data analysis. Nevertheless, all samples were genotyped at 9 DNA microsatellite loci.

Table 1: List of samples used for the genotyping study. OI = Orpheus Is NE, NF = North Fantom, PI = Pelorus Is SE. The number indicates the collection year (1997 or 2004)

Species, collection location and year	Sample size	Sample size after removal of clone mates
A. aspera OI 2004	9	9
A. aspera NF 2004	4	4
A. aspera PI 1997	6	6
A. millepora PI 2004	50	50
A. millepora OI 2004	50	50
A. millepora mil NF 2004	50	50
A. millepora PI 97	18	18
A. millepora OI 97	17	17
A. spathulata PI 97	11	11
A. spathulata PI 2004	50	49
A. spathulata OI 2004	50	50
A. spathulata NF 2004	45	45
A. pulchra PI 97	35	30
A. pulchra PI 2004	49	33
A. pulchra OI 2004	6	6
A. pulchra NF 2004	53	43
A. papillare PI 97	5	5
A. papillare PI 2004	50	33
A. papillare OI 2004	25	21

In *A. pulchra,* 8, 7 and 3 genotypes were repeated between two and six times in the Pelorus 2004, Fantome 2004 and Pelorus 1997 populations, respectively. The probability of these multilocus genotypes being produced by random mating (PID) in each of the populations was generally low (< $1x10^{-5}$), indicating that these they are likely to have been produced asexually through fragmentation. Six and three genotypes were observed 2-10 times for *A. papillare* from Pelorus and Orpheus Is., respectively. The PID in each of the populations was higher than for *A. pulchra* (0.016-0.0004), but based on the sample sizes far fewer identical genotypes would have been expected if these were produced sexually. Hence, the most likely explanation is that fragmentation is also common for *A. papillare*. One genotype was found twice in the *A. spathulata* population from Pelorus Island, and it was produced asexually (PID=4.6 $x10^{-10}$). Clone mates were not observed in any of the other sampled populations. All but one of the clonal specimens within a population were removed from the data set prior to analysis. The final data set therefore comprised the multilocus genotypes of 530 specimens.

The Pelorus and Orpheus Island 2004 *A. pulchra* populations shared one multilocus genotype, suggesting recent migration across the channel that separates Orpheus and Pelorus Islands. The same was observed for *A. papillare* from these locations. This is

supported by the lack of significant genetic differentiation between *A. papillare*, *A. millepora* and *A. spathulata* populations from Pelorus SE and Orpheus NE (see below).

On three occasions the same multilocus genotype found in 1997, was also observed among the 2004 samples, indicating that certain genotypes have survived the 1997 bleaching event. This was the case for two *A. aspera* colonies from Pelorus Is. 1997 and Orpheus NE 2004, repectively, two *A. millepora* colonies from Pelorus Is., one collected in 1997 and one in 2004, and two *A. papillare* colonies from Pelorus Is., one collected in 1997 and one in 2004.

Preliminary analysis of the data (there are likely to be null alleles at some of the loci in some of the species, and the data will still need to be checked and corrected for those) for populations with sufficiently large sample sizes shows the following patterns:

- *A. millepora* populations from Pelorus SE and Orpheus NE are panmictic. *A. spathulata* populations from Pelorus SE and Orpheus NE are also panmictic. Small, but statistically significant levels of genetic differentiation are present between those populations and their conspecific North Fantom population.
- Small, but statistically significant levels of genetic differentiation are present between the *A. pulchra* populations from Pelorus SE, Orphues NE and N Fantome. Hence, the highest level of spatial structure was found for this species.
- *A. papillare* populations from Pelorus SE and Orpheus NE are not significantly different from one another.
- Sympatric populations of *A. millepora* and *A. spathulata* show high levels of genetic differentiation (Fst ~ 0.2, $p < 0.001$), confirming the species status of A. spathulata (previously named *A. millepora* 'thick morph' and recognized as separate from *A. millepora* (Wallace 1999) based on research into breeding (Willis *et al.* 1997) and detailed morphology (Wallace 1999).
- The only species for which sufficiently large sample sizes were available pre-1998 bleaching, is *A. pulchra*. The pre- and post-bleaching populations of this species from Pelorus Is. are genetically distinct, indicating that the population has changed either through genetic drift following the bleaching-related bottleneck or through recovery from external recruits. Levels of genetic diversity, as indicated by expected heterozygosity and allelic diversity do not appear to have diminished following bleaching.

- **Preliminary findings of optimization of microsatellite loci for *Symbiodinium* species [(a) JCU] and Contribute to JCU report on preliminary findings of microsatellite genotyping of populations of the corals *Acropora millepora,A.spathulata, A. pulchra, A. aspera, A. papillare* from the Palm Islands [(a) AIMS]**

Enriched microsatellite libraries for three *Symbiodinium* strains (C1, C2 and D) commonly hosted by hard corals on the GBR have been sequenced and 384 clones obtained from Clade C1 and D respectively and 192 clones of Clade C2 *Symbiodinium.* These clone libraries were found to have a low redundancy and to contain many microsatellites. 65 clones had enough flanking region for specific primers to be designed and 29 of these loci amplify in a single product in Clade C1, C2 or D Symbiodinium DNA. 15 loci amplified in coral sperm samples suggesting that they are of coral host origin and 21 loci failed to amplify any or single products and were consequently abandoned. The successful primers vary in their specificity with some amplifying solely in the Clade for which they were developed and some across clades. Screening of levels of polymorphism both within and among coral host species is currently being undertaken and a technical note reporting on these primers in under preparation.

- **Report on results from modelling of bleaching resistance evolution [(b) AIMS]**

The modeling framework for the evolution of bleaching resistance in corals that was reported on in the previous milestone report has since been developed into a population genetics model of the dynamics of bleaching resistant alleles both in the coral hosts and the their mutualistic symbionts. Our goal was to better understand factors that might affect the potential evolution of bleaching resistance in corals, in response to increased average sea temperatures.

The model indicates that there is no necessary impediment to trait evolution within mutualisms, but that the details of the interactions between hosts and symbionts will be important in determining the relative rates of the evolution of bleaching resistance. The model explores the evolutionary consequences of four factors in some detail:

(i) Tradeoffs among fitness components can impede the evolution of bleaching resistance particularly where the population size of free-living zooxanthellea is relatively large.

(ii) Different proximate mechanisms of coral bleaching are possible whereby, either the host and symbiont dies during bleaching, or merely disassociate. Where dissociation occurs, non-resistant alleles in the zooxanthellea populations are not removed and will impede resistance evolution if they are able to recolonize coral hosts.

(iii) The mechanism of genetic determination of bleaching resistance is also likely to influence the rate at which resistance evolves. Three mechanisms were explored where the effects of alleles in the host and symbiont interact additively, and with positive and negative epistasis, that is where there are synergistic and antagonistic effects among alleles, respectively. Overall, in a set period, negative epistasis leads to greater bleaching resistance.

(iv) Sexual reproduction impedes resistance evolution compared to asexual reproduction in all cases except where there is negative epistasis and vertical transmission of zooxanthelle into new hosts. Even when this occurs the effect is small.

Because this model explores evolution of traits that can be influenced by two separate genomes, that of the host and the symbiont, its construction required the development of two novel concepts, interspecific epistasis and interspecific linkage disequilibrium. Overall, this model suggests that some proximate mechanisms of bleaching yield faster evolutionary responses to temperature stress, and that the nature of the interspecific control of bleaching resistance and the mode of sexual reproduction interact to strongly influence the rate of spread of resistance alleles.

These qualitative theoretical results highlight important future directions for empirical research in order to quantify the potential for coral reefs to evolve resistance to thermal stress.

This research was the subject of a media release during the reporting period. It received considerable media attention and was featured on the Census of Marine Life's website.

This project is ahead of schedule and has already delivered on its next milestone. We are continuing to explore how resistance evolution might be better understood by putting this style of mutualism in a broader context of the diversity of mutualisms that have evolved. We are also now considering options for empirical studies in Year 3 of the MTSRF Program that will help to address some of the issues highlighted by modeling.

- **Progress report on developing a modelling framework for investigating the relationship between coral disease abundance and ocean warming [(c) JCU]**

Funding for Program 2.5i.3(c) commenced in the second year of the MTSRF grant (2007-2008). Surveys of coral disease prevalence were completed on nine Northern sector reefs, three Capricorn Bunker reefs and four Central sector reefs. Surveys are currently underway at the remaining five Central sectors reefs. The AIMS LTMP has or is planning to survey all non-RAP sites for coral disease in the survey year 2007-2008.

A workshop focusing on modeling the relationship between thermal anomalies and coral disease was held at Cornell University, 3-5 June 2007. Workshop participants were modelers (P. Mumby, Univ. Exeter; J. Bruno, Univ. North Carolina), NOAA researchers (M. Eakin, S. Heron), and coral disease experts (B. Willis and C. Page, James Cook Univ.; D. Harvell, Cornell Univ.).

During this workshop the potential positive and negative impacts of both anomalously high and low water temperatures on the health of coral hosts and virulence of pathogens was reviewed. A number of temperature metrics were developed which incorporate the magnitude and duration of temperature anomalies in both winter and summer. Preliminarily comparisons of the capacity of these metrics to explain variation in disease levels were completed.

An additional four years of disease data was acquired from AIMS to extend the timeframe over which disease records are available from the GBR to nine years (1998-2007). Additional data on the cover of acroporid corals were also acquired from AIMS. These data allowed corals not highly susceptible to disease to be excluded from analyses and enabled a more detailed analysis of the relationship between disease levels and the number of highly susceptible acroporid hosts.

Data on current strengths on GBR reefs were obtained from NOAA to incorporate into the model. Currents may influence the time pathogens spend near a susceptible host and hence the number of cases of disease. Fast currents may allow rapid pathogen spread but are also likely to minimise the time available for the pathogen to adhere to host. Slow currents may allow greater pathogen build up and greater adhesion to host, but result in slower spread of pathogens between hosts.

An abstract has been accepted for an oral presentation at the 11th International Coral Reef Symposium in Fort Lauderdale USA, 7-11 July 2008. Abstract title: *Developing an expert system for predicting coral disease risk on Indo-Pacific reefs*. Authors: B. L. Willis, S. F. Heron, C. A. Page, W. J. Skirving, C. M. Eakin, C. D. Harvell, D. Jacobsen, G. Coleman, I. Miller, H. Sweatman.

- **Preliminary findings of quantification protocol for identifying critical functional groups and measuring the capacity of reef fishes to respond to increased macroalgae on the GBR [(d/e) JCU]**

Recent advances in the study of reef fish herbivory have revealed limitations in the application of visual censuses for measuring rates of macroalgal removal by reef fishes. Basically, the fishes that eat macroalgae avoid divers. This discovery was based on the use of underwater video techniques. However, the application of these methods varied among studies and, in some cases, was impractical for extensive replication. In 2007 therefore, a series of dedicated trips were undertaken to Orpheus Island to trial a standardised macroalgal bioassay that would permit spatial variation in the extent and nature of herbivory on macroalgae to be evaluated. The standardized method is based on a three-hour algal deployment with herbivore feeding activity recorded using remote digital videos. The trials

revealed up to seventy percent removal of algae in the three-hour period with sufficient sensitivity to detect both within and between bay variation in algal removal. Ten fish species were found to feed on the algal assays although there was marked location-specific variation in feeding activity. Following the trials a fully replicated study was undertaken with to compare patterns of herbivory within and between bays. These data will provide a preliminary indication of the spatial variability in the ability of local fish populations to remove adult macroalgae.

- **Preliminary report on long term recovery and resilience of reef fish communities to climate change induced habitat degradation**

Program 2.5i.3(f) did not receive funding until the second year of the MTSRF grant (2007-2008) and has only just commenced proposed activities. In late January, Pratchett, Wilson and three of their graduate students conducted the first survey of fish and coral communities at Trunk Reef since late summer 2005, and a complete report of their findings will be submitted by end of March 2008. Currently, there is considerable lab work required to assimilate the data, especially information on coral cover and composition, which is the most critical element of the project. During this latest survey, benthic communities were sampled using extensive photographic records. A total of 1,500 photographs were taken along thirty replicate transects, each of which now need to be viewed to record the specific coral or benthic habitat underlying a specified point within each frame. This technique essentially provides the same information as fifty-metre point-intercept transects, except that minimal training is required for the person who took the photographs, such that Pratchett (the team leader and only person with sufficient skills in coral taxonomy to complete benthic sampling in the field) could coordinate sampling of other biophysical variables. It is apparent however, that while coral communities have exhibited some level of recovery from the 2001-2002 bleaching event, the recover of butterflyfish assemblages is lagging behind, such that there are fewer butterflyfish than expected for current levels of coral cover.

- **Provision of JCU data (coral samples, experimental results) to AIMS [Responsible Officer: B. Willis, JCU.]**

Alcohol preserved tissue samples of corals collected in 1997 (before the 1998 bleaching event) have been transferred to AIMS for DNA extraction and genotyping.

- **Provision of AIMS data (theoretical model, experimental results) to JCU [Responsible Officer: J. Caley and M. van Oppen, AIMS]**

Population genetic data on *Acropora* species from the Palm Islands have been communicated to JCU.

4. Summary of communication activities

(b) 23 October 2007
Meeting between Line Bay and Bette Willis, JCU. Sampling design for Line's gene expression work and general progress of the research was discussed.

(b) 13 November 2007
Lunch meeting between Line Bay, Madeleine van Oppen and Bette Willis at C-Bar, Townsville. During this meeting we discussed issues regarding Line's gene expression work, the progress of the zooxanthellae microsatellites and details regarding coral spawning.

(b) 16 January 2008
Meeting between Line Bay, Madeleine van Oppen and Bette Willis at ARC Centre of Excellence for Coral Reef Studies, Townsville. Progress and potential application of the zooxanthellae microsatellites in addition to future grant applications was discussed.

5. Summary of annual project achievements for 2006/2007

5.1 Resilience of coral assemblages to climate change

The MTSRF proposal for objective (a) in 2006/2007 was to complete an assessment of the genetic connectivity of *Symbiodinium* populations hosted by a soft coral on the Great Barrier Reef (GBR) and develop microsatellite markers for additional strains of *Symbiodinium* which are commonly hosted by hard corals in this region. This commenced with a preliminary assessment of the results of an honours project on genetic diversity and differentiation of twelve reef populations of *Symbiodinium* hosted by the soft coral, *Sinularia flexibilis*, spanning 1,300 km of the GBR during 2006.

Additional molecular genotyping, subsequent data analysis and write-up during early 2007 led to the achievement of a manuscript of publishable quality, to be submitted in August. This publication was the first investigation of the genetic diversity and connectivity of *Symbiodinium* populations in the GBR region, and contributes to a very limited body of knowledge on the natural population ecology of coral endosymbionts. The major findings were that while high levels of genetic diversity exist within *Symbiodinium* reef populations, barriers to gene flow prevent this diversity form being uniformly distributed across the GBR, and over time significant genetic differences have accumulated among all twelve surveyed populations. Population structure was consistent with restricted hydrodynamic transport via the broad-scale patterns of water circulation within the GBR lagoon.

It is proposed that restrictions to dispersal in this particular clade C strain of *Symbiodinium* arise from a short duration in the water column due to either, or a combination of, a benthic free-living existence in the sediments, negative buoyancy (non-motile phase) and limited migrations into the water column (flagellated phase), or poor survival outside of a nutrient-rich host environment. In the face of global warming, barriers to gene flow among the investigated populations of *Symbiodinium* indicate that this zooxanthella strain is particularly susceptible to losses of genetic diversity (potentially experienced during coral bleaching) as there is little opportunity for any losses of genetic diversity within populations to be mediated by migration.

To develop a wider understanding of the importance of different factors that drive patterns of *Symbiodinium* population connectivity and resilience for different host-zooxanthella combinations, it is necessary to develop population-level molecular markers that target the *Symbiodinium* strains commonly hosted by a range of corals on the GBR. For three of the

most common strains of *Symbiodinium* (C1, C2, D) hosted by hard corals on the GBR, microsatellite libraries were developed during 2006/2007 and a number of specific primers were developed. During the next year, additional specific primers will be developed (approximately forty primers per strain) and subsequently tested for their applicability in detecting genetic variation. In combination with markers targeting host DNA, this will enable connectivity and resilience to be examined in various host-zooxanthella partnerships that differ in aspects of both host and symbiont ecology, and the susceptibility of the partnership to disturbance (e.g. coral bleaching).

For objective (b), a modeling framework for understanding the potential for corals to evolve greater resistance to bleaching under temperature stress is now complete, and population sampling of corals for experiments measuring gene expression levels in coral-*Symbiodinium* partnerships originating from different thermal environments has commenced. Initial tagging and collecting of coral colonies from different thermal environments commenced in 2007 for analysis of baseline gene expression patterns in 2007/2008.

While there was no funding or research activity for objective (c) in the 2006/2007 year, this project will be kick-started with a workshop on modelling the relationship between thermal anomalies and coral disease at Cornell University (Ithaca, NY), 3-5 June 2007. Workshop participants will include modellers (P. Mumby, Univ. Exeter; J. Bruno, Univ. North Carolina), NOAA researchers (M. Eakin, S. Heron), and coral disease experts (B. Willis and C. Page, James Cook Univ.; D. Harvell, Cornell Univ.). The workshop will focus on modelling disease outbreaks following the 2005 bleaching event in the Caribbean. In year 2, we will develop the model to explore the relationship between disease and temperature on the GBR.

5.2. Resilience of reef fish assemblages to climate change

For objectives (d) and (e) the main focus this year has been to thoroughly review the available literature so that we may more effectively quantify current levels of herbivory by reef fishes on the GBR. The results identified significant knowledge gaps, particularly in identifying herbivores, obtaining robust quantification of abundances and, primarily, in quantifying variation in the nature and intensity of herbivory across the reef. Herbivory on macroalgae was particularly poorly understood in terms of the taxa responsible for algal removal.

One of the key objectives is to evaluate the extent to which reefs across the GBR shelf are vulnerable to ecosystem phase-shifts and domination by macroalgae as a result of climate change. It was clear from the existing literature that our knowledge base was extremely limited in terms of both the spatial scale of studies and taxonomic resolution. Although research on herbivory on the GBR quantitatively lags behind that of other countries, probably reflecting the relatively intact nature of the GBR compared to collapses elsewhere, recent findings have emphasised the potential for reef resilience. In addition to a comprehensive literature search and a through evaluation of the available evidence, work in the current year included preparation for an intensive field season in the 2007/2008 year.