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Program 5(i): **Climate Change: Understanding the threat, ecosystem impacts and mitigation of the Great Barrier Reef**

Project 2.5i.3: Resilience to climate change

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Contents

1. Summary

Specific primers have been developed for population-level markers targeting additional strains of *Symbiodinium* commonly hosted by corals on the Great Barrier Reef, and a primer note on these markers has been submitted for publication.

In addition to work towards the specific milestones listed for Objective (a), a paper has been published in the journal *Coral Reefs*, presenting genetic analyses of Great Barrier Reef populations of clade C *Symbiodinium* hosted by the alcyonacean coral, *Sinularia flexibilis* (results and their implications are summarised below in Section 6 *Summary of annual project achievements for 2008/2009*).

Also, in addition to the specific milestones listed for Objective (a), a manuscript was submitted in May 2009 to the journal *Conservation Genetics* on spatial and temporal patterns in population genetic structure for four scleractinian coral species of the *Acropora aspera* group, *A. millepora*, *A. papillare*, *A. pulchra* and *A. spathulata*, at three locations within the Palm Islands group in the central Great Barrier Reef (results and their implications are summarised below in Section 6).

A manuscript on a complete common garden experiment of *Acropora millepora* from Davies and Orpheus Island to assess the extent of fixed population differences in gene expression was published in *Molecular Ecology* (see Section 3 *Project results*).

In addition to work towards the specific milestones listed for Objective (b), an oligonucleotide microarray has been developed for coral gene expression studies, which includes 10,920

A. millepora ESTs and 1,269 *Symbiodinium* ESTs. Heat stressed and unstressed samples have been tested on the array, and the results are robust for both the coral and *Symbiodinium*. This array is available for future coral and *Symbiodinium* gene expression studies.

Also in addition to the specific milestones listed for Objective (b), a new and efficient method for high-throughput gene expression analysis has been developed based on recently purchased hard- and software at the Australian Institute of Marine Science. Preliminary trials indicate that the method was successful for 17 of the 18 genes tested and results are highly reproducible. A manuscript reporting this method is in preparation.

A framework for modelling disease risk has been developed based on heating rate analyses of SST data based on the product suite, *ReefTemp,* to identify anomalously high sea temperatures in the year proceeding each summer to predict the likelihood of a disease outbreak. A final report providing an overview of the model and figures showing outbreak likelihood for 2006-2009 was completed and will the basis for a manuscript to be submitted shortly to *Global Change Biology*. Images produced will be made available in the coming month through a webpage found within the *ReefTemp* area of the CSIRO Marine and Atmospheric Research website with links to the JCU ARC Centre of Excellence for Coral Reef Studies, the Great Barrier Reef Marine Park Authority and the Reef and Rainforest Research Centre/Marine and Tropical Sciences Research Facility webpages. The images can be viewed through a standard web browser as well as through Google Earth™, enabling users to search for, navigate to, and store locations of interest.

In 2008/2009, an extensive field programme extending approximately 1,000 km along the Great Barrier Reef was undertaken to examine regional variation in the response of herbivore populations to localised increases in macroalgae on inshore reefs. Preliminary results indicated that the key functional groups remained similar yet the rate of herbivory varied markedly among regions.

Regional comparisons have established a foundation for identifying multiple thresholds in coral-macroalgal dynamics with extensive regional and taxonomic variation.

Ongoing field sampling of fish (specifically, butterflyfishes) and coral assemblages was advanced in January 2009 at three reefs (Bramble, Rib and Trunk Reefs) in the central Great Barrier Reef to assess recovery and resilience of coral communities and butterflyfish assemblages in the aftermath of the 2001/2002 bleaching event. Coral cover varies greatly among sites within and between reefs, reflective of significant but very patchy recovery. Recovery is due mainly increased abundance of acroporid corals, which provide critical food and habitat for coral reef butterflyfishes. There has not however, been any apparent increase in the abundance of butterflyfishes over the last three years. Results of this research form the basis of a paper that was accepted for publication in the *Proceedings of the 11th International Coral Reef Symposium.*

2. Summary of project objectives

2.1 Resilience of coral assemblages to climate change

(a) Estimate genetic connectivity among Great Barrier Reef population 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 Great Barrier Reef 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. Differential gene expression may occur 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). Microarray and quantitative real time PCR analyses will be used to examine gene expression differences between geographically distinct coral populations. Common garden and reciprocal transplant experiments will be used to assess the relative importance of local environmental variation (acclimatisation) and genetic differentiation (adaptation) in producing gene expression variation. This will allow for an assessment of the environmental and genetic drivers of observable phenotypic variation in bleaching resistance and whether these processes vary among geographically distinct coral 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 Great Barrier Reef 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 Great Barrier Reef. 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 Great Barrier Reef and evaluate the extent to which reefs across the Great Barrier Reef 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 Great Barrier Reef and to evaluate the extent to which reefs across the Great Barrier Reef 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 Great Barrier Reef, 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 Great Barrier Reef 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 Great Barrier 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 Great Barrier Reef 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 Great Barrier Reef, 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. To further improve current understanding of limitations to recovery and longer-term consequences of acute disturbances, we also propose to study patterns of recruitment (for fish and corals) and begin looking at the genetic diversity of recovering fish populations, to test the hypothesis that increases in the abundance of fishes may occur, but these populations could be more susceptible to future disturbances.

3. Project results

3.1 Resilience of coral assemblages to climate change

(a) Submit manuscript (with appropriate attribution of MTSRF funding) on newly developed microsatellites for Symbiodinium species (AIMS, JCU).

The health and productivity of coral reefs is underpinned by the symbiosis between corals and dinoflagellates (*Symbiodinium* spp.). To enable population genetic analyses of *Symbiodinium* spp., required for the conservation, seven microsatellite loci were isolated from *Symbiodinium* clade C from the Great Barrier Reef, Australia. These microsatellite primer pairs consistently amplified between 1-8 alleles per coral host colony, with mean number of alleles ranging from 1.9-4.0 and generally high genetic diversities (Shannon's Index = 0.71-2.76). The novel microsatellite loci amplified between 1-10 alleles in four other C strains, but did not amplify a D strain. Three of six previously published clade C microsatellite loci amplified 2-6 alleles in two or more of five C strains tested. The primers and cross amplifications presented here therefore provide a useful tool for elucidating the population genetic structure of clade C *Symbiodinium* populations.

A manuscript reporting these new primers will be submitted in the next few weeks. The manuscript has almost been finalised but the testing of our new as well as published microsatellite loci across a range of Great Barrier Reef species has taken longer than anticipated.

Nevertheless, we feel these data are important for the wider *Symbiodinium* research community. The missing data consist of information for two microsatellite loci for a small number of samples, which will be analysed at the Genetic Analysis Facility at James Cook University in the next two weeks. After this, the manuscript will be submitted for publication as soon as possible.

(b) Submit manuscript (with appropriate attribution of MTSRF funding) on complete common garden experiment of *Acropora millepora* from Davies and Orpheus Island to assess extent of fixed population differences in gene expression (AIMS, JCU).

Manuscript published in *Molecular Ecology*:

Bay, L., Ulstrup, K., Nielsen, H., Jarmer, H., Goffard, N., Willis, B., Miller, D. and van Oppen, M.J.H. (2009) Microarray analysis reveals transcriptional plasticity in the reef building coral *Acropora millepora*. *Molecular Ecology* 18: 3062-3075. [doi:10.1111/j.1365-294X.2009.04257.x]

Abstract: We investigated variation in transcript abundance in the scleractinian coral, *Acropora millepora,* within and between populations characteristically exposed to different turbidity regimes and hence different levels of light and suspended particulate matter. We examined phenotypic plasticity by comparing levels of gene expression between source populations and following 10 days of acclimatization to a laboratory environment. Analyses of variance revealed that 0.05% of genes were differentially expressed between source populations, 1.32% following translocation into a common laboratory and 0.07% in the interaction (source population-dependent responses to translocation). Functional analyses identified an over-representation of differentially expressed genes associated with metabolism and fluorescence categories (primarily downregulated), and environmental information processing (primarily upregulated) following translocation to a lower light and turbidity environment. Such metabolic downregulation may indicate nonoxidative stress, hibernation or caloric restriction associated with the changed environmental conditions. Green fluorescent protein-related genes were the most differentially expressed and were exclusively downregulated; however, green fluorescent protein levels remained unchanged following translocation. Photophysiological responses of corals from both locations were characterized by a decline when introduced to the common laboratory environment but remained healthy (F_v/F_m > 0.6). Declines in total lipid content following translocation were the greatest for inshore corals, suggesting that turbid water corals have a strong reliance on heterotrophic feeding.

(c) Report (with appropriate attribution of MTSRF funding) on a framework for modelling the relationship between coral disease abundance and sea temperature to predict the impacts of ocean warming (JCU).

Knowledge of disease risk on coral reefs is becoming increasingly important as ocean warming enhances levels of stress and disease susceptibility of corals. We explored the links between temperature and abundance of the coral disease, white syndrome, using high-resolution sea surface temperature data collected by environmental monitoring satellites and a ten-year dataset on white syndrome abundance collected by the AIMS Long-term Monitoring Program (AIMS LTMP). We found that greater than 85% of the observed variability in white syndrome abundance can be explained by a combination of the rate at which temperature stress accumulates, i.e. the 'heating rate', combined with percent cover of *Acropora* species, the primary hosts for white syndrome. Heating rate describes how anomalous a temperature regime is in comparison to the average temperatures experienced in the previous ten years. One hundred percent of the sites monitored by the AIMS LTMP in the last ten years, that had greater than fifty percent cover and experienced a summer heating rate greater than 0.3, suffered a severe white syndrome outbreak (>200 cases). Only four sites met these criteria and outbreaks occurred at all of these sites in late 2002.

Based on retrospective calculations of summer heating rates, we have developed an early warning system for white syndrome outbreaks that takes the form of a web-based tool, which colour-grades white syndrome outbreak risk as low or high. The model uses heating rate analyses of SST data based on the product suite, *ReefTemp,* to identify anomalously high sea temperatures in the year proceeding each summer to predict the likelihood of a disease

outbreak. The images produced will be made available in the coming month through a webpage found within the *ReefTemp* area of the CSIRO Marine and Atmospheric Research website with links to the JCU ARC Centre of Excellence for Coral Reef Studies webpage, Great Barrier Reef Marine Park Authority webpage and the Reef and Rainforest Research Centre /Marine and Tropical Sciences Research Facility webpage. The images include reef, park and marine reserve boundaries to facilitate interpretation. The images can be viewed through a standard web browser as well as through Google Earth™ enabling users to search for, navigate to, and store locations of interest. A paper is in preparation for *Global Change Biology*.

The capacity to predict where white syndrome outbreaks are likely to *have* occurred, as well as where they are likely *to* occur, will enable targeted research and monitoring in order to answer questions that have been difficult to address using available datasets. The resulting improved understanding of white syndrome outbreaks may help managers understand whether actions can be taken to reduce both susceptibility to white syndrome and recovery timeframes. The white syndrome outbreak prediction tool package, a world first for coral diseases, has been developed collaboratively with managers, and forms a critical component of the early warning systems within a new Great Barrier Reef-wide coral disease response plan.

3.2 Resilience of reef fish assemblages to climate change

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

- *Report (with appropriate attribution of MTSRF funding) on progress of regional scale evaluation of the potential of herbivores on inshore reefs to respond to increases in macroalgae (JCU).*

A full scale deployment of algal bioassays extending from the Low Isles in the northern sector of the Great Barrier Reef, through the Whitsundays (central Great Barrier Reef) to the Kepple Islands (southern Great Barrier Reef) revealed marked variation in the extent but not the nature of ecosystem processes. Using over 270 algal bioasseys, the southern reef sites were found to have only half the number of fish herbivore species feeding on the asseys and a markedly lower number of bites. As a consequence algal removal rates on the southern reefs were approximately one quarter of those on the northern reefs. However, surprisingly, of the more than 62,000 feeding events recorded using underwater remote video bioasseys the vast majority were restricted to just four species. Furthermore these species were the same at all three study locations. Thus the critical functional groups responsible for the removal of adult macroalgae appear to be the same in all three regions. The results suggest that nature of ecosystem processes remains similar over almost 1,000 km of the Great Barrier Reef but that the extent of this activity can vary markedly.

- *Provide initial report on the capacity to identify thresholds in algal-herbivore interactions (JCU).*

As noted above there was marked variation in the number of species feeding on algae at the three study locations and in rates of algal removal. However, the nature of the removal revealed considerable complexity in patterns of removal with marked differences in the response of key herbivores to algae. On northern reefs most fishes would feed on algae when encountering it. On southern reefs more fishes swam past the algal assays than fed upon them. The results suggest that some Great Barrier Reef reefs may be approaching a threshold where herbivores have a limited capacity to respond to increases in algae. These

results highlight the vulnerability to marginal reefs, including some southern reefs, to rapid increases in macroalgae.

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

- *Report (with appropriate attribution of MTSRF funding) on status and trends in recovery of fish communities following ongoing recovery in coral habitats, including preliminary assessment of key factors promoting or limiting recovery of fish communities (JCU).*

Ongoing sampling of fish and coral assemblages was continued in January 2009 to further assess recovery of coral assemblages and fish communities (specifically, butterflyfishes), following severe coral bleaching in the central Great Barrier Reef in 2001/2002. Coral cover declined by ninety percent from 2001 to 2005, but since has started to recover. Importantly, recovery has been highly variable among sites (within reefs) and among reefs, reflecting patchy recovery caused by differential settlement of the main habitat-forming taxa *Acropora* spp. Despite recent increases in the abundance of corals there has been no apparent increase in abundance of butterflyfishes. If anything, overall densities of butterflyfishes declined even further between 2005 and 2009, due to longer term declines in the abundance of some non-coral feeding butterflyfish. Although there are some signs of coral recovery, it is clear that severe episodes of coral bleaching can have enduring effects on coral reef ecosystems, and that recovery typically takes many years (more than five years). Protracted declines and limited recovery of coral and fish communities indicate that reef ecosystems will gradually deteriorate as bleaching events become more frequent and more severe.

A manuscript arising from these surveys has been accepted for publication, which acknowledges financial support from MTSRF:

Pratchett, M.S., Baird, A.H., McCowan, D.M., Coker, D.J., Cole, A.J. and Wilson, S.K. (2009) Protracted declines in coral cover and fish abundance following climate-induced coral bleaching on the Great Barrier Reef. *Proceedings of the 11th International Coral Reef Symposium.*

4. Summary of communication activities

- *Summary of any communication activities undertaken, including minutes of meetings/ workshops if applicable (AIMS, JCU).*

(Objective) Date: Event

- (a) 3 December 2008: Meeting between Emily Howells, Madeleine van Oppen, Bette Willis and Line Bay, Australian Institute of Marine Science, Townsville.

  During this meeting we discussed issues related to Emily's work using the zooxanthellae microsatellites under development.
- (a) 16 January 2009: Meeting between Madeleine van Oppen, Bette Willis, Petra Souter and Greg Torda, Australian Institute of Marine Science, Townsville.

  During this meeting we discussed issues relating to the commencement of Greg's PhD.
- (a) 16 April 2009: Meeting between Emily Howells, Madeleine van Oppen and Line Bay, Australian Institute of Marine Science, Townsville.

  During this meeting we discussed lab work requirements for the finalisation of the zooxanthellae microsatellites paper.

- (b) 25 February 2009: Meeting between Emily Howells, Madeleine van Oppen, Bette Willis and Line Bay, Australian Institute of Marine Science, Townsville.

  During this meeting we discussed Emily's PhD.
- (b) 20 April 2009: Meeting between Line Bay and Madeleine van Oppen, Australian Institute of Marine Science, Townsville.

  Results of microarray analyses and paper revisions were discussed.
- (b) Wed 13 May 2009: Meeting between Line Bay and Madeleine van Oppen, Australian Institute of Marine Science, Townsville.

  During this meeting the results of the clonal variation study were discussed.
- (f) 4 February 2009: Meeting between Morgan Pratchett, Dominique McCowan, Darren Coker and Andrew Cole, ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville.

  Arrangements were made to progress data analyses from the January survey trip. Andrew Cole was to take primary responsibility for compiling and undertaking preliminary analyses for fish communities, while Morgan Pratchett would do the same for coral communities.
- (f) 26 March 2009: Meeting between Morgan Pratchett, Line Bay and Rebecca Lawton, ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville.

  Ms Rebecca Lawton reported on current progress in developing a microsatellite library for key species of butterflyfishes (C. trifascialis and C. lunulatus) from the Great Barrier Reef. This project is nearing completion with two separate publications detailing microsatellite libraries for each species to be submitted by end of 2009.

5. Completion plan for remaining activities in out years (JCU, AIMS)

Objective	Targeted Activity	Completion Date
(a)	Genotyping of *Symbiodinium* C2 within *Acropora millepora* coral populations using developed *Symbiodinium* microsatellites to infer spatial connectivity of populations on reefs within and between the Central and Southern regions of the GBR.	March 2010
(a)	Development of new microsatellite markers for *Seriatopora hystrix* on the GBR for parentage analysis in low diversity populations.	March 2010
(a)	Examination of small-scale population genetic structure of Lizard Island and Palm Island *S. hystrix* populations, a comparison of habitats (i.e. exposed vs. sheltered) and regions.	June 2010
(a)	Genotyping of *Symbiodinium* C2 within healthy and stressed (=bleached) colonies of *Acropora millepora* from different reefs using developed *Symbiodinium* microsatellites to assess temporal variation in the genetic composition of *Symbiodinium* assemblages hosted by corals and how genetic variation is impacted by coral bleaching.	June 2010
(b)	Development of high through-put multiplex oxidative stress gene expression method in corals.	March 2010
(b)	Development of new generation microarray technology for high through-put gene expression screening in corals.	March 2010
(b)	Examination of the clonal sources of gene expression variation in corals.	June 2010
(c)	Completion of surveys of coral disease prevalence and coral recovery following the 2009 low salinity event at key sites. (dependent on funding).	March 2010

Objective	Targeted Activity	Completion Date
(c)	Testing of the disease-temperature model to predict the likelihood of white syndrome outbreaks in response to SST anomalies (dependent on funding).	March 2010
(c)	Delivery of report on the vulnerability of GBR corals to disease in relation to ocean warming (dependent on funding).	June 2010
(d), (e)	Delivery of an initial report on regional scale variation in inshore reef susceptibility to coral-algal phase-shifts and ecosystem collapse; including an initial evaluation of herbivore abundances and ecosystem thresholds.	March 2010
(d), (e)	Completion of field and experimental evaluation of algal ecosystem thresholds, modeling of coral algal phase shifts under different climate change scenarios.	June 2010
(d), (e)	Delivery of final 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.	June 2010
(f)	Publish scientific paper on appropriate genetic markers to assess genetic variation within recovering populations of specialist butterflyfishes as a measure of population resilience. Compare fish and coral communities at Trunk Reef to pre-disturbance structure, as well as against other reefs with contrasting disturbance histories.	March 2010
(f)	2010 surveys of fish and coral assemblages, with sampling at three mid-shelf reefs (Trunk, Rib and Bramble). Sampling will focus on measuring differential rates of settlement with a view to separating pre- versus post-settlement processes in limiting recovery. Analyses population genetic structure for remnant and recovering populations of butterflyfishes to assess long-term consequences of the bleaching event (e.g., genetic variation within the population).	June 2010
(f)	Prepare final publications and report on findings to end-users. Proposed publications include a meta-analysis of rates of recovery for coral communities and factors that regulate recovery of coral reef communities.	December 2010
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

6. Summary of annual project achievements for 2008/2009

6.1 Resilience of coral assemblages to climate change

For Objective (a) in 2008/2009, a paper was published in the journal *Coral Reefs*, presenting genetic analyses of Great Barrier Reef (GBR) populations of clade C *Symbiodinium* hosted by the alcyonacean coral, *Sinularia flexibilis,* in addition to the primer note manuscript described above. Allelic variation at four newly developed microsatellite loci demonstrated that *Symbiodinium* populations are genetically differentiated at all spatial scales from 16-1,360 km; the only exception being two neighbouring populations in the Cairns region separated by 17 km. This indicates that gene flow is restricted for *Symbiodinium* C hosted by *S. flexibilis* on the GBR. Patterns of population structure reflect longshore circulation patterns and limited cross-shelf mixing; suggesting that passive transport by currents is the primary mechanism of dispersal in *Symbiodinium* types that are acquired horizontally. There was no correlation between the genetic structure of *Symbiodinium* populations and their host *S. flexibilis*, most likely because different factors affect the dispersal and recruitment of each partner in the symbiosis. The genetic diversity of these *Symbiodinium* reef populations is on

average 1.5 times lower on inshore reefs than on offshore reefs. Lower inshore diversity may reflect the impact of recent bleaching events on *Sinularia* assemblages, which have been more widespread and severe on inshore reefs, but may also have been shaped by historical sea level fluctuations or recent migration patterns was "Assessment of small scale population structure and genetic connectivity among populations in the *Acropora aspera* group". Samples from members in this species group occurring in the Palm Islands were collected in 1997 and 2004 and their population genetic characteristics assessed using nine DNA microsatellite loci. Because four of the nine loci suffer from the presence of non-amplifiable alleles (null alleles), null allele frequencies will have to be estimated and the data re-analysed. This analysis will be conducted in the next year and a small scientific publication will be written.

Also, a manuscript has been submitted in May 2009 to the journal *Conservation Genetics* on spatial and temporal patterns in population genetic structure for four scleractinian coral species of the *Acropora aspera* group, *A. millepora*, *A. papillare*, *A. pulchra* and *A. spathulata*, at three locations within the Palm Islands in the central Great Barrier Reef. Species boundaries and spatial genetic structure were evaluated from samples of all four species collected in 2004, six years after the mass bleaching event of 1998. *A. millepora* and *A. pulchra* were also sampled in 1997, enabling a temporal comparison across a major disturbance event. All pairwise comparisons between species showed significant genetic differentiation, supporting species delineations. Conspecific populations examined from Orpheus and Pelorus Island (separated by ~1 km) was panmictic in both 1997 and 2004, but the Fantome Island populations were genetically distinct, despite being located only 11 km away. A change in the genetic composition, measured as significant pairwise F_{ST} of *A. millepora* and *A. pulchra* populations was observed between the 1997 and 2004 samples. Even though the 1998 coral bleaching event caused extensive mortality, only marginal changes in levels of genetic diversity were detected between 1997 and 2004 population samples and neither species displayed evidence of a recent genetic bottleneck in 2004. These results suggest that recovery has mainly occurred through re-growth of cryptic patches of remnant tissue. *A. papillare* exhibited significantly lower genetic diversity compared to the other three species, consistent with its rare occurrence in the Palm Islands and throughout its distributional range, and was the only species to display evidence of a genetic bottleneck in 2004.

For Objective (b), two microarray studies have been undertaken to understand the potential for acclimatization, and levels of clonal variation in gene expression in corals. The first study found substantial potential for acclimatisation in metabolic gene expression and has been accepted for publication in *Molecular Ecology*. The second dataset is currently being analysed and reveals large variation between replicate branches taken from the same coral colonies. This has important implications for the design of future microarray studies. Significant progress has been made in developing a multiplex gene expression assay that targets oxidative stress genes important in the coral bleaching response.

Also, an oligonucleotide microarray has been developed for coral gene expression studies, which includes 10,920 *A. millepora* ESTs and 1,269 *Symbiodinium* ESTs. Heat stressed and unstressed samples have been tested on the array, and the results are robust for both the coral and *Symbiodinium*. This array is available for future coral and *Symbiodinium* gene expression studies. Furthermore, a new and efficient method for high-throughput gene expression analysis has been developed based on recently purchased hard- and software at AIMS. Preliminary trials indicate that the method was successful for 17 of the 18 genes tested and results are highly reproducible. A manuscript reporting this method is in preparation.

For Objective (c), a modelling framework for predicting outbreak risk for the coral disease, white syndrome, in relation to seasonal seawater temperature anomalies has been

developed and a final report on the predictive tool submitted with the June 2009 report. The images produced will be made available in the coming month through a webpage found within the *ReefTemp* area of the CSIRO Marine and Atmospheric Research website with links to the JCU ARC Centre of Excellence for Coral Reef Studies, Great Barrier Reef Marine Park Authority and the Reef and Rainforest Research Centre/Marine and Tropical Sciences Research Facility webpages. The images include reef, park, and marine reserve boundaries to facilitate interpretation. The images can be viewed through a standard web browser as well as through Google Earth™ enabling users to search for, navigate to, and store locations of interest. A paper is in preparation for *Global Change Biology*. Also, seasonal surveys of disease prevalence in the northern, central and southern Great Barrier Reef have been completed in 2008/2009, continuing the integrity of long-term datasets to further explore the links between temperature and disease in coral populations and to evaluate the efficacy of the predictive tool.

6.2 Resilience of reef fish assemblages to climate change

For Objectives (d) and (e), the main focus this year was to expand the spatial scale of our observations to examine regional variability in the ability of herbivorous fish populations to respond to local increases in macroalgae. We used a recently developed methodology to examine the ability of reef fish populations to remove adult macroalgae from reefs in the northern, central and southern regions of the Great Barrier Reef. The results were striking with a four-fold increase in removal rates on northern reefs compared to their southern counterparts. Despite regional variation in algal removal raters, local fish population densities, and reef fish community structure, the underlying ecosystem function or ecosystem processes remained remarkably consistent at sites over 1,000 km apart. It appears that processes are consistent but rates of activity vary and that some marginal reefs may be close to macroalgal consumption thresholds.

For Objective (f), this year (2008/2009) combined ongoing monitoring of standard state variables (e.g. coral cover and fish abundance) as well as developing new tools for measuring of population status (e.g. genetic structure of remnant and recovering populations) to establish long-term consequences of disturbances to coral reef communities. Sampling was undertaken in January 2009, involving complete surveys of fishes (using visual surveys along fifty-metre belt transects) and corals (photographic records spaced one metre apart along fifty-metre transects) in reef crest and reef slope habitats at three sites at each of three reefs (Trunk, Rib and Bramble) in the central Great Barrier Reef. Results from these surveys have already contributed to one publication (accepted for publication in the *Proceedings of the 11th International Coral Reef Symposium*) with another more detailed publication to follow within the next six months. Moreover, extensive sampling and detailed analyses of our survey data has provided clear direction for further expansion of this project to, i) continue detailed annual monitoring of corals and butterflyfishes, ii) increase focus on processes of recovery, by measuring recruitment rates, not just adult abundance, and iii) consider resilience of populations, rather than previous emphasis on community resilience, by looking at genetic variation and fitness of recovering populations.