



2022 Student
Seminar Day

Abstract
Booklet

Museum of
Tropical Queensland

AIMS@JCU 2022 Student Seminar Day Schedule

| Time | Abstract title | Presenter/Chair |
|---------|---|----------------------------------|
| 10.00am | Welcome to Country & dance presentation | Wulgurukaba Walkabouts |
| 10.15am | Official launch of AIMS@JCU Triennial plan | JCU/AIMS/ Libby Evans-Illidge |
| 10.45am | Morning tea | |
| 11.15am | Opening Remarks | Cherie Motti |
| | Session 1 | Chris Brunner - Chair |
| 11.20am | Scale matters: Incorporating a multiscale framework into genotype-environment associations to investigate coral adaptation | Annie Guillaume |
| 11.35am | Exploring an integrated aquaculture approach to coral grow-out | Rachel Neil |
| 11.50am | Demographic Drivers of Coral Population Persistence: An Integral Projection Modelling Approach | Kevin Bairos-Novak |
| 12.05pm | Which receptors are responsible for settlement of <i>Acropora millepora</i> larvae? | Ramona Brunner |
| 12.20pm | How variations in pCO ₂ influence calcification rates of corals and carbonate structures | Stephanie Di Perna |
| 12.35pm | Lunch | |
| | Session 2 | Bettina Glasl - Chair |
| 1.05pm | Environmental and host drivers of coral symbiont diversity in thermally distinct reefs | Magen Marzonie |
| 1.20pm | Determining the transmission dynamics of expelled heat-evolved symbionts and their implications for coral reef restoration | Bede Johnston |
| 1.35pm | Symbiosis under climate change: integrating host, Symbiodiniaceae and bacteria responses in coral reef invertebrates | Emma Maragon |
| 1.50pm | Functional signatures of seawater microbes show increased stress response in degraded reefs | Marko Terzin |
| 2.05pm | Posters and Afternoon Tea | |
| | Session 3 | Cherie Motti - Chair |
| 2.35pm | AIMS@JCU and me | Yui Sato - Keynote Speaker |
| 3.05pm | Assessing the use of "Assisted gene flow" to enhance heat tolerance of multiple coral species across the Great Barrier Reef | Alex Macadam |
| 3.20pm | Large-scale patterns of thermal tolerance in two species of <i>Pocillopora</i> on the Great Barrier Reef | Josephine Nielsen |
| 3.35pm | Do coral populations harbour genetic variation to adapt to climate change? | Rhys Cornish |
| | Session 4 | Marina Santana - Chair |
| 3.50pm | Impacts of ocean warming on echinoderms, with a focus on crown-of-thorns starfish (CoTS; <i>Acanthaster cf. solaris</i>) | Bethan Lang |
| 4.05pm | eReefs modelling suggests <i>Trichodesmium</i> may be a major nitrogen source in the Great Barrier Reef | Chinenye Ani |
| 4.20pm | Can supplementation with DMSP & acrylate promote coral recruit growth? | Geoffrey Yau |
| 4.35pm | Understanding plasticiser leaching from microplastic polymers | Alexandra Gulizia |
| | Session 4: Speed talks | Heidi Luter - Chair |
| 4.50pm | Using environmental predictors of wave energy to understand the influence of grazing fish on coral survival to optimise coral seeding | Taylor Whitman |
| 4.55pm | Connectivity modelling for informed deployment of enhanced coral larval slicks in the Great Barrier Reef | Chinenye Ani |
| 5.00pm | Striking a balance: maximising Symbiodiniaceae uptake while minimising risk of bleaching-induced mortality in corals | Corinne Allen |
| 5.05pm | Never ask a starfish its age | Sarah LT Kwong |
| 5.30pm | Present awards & closing remarks | Cherie Motti |
| 5.40pm | End of Year celebration | |

11.20am

Scale matters: Incorporating a multiscale framework into genotype-environment associations to investigate coral adaptation

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Genome–Environment Association (GEA) methods are quickly becoming popular tools for identifying signatures of local adaptation in natural populations. These methods look to associate genetic variations between individuals or populations with environmental variables of interest. In this way, organisms with a potential to adapt to future conditions may be identified, such that populations hosting tolerant individuals may be managed and protected going into the future. While GEA methods are benefiting from increases in accessibility of high resolution genetic and environmental data sets, a current limitation is that role of spatial scale has largely been neglected. Indeed, spatial scale is known to affect evolutionary-ecology model outcomes, with impacts on subsequent interpretations and management decisions. In my thesis, I investigate the sensitivity of these models to spatial resolutions, looking to improve model performance and create frameworks for incorporating multiscale variables. Here, we look to apply multiscale frameworks developed for terrestrial landscape genomic analyses to perform multiscale seascape genomic analyses. Using a case study of a coral species in the Great Barrier Reef (GBR), Australia, we demonstrate how a multiscale seascape genomic analysis can be performed using multivariate redundancy analyses, to obtain a more complete understanding of how corals may be adapting to thermal stressors.

11.35am

Exploring an integrated aquaculture approach to coral grow-out

Rachel Neil^{a,b,c}, Jonathan Barton^{a,c}, David Bourne^{a,b,c},
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Integrated aquaculture is the approach of rearing two or more species alongside each other, typically using the wastes of one species to supply nutrition to the other. There is evidence that wild corals derive benefits from associated fish, including increased growth and resistance to bleaching. To test if similar effects could be applied in *ex situ* environments, growth, photosynthetic activity, protein and lipid content of two fish-associated corals, *Acropora tenuis* and *Pocillopora verrucosa*, and two non-fish-associated, *Porites lutea* and *Platygyra daedalea*, were assessed in aquaria over 3 months under different treatments. These included corals 1) kept with a school of *Chromis viridis* fed on a pelleted diet, 2) supplied filtered water from a tank with a school of *C. viridis*, 3) fed live feeds whilst maintained with *C. viridis*, 4) no fish but supplied with live feeds, 5) no fish but supplied with pelleted fish diet, and 6) control treatment with no feeds or fish. The pelleted fish diet suppressed coral growth as measured by buoyant weight, while live feeds, fish or fish-water treatments improved growth by ~1.5 – 2x compared to the lowest treatment for each species. Exposure to fish, fish-water or live feeds typically increased photosynthetic capacity of the Symbiodiniaceae within the corals. Tissue protein in *P. verrucosa* was higher under live feeds, while lipid content increased in fish, fish-water and pellet treatments. The interaction of supplied nutrients and the coral holobiont's physiological response is complex, with further avenues of analysis planned to fully understand these relationships.

This research was undertaken on the lands and sea country of the Wulgurukaba, Bindal and Wadawurrung peoples.

11.50am

Demographic Drivers of Coral Population Persistence: An Integral Projection Modelling Approach

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Projecting the long-term trajectories of coral populations requires a comprehensive knowledge of population demography. Population models increasingly adopt an integral projection model (IPM) framework, which allows more realistic characterization of size-dependent demography than traditional matrix models. However, a better understanding of how model architecture and parameterisation affect population trajectories is required before IPMs can be used to project coral population trajectories. Here, we construct a size-structured, density-dependent IPM of a single population of corymbose *Acropora* corals, parameterised with demographic data from the northern and central Great Barrier Reef. We then analyzed population extinction risk and long-term equilibrium coral cover in response to different size-dependent demographic relationships, and quantified the contribution of each process to uncertainty in model predictions. Relative to growth, survival, and fecundity, data on recruit intra-cohort density-dependence is rarely collected and included in coral IPMs. Yet, in the absence of density-dependent interactions among recently-settled individuals, our model predicted realistic levels of cover only at ecologically implausible larval survival and settlement probabilities. In contrast, when recently-settled corals interact in a density-dependent way, plausible levels of coral cover occur over a much broader range of parameter space. Additionally, we found that coral dynamics depend most on processes associated with the establishment of first-year recruitments (e.g., intra-cohort density dependence, probability of successful settlement), but are also sensitive to uncertainty related to growth and survival functions. Our study suggests an increased focus on recruitment processes and juvenile demography is warranted to improve the realism of coral population models.

12.05pm

Which receptors are responsible for settlement of *Acropora millepora* larvae?

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Coral reproduction is vital for reef recovery. Corals reproduce by releasing gametes or larvae into the water column. Successful recruitment depends primarily on the ability of larvae to find suitable habitats for permanent attachment to the reef substrate (settlement) since this determines the survival rate after metamorphosis into sessile polyps. Larvae follow environmental cues to appropriate settlement spots. Most research on coral settlement focused on the identification of natural settlement cues, however, the cellular structures of coral larvae to sense these cues are still unknown. This study investigated the receptors responsible for coral larvae settlement of *Acropora millepora* by combining the methods of proteomics, transcriptomics, phylogenetics and pharmacological settlement assays. The settlement receptor search was based on two assumptions. Firstly, the settlement receptors are predicted to be present at the aboral larval part because this is the region that probes and attaches to the substratum. For this reason, transcriptomics was applied to investigate gene expression differences between aboral and oral larval parts. Secondly, the receptors that receive settlement cues are assumed to be present in the ectodermal or ciliary membranes of competent larvae and absent in the pre-competent stage. Therefore, mass spectrometry techniques were used to investigate changes in protein expression between pre-competent and competent larvae in membrane samples originating from larvae and isolated cilia. The identification of settlement receptors would be the first step to reveal the molecular signalling pathways of settlement induction and could increase settlement efficiency for coral aquaculture.

12.20pm

How variations in pCO₂ influence calcification rates of corals and carbonate structures.

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Coastal environments have highly dynamic carbonate chemistry trends, often with much greater ranges in pH and pCO₂ than what is recorded in the open ocean. However, our understanding of the impact of diurnal variability on coral reefs and their constituents is still in its infancy, as this natural variability has not until recently been considered in most coral reef acidification research. This study aimed to understand how pCO₂ variability influences calcification of carbonate functional groups (coral, sediment and rubble) under pre-industrial (mean 270 +/- 50 µatm), contemporary (mean 410 µatm +/- 50 and 150 µatm) and ocean acidification conditions (mean 900 µatm +/- 50, 150 and 300 µatm). Corals (*Acropora millepora* and *Montipora aequituberculata*), sediments and rubble were kept in conditions for 10 weeks, and net calcification was assessed via buoyant weight. For corals, respirometry was used to separate day and night metabolic rates. Under contemporary conditions, increased variability led to greater net calcification (N_{calc}) for the two coral species and the sediments. In OA conditions, increased variability led to lower N_{calc} for *M. aequituberculata*, sediment and rubble. Pre-industrial conditions minimized weight loss of sediments but had less impact on weight of corals and rubble. *A. millepora* day calcification rates and *M. aequituberculata* night calcification rates increased with variability in contemporary conditions but decreased with variability in OA conditions. The results demonstrate how important natural variability is on the health and metabolism of our coral reefs, and that it is critical to include variability in monitoring efforts and predictive tools.

I wish to acknowledge the Wulgurukaba and Bindal people as the traditional owners of the land where I conducted my experiment as well as the sea country where the corals originated.

1.05pm

Environmental and host drivers of coral symbiont diversity in thermally distinct reefs

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The diversity and distribution of coral endosymbiotic algae (Symbiodiniaceae) can mitigate coral heat tolerance at local-to-regional scales. However, it is still uncertain whether symbiont genetic diversity, host effects or environmental drivers shape the coral response to heating events. The Coral Sea Marine Park is a unique seascape, where isolated reefs and low connectivity can act to naturally detect variation in response to environmental gradients and thermal history. Here we collected three coral species (*Acropora humilis*, *Pocillopora verrucosa* and *Pocillopora meandrina*) from 13 reefs that spanned over 1300 km. We used ITS2 and psba genetic markers to identify Symbiodiniaceae to species-level resolution. For all host species across the Coral Sea, symbionts almost exclusively belonged to the genus *Cladocopium*. We found that symbionts were highly structured according to their coral host. Symbionts hosted by *Acropora* were very sensitive to local environmental conditions and recent bleaching events. In contrast, symbionts of *P. meandrina* were highly partitioned by latitude, whereas *P. verrucosa* communities had little influence from any environmental factors. Overall, host species was a key player in shaping symbiont genetic diversity across reefs, followed by environmental drivers including latitude, recent thermal history and depth. The variable patterns of symbiont distribution identified here highlight the importance of coral species-level comparisons of symbiont communities across large environmental gradients. These interactions will enable detection of coral responses relative to prospective heatwave anomalies in the future.

Traditional Owners to be acknowledged:

Wulgurukaba and Bindal Traditional Owners of Australia; Meriam Traditional Owners of Torres Strait where experiments were conducted (Coral Sea).

1.20pm

Determining the transmission dynamics of expelled heat-evolved symbionts and their implications for coral reef restoration

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Faced with recurring sea surface temperature anomalies the ecological success of coral reefs is becoming increasingly dependent upon the physiological performance of their hosted dinoflagellate symbionts of the family Symbiodiniaceae. In light of this, experimental evolution strategies have recently been applied to symbionts *in vitro* in an attempt to generate heat-evolved (SS) strains capable of enhancing the thermotolerance of their coral hosts. While this strategy has proven successful for coral larvae, recruits, and adults, whether SS Symbiodiniaceae-coral associations can be established in the environment at scales capable of generating significant restoration outcomes is yet to be tested. Host-host expelled symbiont transmission through the water-column has the potential to upscale the outcomes of this restoration approach to ecologically relevant levels, however, its mechanism is poorly understood in corals. To begin to address this knowledge gap I first chemically removed the native symbionts of the coral *Galaxea fascicularis* before inoculating them with SS symbionts. Following the resumption of a functional SS Symbiodiniaceae-coral symbiosis, I then collected the Symbiodiniaceae expelled from *G. fascicularis* over a 24-hour period and took the following measurements: expulsion rate, species composition, life-stage, and photosynthetic and morphological viability. While symbiont expulsion rate was observed to be highly variable over time, the photosynthetic viability of expelled symbionts displayed a significant diel rhythm. The results from these tests will then be used to inform future experiments where I will characterise the ability of expelled SS symbionts to be acquired by and improve the thermotolerance of downstream adult *G. fascicularis* colonies.

The authors would like to acknowledge the traditional owners of the land and sea country on which this research took place and thank the Wulgurukaba and Bindal people for their contribution as the original scientists and custodians of the land (Gurumbilbarra and Thul Garrie Waja).

1.35pm

Symbiosis under climate change: integrating host, Symbiodiniaceae and bacteria responses in coral reef invertebrates

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The ecological success of many coral reef invertebrates relies on their metabolic exchanges with microbial symbionts. These essential host-microbe relationships can be disrupted under increasing environmental pressures, with implications for host health. Here, we experimentally explored the stability and molecular mechanisms underpinning host-symbiont interactions in the thermotolerant coral *Porites lutea* and sponge *Cliona orientalis* under increasing heat stress (28 - 32 °C) using physiological and omics-based tools (16S rRNA gene sequencing and transcriptomics). Comparative analysis revealed that holobiont responses to heat stress are host-specific, varying also among holobiont members (i.e. host, Symbiodiniaceae and bacteria). While host transcriptomic responses to moderate heat stress (31 °C) differed markedly between the coral and sponge species, similar gene expression patterns were observed in Symbiodiniaceae within both holobiont hosts. Symbiodiniaceae also showed stronger transcriptional changes than the host in both species under heat stress. Physiological stress signatures were coupled with a shift in the microbial community in the coral, whereas the sponge microbiome was highly stable under increasing temperatures. Overall, our study indicates that mechanisms at the basis of thermal tolerance may be distinct across reef species, and highlights the importance of multi-omics approaches to better understand holobiont functioning under environmental stress.

1.50pm

Functional signatures of seawater microbes show increased stress response in degraded reefs

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Coral reefs are impacted by both local and global human-induced stressors. To understand/quantify how environmental impacts correlate to changes in reef communities, long-term monitoring is a necessity. Most reef monitoring programs implement visual surveys (i.e. coral cover, bleaching or disease assessments), however, visual cues become evident at a point when ecosystem change may be irreversible and management interventions are reactive. Marine microbial communities respond rapidly to environmental shifts and represent a potential early warning indicator of ecosystem stress. Here we detail how seawater microbes can be used in reef monitoring, through collection of seawater at 48 sites across the GBR for metagenomic sequencing, paired with *in situ* reef health survey data. Seawater microbial taxonomic/functional signatures were directly correlated with environmental data on benthic cover and water quality to identify microbial indicators of degraded reef health. Our results indicate that traditionally characterised opportunistic/potentially pathogenic microbes (e.g. *Flavobacteriaceae*, *Cryomorphaceae* and *Rhodobacteraceae*) and functions (motility elements, response to stress, virulence factors) are enriched in reefs with elevated temperature and nutrient loads, as well as reef sites where coral bleaching and disease were observed. While both microbial taxonomic and functional information provide a robust indicator of coral reef health status, multivariate linear regression-based modelling identified that functional information is a more stable predictor of coral health compared to taxonomy. Our results demonstrate the potential of reef seawater microbes to inform reef health status, and that microbial function may be more informative for reef monitoring purposes compared to microbial taxonomy.

3.05pm

Assessing the use of “Assisted gene flow” to enhance heat tolerance of multiple coral species across the Great Barrier Reef

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Coral cover in the tropics has declined by at least 50% in the last 30 years, with reefs projected to bleach yearly by 2050. If population sizes of coral remain high, adaptation may keep pace with warming. However, restoration may be needed in the short term to supplement natural adaptive capacities given the fast rate of warming. Genetic restoration methods like Assisted Gene Flow (AGF) utilise the heritability of heat tolerance to speed up adaptation and gene flow between resilient and sensitive reefs. To test this, we reproductively mixed eggs and sperms from a range of reefs along a thermal gradient on the Great Barrier Reef and compared acquired heat tolerance in purebred and crossbred offspring from two corals species (*Acropora tenuis* and *A. hyacinthus*) compared to their parents. Moreover, juveniles were inoculated with different algal symbiont treatments (*Durusdinium trenchii*, a heat-evolved selected strain of *Cladocopium goreaui*, and “wild” symbionts from warm reef sediments) to assess the impact of symbiosis on acquired heat tolerance of the coral offspring from a range of crosses. We measured survival, growth, and colour (as a proxy for bleaching), as well as photosynthetic efficiency using microscopy pulse amplitude modulation (PAM). Survival was improved in both *Acropora tenuis* and *A. hyacinthus* at elevated temperature for juvenile (32°C) life stage, and in *A. tenuis* larvae (35.5°C) when comparing inter-population crosses with intra-population crosses from cooler reefs. However, survival was not improved in *A. hyacinthus* larvae. Further work will identify the key underlying genomic and transcriptomic drivers of these traits in coral larvae and juveniles.

I acknowledge the traditional custodians of the land on which I have worked, Wulgurukaba, Bindal, Manburra, Ngurruumungu, Walambaar, Gunggandji, Wuthathi, Cape Melville, Flinders & Howick Island Aboriginal Corporation, and pay my respects to their Elders past, present, and emerging. I extend that respect to any Aboriginal and Torres Strait Islander peoples here today.

3.20pm

Large-scale patterns of thermal tolerance in two species of *Pocillopora* on the Great Barrier Reef

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Rising seawater temperatures pose a significant challenge to the continued survival of many tropical corals due to the increased risk of coral bleaching. However, corals exhibit differential thermal tolerance and resilience to bleaching both within and among species and across populations. The causes of this variation are not well-understood. It is likely that genetic and physiological mechanisms as well as the capacity for plasticity in organismal stress responses underpin differential thermal tolerance and bleaching resilience in tropical corals.

To assess the variation in thermal tolerance between coral species and across multiple populations, we conducted acute thermal stress assays along the latitudinal gradient of the Great Barrier Reef (GBR) on two coral species (*Pocillopora verrucosa* and *P. meandrina*). Corals were distributed across four treatments (Max Monthly Mean; MMM, +3°C, +6°C and +9°C) following standardised protocols. We quantified photosynthetic efficiency (F_v/F_m), tissue colour change, chlorophyll content, and Symbiodiniaceae densities to provide insight into coral responses to acute thermal stress. Thermal tolerance between populations and species was compared by calculating ED₅₀ temperature thresholds for multiple traits. For photosynthetic efficiency, ED₅₀ temperatures varied by 2.4°C above site-specific MMM in *P. verrucosa* and by 2.62°C above MMM in *P. meandrina*. We discuss differences in thermal tolerance with respect to community composition of Symbiodiniaceae of each sampled colony. Finally, we combine data from physiology and symbiont communities with environmental drivers of tolerance such as thermal history to provide an overview of where to find tolerant populations of each species across the GBR.

3.35pm

Do coral populations harbour genetic variation to adapt to climate change?

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Marine heatwaves are increasing in frequency and intensity causing widespread coral bleaching. Temperature tolerant genotypes may hold the key to adaptation to marine heatwaves, however, we have poor understanding of where these individuals occur, the mechanisms of thermal tolerance and how this variation in thermal tolerance may contribute to adaptation of populations. Approaches based on predictive modelling and remote observations lack the spatial resolution required to detect variation at smaller scales such as among genotypes. Furthermore, we lack understanding of the heritability of these traits, and what trade-offs may come with thermal tolerance. To address this knowledge gap, we tagged 350 *Acropora millepora* colonies across the Keppel Islands. These colonies varied in their level of bleaching level in April 2020 with ~94% of tagged colonies recovering. We exposed these colonies to a rapid heat stress assay using PAM chlorophyll fluorescence to measure photosynthetic efficiency (bleaching response). By combining these results with natural bleaching data, we identified “top” and “bottom” performers in terms of thermal tolerance. With this, we then conducted selective breeding trials on sea country in November 2022. We conducted heat-stress experiments on coral larvae from thirty-nine family crosses sampling for survivorship and allele frequencies. We then settled 32 families to outplant juvenile corals for later heat stress experiments during the juvenile life stage. This research will reveal heritability of thermal tolerance for larvae and juvenile corals and associated trade-offs. This study will contribute data to model how populations may recover from marine heatwaves and adapt to climate change.

3.50pm

Impacts of ocean warming on echinoderms, with a focus on crown-of-thorns starfish (CoTS; *Acanthaster cf. solaris*)

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Ocean warming is threatening marine species and populations globally, and marine ectotherms are particularly vulnerable. Echinoderms (including starfish, sea urchins, sea cucumbers and brittle stars) are marine ectotherms that are both ecologically and economically important. Shifts in their population dynamics can have profound impacts on the marine environment. Firstly, I will discuss a recent meta-analysis conducted, exploring the impacts of elevated temperature on echinoderms. I find that vulnerability to ocean warming varies based on the traits measured, as well as the collection latitude, life stage and taxonomic class. Notably, I find that starfish and tropical echinoderms are particularly vulnerable to ocean warming. Secondly, I will draw my attention to the effect of warming on one such tropical starfish, the crown-of-thorns starfish (CoTS; *Acanthaster cf. solaris*), which has caused substantial damage to coral reefs across the Indo-pacific, as a result of their preference for feeding on coral, and their tendency to reach outbreak densities. As expected, I find that the survival of CoTS significantly declines with only moderate increases in temperature, that are expected to commonly occur on the reef in the near-future. These observations indicate that populations contractions or redistributions of CoTS may occur over the coming decades.

4.05pm

eReefs modelling suggests *Trichodesmium* may be a major nitrogen source in the Great Barrier Reef

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Trichodesmium can fix nitrogen that is later released into the water column. This process may be a major source of ‘new’ nitrogen in the Great Barrier Reef (GBR), but to date this contribution is poorly resolved. We have estimated the seasonal, spatial and annual contributions of *Trichodesmium* to the annual nitrogen budget of the GBR using the eReefs marine models. Models were run for the interval December 2010 to November 2012. During this period La Niña conditions produced record rainfalls and widespread flooding of GBR catchments. Model outputs suggest nitrogen fixation by *Trichodesmium* in the GBR (which covers about 348,000 km²) contributes approximately 0.5 MT/yr, exceeding the total average annual riverine nitrogen loads (0.05 -- 0.08 MT/yr). Nitrogen fixation loads are exceeded by riverine loads only if the comparison is restricted to inshore waters and during the wet season. This result is provisional but reinforces the need for more detailed assessment and reliable quantification of the annual nitrogen contribution from nitrogen fixation in the GBR and other coastal waters. Such advances will improve understandings of the role of terrestrial nitrogen loads in the GBR and of terrestrial phosphorus and iron loads which can modulate *Trichodesmium* abundance. These findings will help to broaden the focus of water quality management programs and support management to improve GBR water quality.

4.20pm

Can supplementation with DMSP & acrylate promote coral recruit growth?

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Corals are one of the largest producers of dimethylsulfoniopropionate (DMSP), an organic sulphur compounds that has important ecological functions in marine ecosystems and is central to global sulphur cycling. DMSP serves as an antioxidant and stress protectant alongside its breakdown products dimethylsulfide (DMS) and acrylate. High concentrations of DMSP and acrylate are present in fast growing Acroporids in contrast to slower growing non-Acroporid species which have low or undetectable concentrations. The biological function of the high concentrations of acrylate in Acroporid coral tissues is unknown though has been postulated to be linked with coral calcification. This study therefore investigated the potential role of DMSP and acrylate in coral calcification. Supplementation of exogenous DMSP to *Acropora kenti* and *Goniastrea retiformis* showed no difference in survival and growth compared to non-supplemented controls, though acrylate supplementation demonstrated negative toxicity effects on the coral recruits. DMSP concentrations in the tissues of the *A. kenti* recruits was similar across supplemented and control treatments indicating that this family can produce endogenous DMSP. In contrast endogenous DMSP was not detectable in *G. retiformis* tissues, though supplemented recruits were able to uptake exogenous DMSP. Despite uptake no increased growth was observed for *G. retiformis* recruits relative to the control treatment across the 8-day exposure period. Overall, chemical supplementation of DMSP and acrylate did not promote the growth of coral recruit, though further studies to resolve the form, and uptake pathways into the coral tissue spaces to allow coral calcification is warranted.

4.35pm

Understanding plasticiser leaching from microplastic polymers

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Microplastic contamination in our oceans is of growing concern particularly due to the presence of toxic chemical additives, such as plasticisers. Plasticisers are incorporated into plastic materials during manufacturing to tailor the mechanical and thermal and thermal properties of the polymer. However, exposure to plasticisers, both alone and in combination with microplastics can lead to severe physiological and behavioural changes in aquatic organisms. Moreover, through leaching behaviours, microplastics represent a significant source of plasticisers into marine environments, and further contributing to environmental and wildlife toxicity. Understanding the reactivity of plasticised polymers in aqueous media over time will help mediate the ecotoxicological concerns associated with microplastic contamination in marine environments. In this study, the leaching behaviours of common phthalate acid ester (e.g., DEHT and DEHP) and diphenol (e.g., BPA and BPS) plasticisers from polystyrene microplastics was investigated, and a model developed which explains these behaviours in different aqueous media. This model was then applied to degraded microplastics, as well as other polymers prevalent in marine ecosystems (e.g., polyvinyl chloride). Results obtained here will help to further understand the reactivity of marine microplastic and plasticiser contamination under relevant conditions, clarifying exposure and toxicity pathways to wildlife.

We would also like to acknowledge the Wulgurukaba, Bindal, Djabugay, Yirrganydji, and Gimuy Yidinji people as the traditional Owners of the lands on which we are located and where we conducted this research. We pay our respects to ancestors and Elders, past and present.

4.50pm Speed Talk

Using environmental predictors of wave energy to understand the influence of grazing fish on coral survival to optimise coral seeding

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Coral seeding, harnessing the high fecundity of sexually propagating corals, offers one solution to help reefs persist in an uncertain future. However, grazing-induced coral mortality from fish are challenging the effectiveness of this technique. We tested the ability of seeding devices with micro-refugia to protect recruiting corals from grazing and seeded them to reefs with varying wave energy. We identified sites with high wave energy had less coral predation and increased survival (2.5-fold). Corals at low energy sites were 9x more likely to suffer from grazing mortality. Protective devices and strategic site selection are required for successful restoration via seeding.

Traditional Owners to be acknowledged: Wulgurukaba, Bindal, Gunggandji.

4.55pm Speed Talk

Connectivity modelling for informed deployment of enhanced coral larval slicks in the Great Barrier Reef

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We used OceanParcels, a particle tracking simulator using outputs from the high resolution hydrodynamic-biogeochemical marine model, Relocatable Coastal Model (RECOM), to simulate the spawning, dispersal and settlement of coral larvae considering the timing of annual spawning, larval behaviour and mortality in the Great Barrier Reef for 2015, 2016 and 2017. Our results will help to identify reefs that are strongly connected to surrounding reefs within a cluster or subregion of the Great Barrier Reef for informed deployment of enhanced coral larval slicks. Our findings highlight the need to consider different conditions when assessing connectivity.

5.00pm Speed Talk

Striking a balance: maximising Symbiodiniaceae uptake while minimising risk of bleaching-induced mortality in corals

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To combat the rapid loss of corals due to climate change, coral thermal resilience may be enhanced through the introduction of heat-evolved algal symbionts (Symbiodiniaceae) into bleached corals. However, it is unknown whether heat-evolved Symbiodiniaceae can establish symbiosis and proliferate in the presence of competing homologous Symbiodiniaceae occupying mildly bleached corals. Here, I assess how the extent of bleaching in the coral *Platygyra daedalea* impacts a) host health and b) uptake of heat-evolved *Cladocopium* and *Durusdinium*. Results will provide insight into competitive outcomes of Symbiodiniaceae communities and contribute to optimisation of this assisted evolution approach for implementation into reef restoration practices.

I would like to acknowledge the Wulgurukaba and Bindal people as the Traditional Owners of the sea country and land where this research takes place, and pay my respects to Elders past, present, and future.

5.05pm Speed Talk

Never ask a starfish its age

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Population irruptions of crown-of-thorns seastar (CoTS, *Acanthaster* spp.) represent a perennial threat to coral reefs in the Indo-Pacific region. Age determination of CoTS has been challenging in the past, thus hindering the understanding of population dynamics and the development of corresponding management strategy. My PhD project aims at developing DNA-based tools to determine the chronological age of CoTS. Telomere lengths and DNA methylation patterns, which are newly emerged age markers for a diverse array of taxa, will be explored as age proxies in CoTS.

I acknowledge the Wulgurukaba and Bindal people as the Traditional Owners of the land I work on.

Downstream Effects of Variable Coral Bleaching on Natural Recovery Potential in the Keppel Islands

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Future reef recovery relies on reproduction by coral survivors of major disturbances, but increasingly frequent and severe bleaching events are impacting recovery by decreasing larval inputs to reef systems. Furthermore, sublethal effects on corals that do survive bleaching may be further suppressing recovery, although these effects often go undetected. We investigated sub-lethal effects of the 2020 mass-bleaching event on inshore, turbid corals in Woppaburra sea country (Keppel Islands). *Acropora millepora* experienced high bleaching incidence but low mortality across the island group. We decalcified and dissected samples from fate and phenotype-known *A. millepora* colonies collected prior to spawning and 6 months after bleaching. We found a no significant decrease in average egg size in severely bleached colonies across all bleaching scores from 1-6, but a 20% reduction in polyp fecundity in the most extreme bleached colonies. We also present results on the variable impacts of the 2020 bleaching event on Woppaburra coral populations. Results will be presented against historic data on coral fecundity. Identifying sub-lethal impacts of coral bleaching on survivors provides valuable insights into their capacity to contribute to recovery of coral populations.

Spatial dynamics of macroalgae in the Central GBR

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The combined effect of climate change and local anthropogenic stressors have led to global declines in coral cover. Available substratum is often colonised by fast-growing organisms such as macroalgae. While algae are natural reef components, large increases in the cover and/or biomass of macroalgae are often related to lower coral recruitment. Thus, there is growing interest in understanding the effect of macroalgae on coral early-life stages. However, little is known about the spatial and seasonal dynamics of tropical macroalgae, limiting our ability to understand how corals respond to different algal communities. This project aims to quantify the seasonal and spatial dynamics of macroalgal assemblages in the Central GBR, as well as natural occurrences of coral-algal interactions, and coral juvenile occurrence in macroalgal habitats.

Traditional Owners to be acknowledged: Manbarra and Wulgurukaba

Incorporating bleaching sensitivity through thermal history into coral bleaching prediction models

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On the Great Barrier Reef, predicting coral bleaching events has been a key component of reef conservation and management efforts. Current bleaching prediction models, although useful, continue to yield results of varying accuracies when compared to in situ bleaching observations. This has largely been attributed to the simplistic nature of these models, which focus solely on heat exposure during the summer, omitting the adaptive potential of corals and the bleaching sensitivity that varies depending on this. With thermal history being identified as the primary influencer of bleaching susceptibility, incorporating acclimatisation to heat stress as a metric is proposed as a target for improving prediction models. Using satellite-derived SST data, various pre-summer metrics speaking to acclimatisation to anomalous temperatures are developed and tested to assess the potential for their implementation into future models. The inclusion of each of these metrics were recorded to significantly increase the goodness of fit of the prediction model by an average of 2.2%. The importance of including these metrics was significant in predicting the occurrence of coral bleaching on reefs exposed to low (0-2 DHWs) and high (6+ DHWs) levels of heat stress, but not in predicting bleaching on reefs exposed to medium (2-6 DHWs) levels of heat stress. This suggests that the importance of incorporating acclimatization to heat stress in prediction models varies across different DHWs. Current and future research efforts aim to identify novel metrics that test the effect of different SST trends, temperature variability, and the speed of heating seen during the summer.

I would like to acknowledge the 70 Traditional Owners groups of the Great Barrier Reef and their leaders, past, present, and emerging, whose sea country this data were collected from. I would also like to acknowledge the Wulgurukaba people as the Traditional Owners of Yunbenun, the land on which I conduct my research.

Distribution and Function of Bacterial Aggregates Within Tissues of the Coral *Acropora loripes*

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While the diversity of coral microbiomes has been studied extensively, knowledge about their structure and ecological role within the holobiont remains scarce. Bacteria from the genus *Endozoicomonas* are well-known coral symbionts commonly found as cell-associated microbial aggregates (CAMAs) in a wide range of coral species, however, their spatial distribution and function within the coral holobiont remain largely underexplored. In this study, CAMAs associated with the common reef-building coral *Acropora loripes* were characterized to provide novel insight into their distribution and functional potential. Twelve distinct coral genotypes were obtained from two separate reef sites in the central Great Barrier Reef and 16S rRNA gene metabarcoding demonstrated that all genotypes harboured *Endozoicomonas* as their dominant bacterial symbiont. A combination of RNA hybridization chain reaction fluorescence *in situ* hybridization (HCR-FISH) and whole-mount FISH revealed bacterial clusters to be comprised of members of *Endozoicomonas* using taxon-specific probes. While no significant differences were observed in the occurrence or morphology of CAMAs between reef sites or genotypes, CAMAs were more prevalent in tissue structures found in the upper and lower gastric cavity. The ten most prevalent *Endozoicomonas* strains revealed by 16S rRNA gene metabarcoding were cultured, and high-quality genomes have been assembled. This will allow us to investigate their functional potential and develop strain-specific FISH probes to explore whether multiple *Endozoicomonas* phylotypes coexist inside a single CAMA. This work contributes to the understanding of how tissue-associated bacterial communities influence coral holobiont functioning.

I acknowledge and respect all of the Traditional Owners of Australian lands, especially recognising those on the land on which I live and work: the Wulgurukaba and Bindal people of the Magnetic Island/Townsville region.

Variation in the size structure of 6 dominant coral morpho-taxa in the Central Great Barrier Reef

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Sustained and widespread degradation of coral reef ecosystems is threatening the viability of coral populations and communities. Changes in percent cover is largely used to assess population viability, however variations in the size-frequency distribution of coral colonies would provide more nuanced ecological data especially at large spatial scales and/or for large sampling sizes. Here, we report the size structure of six dominant coral morpho-taxa at three offshore and two inshore reefs of the central region of the Great Barrier Reef. We explored the variation in size structure among depths, sites and reefs, as well as between years. Our results suggest an overall increase in colony size between 2021 and 2022 for all morpho-taxa and highlight strong differences in the size structure with marked variation among locations but not between depths. We found that the size structure of tabular *Acropora* was fundamentally different from the other taxa, suggesting that other factors such as pulse recruitment are likely modifying the size structure.

We would like to acknowledge the Wulgarukaba and Bindal people, Traditional Custodians of the land on which we meet and work, as well as the Traditional Custodians of the Great Barrier Reef whose sea country this data is collected from and pay our respects to their Elders past and present. We would like to extend that respect to the Aboriginal and Torres Strait Islanders peoples.

The coral holobiont responses to heat-stress: a multi-omics approach

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Coral reefs globally are threatened by ocean warming, as high temperatures disrupt the symbiotic relationship between corals and their dinoflagellate algae (Symbiodiniaceae). Although the interactions between host, Symbiodiniaceae and microbes are at the basis of coral thermal acclimatisation, their relationships under early heat stress are poorly understood. Here, we exposed the coral *Porites lutea* to increasing temperatures over 2 months, from 28°C to 32°C (0 – 8 Degree Heating Weeks, DHW), and assessed the stability of the host-symbiont relationship through coral host and Symbiodiniaceae transcriptomics, microbial 16S rRNA gene sequencing and physiological measurements. We observed a physiological decline in host health at > 1 DHW coupled with a shift in the microbial community composition. Specifically, a loss of bacterial Endozoicomonadaceae affiliated taxa was identified as a driver of microbial community changes, while also observing an increase in Rhodobacteraceae under high temperatures. Furthermore, reference-based transcriptomic analyses revealed changes in gene expression in Symbiodiniaceae prior to any signs of coral health decline, suggesting Symbiodiniaceae may respond earlier than the host to thermal stress. While Symbiodiniaceae response was incremental as thermal stress increased, the host showed distinct gene expression patterns depending on stress severity. Overall, our study provides new insights into the molecular processes underlying the interactions among the coral holobiont components during heat stress.

Bayesian estimation of community dynamics reveals largely individualistic dynamics in high-diverse reef fish assemblages

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Understanding biodiversity on coral reefs is crucial as millions of people's livelihoods depend on them. Reef fishes play vital roles on coral reefs, and identifying what mechanisms drive the dynamics of fish populations is critical to ensure biodiversity maintenance. Species-to-species and species-to-environment interactions are considered key drivers of community dynamics. However, disentangling these drivers in species-rich assemblages, like coral reefs, is challenging due to the high number of potential interacting species. To address this issue, we developed a process-based model that can quantify how intra-specific competition, interspecific interactions, and species' covarying responses to environmental fluctuations jointly drive temporal community dynamics. To reduce the dimensionality of the model we implemented a factor analysis approach and a shrinkage prior within a Bayesian framework. Here, we fitted the model to time series of abundances on 41 reefs of the Great Barrier Reef. We found that most reef fish species are, on average, weakly positively correlated in their responses to environmental fluctuations, with considerable variability in the magnitude of species pairwise correlations. However, interspecific interactions are negligible, whereas intraspecific interactions are strongly density dependent. Among species, there are strong, detectable differences in both overall average and magnitude of temporal fluctuations in intrinsic growth rates, as well as intraspecific density dependence; however, within species, there is no detectable among-reef variation in these parameters in the model. These findings reveal largely individualistic species dynamics, and strong geographically consistent niche structure in reef fish communities, on the Great Barrier Reef.

Traditional Owners to be acknowledged: Wulgurukaba and Bindal people and the traditional custodians of the Great barrier Reef

Improved microplastic processing from complex biological samples using customized vacuum filtration apparatus

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Plastics, the majority of which are non-biodegradable in nature, represent the largest component of marine debris globally. In this context, it is important to understand the current extent of plastic pollution in marine environments and within biota. Despite the many approaches reported in the scientific literature to extract plastics from marine samples, field studies still face methodological impediments to establishing accurate and standardized protocols to process and analyse microplastic items (i.e. < 5 mm). Presented here is a custom-made stainless-steel vacuum filtration apparatus designed to perform tiered separation of MPs from a variety of environmental sample matrices. Incorporating this apparatus into a standard MP workflow achieved efficient graduated separation of commonly found MP fragments and fibres, validated by spike-recovery tests. As a case study, the gastrointestinal tracts of three juvenile Australian sharpnose sharks, *Rhizoprionodon taylori*, were processed using the filtration apparatus, and 46 anthropogenic items ranging from 0.021 mm to 8.87 mm were retrieved. This study demonstrates the effective use of the tiered stainless-steel vacuum filtration apparatus and improved efficiency in downstream microphotography and spectroscopic analyses of MPs from a complex sample matrix. Finally, it contributes to the MP research field by delivering more reliable estimates of MP contamination in marine ecosystems.

Coral Reef Microbial Observation: Moving Towards Predictive Ecosystem Monitoring

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Marine microorganisms underpin the health and function of coral reefs and are sensitive to environmental changes that affect ecosystem stability. This rapid response of microbes to environmental perturbations can provide a robust indicator of reef health. While certain microbial taxa persistently associate with degraded reefs (e.g. increased temperature, nutrients, and macroalgae cover), a major limitation in using microbes to report on coral health is that we have an incomplete understanding of how environmental change affects microbial community structure, and how changes in microbial functions may translate to changes in reef ecosystem services. The functions of free-living (seawater and sediment) reef microbes are poorly characterised, though recent studies suggest free-living microbes have a higher diagnostic potential to predict temperature and eutrophication states in the reef compared to host-associated microbiomes. Through positive feedback mechanisms and cascading effects, changes in functioning of free-living reef microbes may drive benthic organisms towards the limit of their resilience and translate into shifts in biogeochemical cycles and marine food webs, ultimately affecting entire reef ecosystems. Current research has largely focused on changes in microbial community profiles (taxonomy) for (1) ‘early detection’ of changes in the environment. Here, we highlight that incorporating information on microbial function (via genetic analysis) in reef monitoring may (2) ‘substitute’ environmental measurements that are absent; and (3) ‘predict’ how altered microbial activity can affect the functioning of reef ecosystems. Microbial observation of free-living reef microbes (using functional -omics) would complement current reef monitoring programs, moving from ‘descriptive’ to ‘predictive’ science and from reactive to proactive reef management.

Functional signatures of seawater microbes show increased stress response in degraded reefs

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Coral reefs are impacted by both local and global human-induced stressors. To understand/quantify how environmental impacts correlate to changes in reef communities, long-term monitoring is a necessity. Most reef monitoring programs implement visual surveys (i.e. coral cover, bleaching or disease assessments), however, visual cues become evident at a point when ecosystem change may be irreversible and management interventions are reactive. Marine microbial communities respond rapidly to environmental shifts and represent a potential early warning indicator of ecosystem stress. Here we detail how seawater microbes can be used in reef monitoring, through collection of seawater at 48 sites across the GBR for metagenomic sequencing, paired with *in situ* reef health survey data. Seawater microbial taxonomic/functional signatures were directly correlated with environmental data on benthic cover and water quality to identify microbial indicators of degraded reef health. Our results indicate that traditionally characterised opportunistic/potentially pathogenic microbes (e.g. *Flavobacteriaceae*, *Cryomorphaceae* and *Rhodobacteraceae*) and functions (motility elements, response to stress, virulence factors) are enriched in reefs with elevated temperature and nutrient loads, as well as reef sites where coral bleaching and disease were observed. While both microbial taxonomic and functional information provide a robust indicator of coral reef health status, multivariate linear regression-based modelling identified that functional information is a more stable predictor of coral health compared to taxonomy. Our results demonstrate the potential of reef seawater microbes to inform reef health status, and that microbial function may be more informative for reef monitoring purposes compared to microbial taxonomy.

Bisphenol A (BPA) leachate from polystyrene microplastics has species-specific impacts on scleractinian corals

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Improper disposal of plastic waste has caused pervasive environmental contamination, including coral reef ecosystems on a global scale. This study aimed to determine the toxicity of polystyrene (PS) microplastics and associated bisphenol A (BPA) leachate to the framework-building corals, *Pocillopora damicornis* and *Dipsastraea pallida*. Intermittent exposure over 14-days to plain PS and PS with BPA which was 'pre-leached' had minimal effect on corals, however, BPA leachate had negative effects on the tissue composition of *P. damicornis* fragments (i.e., decreased chlorophyll a content, *Symbiodiniaceae* density and total protein content compared to controls), as well as decreases in photosynthetic yield (F_v/F_m). Conversely, BPA leachate did not compromise health of *D. pallida* fragments. These results reveal that exposure to chemicals leaching out of microplastics can be a major driver of the negative effects of microplastic exposure rather than physical mechanisms due to ingestion, and that there is variability in the response of different taxa to chemical additives. Further studies are therefore required to determine if toxic effects are observed in other coral species, and if toxicity varies among polymer and chemical additive type at environmentally relevant concentrations.

The authors would like to acknowledge the Traditional Owners of the lands on which research has been conducted, specifically the Manbarra people of Goolboddi Island and the Bindal people of the Birrigubba nation.

Does hosting a specific species of Symbiodiniaceae enhance coral growth & DMSP concentration?

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Coral is one of the largest producers of dimethylsulfoniopropionate (DMSP) with most derived from the endosymbiotic Symbiodiniaceae within the tissues, though the coral animal is also able to produce DMSP. DMSP and its breakdown products dimethyl sulphide and acrylate have important ecological function in global sulphur cycling. High levels of DMSP and acrylate are present in fast growing Acroporids while low or undetectable levels are found in slower growing non-Acroporid species. These compounds are hypothesised to be critical in rapid skeleton formation. Here I investigate if DMSP has an additional function in the coral calcification process, through measuring DMSP concentration within newly settle coral juvenile tissue with and without symbionts. Hence, if higher DMSP concentration would correlate to faster coral growth. This study will provide crucial information on potential factor that may affect coral recruit growth in their highest mortality life stage.

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Rachel Neil

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