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ABSTRACTS

How does salinity affect growth, lipid and pigment composition of Australian *Botryococcus braunii*?

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The unusual green alga *Botryococcus braunii* is of great interest for renewable fuels as it produces abundant hydrocarbons that have the potential for a 'drop-in' fuel. However, *Botryococcus* grows slowly in culture, severely limiting its potential for development as a bioresource. Undertaking a biodiscovery program we found *Botryococcus* in locations from tropical to temperate Australia in both freshwaters and brackish waters. As part of characterisation of this new biodiversity and to investigate factors affecting growth, the effects of salinity on growth, lipid and pigment compositions were studied on six strains from 6 different locations. The strains were inoculated into either fresh-water based medium or saline medium (salinity of 4) and maintained over 150 days. Growth of cultures was studied continuously while lipid and pigment composition were analysed at final harvest at day 150. Some strains were more tolerable of saline conditions than others, with a link between salinity tolerance and original location. The strain originating from a coastal lagoon (<300m from coastline) grew to higher densities in saline medium than strains from the freshwater locations. However, growth rates of <0.23 div day⁻¹ were similar in both fresh and saline media. Salinity had a minimal effect on lipid composition, with only one of the six strains showing a different hydrocarbon profile in comparison the other strains. While pigment composition showed only minor variations between fresh and saline cultures, the concentrations varied significantly, with the fresh cultures showing higher levels of pigment concentrations in comparison to the saline cultures.

Diatom distributions delineated by lipid, genomic and microscopic observations between the Sabrina Coast and Antarctica

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In 2014 the RVIB *Nathaniel B. Palmer* was used to undertake a US-led voyage focused on a geological and oceanographic survey of the George V and Sabrina coastlines with respect to the history of the East Antarctic glacial ice drainage basins (NBP14-02). During this voyage biological survey work was undertaken to broaden methodological applications of the phytoplankton community beyond microscopic observations in an attempt to help with providing ground-truth data for both modern biological distributions and palaeo-oceanographic interpretations. Surface water, sampled and concentrated from the ship's intake line, was filtered for algal lipid (isoprenoid) and genomic analysis. Preliminary results from all three applications are presented and considered against sea-ice cover.

Patterns of diatom activity in coastal Australian waters using the fluorescent probe PDMPO

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Coastal waters tend to be dominated by microscopic phytoplankton known as diatoms who contribute approximately one-fifth of photosynthesis on Earth. Diatom cell walls (frustules) are comprised of hydrated silica, which form mineral ballast and affect cell sinking rate. Changes in frustule silicification due to environmental factors may alter the biological carbon pump by changing current rates of diatom-mediated carbon sequestration. We can measure diatom silicification using the fluorescent probe, PDMPO and can use the incorporation of this stain as a proxy of diatom activity. In this study, we use this stain to measure diatom activity in coastal Australian waters; extending from the warmer oligotrophic waters of the Aegean and Coral Seas to the colder nutrient rich waters off Sydney, NSW. We then relate these changes in diatom activity to physiochemical parameters such as temperature, salinity and nutrient concentration.

Thermal performance curves reveal alternative energy pathways at stressful temperatures: a multi-trait analysis of phenotypic plasticity in *Thalassiosira pseudonana*

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Temperature drives algal function at levels of organisation from molecules to ecosystems. Understanding the underlying mechanisms influencing function will enable better prediction of responses to contemporary environmental change. Thermal performance curves (TPCs) quantitatively describe the relationship between biological rate processes (e.g. growth) and temperature. There has been a renewed interest in TPCs because of their success in predicting population or species-specific responses and the potential incorporation of empirical temperature-dependent relationships into mechanistic models. For the first time, we present a multi-trait analysis of thermal sensitivity in the cosmopolitan diatom *Thalassiosira pseudonana* and demonstrate the activation of alternative energy allocation under sub/supra

optimal temperatures. *T. pseudonana* was exposed to a range of temperatures between 11 and 34°C where multiple traits describing fitness and biogeochemical function were measured. We found that the optimum temperature for growth was ~19 °C (0.8 d⁻¹) different from that of carbon fixation (~20 °C) and silicification (~16.5 °C). Growth was impaired by approximately 50% at hot and cold extremes, suggesting similar magnitudes of stress but with different photophysiological implications. Our study increases our understanding of the trade-offs between different biogeochemical functions under thermal stress by demonstrating that the thermal optima for phytoplankton traits can differ from the whole organism response. We advocate for the incorporation of performance curves into contemporary evolution experiments, to explore adaptation mechanisms in order to be able to further understand the constraints on how phytoplankton will respond to long-term ocean change.

Development of a microsatellite library for *Hormosira banksii* and examination of the appropriate spatial scale in which to sample for population genetics studies

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In recent years there has been a dramatic increase in the number of studies that are using molecular approaches to address ecological questions, such as those related to connectivity and dispersal dynamics, biodiversity, resilience and adaptation. Whilst the application of molecular techniques to phycology has been hampered by difficulties in extracting good quality DNA from polysaccharide-laden algal tissues, progress is now being made through technological advances. The intertidal fucoid *Hormosira banksii* has been a particularly challenging species to develop a reliable microsatellite analysis for but we have finally succeeded! Where dispersal is potentially very limited or life histories are such that clonality might be prevalent, population genetic studies may benefit from an understanding of the spatial scales at which clonality or relatedness breakdown. In this presentation will highlight some of the difficulties in molecular analysis of *H. banksii*, the lessons learnt and present data that should guide the appropriate spatial scale at which to sampling for population genetics studies of *H. banksii*, and inform a sampling approach for other taxa.

The Australian National Algae Culture Collection: Research and development for microalgae for bioenergy and bioresources

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Microalgae as a resource for bioenergy and bioresources continues to be of great interest, with the recognition that bioproducts and other applications need to be developed in parallel along with development of renewable fuels, due to the economics of algal production not matching the commodity pricing needed for fuels. CSIRO holds the Australian National Algae Culture Collection, ANACC, as one of CSIRO's National Research Collections. Over 50 years of development and research in ANACC provides a strong knowledge base on Australian microalgal diversity to inform decisions on target microalgae for different bioapplications. For 30 years ANACC has underpinned the aquaculture industry nationally, and supplied 70 countries globally, where microalgae are used as a feed for many juvenile and larval aquaculture animals. The more recent interest in algae as a source for biofuels promoted lipid screening of ANACC microalgae – genera, species, strains – for lipid composition. These data, along with growth and other physiological information, is sought by industry aiming to develop oil-based applications for microalgal production in Australia. As well, new biodiscovery for potential biofuel species has utilised ecosystem knowledge and historical records in seeking strains of high lipid producing microalgae such as the hydrocarbon producing green alga *Botryococcus braunii*, as well as microalgae that can grow in wastewaters, offering both bioremediation and also bioproducts potential. Growth strategies include both photosynthetic (autotrophic) and heterotrophic approaches. In addition engineered microalgae for production of particular compounds, and suitable growth technologies in which to grow such modified microalgae are part of CSIRO's current R&D.

Strain variation in the green alga, *Haematococcus pluvialis*

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The freshwater green alga, *Haematococcus pluvialis* is well known to accumulate high concentrations of the ketocarotenoid astaxanthin, especially in the aplanospore stage. *H. pluvialis* can be grown photoautotrophically, mixotrophically and heterotrophically. In culture the alga goes through part of the life cycle changing from a fragile motile flagellate to a thick-walled, non-motile, astaxanthin-containing, aplanospore. As part of a large scale screening programme strains of *H. pluvialis* from culture collections as well as newly isolated strains from around the world were grown in several media under a range of culture conditions to assess the variation in growth pattern (i.e. cell types), growth rates and carotenoid content. The variation between strains was much greater than that observed in any other species of algae. We observed very large differences between the strains in their carotenogenic capacity, their ability to use acetate as an organic carbon source and in their growth rates. For example, in mixotrophic growth the optimum concentration of acetate for growth and carotenogenesis ranged from 0.5% (w/v) to 2%, and the cell astaxanthin content ranges from 0.7 to 4.25% of dry weight, depending on the strain. Unlike other carotenogenic green algae such as *Dunaliella salina*, very significant improvements in biomass and carotenoid (astaxanthin) productivity can be achieved the strain selection in *H. pluvialis*. The

reasons for this high physiological diversity are not known, but this strain variation is important for commercial exploitation of this alga and is also an interesting future research topic.

Physiological diagnosis of phytoplankton responses to future complex ocean conditions

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A changing climate is altering many ocean properties that consequently will modify marine productivity. Prior phytoplankton manipulation studies have focussed on individual or subsets of these properties. Here, we investigate the cumulative effects of multi-faceted change on a subantarctic diatom *Pseudonitzschia multiseries* by concurrently manipulating five stressors (light/nutrients/CO₂/temperature/iron) that primarily control its physiology, and explore underlying reasons for altered physiological performance. Climate-change enhances diatom growth mainly due to warming and iron-enrichment, and both properties decrease cellular nutrient quotas partially offsetting any effects of decreased nutrient supply by 2100. Physiological diagnostics and comparative proteomics demonstrate the joint importance of individual and interactive effects of temperature and iron, and reveal biased future predictions from experimental outcomes when only a subset of multi-stressors is considered. Our findings for subantarctic waters illustrate how composite regional studies are needed to provide accurate global projections of future shifts in productivity and distinguish underlying species-specific physiological mechanisms.

Codium fragile: defining subspecies using tufA DNA analysis and morphology

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Codium fragile subsp. *fragile* has been referred to as an invasive, cryptic, or cryptogenic species in many parts of the world. It is definitely present in Victorian waters, but is difficult to identify correctly in the field. This is due to the presence of two local, morphologically similar, subspecies: subsp. *tasmanicum* and subsp. *novae-zelandiae*. The correct identification of all the subspecies may also be obscured by the influence of environmental conditions on morphology. We use *tufA* DNA sequences of *C. fragile* samples from Australian and worldwide collections to examine the boundaries between potential subspecies and relate these boundaries to morphological measurements. Our data indicate that the native

local subspecies is clearly distinct from the invasive one based on DNA, and that this boundary correlates with morphological and ecological features. In fact, the boundary is large enough to consider the possibility that the invasive *C. fragile* subsp. *fragile* is a separate species from our local Australian lineage. We are now looking into the possibilities for defining ‘spotting characters’ for field identification, or it may be that only DNA can differentiate between the entities with confidence.

Data, Data Everywhere – How to access phytoplankton taxonomic and pigment composition data for the Australian region

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For decades phytoplankton taxonomic observations have been recorded in Australian waters and in more recent times (past 20-25 years) phytoplankton pigment composition has also been recorded. Both types of observations are complimentary; the taxonomic observations are microscopic identification to species level, while the pigment composition is used to estimate phytoplankton community composition to class level. Pigments which relate specifically to an algal class are termed marker or diagnostic pigments and the presence or absence of these diagnostic pigments can provide a simple guide to the composition of a phytoplankton community, including identifying classes of small flagellates that cannot be determined by light microscopy techniques. Until recently both types of observations have not been generally available to anyone other than the scientists who were responsible for their collection. Small, individual datasets alone may have a great localised impact, but when collated can provide valuable additions to large scale spatial and temporal studies. The recent development of several databases has now made these data publicly available, allowing scientists to study regional differences within the Australian environment as well as the impact of changes in environmental parameters on the taxon within a specific region. The presentation will discuss the databases and how to access them.

Phylogenomics of the red algal order Nemaliales

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The order Nemaliales is part of the highly diverse red algae subclass Nemaliophycidae that is believed to be the oldest group in the Florideophyceae. Distributed from subantarctic to all tropical seas it comprises both calcified (in most genera of the Liagoraceae *sensu lato* and the Galaxauraceae) and uncalcified (Scinaiceae) taxa. These characteristics make it a great model to study evolutionary dynamics. Despite significant improvements in the higher-level systematics, and the proposal of several new genera and families in recent years based on analyses of morphology and one or two genes, the phylogenetic relationships among families

and genera are not fully resolved. We have approached the inter-generic and familial relationships with high-throughput sequencing of organelle genomes. Using Illumina technology we assembled the chloroplast genome of representatives belonging to 19 genera of the Nemaliales, and extracted >190 genes concatenated in a >49k aminoacid alignment. Our results show a highly conserved plastid genome across families with an identical composition and architecture and our ML phylogeny recovered a fully resolved tree with very high bootstrap values at all nodes. The data shows that Liagoraceae *sensu lato* is a monophyletic group and that the exclusively calcified Galaxauraceae family is more closely related to the exclusively uncalcified Scinaiceae than to the Liagoraceae *sensu lato*. I will present new insight into the evolution of the Nemaliales and explore their radiation on the light of earth history.

Taxonomic revision of *Halimeda* in southwestern Australia

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Halimeda Lamouroux is a tropical green algal genus that is an important component of reef and lagoons. While the genus does not generally occur outside the tropics, one species (*Halimeda cuneata* Hering) is known to extend southwards along the west coast, around Cape Leewin and on to the south coast of Western Australia. Previous molecular study revealed that this particular species exhibit pseudo-cryptic species diversity and most of the cryptic entities are geographically isolated from others. In Western Australia, *H. cuneata* is the name applied to specimens from southwestern Australia, where it reaches its eastern limit at the Recherche Archipelago. Field observations indicated that there might be two forms of *Halimeda* in the region. Using a combination of morphological observations and assessment of species boundaries based on a plastid gene (*tufA*) and a nuclear protein-coding gene (HSP90), we reassess the diversity of *H. cuneata* in the region. We show the existence of two different species of *Halimeda* in the region, confirming the field observations. We describe *H. gigas* Taylor as one of the two *Halimeda* species found in the region and we reinstate *H. versatilis* Agardh for those species previously identified as *H. cuneata* in southwestern Australia. Morphological similarities and differences between the two species of *Halimeda* in southwestern Australia are discussed as well as how they compare to the type specimens.

Developing seaweed production techniques for integrated multi-trophic aquaculture in Port Phillip Bay, Victoria

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Seaweeds have complex life cycles but with significant variations amongst different taxonomic groups. Because of the sheer diversity of southern Australian seaweeds, the life history dynamics are poorly understood for many species of potential commercial value. There are many factors that can affect the yield and quality of seaweeds grown in aquaculture, including Integrated Multi-Trophic Systems (IMTA). For example stocking densities have been shown to affect biomass production through competition for light and nutrients and alterations to flow. Similarly natural nutrient, light and mixing environments can influence the growth of seaweeds, such that some locations may be more conducive to high sustainable yield/ quantity seaweed production than others. Other studies have shown differences in the nutritional value of seaweeds in aquaculture compared to the same species from wild harvest, with a variety of contributing factors identified. IMTA systems are ideally designed to approach stability for sustainable yields of co-cultured crops, but interactions amongst different elements in the system can disrupt balance. Thus in order to maximize sustainable yields and nutritional quality of seaweeds in aquaculture it is essential to identify (through carefully designed experiments) the ideal growth conditions and any factors that may adversely affect production at all stages of the life cycle. This presentation will outline what I endeavor to complete throughout my PhD, which includes 1) the expansion of sustainable aquaculture in southern Australia through the development of commercial endemic seaweed production, and 2) provision of knowledge for farmers to diversify and expand current business and boost economic productivity.

Comparative performance of different immunological kits for paralytic shellfish toxin testing in Australian shellfish

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Algal blooms producing paralytic shellfish toxins (PST) are mainly caused by the dinoflagellates *Gymnodinium catenatum* and *Alexandrium* sp. in Australia. These algal strains differ from the Northern Hemisphere strains in the production of different PST analogues, including GTX1,4, GTX2,3 and C1,C2. Four brands of PST detection kits (Abraxis™, Europroxima™, Neogen™ and Scotia™) possess different cross-reactivity for each toxin analogue, and their suitability for PST testing in Australian shellfish was compared. The two ELISA kits Abraxis and Europroxima did not perform well as they underestimated the toxin levels by 3 and 7 times, respectively, in shellfish samples. These ELISA kits are microplate-based and laboratory experience is essential, user error can be high and they are time-consuming. The Scotia kit showed good detection for GTX2,3, however, the detection range is between 0.2 and 0.7 mg/kg, which may give false non-compliance positives at 0.2 mg/kg which is four times lower than the regulatory limit and still safe for human consumption. This kit possesses low reactivity for GTX1,4 (1.8%), which can be increased with an extra hydrolysis conversion step (to 26%), that also adds 1 hr to the protocol (total of 1 hr 35 min). However, spiked samples with GTX1,4 (at ~0.7 mg STXeq/kg) gave false negatives after performing the extra step. The Neogen test was the best kit because of its high sensitivity and ease of use. Although it has low reactivity for GTX1,4, this was overcome by performing an extra hydrolysis step to convert it to neosaxitoxin, which has very high sensitivity and is

easily detected. Performance of the Neogen test kits during the July-Sept 2015 *Alexandrium* bloom event and resulting shellfish farm closures is discussed.

Applications and implications of macrophytes for biomonitoring: A case study of the Derwent estuary, Tasmania

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Understanding the differences in metals uptake by macrophytes is important in designing biomonitoring programs. This investigation determined spatial and temporal changes in heavy metal load in different species of macrophytes from an impacted estuarine system (Derwent Estuary) and used this information to identify potential bioindicators of metal pollution. This study compared the pro and cons of macrophytes as bioindicators of metal pollution, with respect to their application and implications for biomonitoring. *Ulva* sp. was found to be widely distributed within the middle and lower estuary, and showed a clear spatial gradient of metal concentration throughout the study area. While, there were other species, which also appeared to reflect the gradient of metals in the system, *Ulva* sp. was the only species that was ubiquitous throughout the middle-lower estuary. This perennial species was selected for further study as i) it can give information on the pollution status in the area at a given point in time (i.e. a contamination snapshot), and ii) can be used to compare conditions across the estuary. Consequently it is suggested as a suitable bioindicator for metal pollution. In the upper estuary seagrasses were identified as potential indicators as they too concentrated high levels of metals in their tissues. However, this group of macrophytes differs from *Ulva* sp. as they provide a longer-term integrated picture of metal availability. The advantage of some species and the disadvantages of other species are compared to provide a comprehensive overview of the potential to use macrophytes as bioindicators of metal pollution.

Fine-tuning transmission electron microscopy methods to evaluate the cellular architecture of Ulvales

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To analyse changes in the ultrastructure of seaweeds chemical fixation is a critical step; the wrong approach can compromise the ability to distinguish fine-scale cellular composition. Fixation agents, fixation time and type of tissue are important factors to consider for transmission electron microscopy (TEM), and not every protocol will suit all types of cells.

To determine a TEM protocol for Ulvales, we evaluated a range of fixation agents, post-fixation time and dehydration solutions. We assessed *Ulva lactuca* under 5 protocols 1) Fixation in glutaraldehyde + 0.1M buffer (4 hr). Overnight treatment in osmium tetroxide and then dehydration with ethanol; 2) Glutaraldehyde + 0.1M buffer overnight prior to treatment 8h in osmium tetroxide followed by ethanol dehydration; 3) Glutaraldehyde + 0.05M buffer + Paraformaldehyde (4 h), followed by overnight treatment in osmium tetroxide and dehydration in ethanol; 4) Glutaraldehyde + 0.05M buffer overnight then treatment in osmium tetroxide for 8 hr, before dehydration in ethanol; 5) Glutaraldehyde + 0.1M buffer + Sucrose overnight before 4 h in osmium tetroxide and dehydration in acetone. The preservation obtained using these fixation methods differed markedly. The best result was obtained with fixation option 4 (Fixative - Glutaraldehyde, buffer and paraformaldehyde). This formula, glutaraldehyde (2.5%), buffer and paraformaldehyde, ensured that the membranes, especially the thylakoid membranes of chloroplasts, remained intact. The use of acetone for dehydration resulted in the collapse of membranes so ethanol is recommended for dehydration. This new protocol will ensure the ultrastructures of Ulvales can be clearly ascertained in the future.

Effect of nitrogen source on nutrient uptake and pH change at the surface of *Macrocystis pyrifera* blades

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Inorganic nitrogen (Ni) availability plays an important role in the productivity of ecosystems and in the physiology of marine algae. The most common sources of Ni to algae are NO_3^- and NH_4^+ . The transport of nutrients from the bulk seawater to the seaweed blade surface occurs across the diffusion boundary layer (DBL). Therefore, the DBL plays an important role in the flux of ions and molecules (e.g. C: CO_2 ; HCO_3^- or N: NO_3^- ; NH_4^+) to/from the thallus surface. Under slow flow (thicker DBL) the chemistry of seawater near to thallus surface could be influenced by the different charges of ions due to the efflux of dissolved metabolic materials, which may modify the pH within the DBL. Physiological processes such as photosynthesis and NO_3^- uptake could increase the pH within of the DBL whereas respiration and NH_4^+ uptake could reduce it. In this study, we hypothesized that (1) NO_3^- uptake will increase the pH within of the DBL under slow flow conditions whereas NH_4^+ uptake will decrease it, (2) under a low pH simulating ocean acidification (OA, pH=7.6) the pH will be more affected than under today's seawater pH (pH=8.1) due to a higher nutrient uptake and photosynthetic rate. After a short nutrient uptake experiment (75 min) there was no significant effect of Ni source on the pH within the DBL, with pH increasing for both nutrient sources (NO_3^- and NH_4^+). However, the change in pH (ΔH^+) within the DBL was always higher under OA conditions than at pH 8.1. NH_4^+ uptake was significantly higher under OA conditions. Overall, carbon acquisition was significantly affected by pH treatment but not by Ni source. CO_2 - consumption was higher at pH 7.65 than at pH 8.1 whereas HCO_3^- consumption was the same under both pH treatments. Our findings suggest that the main

changes in pH within the DBL are due to photosynthesis rather than nitrogen uptake. The increased availability of CO₂ at pH 7.65 could stimulate NH₄⁺ assimilation to support higher photosynthetic rate under OA.

The energy allocation principle in marine macroalgae: Estimating the physiological cost of reproduction in the seaweed *Gracilaria chilensis*

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The extent of changes in basic physiological and demographic traits associated with reproduction was investigated in the highly cultivated haploid–diploid red alga, *Gracilaria chilensis*. Sixty individuals bearing vegetative and reproductive fronds collected in the natural population in Chile (39°52'S, 73°23' W), were cultivated under controlled culture conditions. Our results demonstrated that vegetative fronds have a higher survival rate and a better growth rate than reproductive ones irrespective of the type of individual analysed (male gametophyte, female gametophyte, and tetrasporophyte). Moreover, the reproductive fronds clearly showed a decrease in photosynthetic activity compared to non-reproductive ones. In males and tetrasporophytes, the photosynthetic reduction in reproductive individuals could be explained by a physical effect of reproductive structure development as well as spores release, disrupting the continuity of the photosynthetic cortical tissues. Translocation of photoassimilates from nearby vegetative tissue or the previous accumulation of photosynthetic products seems to be a prerequisite for reproductive structure development in this species. Altogether, these results document for the first time in *G. chilensis* that reproduction has a strong physiological effect on male, female, and tetrasporophyte fronds. This trade-off between reproduction, growth, and survival suggest the existence of reproductive costs in the life history of *G. chilensis*.

The potential ecological impacts of some newly described true fungal and fungal like parasites on the composition of phytoplankton, invertebrate and vertebrate populations in marine food webs

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Recently, a large number of species of newly discovered fungal, fungal-like and protozoan microbes have emerged as important contributors to marine food webs. Some of these species are highly infective, have short generation times, can cause rapid declines in host population sizes and can significantly change the species composition of aquatic ecosystems. Frequently, several species of parasites simultaneously infect populations of the same host species in the same or in different parts of their life cycles, and many parasites have broad host specificity. Despite increasingly sophisticated microbiological techniques, the basic knowledge to fully appreciate the ecological importance of microbial parasites is lacking. In this presentation,

fungus and fungus-like parasites of some cyanobacterial, diatom, dinoflagellate, invertebrate and vertebrate hosts in marine ecosystems will be considered. In particular the *Ichthyodinim* and parasites which attack eggs and larvae of fin fish in the ichthyoplankton and *Hematodinium* parasites of shellfish will be described. Many of these parasites have been recognized as agents of emerging infectious diseases. The possible ecological, economic and social impacts of introduction into new ecosystems, habitat destruction, and global climate change on the prevalence of these parasites will be considered.

Symbiotic associations in Australian tropical marine microplankton

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Symbiotic associations between various groups of protists have played a critical role in the evolution of marine microplankton biodiversity. Dinoflagellates have been the most successful in engaging in numerous associations with cyanobacteria, cryptomonads, chrysophytes, pelagophytes, haptophytes, diatoms and chlorophytes. In the 1980s-1990s the phylogenetic identity of these symbionts was partially resolved by transmission electron microscopy of pipette-picked cells, but in the 2000s numerous definitive molecular sequences have become available. Non-photosynthetic dinophysoid dinoflagellates of the genera *Histioneis*, *Ornithocercus*, *Citharistes* exhibit elaborate sulcal and cingular list modifications that support extracellular cyanobacterial consortia of 4 genotypes of *Synechococcus* and *Prochlorococcus* as a means of sustenance in oligotrophic tropical oceans. The dinoflagellate genus *Amphisolenia* contains intracellular pelagophyte symbionts and *Dinophysis miles* can contain up to three different types of plastids of cryptophyte, haptophyte and cyanobacterial origin. Diatoms have explored symbioses to a much lesser extent, with the best known the *Rhizosolenia clevei*-*Richelia intracellularis* diatom-cyanobacterial association. We recently examined in detail from Moreton Bay the unique association between the large diatom *Palmerina ostenfeldii* and the epiphytic ciliate *Vaginicola* attached in a host-specific subapical fold of the diatom cell wall. Observations on living diatom-ciliate associations suggests that rotational movement of the large discoid diatom cells driven by the ciliates may enhance exposure of chloroplasts to light and promote diffusive uptake of nutrients. Much of this ecophysiological information would be lost working with preserved samples, or misinterpreted working with pigment proxies or molecular approaches when not supported by careful microscopy.

Invisible Indicators for determining nutrient response (Impact) in coastal macroalgal reefs – Implications for spatial ecosystem-based management

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Location-specific physical variations and underpinning macroalgae ecophysiology are crucial in determining the extent of impacts associated with nutrient loads in coastal habitats. The interactions between these factors can determine the capacity of coastal systems to cope with nutrient inputs. This study examined the extent to which a set of prevailing environmental factors within a sheltered water body can modulate susceptibility/resistance of reefs to additional nutrient impacts and used the findings to discuss potential management implications for human-induced nutrient sources in the coastal environment. The influence of nutrient loads on macroalgal ecology and physiology was experimentally evaluated at three reefs with different prevailing environmental conditions. Baseline light, salinity, temperature and nutrients were evaluated *in situ*, while wave exposure was quantified using a wave-fetch model. The influence of increased nutrient loading was examined by manipulation of nutrient through the addition of a slow-release fertilizer to experimental plots within these reefs. Increasing exposure saw a gradual change in the dominant macroalgal community from one characterised by Caulerpales/Fucoids/Laminariales to one where Fucoids/Encrusting algae were the characterising taxa. Habitat-specific variations in physical drivers as wave exposure and light modulated not only the abundance of opportunistic species but also the nutrient composition of several key habitat-forming macroalgae (i.e., *Sargassum fallax*, *Ecklonia radiata*), and this were also evident where nutrients were enhanced. Although the set of abiotic factors influenced the macroalgal community, wave climate was an important driver of both ecological and physiological responses and as such needs to be considered when assessing the impact response of the reef systems. Understanding the spatial-temporal variations of prevailing physical factors (e.g., wave exposure, light) can provide insightful information on the responses of macroalgal communities to changes in nutrient availability and may be critical for assessing reef susceptibility/resilience. This should be a key element in ecosystem modelling and coastal planning.

Tasmanian seaweed communities have an unusually high proportion of CO₂-only users: implications for ocean acidification

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Productivity of most marine macroalgae is not currently considered limited by dissolved inorganic carbon (DIC), as the majority of species have CO₂-concentrating mechanisms (CCM) allowing the active uptake of DIC. The alternative, diffusive uptake of CO₂ (non-CCM), is considered rare (0–9 % of all macroalgal cover in a given ecosystem). CCM activity has higher energetic requirements than diffusive CO₂ uptake, therefore when light is low, CCM activity is reduced in favour of diffusive CO₂ uptake. We hypothesized that (1) the proportional cover of macroalgae without CCMs (red and green macroalgae) would be low (<10 %) across four sites in Tasmania, southern Australia, at two depths (4–5 and 12–14 m); (2) the proportion of species lacking CCMs would increase with decreasing depth and (3) the $\delta^{13}\text{C}$ values of macroalgae with CCMs would be more depleted with depth. We found the proportion of non-CCM species ranged from 0 to 90 % and included species from all three macroalgal phyla: 81 % of red (59 species), 14 % of brown (three species) and 29 % of green macroalgae (two species). The proportion of non-CCM species increased with depth at three of four sites. 35 % of species tested had significantly depleted $\delta^{13}\text{C}$ values at deeper depths.

Non- CCM macroalgae are more abundant in some temperate reefs than previously thought. Ocean acidification is predicted to ‘benefit’ non-CCM species and so the ramifications for subtidal macroalgal assemblages dominated non-CCM species, such as those in Tasmania, could be larger than previously considered.

Taxonomy and bioinformatics at the Australian National Algae Culture Collection ANACC

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Growing out of a small bio-oceanographic project in the mid 1960’s, the Australian National Algae Culture Collection, ANACC has evolved to be a significant bio-resource centre for living microalgae, supporting projects within CSIRO and more broadly nationally and internationally through research collaborations and via the Australian National Algae Supply Service, ANASS. Our recent studies on the taxonomy and biogeography (morphology + 18S and rbcL) of the marine coccoid eustigmatophyte *Nannochloropsis*, of great interest in microalgal bioapplications, will be made. This includes identification of a novel Tasmanian sourced species, *N. australis* and the proposition of a new genus, *Microchloropsis* for the existing species *N. gaditana* and *N. salina*. A similar taxonomic perspective on an Australia wide collection of freshwater *Botryococcus braunii* will be made. An initiative made possible by CSIRO’s National Research Collections Australia (NRCA) in mid 2015 saw the commencement of an intensive genomic survey of 800 ANACC strains (95% DNA extracted) with an analysis of 18S, 28S, ITS, COI and rbcL amplicons. Microbial metabarcoding of algal and cyanobacteria strains was undertaken as a basis for typification of algal-bacterial interactions and confirmation/rejection of nominally axenic strains. Several genera were selected for variable marker development using Single Nucleotide Polymorphisms (SNP) for future population genetics. ANACC shares challenges experienced by most living collections in striving to maintain and expand existing resources and incorporate the growth in bioinformatics stemming from multiple lines of strain characterisation. Integration of such varied project data combined with regulatory compliance into the ANACC database is being used within CSIRO as a fundamental project based tool. <http://www.csiro.au/ANACC>.

Phase shift from kelp bed to turfing algae represents alternative stable states with hysteresis, and the risk of transition increases with multiple stressors

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The transition from kelp-beds to turfing algae on shallow temperate reefs is increasingly reported around the globe, and represents a significant loss of biodiversity and ecosystem services. Effective management of this issue requires knowledge of: (1) whether the shift is continuous in response to a changing environment or instead represents a discontinuous shift with hysteresis so that either state can persist under identical environmental conditions; (2) whether anthropogenic stressors influence the likelihood of the shift from a kelp- to turf-dominated state; and (3) if the shift is discontinuous, where the tipping points in the system lie. Validated simulation models can provide useful answers to all 3 questions provided independent parameter estimates are available. We modelled kelp (*Ecklonia radiata*) - turf dynamics on shallow South Australian reefs, which showed clearly that the kelp-turf transition in this region represents a discontinuous phase shift with hysteresis and therefore that the kelp and turf states represent alternative stable community configurations, and that the likelihood of a shift to domination by turf algae increases with nutrification, acidification and warming. Moreover, as multiple stressors arise increase in the risk of transition to turfing algae is additive, and tipping points shift so that the transition to turf is much more likely.

Use of heterotrophy and mixotrophy for algal biomass production

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Considerable research has been carried out on the potential for algal-derived biofuels, yet this has not yet been made a commercial reality due to the high cost and low biomass productivity of algal biofuels. Research conducted so far has mainly focused on optimizing phototrophic cultivation of algal biomass. However, the maximum algal biomass one can achieve using phototrophically grown algae is restricted by light or inorganic carbon availability, and sometimes both. Therefore other modes of growing algae such as heterotrophy and mixotrophy need to be investigated. We grew *Scenedesmus* sp. in complete darkness using molasses as the growth medium and found that heterotrophy led to bigger cells, faster growth rates and denser cultures as compared to phototrophically grown cultures. Moreover, these heterotrophically grown cultures surprisingly retained their photosynthetic apparatus with similar values in all the photosynthetic parameters measured. Exposing molasses-grown cultures to light during the late exponential phase further boosted growth rate and biomass production significantly. As a result the biomass obtained through this process (mixotrophy) is twice as large as with heterotrophically grown cultures and three times larger than with photosynthetically grown cultures. We also observed some interesting changes in the photosynthetic apparatus under heterotrophic and mixotrophic conditions that allow the cells to keep their photosynthetic rates on par with photosynthetically grown cultures. Furthermore, calculations suggest that the molasses addition to growth media will only cost ~ 1 cent per litre. Overall this study provides promising leads for a greener future.

Revision of Korean *Papenfussia japonica* (Delesseriaceae, Rhodophyta), with *Augophyllum japonicum* comb. nov.

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Papenfussia japonica (Yoshida & Mikami) M.J.Wynne, recognized as a Japanese endemic species, is characterized by polystromatic thalli, growth by transversely dividing an apical cell with intercalary cell division of primary and higher order cell rows, and *Papenfussia*-type procarp which is composed of a four-celled carpogonial branch, a supporting cell and one-celled sterile cell group without cover cell. Among our collections from the southern coast of Korea, there is similar species with the original description of *P. japonica* based on morphological evidences, except that *P. japonica* from Korea has not *Papenfussia*-type but *Nitophyllum*-type procarp which have a cover cell. The development of female reproductive structure of the species indicates the same pattern with the recently described genus, *Augophyllum* S.M.Lin, S.Fredericq, M.H.Hommersand. Furthermore, molecular phylogenetic analyses based on *rbcL* gene sequence reveal the close phylogenetic relationships between *Papenfussia japonica* and several species of the genus *Augophyllum*. Therefore we propose to transfer of *P. japonica* to the genus *Augophyllum*, as *A. japonicum* com. nov.

Preliminary data on species delimitation of the genus *Pyropia* (Bangiophyceae, Rhodophyta) from Korea

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Species delimitation of the red algal genus *Pyropia* has been confused by morphological variation and lack of reliable diagnostic characters. We collected three species of the genus *Pyropia*: *P. "tenera"* from Jeju Island of the southern Korea, and *Pyropia* sp.1 and *Pyropia* sp.2 from Ulleung Island in the most eastern part of Korea, and analysed them based on the morphology and *rbcL* gene molecular analyses. As the result, *P. "tenera"* is closely related to *P. suborbiculata* (GQ427219: China and Korea; AB287947: Japan), as shown by 0.1~0.8% sequence divergence with *P. dentata* (GQ427222: China) and *P. ishigecola* (GQ427225: China). *Pyropia* sp.1 is identical with *Pyropia* sp. from Japan (as *Porphyra* sp.) and is closely related to *P. ishigecola* (HQ687524: Japan), *P. oligospermatangia*, *P. tenera* (AB287950, AB366149: Japan) and *P. yezoensis* as shown by 0.7~1.1% sequence divergence. *Pyropia* sp.2 is related to another Japanese *Pyropia* sp. (as *Porphyra* sp.) showing 9.5% sequence divergence with the *rbcL* sequence of that taxon. We are continuing this project to find more species and to understand the phylogenetic relationships within the genus *Pyropia*.

Biodiversity of the Red Algal Order Halymeniales in Australia

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The southern coasts of Australia are known for their rich diversity of marine macroalgae, particularly representatives of the dominant phylum Rhodophyta of which some 80% of species are endemic. Many of the most bizarre and attractive members of this group belong to the order Halymeniales, which consists of the two families Halymeniaceae and Tsengiaceae. The former occurs in tropical to cold-temperate waters of both hemispheres and is richly represented in Australia, where some 15 genera and 28 species were known prior to

our molecular-assisted alpha taxonomic studies. Our findings have doubled the number of definable species-level taxa in the family present there. The Tsengiaceae has been a monotypic family comprised of the rare genus *Tsengia*, which is currently represented worldwide by five species, three of which were previously known from Australia. Our studies show that Australia harbours even greater richness for the Tsengiaceae than was suspected, with at least four new species and one new genus being added as a result of our molecular analyses. Highlights of some new taxa will be briefly covered, and thoughts on the importance of basic taxonomy and phylogenetics, even in relatively obscure groups, presented.

Why Every Patriotic Australian Should Salute the Genus *Mychodea*

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The obscure genus *Mychodea* is the sole member of the red-algal family Mychodeaceae and has long enjoyed the distinction of being the largest wholly endemic genus and family of any algal group anywhere in Australia. Further reflection along these lines suggests that it is also almost certainly the largest genus and family wholly endemic to the shores of any continental landmass in the world, a claim that surely makes it worthy of note and reverence. Over 40 years ago Kraft completed a morpho-taxonomic monograph the genus and attributed 11 species to it, all but one of which had been described by European phycologists prior to the 20th Century. Kraft synonymized many early species, and all extra-Australian records (from Mauritius, Chile, South Africa, the Caribbean and California) were eliminated or discounted. Thoughts on phylogenetic relationships in the published 1978 monograph were based strictly on “educated” guesswork, which remained the unsatisfactory situation until the advent of molecular-taxonomic methodologies that the second author has now applied to the complex following extensive recent collecting across the whole of southern Australia, including Tasmania. Some 16 distinguishable species and several cryptic ones now comprise *Mychodea*, including three new species and two that are resurrected. Many have highly distinctive morphological and anatomical features, and a cherry-picked selection of these will be illustrated.

Morphology and phylogenetics of *Gambierdiscus* sp. nov. (Gonyaulacales): a new dinoflagellate associated with toxins from the Great Barrier Reef (Australia)

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Gambierdiscus is a genus of benthic dinoflagellates which is found worldwide and forms harmful algal blooms (HABs). Some species produce neurotoxins (maitotoxins (MTX) and ciguatoxins (CTX)) which bioaccumulate and cause ciguatera fish poisoning (CFP). In this study we characterised 6 strains of *Gambierdiscus* collected from Heron Island, Australia, a region in which CFP is endemic. Clonal cultures were processed using (i) light microscopy;

(ii) scanning electron microscopy; (iii) DNA sequencing based on the nuclear encoded ribosomal SSU and D8-D10 LSU regions and, (iv) toxin profile as determined by LC-MS. Correlation of morphological and phylogenetic data has ascertained that these strains represent a new ribotype of *Gambierdiscus*, and possibly a new species. Cultures produced MTX but no known congener of CTX, however the CTX toxin profile requires further investigation. The toxicity of CTX and MTX phases are under investigation via mouse bioassay. The investigation of toxigenic species of *Gambierdiscus* in CFP endemic regions continues the investigation for the causative agent of CFP in Australia.

Understanding the Ecological Niche of Toxin Producing Epibenthic Dinoflagellates

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Some microalgal species produce potent toxins that can accumulate in the food web and when consumed by humans can cause illness and death. Ciguatera Fish Poisoning (CFP) is a human illness which arises from consumption of marine fish whose flesh and viscera have been contaminated with ciguatoxins produced by dinoflagellates from the genus *Gambierdiscus*. Species from this genus are usually found in tropical reef environments and have been documented throughout the Great Barrier Reef, Queensland Australia; however in recent years a population of *Gambierdiscus carpenteri* was identified as far south as Merimbula, New South Wales, Australia. Monoclonal isolates of *Gambierdiscus carpenteri* were established from temperate Merimbula and species classification was confirmed using species-specific semi-quantitative polymerase chain reaction (qPCR) assays. Targeted Liquid Chromatography-Mass Spectrometry (LC-MS) analysis designed to detect toxins implicated in CFP occurrences revealed established strains of *Gambierdiscus carpenteri* from Merimbula do not produce toxins known to be associated with this illness. However, a high level of cytotoxicity toward the SH-SY5Y human derived neuronal cell line was identified using the neuroblastoma cell based assay suggesting the presence of an unknown toxic compound. In order to characterise the thermal niche of this temperate *Gambierdiscus carpenteri* population, five strains were used to measure growth rate at six temperatures across a thermal gradient ranging from 15-30°C. The thermal niche width extended across all temperatures tested and the measured thermal optima (24-27°C) was found to be several degrees above the ambient average water temperature. Here we describe the species identity, assess the toxin profile, cytotoxicity and thermal niche of monoclonal isolates of *Gambierdiscus* sp. collected from a recently discovered marginal population in temperate Australia. Studies such as this are fundamental to assist in mitigating the risk of human exposure to CFP and predicting areas of future concern.

Interactive effects of seawater pH, temperature and copper exposure on the development of meiospores of the kelps *Macrocystis pyrifera* and *Undaria pinnatifida* (Laminariales)

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Anthropogenic CO₂ emissions are driving a temperature increase of 4°C and a pH reduction from 8.10 to 7.65 (ocean acidification, OA) in the ocean surface by 2100. The concentration of free toxic Cu²⁺ is also increasing due to OA. These changes may affect the physiology of macroalgae, especially their susceptible early life stages. Our objective was to evaluate the interactive effects of pH, temperature and copper exposure on the kelps *Macrocystis pyrifera* and *Undaria pinnatifida* meiospore development. Meiospores of both kelps were separately cultured for 18 days under two temperature treatments (12°C, ambient temperature and 16°C, projected temperature for 2100), in two seawater pH treatments (pH_T 7.65, OA predicted for 2100 and pH_T 8.16, ambient pH), and two copper concentrations (species-specific germination EC₅₀). Meiospore germination for both species decreased by 10–15% in the presence of copper compared to the controls, irrespective of pH and temperature treatments. Germling growth rate under copper exposure was 50% lower than that in controls for both species under all pH and temperature treatments but higher for *M. pyrifera* than *U. pinnatifida* in all treatments. Gametophyte development for both species was inhibited by copper in all pH and temperature treatments. Results indicate that meiospore germination, germling growth rate and gametophyte differentiation are tolerant to the pH-temperature interaction but copper negatively affects these processes. The native kelp *M. pyrifera* was more tolerant to the three-factor interactions than the invasive kelp *U. pinnatifida*. Long-term, multiple-factor experiments are needed to understand how macroalgal microscopic life-stages are responding to global climate change.

Molecular data provide Korean species diversity and phylogenetic relationships of the order Halymeniales (Rhodophyta)

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The red algal order Halymeniales, having morphological divergence according to environments, is examined as the subject to revisions based on molecular approaches. Among our collection from intertidal to subtidal up to 25 m in Korea, we acquired results from the plastid *rbcL* analysis revealing seven generic groups of the order Halymeniales: *Cryptonemia*, *Grateloupia*, *Kintokikocolax*, *Pachymeniopsis*, *Polyopes*, *Prionitis* and another *Grateloupia* group. *Pachymeniopsis* contains eight species with various morphology, such as terete type (*Pa. angusta*), subdichotomous type (*Pa. imbricata*), and foliose type with simple or marginal lanceolate bladelets. *Prionitis* includes three species, which has mostly slightly terete below flattened blades and bushy type with irregularly pinnate branchlets. *Grateloupia*

subpectinata and *G. turuturu* are positioned in another *Grateloupia* with Japanese *G. sparsa*, which is different node from the *Grateloupia* group including generic type *G. filicina*. *Cryptonemia asiatica*, having foliose and undulate blades with clearly visible stems, is occurred in the subtidal up to 25 m. The parasitic species, *Kintokiocolax aggregato-cerantha*, is also confirmed. To reveal phylogenetic relationships among 17 species of Halymeniales from Korea, it is necessary to conduct a detailed morphological comparison with molecular data.

A revision of Korean *Scinaia* (Nematales, Rhodophyta): *rbcL* gene sequences reveal six species

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The red algal genus *Scinaia* Bivona-Bernardi from Korea is re-evaluated based on recent collections. *Scinaia* has been reported fifteen species in the northwestern Pacific, most of them incompletely described, and is characterized by an uncalcified, dichotomously or subdichotomously branched thallus with a consolidated cortex. A molecular-assisted alpha taxonomy approach, *rbcL* gene sequences, is used for the species segregation, and the result is revealed six species: *Scinaia japonica* Setchell, *S. johnstoniae* Setchell, *S. latifrons* M.A.Howe, *S. okamurae* (Setchell) Huisman, *S. okiensis* Kajimura and unknown species. The minimum interspecific divergence is 6.0-6.1% between *S. okamurae* and *S. okiensis*, and the maximum is 14.6-14.9% between *S. okamurae* and *S. johnstoniae*. Diverse species of *Scinaia* occur in the subtidal regions at depths of 5 to 20 m on Jeju Island. This revision continues to clarify the species delimitation and phylogenetic relationships of the genus *Scinaia* in having very similar and highly variable morphology.

Inorganic carbon acquisition and photosynthetic characteristics of Australian freshwater microalgae from a subtropical reservoir

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Most microalgae from marine and freshwater environments possess CO₂ concentrating mechanisms (CCMs) that render them relatively unaffected by CO₂ levels in the environment. Nonetheless, different species express CCMs to varying extents and thus future rises in atmospheric CO₂ could potentially influence species composition in algal populations. In an attempt to understand the potential effects of elevated atmospheric CO₂ on algal growth and populations in freshwater systems we investigated some of the carbon acquisition characteristics of six strains of freshwater phytoplankton from Lake Wivenhoe, South East Queensland, Australia. These included *Cyclotella* sp. (Bacillariophyceae), *Cylindrospermopsis raciborskii* (Cyanophyceae), *Monoraphidium* sp. (Chlorophyceae), *Nitzschia* sp. (Bacillariophyceae), *Staurastrum* sp. (Zygnemophyceae), and *Stichococcus* sp. (Chlorophyceae). We determined rates of gross photosynthesis, respiration and the half-saturation rate constants for light (K_{0.5, I}) and DIC (K_{0.5, CO2}) by oxygen electrode and rates of electron transport by chlorophyll fluorescence (Walz PhytoPAM). Internal carbon pool and

the cells' ability to concentrate CO₂ was determined directly via the silicon oil centrifugation technique.

Effects of elevated CO₂ and N-limitation on sinking rates and macromolecular composition in marine phytoplankton

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Approximately 1-3% of the yearly 50–60 Pg C of marine primary production currently settles in the deep ocean, due in part, to the activity of the biological carbon pump. Central to the strength of the biological carbon pump is sinking of phytoplankton cells. In order for accurate predictions to be made about the likely extent of future climate change, it is important to know whether the biological carbon pump will continue to operate at its existing capacity or whether it will change its drawdown capabilities as a consequence of anthropogenic activities. We have investigated the effects of elevated CO₂ and N-limitation on macromolecular composition and sinking rate of the coccolithophorid *Emiliania huxleyi* and the diatom *Chaetoceros didymus*. For *E. huxleyi* size rather than macromolecular composition was the determining factor for sinking velocity and cells followed Stokes Law tightly. For *C. didymus*, the situation was more complex and changes in form resistance, largely chain formation, played a significant role in controlling sinking velocity.

A new molecular phylogeny of the *laurencia* complex (rhodophyta, rhodomelaceae) and a review of key morphological characters results in a new genus: *coronaphycus*, and a description of *c. novus*

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Within the *Laurencia* complex (Rhodophyta, Rhodomelaceae), six genera have been recognized based on both molecular analyses and morphology: *Laurencia*, *Osmundea*, *Chondrophycus*, *Palisada*, *Yuzurua* and *Laurenciella*. Recently new material from Australia has been collected and included in the current molecular phylogeny, resulting in a new clade. This study examined the generic delineations using a combination of morphological comparisons and phylogenetic analysis of chloroplast (*rbcL*) nucleotide sequence. The molecular phylogeny recovered eight (rather than six) clades; *Yuzurua*, *Laurenciella*, *Palisada* and *Chondrophycus* showed as monophyletic clades each with strong support. However, the genera *Osmundea* and *Laurencia* were polyphyletic. Consequently, the new genus *Coronaphycus* is proposed, resulting in the new combination *Coronaphycus elatus* and a description of the new species *C. novus*.

Contrasting Zn toxicity effects to model extremophilic and neutrophilic freshwater algal species

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Acidophilic microalgae are often found at sites heavily affected by acid mine drainage and in naturally occurring acidic environments, and are often metal tolerant. Microalgae employ various coping strategies when subjected to metal stress, which determine their threshold of metal tolerance. An alga with a high level of metal tolerance is the extremophilic red alga *Cyandium caldarium*. In this study, we have looked at the coping mechanisms *C. caldarium* employs to cope with zinc stress, and have compared it to the more susceptible mesophilic green alga *Chlamydomonas reinhardtii*. Measurements of gross photosynthesis, respiration, pigment levels, oxidative stress, stress protein and FTIR, as a phenomics approach, show that these species, with contrasting Zn tolerances, also have a contrasting approach to coping with Zn-induced oxidative stress. Despite its significantly lower tolerance to Zn, *Chlamydomonas reinhardtii* was able to regain gross photosynthetic capacity after an acclimation period, which it also maintained when subjected to further zinc stress. This was not seen in the much more tolerant *Cyandium caldarium*, which reduced its photosynthetic capacity when subjected to Zn stress, even after an acclimation period. The coping strategy of *Cyandium caldarium* resulted in down-regulation of photosynthetic capacity, and its ROS production depended on the Zn-dose. FTIR analysis shows that Zn acclimation and stress results in modification of cellular macromolecular composition. These results open up questions of the role ROS signalling might play in different coping strategies seen in microalgae and the wider implications of metal-stress induced alterations in nutritional quality of microalgae.

Variations in the diffusive boundary layer of kelp blades in different conditions of pH and water motion

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Seaweeds are able to modify the chemical environment at their surface, in a micro-zone called the diffusive boundary layer (DBL) via their metabolic processes controlled by light intensity. Living at the surface of kelp blades, sessile invertebrates such as calcifying bryozoans or tube-forming polychaetes can be affected by the chemical variations occurring in this layer, depending their size and the thickness of the DBL. The physico-chemical conditions of the surrounding seawater such as flow velocity are known to affect the characteristics of the DBL but how ocean acidification, one of the major threat in the current climate change, can affect DBL thickness and the organisms living inside is currently poorly understood. The thickness and the characteristic of the DBL have been assessed in different pH levels (current one, pH 8.1 and a condition predicted for the end of the century, pH 7.6) and seawater motion condition (slow and high flow) on kelp samples. Oxygen and pH profiles were measured with microprobes in both bare kelp blades and bryozoan colonized ones to see the differences in DBL characteristics under ocean acidification conditions. It is expected that (1) kelp photosynthesis will be boosted and the thickness of the DBL will increase under slow flows and low pH conditions and (2) the DBL would be thinner at the top of bryozoans colonies than in bare blades not only because the lophophores can create

turbulence which alter the DBL but also because bryozoan decrease the light intensity received by the blade and so limit the productivity of the kelp.

Three new red algal parasites and the complex evolutionary history in the red algal parasite *Pterocladophila hemisphaerica* from New Zealand

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Red algal parasite have a reduced morphology and unique development and are common on other red algae. Red algal parasites are often closely related to their hosts but also switch hosts. There are nine parasites described in New Zealand but preliminary studies indicate a much higher number of red algal parasite. This study details three undescribed parasites growing on *Polysiphonia atterrima*, *Cladhymenia oblongifolia* and *Phycodrys novae-zelandiae*. Microscopy and molecular markers (mitochondrial, nuclear, plastid) were used to study the morphology and genetic variation of these parasites. All three parasites show a close relationship to their hosts: 1) the *Cladhymenia* parasite is a sister species to its host, 2) the *Polysiphonia* parasite seems to be nested within the host species, which is not monophyletic, and 3) the *Phycodrys* parasite is nested within the host species. The close relationships between all parasite and host combinations suggests that each parasite evolved from its host and relatively recently. The evolutionary history between the previously described red algal parasite *Pterocladophila hemisphaerica* and its host *Pterocladia lucida* were investigated. The parasite is taxonomically in the order Gracilariales and parasitizes *Pterocladia lucida* in the order Gelidiales. Based on nuclear markers the parasite probably evolved from neither the Gracilariales nor Gelidiales. Mitochondrial genes indicate that the mitochondrion is within the Gelidiales but not from the genus *Pterocladia*. While the plastid markers indicate that the parasite probably retains plastids of its host. These three organelle genomes, all in the same organism, but with different origins has not been seen before and shows the complexity that exists in parasitic algal evolution.

Chloroplast function in the absence of genes encoding chloroplast proteins

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About 5% of the chloroplast proteome is encoded by the chloroplast genome; the remainder are encoded by the nuclear genome. In both cases there is evidence of breakdown of the proteins, so retention of chloroplast function is expected to depend on the retention of the genes, or at least the derived mRNAs, encoding the proteins. Chloroplasts from the food algae remain functional as kleptoplastids in a range of saccoglossan gastropods for days to months. Despite previous suggestions that some genes from the food alga have been transferred to the saccoglossan, current opinion is that there has been no such transfer. There is no evidence on the occurrence of long-lived algal mRNA transcribed from nuclear genes that are translated into chloroplast proteins, so explaining the long-term retention of kleptoplastid function requires further work. Some chloroplasts in growing *Acetabularia* lose

their DNA but still retain function for days to weeks; other chloroplasts retain their DNA and act as the ‘germ line’, contributing to the next generation. There is evidence of long-lived (weeks) mRNA (from nuclear genes) in *Acetabularia*, but there is no evidence on such long-lived mRNA from chloroplast genes. As with kleptoplastids, more work is needed on how the inevitable damage to chloroplast proteins is countered and protein function is retained.

***Gambierdiscus*, the producer of ciguatera fish poisoning toxins, in the Pacific region**

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Ciguatera fish poisoning (CFP) is caused by consumption of fish contaminated with ciguatoxins and maitotoxins. The illness can be severe and deaths have occurred. Herbivorous fish accumulate the toxin producing dinoflagellates, species in the genus *Gambierdiscus*, as they graze on macroalgae and corals. If the dinoflagellates are toxic, the toxins will pass up the food chain and are bio-transformed into more toxic forms. Both *Gambierdiscus* sp. and the related *Fukuyoa paulensis* (= *G. yasumotoi*) have been detected in northern sub-tropical coastal waters of New Zealand and also in the more northern Kermadec Islands. With warming oceans predicted, New Zealand is expecting and preparing for CFP in the future. New molecular tools and chemical tests have been developed and extensive sampling has been carried out in the Cook Islands, both to determine the situation there and to trial the new technologies. Testing includes determining whether toxin levels in fish correlate with dinoflagellate cell numbers at selected sites. Two new *Gambierdiscus* species were isolated during a 2014 sampling trip. The longer term aim is to have real-time tools to assess CFP risk and so reduce the number of illnesses.

Nutrient enrichment and extreme depths (light deprivation) influence C and N incorporation of marine macroalgae

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The ratios of the stable isotopes of carbon (C) and nitrogen (N) in algal material provide information describing both the activity of physiological processes occurring within the alga (in particular the mode of inorganic carbon uptake), and the potential origin of inorganic N taken up by the alga. Analysis of organic material for total C and N, and their stable isotopes is a relatively inexpensive and routine process that can provide a wealth of data. In this presentation I discuss a selection of concepts where stable isotope ratios can be used to address specific biological issues and support the discussion with data collected from a variety of environments, as part of manipulative nutrient enrichment (N, P, N+P) experiments, across natural gradients of irradiance, latitude and anthropogenic impact, and

from field collections . Finally I speculate on future research that might benefit from the study of C and N stable isotopes in algae.

Genomic Copy Number Variability and the use of a qPCR assay based on *sxtA* for the detection of *Alexandrium* species

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Many marine biotoxins are synthesised by dinoflagellates, a group of marine microalgae, and are associated with significant ecological and human health impacts worldwide. In Australian marine waters, *Alexandrium minutum*, *Alexandrium fundyense*, *Gymnodinium catenatum* and *Alexandrium pacificum*, are known to produce paralytic shellfish toxins that can cause Paralytic Shellfish Poisoning (PSP) in humans after shellfish consumption. A qPCR based genetic tool based on the genes involved in the saxitoxin biosynthesis pathway (STX) can detect and quantify STX biosynthesis genes in marine waters. This tool has been successfully used to detect and quantify blooms of *Alexandrium* spp. from France, Australia, China and the US. Previous studies in dinoflagellate genome imply that many genes have multiple copies in their genomes. This also includes the *sxtA* gene. Understanding the gene copy variation of STX biosynthesis genes are important in order to accurately determine the cell number in the environmental samples. In this project, multiple approaches will be applied to quantify the ribosomal and *sxtA* gene copy numbers in several *Alexandrium* spp. species and strains as well as saxitoxin producing *G. catenatum*. The application of qPCR detection assays in environmental samples will also be demonstrated.

An Australian based Edible Seaweed Company a Reality?

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Worldwide, the seaweed industry is estimated to have an annual value of some US\$6 billion and the largest share of this is for food products (McHugh 2003). It is estimated that US\$5 billion of this is used for human consumption. The other US\$1 billion is largely based upon extracting seaweed products such as hydrocolloids for use in products such as animal feeds and fertilizers, bioactives. (Lee 2008). Wild harvest of seaweeds only accounted for about 4.5% of the total seaweed production in 2010. While cultivated seaweed production has grown by about 50% in the last 10 years, seaweeds harvested from the wild have declined significantly. Even with seaweed farming growing rapidly, the global demand for seaweed based products has surpassed supply (Lee 2008). There is minimal commercial utilization of Australian seaweeds, despite globally significant levels of biodiversity. To date, Australian research monies are often directed at algae based on very speculative claims about a seaweeds potential value. When will an Australian based industry evolve to justify these speculative claims? A company has been established in Tasmania that is specializing in marketing edible seaweeds: Kai Ho Oceantreasure or Tasmanian Sea Vegetables. This company is targeting local Australian markets. The company was started in 2012 and is experiencing a steady increase in trade. The principle seaweed products for Tas Sea Veges are based on the introduced alga *Undaria pinnatifida* and are Wakame and Mekabu. These

products are sold fresh, frozen and dry. A second introduced alga: *Grateloupia turuturu* or Red Lettuce is also subject to strong demand. Two local species *Lessonia corrugata*, sold as Tasmanian Kombu and *Chaetomorpha coliformis* or Mermaids Necklace have demonstrated strong market acceptance. Prices for Mermaids Necklace have achieved \$1000/kg. Long term harvesting of the local species will be subject to satisfying conditions of sustainable harvest or culture.

Nutritional Characterisation and Sensorial Properties of Australian Marine Macroalgae

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Temperate southern Australian waters are considered a “biodiversity hotspot”, because of the high diversity and endemism within taxonomic groups. Whilst similar algal species are abundantly harvested commercially elsewhere worldwide, very little is known about southern Australian algae and their commercial exploitation is fundamentally nil. Algae are known to contain nutritionally beneficial compounds that are associated with a number of potential health benefits. Unsaturated fatty acids constitute >70% of the total fatty acids in marine algae, however lipid contents are typically low. Despite the low total lipid content, a large proportion consists of polyunsaturated fatty acids (PUFA) thus making seaweed a healthy low fat food. This study aimed to determine the nutritional profile and sensorial characteristics (palatability) of nine local marine macro-algae, which were compared to four Japanese species traditionally and abundantly consumed. The nutritional parameters investigated included fatty acid and proximate composition (total lipid, protein, moisture, ash, and crude fibre), to identify the overall nutritional values of different species. Lipid, omega-3 DHA and total FA content was highest in Australian species, whilst Japanese species generally contained higher amounts of protein, fibre, and omega-3 EPA. *C. galeatum* met the recommended omega-3 ALA serving guidelines, with all species excluding *P. comosa*, *D. potatorum* and *P. decipiens* classed as being a source of omega-3 fatty acids. There were no significant differences in participant satisfaction between the Australian and Japanese soup dishes. However, there were significant differences in the salad dishes influenced by the general attributes of each species. These results suggest that the Australian marine flora warrants further investigation as a source of novel sea vegetables.

The role of silica in carbon acquisition in the non-silicifying alga, *dunaliella tertiolecta*

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In seawater the conversion of HCO_3^- to CO_2 by external carbonic anhydrase (CA_{ext}) is slow without a buffer. The silica in diatom frustules has been proposed to be a buffer for CA_{ext} , improving the supply of CO_2 to the carbon fixing enzyme RubisCO. The question therefore arises as to whether silica in the external medium buffers CA_{ext} in non-silicifying organisms such as the green alga, *Dunaliella tertiolecta*. We measured growth rate, CA_{ext} activity and photosynthetic parameters in *D. tertiolecta* cultures grown with (Si+) and without (Si-) silica. Whilst there was no difference in growth rate between Si+ and Si- cells, higher apparent CA_{ext} activity was observed for cultures grown in the presence of silica. These findings suggest that silica in the external medium does buffer CA_{ext} in *D. tertiolecta*. Current work is investigating the mechanisms used by *D. tertiolecta* to maintain optimal growth in the absence of silica.

Fatty acids as biomarkers of ciguatera-causing dinoflagellates in marine food chains

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Ciguatera is a human illness associated with the trophic transfer of gambiertoxins produced by the benthic dinoflagellate, *Gambierdiscus* spp. It is hypothesised that the sporadic occurrence of ciguateric-fish is positively related to the wider range of prey consumed by key vectors that migrate between habitats. While some reef fish will remain on a reef other species migrate between habitats. It is therefore predicted that reef fish that have ontogenetic across-shelf migration will feed on a wider range of lower trophic level prey as they transverse habitats such as mangroves, seagrass beds, soft sediment substrates and coral reefs. It has been demonstrated that fatty acids originating from primary producers such as diatoms and dinoflagellates are reliable biomarkers in complex ecosystems. This study presented an important first step in identifying characteristic fatty acids for benthic toxic dinoflagellates and investigated the effect of temperature and salinity on their biochemical profile. Elevated sea surface temperatures have been correlated to an increase occurrence of ciguatera as well as the range expansion of *Gambierdiscus* spp and ciguateric fish. The application of fatty acids to trace benthic toxic dinoflagellates through ciguateric food chains is a novel approach to resolving a complexing trait of ciguatera occurrence.

Resolving the taxonomy of endemic Australian seagrass

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Many seagrass species are endemic to Australia, yet resolution of their taxonomic status lacks consensus among top researchers in the country. Similarly, many herbarium specimens remain incorrectly identified. This may be due to the fact that Australian seagrass have a complicated taxonomic history in Australia, and that there is no agreement from botanists about the roles of morphological and genetic analyses in reaching a resolution. Recently, the status of genera and species in the family Zosteraceae have undergone many years of discussion. Species in the genera *Heterozostera* have caused the most debate, followed by species of *Zostera*. Genetic analyses completed world-wide have resolved 4 phylogenetic

clades within the Zosteraceae family, yet attempts to replicate identification results through use of published taxonomic keys have not been successful. Morphological and geographical evidence of genetic divergences in Australian seagrass have been explored, but are not clearly defined. With the recent acceptance of taxonomic and systematic papers on both sides of this debate (Coyer 2013, Jacobs and Les 2009), taxonomists appear to be no closer to final resolution of this issue. This study reviews evidence on both sides of the debate and suggests a plan for moving forward with a concept for agreement on what constitutes an individual species for seagrass. Resolution in taxonomy can be achieved by focusing on where there are sufficient divergences in morphological and/or geographical characteristics that can be backed up by genetic analyses.

***Corallinapetra novaezelandiae* – an enigmatic non-geniculate coralline alga from the north of New Zealand**

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As part of our studies of coralline algae in New Zealand, collections were made from near Stevenson's Island in the north of the North Island. These collections included a non-geniculate coralline alga exhibiting unusual reproductive features not previously recorded in the group. Phylogenetic analyses based on *nssu*, *psaA*, *psbA* and *rbcL* genes show that this specimen is sister to a clade containing the Hapalidiales and Corallinales, and is excluded from all existing orders in the Corallinophycidae. Here I present what we currently know about this species, which is still known only from a single collection, in terms of morphology, reproduction and relationships with other taxa.

Chemometric perspectives on plankton community responses to natural iron fertilization over and downstream of the Kerguelen plateau in the Southern Ocean

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We examined phytoplankton community responses to natural iron fertilisation at 32 sites over and downstream from the Kerguelen plateau in the Southern Ocean during the austral spring bloom in October-November 2011. Community structure was estimated from chemical and isotopic measurements (particulate organic carbon POC, ¹³C-POC, particulate nitrogen PN, ¹⁵N-PN, and biogenic silica BSi) on size-fractionated samples from surface waters (300, 210, 50, 20, 5, and 1 µm fractions). Higher values of ¹³C-POC (vs. co-located dissolved inorganic carbon ¹³C-DIC source values) were taken as indicative of faster growth rates, and higher values of ¹⁵N-PN (vs. co-located ¹⁵N-NO₃ source values) as indicative of greater nitrate use. These metrics showed good quantitative agreement with classical ¹⁵N and ¹³C incubation results, opening the possibility of spatial mapping of growth parameters from synoptic sampling. Iron fertilised waters over the plateau developed dominance by very large diatoms (50-210 µm) with high BSi/POC ratios, high growth rates, and significant ammonium recycling as biomass built up. In contrast, downstream Polar Frontal waters with similar or higher iron supply were dominated by smaller diatoms (20-50 µm) and exhibited greater ammonium recycling. Stations in a deep water bathymetrically trapped recirculation south of the Polar Front with lower iron levels showed the large cell dominance observed on the plateau, but much less biomass. Comparison to nutrient depletions and mesoscale water mass histories from satellite derived Lagrangian trajectories suggest a difference in impacts between persistent low levels versus punctual high levels of iron fertilisation.

Antarctic sea ice algae: Primary production and carbon allocation

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Research undertaken for this completed thesis details primary production and carbon allocation of ice algal communities in laboratory and field conditions, and discusses the relationships between microbial growth dynamics, responses to physicochemical change, and ecosystem dynamics. The thesis finds that sea ice algae are capable of exuding large quantities of photosynthetically-derived organic carbon. Allocation to exuded organic carbon is highest during times of adverse conditions, such as challenging biochemical and physicochemical conditions. The composition of exuded carbon varies between defined pools, including dissolved organic carbon, colloidal organic carbon, and extracellular polymeric substances. The observed magnitude of changes in carbon allocation indicates that each extracellular carbon pool imparts different ecological roles and/or benefits to the producer organism.

Thermal niche evolution and its relation to latitudinal biodiversity patterns in *Codium* green seaweeds

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Most taxa show latitudinal diversity gradients (LDG) with high species diversity in the tropics and decreasing diversity towards the poles. Seaweeds, however, show a bimodal pattern with highest diversity in temperate waters, offering a great opportunity to test the generality of explanations offered for the typical LDG. Evolutionary processes, i.e. the generation of lineages through speciation and their loss through extinction, are central to explaining LDG patterns. Using the green seaweed genus *Codium* as a test case, we explore the evolution of the thermal niche and its relation to the LDG. We test the spatial coincidence model, which posits that regions with large standing diversity are those with high origination rates. Our results show that this model cannot be generalized across all taxa. In *Codium*, the tropical lineages are young and rapidly diversifying. The higher diversity in temperate regions is in large part due to old, slowly diversifying lineages.

Species diversity of genus *Ostreopsis* Schmidt from Heron Island, Great Barrier Reef, Australia

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Species of the marine benthic- epiphytic genus *Ostreopsis* Schmidt (1902) occur in tropical and temperate waters attached to coral rubble, macroalgae, seagrass and sand. Many *Ostreopsis* species produce highly toxic and complex non-peptide compounds, such as palytoxin (PLTX, C₁₂₉H₂₂₃N₃O₅₄) and its analogues, which are associated with human illnesses by consumption of contaminated seafood and direct contact through aerosolic exposure during blooms. To date, nine *Ostreopsis* species have been described based on their size and thecal plate patterns. The distribution and toxicity of *Ostreopsis* spp. in Australian waters is largely unknown despite reported occurrences from temperate shellfish estuaries. Here we report the diversity of *Ostreopsis* spp. from tropical Heron Island in the Australian Great Barrier Reef (18°S). Microscopic and phylogenetic analysis based on internal transcribed spacer regions (ITS-5.8S) and large ribosomal subunit (LSU) regions were used for identification. Toxicity was analysed using LC-MS/MS and fish gill cell assays. Certain strains were found to produce putative analogues of PLTX. The implications of these findings on aquaculture industry and for understanding the biogeography of *Ostreopsis* are discussed.

Understanding growth and photosynthetic characteristics of phytoplankton species from the Gippsland Lakes, under a dynamic changing environment.

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In the coming decades, algal blooms globally are expected to increase in frequency and intensity due to increasing temperature and storm activity leading to a rise in run-off of nutrients. This is of great concern for the Gippsland Lakes in S.E. Australia, which already suffers from reoccurring nuisance algal blooms. The impacts resulting from these blooms can degrade ecosystems and cause major economic loss for the townships surrounding the water bodies. We are currently examining the physiological performance of key phytoplankton species from the Gippsland Lakes under a range of varying light, salinity, nutrient and temperature regimes, and will present some of our data obtained to date. Our aim here is to better understand the autecology of these species in order to assess environmental conditions which could sustain formation of an algal bloom. Preliminary results for irradiance experiments on a chromophyte (*Sarcinochrysis* sp.), indicate that while this alga can sustain growth at low light levels, maximum growth rates were attained at a light level of 150 $\mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$. Non-photochemical quenching (NPQ) values indicate that when grown at higher light levels above 150 $\mu\text{mol photons} \cdot \text{m}^{-2} \cdot \text{s}^{-1}$, photo-damage can occur. With these results, combined with the results from future salinity, temperature and nutrient experiments, we hope to elucidate which factors more likely influence bloom formation. Understanding the eco-physiology of the phytoplankton in the Gippsland Lake is crucial for predicting future algal blooms and the resilience that they may have to future climate conditions.

Two new species assigned to *Calliblepharis* and *Craspedocarpus* (Cystocloniaceae, Rhodophyta) from the northwest Pacific

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Most species of *Calliblepharis* and *Craspedocarpus*, two closely related genera, occur in the southern hemisphere mainly in Australia and New Zealand. During a survey of Gigartinales diversity from Korea, we found two new species in the family Cystocloniaceae. We analyzed the morphology, chloroplast *rbcL* and nuclear small subunit RNA gene sequences to confirm their taxonomic status. *Calliblepharis* has a compressed thallus bearing alternate branches, which are mostly curved with thorn-like branchlets, without distinct rosettes around the larger cell in surface view, and the cystocarps are on the branches. Whereas *Craspedocarpus* is complanate, irregularly branches, with a visible internal vein, rosettes in surface view, and cystocarps in the margins. Phylogenies indicate that the two species are distinct from conspecifics, and are assigned to *Calliblepharis* and *Craspedocarpus* respectively, which are newly recorded in the northwestern Pacific. Consequently, we describe them as two species, *Calliblepharis saidana* comb. nov., previously known as *Hypnea saidana* from the northwestern Pacific and *Craspedocarpus* sp. nov.

Intra-specific variation in distribution and physiology: small scale patterns affect patterns of diversity

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Molecular studies are revealing an abundance of cryptic species within most morpho-species. Population genetic studies have also shown that many algal populations can be isolated at very small scales of several kilometers or even much less. While rare dispersal events do occur, often small-scale population differentiation is evident. These patterns of differentiations are even seen within populations in single localities. This small-scale population structure leads to several issues. In phylogeographic studies, for example to determine the distribution of diversity and inferring demographic scenarios where sampling is limited, it becomes important to sample all available environments within a site to capture diversity within a population and make accurate conclusions. These microgeographic patterns may also indicate that localized adaptation may occur at these small scales. Studies examining algal distribution with respect to environmental factors need to be more cognizant of these differences, with different cryptic species found in particular areas and genotypes associated with particular environments. We will use the example of *Bostrychia intricata* in New Zealand as an example where these microgeographic patterns are seen and could influence inference about species diversity.

29th ASPAB

Institute for Marine and Antarctic Studies,

20 Castray Esplanade, Hobart.

4-6th November 2015

Venue: The conference will take place on the ground floor of the IMAS building, in the open space as you enter the building.

Oral presentations will be in the Aurora lecture theatre. Lunches and breaks will be in the IMAS flex rooms, opposite the lecture theatre. Posters will also be displayed in the IMAS flex rooms.

Programme

Wednesday Nov 4th 2015

15.00-17.00- ASPAB Executive meeting, IMAS Board room, Level 2. Delegates will need to sign in at the ground floor security desk to receive lanyards.

16.00-19.00- Registration, IMAS Flex rooms; put up poster presentations.

17.00-18.00- Welcome reception and registration, IMAS Flex rooms.

18.00-19.00- AGM, Aurora lecture theatre.

Thursday Nov 5th 2015

08.15- Coffee cart (coffee, tea, hot chocolate) available, IMAS foyer.

08.15-08.55- Registration, IMAS Flex rooms, put up poster presentations.

08.55-09.00- Welcome: Gustaaf Hallegraeff and Catriona Hurd

9.00-09.45- **Philip Boyd Plenary:** Physiological diagnosis of phytoplankton responses to future complex ocean conditions

09.45-10.15 - coffee

10.15 – 12.15 –HARMFUL ALGAE. Chair – Gustaaf Hallaegraaf

10.15-10.30- Juan Dorantes-Aranda: Comparative performance of different immunological kits for paralytic shellfish toxin testing in Australian shellfish

10.30-10.45- Rendy Ruvindy: Genomic copy number variability and the use of a qPCR assay based on *sxtA* for the detection of *Alexandrium* species

10.45-11.00- Lesley Rhodes: *Gambierdiscus*, the producer of ciguatera fish poisoning toxins , in the Pacific region

11.00-11.15- Michaela Larsson: Understanding the ecological niche of toxin producing epibenthic dinoflagellates

11.15-11.30- Anna Liza Kretzschmar: Morphology and phylogenetics of *Gambierdiscus* sp.nov. (Gonyaulacales): a new dinoflagellate associated with toxins from the Great Barrier Reef (Australia)

11.30-11.45-Leanne Sparrow: Fatty acids as biomarkers of ciguatera-causing dinoflagellates in marine food chains

11.45-12.00-Arjun Verma: Species diversity of genus *Ostreopsis* Schmidt from Heron Island, Great Barrier Reef, Australia

12.00-12.15- Susan Blackburn: The Australian National Algae Culture Collection: Research and development for microalgae and bioresources

12.15 – 13.15 – lunch

13.15 – 15.15 – MACROALGAL ECOLOGY & PHYSIOLOGY. Chair – Joe Zuccarello

13.15-13.30- Alecia Bellgrove: Development of a microsatellite library for *Hormosira banksii* and examination of the appropriate spatial scale in which to sample for population genetics studies

13.30-13.45- Craig Johnson: Phase shift from kelp bed to turfing algae represents alternative stable states with hysteresis, and the risk of transition increases with multiple stressors

13.45-14.00- Pablo Leal: Interactive effects of seawater pH, temperature and copper exposure on the development of meiospores of the kelps *Macrocystis pyrifera* and *Undaria pinnatifida* (Laminariales)

14.00-14.15- Fanny Noisette: Variations in the diffusive boundary layer of kelp blades in different conditions of pH and water motion

14.15-14.30- Pamela Fernandez: Effect of nitrogen source on nutrient uptake and pH change at the surface of *Macrocystis pyrifera* blades

14.30-14.45- Juan Diego Gaitán-Espitia: The energy allocation principle in marine macroalgae: Estimating the physiological cost of reproduction in the seaweed *Gracilaria chilensis*

14.45-15.00- John Runcie: Nutrient enrichment and extreme depths (light deprivation) influence C and N incorporation of marine macroalgae.

15.00-15.15- Giuseppe Zuccarello: Intra-specific variation in distribution and physiology: small scale patterns affect patterns of diversity

1515-1545 – coffee

1545-1715 – MICROALGAL PHYSIOLOGY AND BIODIVERSITY. Chair – John Beardall

15.45-16.00- Manoj Kamalanathan: Use of heterotrophy and mixotrophy for algal biomass production

16.00-16.15- Paulina Mikulic: Contrasting Zn toxicity effects to model extremophilic and neutrophilic freshwater algal species

16.15-16.30- Thomas Lines: Inorganic carbon acquisition and photosynthetic characteristics of Australian freshwater microalgae from a subtropical reservoir.

16.30-16.45- Michael Borowitzka: Strain variation in the green alga, *Haematococcus pluvialis*

16.45-17.00- Frank Gleason: The potential ecological impacts of some newly described true fungal and fungal like parasites on the composition of phytoplankton, invertebrate and vertebrate populations in marine food webs

17.00-17.15- Lesley Clementson: Data, Data everywhere: How to access phytoplankton taxonomic and pigment composition data for the Australian region

Friday Nov 6th 2015

08.30 – coffee cart, IMAS foyer

Chair- Philip Boyd

9.00-9.30- **John Raven Plenary: Chloroplast function in the absence of genes encoding chloroplast**

9.30-9.45- Gustaaf Hallegraeff: Symbiotic associations in Australian tropical marine microplankton

9.45-10.00- Heroen Verbruggen: Thermal niche evolution and its relation to latitudinal biodiversity patterns in *Codium* green seaweeds

10.00-10.30 - coffee

10.30 – 12.30 –RED ALGAL TAXONOMY. Chair - Heroen Verbruggen

10.30-10.45- Joana F. Costa: Phylogenomics of the red algal order Nemaliales

10.45-11.00- Young Ho Koh: Preliminary data on species delimitation of the genus *Pyropia* (Bangiophyceae, Rhodophyta) from Korea

11.00-11.15- Lesleigh Kraft: Biodiversity of the Red Algal Order Halymeniales in Australia

11.15-11.30- Gerald Kraft: Why Every Patriotic Australian Should Salute the Genus *Mychodea*

11.30-11.45- Hyung Woo Lee: Molecular data provide Korean species diversity and phylogenetic relationships of the order Halymeniales (Rhodophyta)

11.45-12.00- Yola Metti: A new molecular phylogeny of the *Laurencia* complex (Rhodophyta, Rhodomelaceae) and a review of key morphological characters results in a new genus: *Coronaphycus*, and a description of *C. novus*.

12.00-12.15- Judy Sutherland: *Corallinapetra novaezelandiae* – an enigmatic non-geniculate coralline alga from the north of New Zealand

12.15-12.30- Mi Yeon Yang: Two new species assigned to *Calliblepharis* and *Craspedocarpus* (Cystocloniaceae, Rhodophyta) from the northwest Pacific

12.30 – 13.30 – lunch

13.30 – 14.45 –APPLIED PHYCOLOGY. Chair – Michael Borowitzka

1330-1345- Craig Sanderson: An Australian based Edible Seaweed Company a Reality?

1345-14.00- Vanessa Skrzypczyk: Nutritional Characterisation and Sensorial Properties of Australian Marine Macroalgae

1400-14.15- Luis Henríquez: Invisible Indicators for determining nutrient response (Impact) in coastal macroalgal reefs – Implications for spatial ecosystem-based management

14.15-14.30- Erin Cumming: Developing seaweed production techniques for integrated multi-trophic aquaculture in Port Phillip Bay, Victoria

1430-1445:- Daniella Farias: Applications and implications of macrophytes for biomonitoring: A case study of the Derwent estuary, Tasmania

14.45 – 15.45 MACROPHYTE TAXONOMY AND EVOLUTION. Chair – Michael Borowitzka

14.45-15.00- Maren Preuss: Three new red algal parasites and the complex evolutionary history in the red algal parasite *Pterocladophila hemisphaerica* from New Zealand

15.00-15.15- Margaret Brookes: *Codium fragile*: defining subspecies using *tufA* DNA analysis and morphology.

15.15-15.30- Brooke K. Sullivan: Resolving the taxonomy of endemic Australian seagrass

15.30 – 16.00- coffee break

16.00-17.30 –MICROALGAL ECOPHYSIOLOGY. Chair – Tom Trull

16.00-16.15- Leanne Armand: Diatom distributions delineated by lipid, genomic and microscopic observations between the Sabrina Coast and Antarctica

16.15-16.30- Thomas Trull: Chemometric perspectives on plankton community responses to natural iron fertilisation over and downstream of the Kerguelen plateau in the Southern Ocean

16.30-16.45- Sarah Ugalde: Antarctic sea ice algae: Primary production and carbon allocation

16.45-17.00- Kirralee Baker: Patterns of diatom activity in coastal Australian waters using the fluorescent probe PDMPO

17.00-17.15- Tamsyne Smith-Harding: The role of silica in carbon acquisition in the non-silicifying alga, *Dunaliella tertiolecta*

17.15-17.30 - John Beardall: Effects of elevated CO₂ and N-limitation on sinking rates and macromolecular composition in marine phytoplankton

1900 h conference dinner at Rockwall

89 Salamanca Place, (~50 m from IMAS). **Prize giving.**

Posters: displayed throughout the meeting

***Presenters please stand by your posters during the morning breaks on both days**

***Posters can be A0 or A1 size, landscape or portrait.**

Elisabeth Albinsson: How does salinity affect growth, lipid and pigment composition of Australian *Botryococcus braunii*?

Kirralee Baker: Thermal performance curves reveal alternative energy pathways at stressful temperatures: a multi-trait analysis of phenotypic plasticity in *Thalassiosira pseudonana*.

Chiela Cremen: Taxonomic revision of *Halimeda* in southwestern Australia

Daniela Farias: Fine-tuning transmission electron microscopy methods to evaluate the cellular architecture of Ulvales

Catriona Hurd: Tasmanian seaweed communities have an unusually high proportion of CO₂-only users: implications for ocean acidification

Ian Jameson: Taxonomy and bioinformatics at the Australian National Algae Culture Collection ANACC

Jong Chul Lee: A revision of Korean *Scinaia* (Nematales, Rhodophyta): *rbcL* gene sequences reveal six species

Melissa Wartman: Understanding growth and photosynthetic characteristics of phytoplankton species from the Gippsland Lakes, under a dynamic changing environment.

Jeong Chan Kang Revision of Korean *Papenfussia japonica* (Delesseriaceae, Rhodophyta), with *Augophyllum japonicum* comb. nov.

Instructions for speakers

We have a tight schedule of talks! We ask all speakers to keep within their allocated time.

Talks will be 12 minutes plus 3 minutes for questions and speaker turn-around. The exceptions are the plenary talks (Philip Boyd – 40 minutes plus 5 minutes for questions) and John Raven (25 minutes plus 5 minutes for questions)

The session chair will indicate time to the speaker at 10 minutes; the speaker must then wrap-up their talk within the next 2 minutes.

Loading your talks

- For speakers in the morning sessions, please load your talk onto the Aurora lecture theatre computer at 0830 am on the morning of your talk. A computer technician will be on hand to help.
- Speakers in subsequent sessions can load talks in the break before the session.
- The computer platform is PC. It can be used to give either PDF's or as PowerPoint presentations (Mac or PC). However, if you've used Open Office you should check that your presentation functions in Microsoft Office before the workshop.
- **We strongly recommend that you bring a back-up talk as a PDF document.**