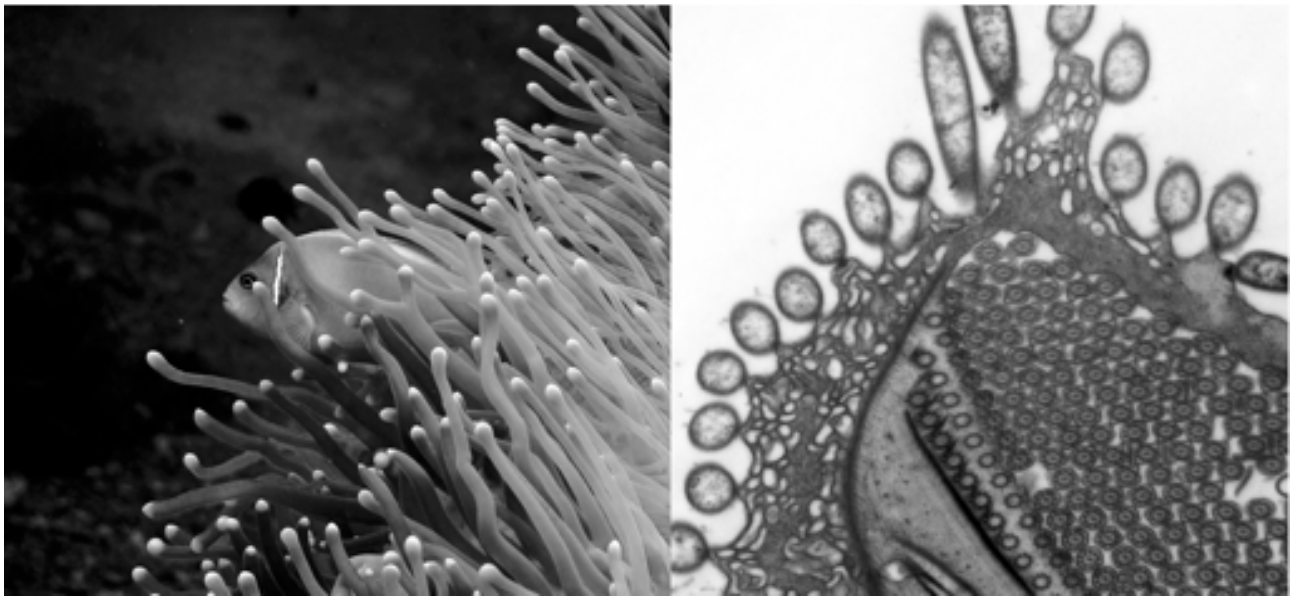

Microbial Symbiosis Meeting

(better together?)

Date And Time

Mon, 16 Dec 2019, 12:00 –
Tue, 17 Dec 2019, 12:00 GMT

Location

Crowne Plaza London - Kings Cross
1 King's Cross Road
London
WC1X 9HX

Protistology UK's Autumn meeting in collaboration with and supported by the Microbiology Society and the Gordon and Betty Moore Foundation.

Meeting Schedule:

Day 1

12:00 - 13:30 ARRIVAL/REGISTRATION/LUNCH

13.30 - 13:40 WELCOME/INTRODUCTION

13:40 - 14:10 **T1 Kathryn Helliwell** (*Marine Biological Association, Plymouth, UK*)
"Evolutionary pathways to aquatic microbial symbioses: metabolic cross-talk, signalling and future perspectives"

14:10 - 14:25 **T2 Matthias Fischer** (*Max Planck Institute for Medical Research, Germany*)
"Virophages as mutualists of heterotrophic flagellates"

14:25 - 14:40 **T3 Charlotte LeKieffre** (*Université d'Angers, France, & EPFL, Lausanne, Switzerland*)
"Kleptoplastic foraminifera: the transformation of heterotrophic unicellular eukaryotes into photosynthetic organisms"

14:40 - 15:10 **T4 Jörg Wiedenmann** (*University of Southampton, UK*)
"Ancestral genetic diversity facilitates a rapid spread of stress-tolerant coral symbionts in response to climate change"

15.10 - 15:30 **Turbo Talks** (3 mins each)

15:30 - 16:00 COFFEE AND POSTERS

16:00 - 17:30 **QMM** Group Leader Laboratory QMMs (5 min introductions to major Questions, Models and Methods)

17:30 - 18:00 **T5 Sinead Collins** (*University of Edinburgh, UK*)
"Potential consequences of evolving in a (maddening) crowd"

18:00 - 18:15 **T6 Johan Decelle** (*University Grenoble Alpes, France*)
"Multimodal subcellular imaging to explore microbial symbiosis at the nanoscale level"

18:15 - 18:30 **T7 Annika Guse** (*Heidelberg University, Germany*)
"Uncovering the Mechanisms of Cnidarian Endosymbiosis using *Aiptasia* as a model system"

18:30 - 19:00 **Discussion 1 Jon Kaye** (*Gordon and Betty Moore Foundation, CA, USA*) – introduction to Symbiosis in Aquatic Systems Initiative and wrap up discussion

19:00 DINNER

Day 2

9:00 - 9:30 **T8 Michael Brockhurst** (*University of Sheffield, UK*)
"Comparison of independent evolutionary origins reveals both convergence and divergence in the metabolic mechanisms of symbiosis"

9:30 - 9:45 **T9 Magali Schweizer** (*Université d'Angers, France*)
"Microbiome of *Amphistegina* (Foraminifera, Rhizaria) subjected to different oxygen levels"

9:45 - 10:00 **T10 Martin Carr** (*University of Huddersfield, UK*)
"Co-evolution of Transposable Elements Codon Usage and Host tRNA Genes in the Choanoflagellate *Salpingoeca rosetta*"

10:00 - 10:15 **T11 Fiona Henriquez** (*University of the West of Scotland, UK*)
"Is *Paramoeba (Neoparamoeba) perurans* both parasite and host in Gill Disease?"

10:15 - 10:30 **T12 Stephane Roberty** (*University of Liège, Belgium*)

"Revisiting the Oxidative Theory of Coral Bleaching two decades later"

10:30 - 11:00 COFFEE AND POSTERS

11:00 - 12:00 **Discussion 2** Key questions in Symbiosis and tools/strategies to address these questions

12:00 ME**ETING CLOSURE AND DEPARTURE**

Turbo Talks and Posters:

Girish Beedessee (Okinawa Institute of Science and Technology)
"Genomic insights on secondary metabolism in symbiotic dinoflagellates"

Emmanuelle Geslin (University of Angers)
"Overview of recent discoveries on kleptoplastic foraminifera"

Elizabeth Hambleton (Heidelberg University)
"Molecular mechanisms of metabolic exchange in animal-algal symbiosis"

Thomas Krueger (University of Cambridge)
"Rearranging the furniture – How does symbiosis alter the cellular spatial proteome of the dinoflagellate coral symbiont?"

Megan Sørensen (University of Sheffield)
"A novel host-symbiont interaction can rapidly evolve to become a beneficial symbiosis"

Abstracts:

T1 Evolutionary pathways to aquatic microbial symbioses: metabolic cross-talk, signalling and future perspectives

Katherine E. Helliwell[1,2], Freddy Bunbury[3], Dominic Absolon[3], Alison G. Smith[3]

[1] Marine Biological Association, The Laboratory, Citadel Hill, Plymouth. PL1 2PB
[2] Biosciences, College of Life and Environmental Sciences, University of Exeter, UK
[3] Department of Plant Sciences, University of Cambridge, Cambridge, CB2 3EA

Aquatic microbes are evolutionarily diverse taxa that underpin marine and freshwater ecosystems. These organisms exhibit a spectrum of ecological lifestyles, from free-living autotrophic phytoplankton to predatory heterotrophic or mixotrophic species. In addition, a complex range of interactions, or symbioses, shape the ecology and evolution of microbes in aquatic communities. However, major knowledge gaps exist in our understanding of the breadth, diversity, and mechanistic underpinnings of microbial symbioses, such as the metabolic basis and signalling processes governing them. I will describe the importance of metabolic auxotrophies for driving nutrient exchanges between microbes, which can forge the establishment of microbial mutualisms. I will focus on evidence drawn from experimental evolution approaches demonstrating that dependency for the organic micronutrient, vitamin B_{12}, can arise rapidly and readily in algal populations. Physiological and biochemical characterisation demonstrates that a newly evolved B_{12} auxotroph is poorly-adapted to coping with B_{12} deprivation. However, we find that long-term co-culture with B_{12}-synthesising bacteria promotes algal survival when B_{12} is absent, and selects for improved resilience to living in a B_{12}-limited environment. This work highlights the importance of the evolution of metabolic cross-feeding for cementing closer associations between microbes, which can shape broader physiological adaptations. Finally I will discuss challenges and new perspectives in the field of aquatic microbial symbioses. In particular, I will describe novel tools we are

currently developing to study algal signalling, and their utility for dissecting symbiosis-signalling mechanisms and cross-talk between aquatic microbes.

T2 Virophages as mutualists of heterotrophic flagellates

Thomas Hackl[1,2] & **Matthias Fischer[1]**

[1] Max Planck Institute for Medical Research, Heidelberg, German
[2] Massachusetts Institute of Technology, Cambridge, USA

Virophages are dsDNA viruses that engage in a mutualistic symbiosis with their protist hosts. These viruses depend for their replication on a co-infecting giant virus of the family *Mimiviridae*. During co-infection, virophages can severely inhibit the production of giant virus particles, which prevents neighbouring host cells from becoming infected and killed by the giant virus. The virophage mavirus integrates efficiently into the nuclear genome of its host, the marine heterotrophic flagellate *Cafeteria roenbergensis*. As an endogenous virophage, the mavirus genome is transcriptionally silent and stably transferred to daughter cells. Only infection with the giant virus CroV is able to reactivate the endogenous virophage and new mavirus particles are produced. Mavirus therefore provides protection from CroV to its flagellate host, and the host enables persistence of the virophage. We have analysed the genomes of natural *C. roenbergensis* populations and found that endogenous virophages are common and diverse, suggesting that virophages actively shape the ecology and evolution of heterotrophic flagellates.

T3 Kleptoplastic foraminifera: the transformation of heterotrophic unicellular eukaryotes into photosynthetic organisms

Charlotte LeKieffre[1,2,*], Thierry Jauffrais[3], Jeremy Lothier[4], Anis M. Limami[4], Caroline Cukier[4], Helena L. Filipsson[5], Anders Meibom[2,6], Emmanuelle Geslin[1]

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[6] Center for Advanced Surface Analysis, Institute of Earth Sciences, University of Lausanne, Lausanne, Switzerland
* Current address: Cell & Plant Physiology Laboratory, University of Grenoble Alpes – CNRS – CEA - INRA, Grenoble, France

Some foraminiferal species are known to sequester chloroplasts, obtained from their microalgal food source (diatoms), in their cell; a process referred to kleptoplasty. The kleptoplasts are shown to be photosynthetically functional in foraminiferal species inhabiting photic zones. To further investigate the role kleptoplasts play in the foraminiferal cell, incubation with stable isotopes ($H^{13}CO_3$ and $^{15}NH_4$) was first combined with TEM and NanoSIMS imaging, revealing an active uptake of both inorganic carbon and ammonium. However, while foraminifera were not able to assimilate C_{inorg} by themselves, they were able to assimilate NH_4. Therefore, the role played by kleptoplasts in the nitrogen metabolism of foraminifera is questioned: do the kleptoplasts contribute to ammonium assimilation in kleptoplastic foraminifera? To answer that question, kleptoplastic and non-kleptoplastic species were incubated with $^{15}NH_4$. Amino acids produced during this incubation were compared after GC/MS analysis. The results revealed different amino acid profiles between kleptoplastic and non-kleptoplastic species: more ^{15}N-glutamine was produced in kleptoplastic species, while ^{15}N-glutamate and ^{15}N-aspartate were the major amino acids produced in non-kleptoplastic species. These findings support the hypothesis of a chloroplastic ammonium assimilation pathway (GS/GOGAT) in kleptoplastic foraminifera. Foraminiferal species sequestering chloroplasts might benefit from this alternative nitrogen source when food competition is high or when food resources in their environment are scarce.

T4 Ancestral genetic diversity facilitates a rapid spread of stress-tolerant coral symbionts in response to climate change

Jörg Wiedenmann

Coral Reef Laboratory, University of Southampton, SO143ZH, Southampton, UK

Reef corals in the Persian/Arabian Gulf (PAG) withstand exceptionally high salinity and regular summer temperatures of ~35 °C that kill conspecifics elsewhere. These thermotolerant communities established themselves within only ~6,000 y under the pressure of rapid climate change and can therefore inform how other coral reefs may respond to global warming. One key to the thermotolerance of PAG corals is their symbiosis with *Symbiodinium thermophilum*. Phylogeographic evidence indicates that this symbiont represents a stress-tolerant subpopulation of an ancestral taxonomic group with surprising genetic diversity that exists at barely detectable levels outside the PAG. Our results highlight the critical importance of present-day biodiversity for future adaptation to climate change for coral reefs and ecosystems in general.

T5 Potential consequences of evolving in a (maddening) crowd.

Sinead Collins

University of Edinburgh, UK

Brief description: I will bring together a range of evolution experiments and simulations to explore how self/non-self recognition, as well as differences in generation times, can affect trait expression and evolution in phytoplankton.

T6 Multimodal subcellular imaging to explore microbial symbiosis at the nanoscale level

Johan Decelle[1], Clarisse Uwizeye[1], Giulia Veronesi[2,3], Benoit Gallet[4], Yannick Schwab[5], Nicole Schieber[5], Charlotte LeKieffre[1], Peta Clode[6,7]

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[2] Chemistry and Biology of Metals Laboratory, Université Grenoble Alpes, CNRS, CEA, IRIG, Grenoble, France.
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[4] Institut de Biologie Structurale, Université Grenoble Alpes, CNRS, CEA; Grenoble, France.
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[6] The Centre for Microscopy Characterisation and Analysis, The University of Western Australia, Crawley, Australia.
[7] UWA School of Biological Sciences, The University of Western Australia, Crawley, Australia.

The advent of electron microscopy was a formidable tool for the detailed exploration of a cell´s structure at nanoscale resolution. Recent methodological advances in single-cell imaging now offer the possibility to unveil the 3D ultrastructural organization of a cell, and to probe its metabolic activity at the subcellular level. These approaches provide spatial information at the nanoscale level and therefore offer the possibility to disentangle the role and function of each partner in symbiosis. More specifically, 3D structural imaging can unveil the architecture of symbiotic cells, and provide morphometric analyses on energy-producing organelles. The physical integration of a symbiont inside a host cell can be also studied to determine communication strategies between both partners. Chemical imaging techniques, such as SIMS (Secondary Ion Mass Spectrometry) and XRF (X-ray fluorescence), enable the visualization and quantification of elements (macronutrients and metals) and molecules. Combined with stable isotopes, SIMS can unveil the uptake and exchange of nutrients between symbiotic cells. This presentation will show the potential and applications of these state-of-the-art subcellular imaging techniques through different examples of symbioses in the marine plankton. A particular focus will highlight the morphological and metabolic transformation of an algal cell from the free-living stage to the symbiotic stage.

T7 Uncovering the Mechanisms of Cnidarian Endosymbiosis using *Aiptasia* as a model system

Annika Guse

Universität Heidelberg, Germany

Centre for Organismal Studies (COS) Heidelberg, Heidelberg University
Many animals establish symbioses with microorganisms to gain an ecological advantage. A remarkable example is the endosymbiosis between corals and dinoflagellates (family Symbiodinaceae), which provide photosynthetically fixed nutrients to enable coral survival in nutrient−poor tropical oceans. Many reef-building corals acquire symbionts via phagocytosis during planula larval stages from the environment anew each generation. I will discuss our advances in developing *Aiptasia*, a marine sea anemone, as a tractable model to dissect fundamental aspects of symbiosis establishment at the mechanistic level. I will summarize our currently available resources and experimental toolkit for *Aiptasia*, and give an overview over the research currently ongoing in the lab. Projects include aspects of symbiont uptake via receptor-mediated phagocytosis, how endosymbionts circumvent the hosts' defensive strategies to persist intracellularly and conversely, how hosts prevent invasion by non-symbiotic organisms and how symbionts integrate into host metabolism. The long-term goal of our research is to dissect the key molecular mechanisms underlying coral-algal symbiosis as a prerequisite to understand its evolution, and combat coral bleaching, the loss of symbionts from the host threatening reefs worldwide.

T8 Comparison of independent evolutionary origins reveals both convergence and divergence in the metabolic mechanisms of symbiosis

Michael A Brockhurst

Department of Animal and Plant Sciences, University of Sheffield, UK

The transient nature of establishment makes study of symbiotic origins difficult, but experimental comparison of independent originations could reveal the degree of convergence in the underpinning mechanisms. We compared independent origins of the experimentally tractable microbial photosymbiosis between the ciliate *Paramecium bursaria* and the green alga Chlorella. Our data suggest that the multiple origins of the *P. bursaria-Chlorella* symbiosis use a convergent nutrient exchange, whereas other photosynthetic traits linked to the functioning of the photosymbiosis have diverged. While convergence enables partner-switching among diverse strains, phenotypic mismatches resulting from divergence of secondary-symbiotic traits could mediate host-symbiont specificity in nature.

T9 Microbiome of *Amphistegina* (Foraminifera, Rhizaria) subjected to different oxygen levels

Magali Schweizer[1], Christine Barras[1], Shai Oron[2]

[1] UMR CNRS 6112, LPG-BIAF, University of Angers, Angers, France
[2] Charney School of Marine Sciences, University of Haifa, Haifa, Israel

Oxygen is one of the parameters likely to decrease in a warming world, and in this context, it seems essential to understand how symbiont-bearing organisms are able to adapt to such evolving conditions.

Among symbiont-bearing organisms, the foraminifera characterised by a large shell size and the presence of symbionts are typical from oligotrophic warm and shallow waters from the tropical and subtropical regions. These foraminifera depend on their symbionts for growth and calcification and contribute approximately 5% to global reef carbonate production. Among them, the cosmopolitan genus *Amphistegina* bears mainly diatoms (Bacillariophyta) and red algae (Rodophyta) as symbionts. Laboratory experiments performed by our team have already demonstrated the ability of *Amphistegina* to survive and calcify in dysoxic or anoxic conditions.

Here, specimens of *Amphistegina* freshly collected in Eilat (Gulf of Aqaba, Red Sea), have been kept in aquaria for 35 days. Each aquarium was subjected to a different level of oxygen: 100%, 50%, 20% and 0% of the present atmospheric level. Live foraminifera were collected at the end of the experiment, extracted for DNA, amplified with 16S and 18S primers and processed with a high throughput sequencer. The results will be presented in the meeting.

T10 Co-evolution of Transposable Elements Codon Usage and Host tRNA Genes in the Choanoflagellate *Salpingoeca rosetta*

Martin Carr & Jade Southworth

Department of Biological & Geographical Sciences, University of Huddersfield, Huddersfield, HD1 3DH

Transposable elements (TEs) are a major component of most eukaryotic genomes. They frequently present a mutational and metabolic burden to their hosts, but may also generate beneficial mutations. Past studies on TEs, mainly conducted in multicellular organisms, have failed to identify any evidence for selection on codon usage, with most TE genes showing a weak bias towards AT-ending codons. The choanoflagellate *Salpingoeca rosetta* harbours a minimum of 20 TE families, most of which appear to be active. In contrast to previous findings on TE codon usage, the *S. rosetta* families show an excess of GC-ending codons and are enriched for host translationally optimal codons. Selection on codon usage is shown to operate at the level of translational efficiency and accuracy. The use of optimal codons appears to benefit the TEs through more efficient protein translation and increased transposition. The choanoflagellate cell benefits from TE codon usage as ribosomes will be more freely available to synthesize host proteins; however this advantage also has a cost to the host, as TEs with strong codon usage are likely to provide a greater source of deleterious mutations

T11 Is *Paramoeba (Neoparamoeba) perurans* both parasite and host in Gill Disease?

David PC MacPhail[1], Rhea Koppenstein[1], Sutherland Maciver[2], Matt Longshaw[3], **Fiona L Henriquez[1]**

1.School of Health and Life Sciences, University of the West of Scotland
2.Centre for Discovery Brain Sciences, Univversity of Edinburgh
3.Benchmark Animal Health Ltd

Amoebic Gill Disease (AGD) is a major problem in the aquaculture industry, as it is responsible for substantial losses of farmed Atlantic salmon in various worldwide locations The disease is caused by the usually free-living *Paramoeba (Neoparamoeba) perurans* compromising the gills through the resulting development of hyperplastic lesions and lamellar fusion. These structural changes result in a reduction in the functional surface area of the gill tissues.

Paramoeba perurans causes amoebic gill disease (AGD) in Salmonid aquaculture. AGD affects the aquaculture industry on a global scale, driving losses of c.100 million dollars per annum. Despite efforts to control disease, little is still known about *P. perurans* biochemistry, which is essential to develop new control measures.

Biochemical characterisation of *P. perurans* is complicated by its close relationship with other microorganisms. A number of bacterial species seem essential to *Paramoeba* survival, as well as a kinestoplastid Perkinsela-like organism (PLO). The PLO has a secondary endosymbiotic relationship with the *Paramoeba* that is unique among eukaryotes.

We have commenced an analysis of the bacteria that survive within P*. perurans* and reveal that some bacteria are potentially pathogenic to fish and hence not only could *P. perurans* be causing gill disease, but pathogenicity could be exacerbated through their bacterial cargo.

T12 Revisiting the Oxidative Theory of Coral Bleaching two decades later

Stephane Roberty[1], Thomas Krueger[2] & Jean-Christophe Plumier[1]

[1] InBioS-Animal Physiology & Ecophysiology, University of Liège, Belgium
[2] Department of Biochemistry, University of Cambridge, United Kingdom

The existence of coral reefs relies on the symbiosis between scleractinian corals and dinoflagellates (Symbiodiniaceae). Although the mutual benefits of this relationship are many, hosting intracellular photosynthetic organisms at a high density causes daily local hyperoxia in both coral host and symbionts. In the presence of excess of energy, high oxygen levels promote the generation of reactive oxygen species, which, if not efficiently scavenged by the antioxidant network, may damage various components of the cells and lead to oxidative stress. Research conducted since the 80's has highlighted a link between oxidative stress and the breakdown of the coral-Symbiodiniaceae symbiosis, thus leading to the conceptualization of the Oxidative Theory of Coral Bleaching (OTB) twenty years ago. However, our knowledge of the mechanisms involved in maintaining redox homeostasis (e.g. signaling, plasticity of the antioxidant network…) is very limited, and some key concepts of the OTB have recently been called into question. During this communication, we would like to highlight some aspects of this area of research that need to be further investigated and whose understanding is critical in the context of the strategies currently developed to increase the persistence and the resilience of coral reefs.

Poster Abstracts:

Genomic insights on secondary metabolism in symbiotic dinoflagellates

Girish Beedessee

Marine Genomics Unit, Okinawa Institute of Science and Technology Graduate University, Onna, Okinawa 904-0495, Japan.

Dinoflagellates play important ecological roles as marine primary producers, coral symbionts and parasites. They also produce a wide variety of secondary metabolites including toxins that are dangerous to man, marine animals, fish and other member of food chains. Our understanding of their metabolite biosynthesis has been hampered by their unusually large genomes. By probing the genomes and metabolomes of three dinoflagellate symbiont of the family Symbiodiniaceae, metabolic similarity is detected only in the late-diverging genera despite their different hosts, suggesting the involvement of metabolites in defense purposes. A comparative genomic analysis with a different symbiotic dinoflagellate of genus *Amphidinium* reveals the conservation of biosynthetic enzymes with the exception of the non-ribosomal peptide synthetase adenylation enzyme that contributes in generating specialized metabolites. A deeper interrogation of the *Amphidinium* genome shed light on the existence of a RNAi machinery and the implication of a miRNA, bdi-miR7721-5p, in post-transcriptionally regulating secondary metabolite biosynthesis. By analyzing these genomes, an iterative mechanism is proposed for metabolite biosynthesis in dinoflagellates that involves the conservation and uniqueness of enzymes. Several evolutionary forces drive chemical diversity in dinoflagellates, but the role and exchange of secondary metabolites in symbiosis remains an open question.

Overview of recent discoveries on kleptoplastic foraminifera

Emmanuelle Geslin[1], Thierry Jauffrais[2], Charlotte Lekieffre[1,3], Bruno Jesus[4], Edouard Metzger[1], Joan M. Bernhard[5], Magali Schweizer[1]

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[5] Woods Hole Oceanographic Institution, Geology & Geophysics Department, Woods Hole, MA, USA

Some benthic foraminifera are capable of sequestering chloroplasts, presumably from their food source, and conserve them in their cytosol. The process of sequestering and sometimes using foreign plastids is referred to as kleptoplasty. Kleptoplastidic foraminifera can be found in photic, and more surprisingly, in aphotic areas.

In photic areas, such as intertidal mudflats, different genera (*Haynesina, Elphidium*) are kleptoplastidic. TEM studies indicated that kleptoplasts are organized differently between foraminiferal species. The kleptoplasts are functional, as demonstrated by net O_2 production and Fv/FM in two species (*H. germanica* and *E. williamsoni*). However, kleptoplast functionality is less efficient in *H. germanica* than in *E. williamsoni*. Furthermore, it was shown that the main short-term photo-regulation mechanism found in diatoms, the xanthophyll cycle, was functional in cells of these two foraminiferal species, although photo-regulation may also be ensured by kleptoplast mobility within foraminiferal endoplasm. C and N assimilation data will be presented by LeKieffre.

A few kleptoplastic genera (*Nonionella, Nonionellina*) are found in aphotic areas such as deep fjords and open oceanic basins. They usually inhabit low-oxygen environments. However, in these genera, kleptoplasts are not photosynthetically active. It was even shown for *N. labradorica* that light is a major stress for the foraminiferal cell, as specimens exposed to light died within a few hours while those exposed to dark did not.

Molecular mechanisms of metabolic exchange in animal-algal symbiosis

Elizabeth Hambleton

Centre for Organismal Studies (COS), Universität Heidelberg, Germany

Animal symbiosis with photosynthetic algae ("photosymbiosis") has significant impacts on physiology, ecosystem function, and evolution. The dominant algal symbionts in animals (*Symbiodiniaceae* dinoflagellates) associate with diverse species including reef-building corals, flatworms, and molluscs. Beyond their ecological importance, these photosymbioses raise fundamental biological questions: how do these very different host organisms interact on the cellular level with the same intracellular algal symbiont? What are the molecular mechanisms underlying these symbioses, particularly complex metabolic exchange? Research has so far focused on cnidarian photosymbiosis, yet almost nothing is known about molecular mechanisms of these photosymbioses outside the cnidarians. To address this, I aim to establish an independent research program to investigate how *Symbiodiniaceae* photosymbioses function on the molecular level by combining functional experimentation in model systems, single-cell transcriptomics, and metabolomics/ lipidomics to compare symbiosis mechanisms in diverse species. This novel approach combines unbiased analyses with candidate- and hypothesis-driven investigations of sterol lipid transfer, which we already demonstrated to be crucial in cnidarian-algal symbiosis. Ultimately, I seek to uncover fundamental principles for the selective establishment of photosymbiosis in some lineages yet not others. This work will be key to understanding a

globally widespread and evolutionarily important symbiosis and how it will respond to environmental change.

Rearranging the furniture – How does symbiosis alter the cellular spatial proteome of the dinoflagellate coral symbiont?

Thomas Krueger[1], Marija Kupresanin[2], Kathryn Lilley[1], Helena Knowles[3], Mete Atatüre[3], Michael Sweet[2], Ross Waller[1]

[1] Department of Biochemistry, University of Cambridge, UK
[2] Environmental Sustainability Research Centre, University of Derby, UK
[3] Department of Physics, University of Cambridge, UK

Most tropical reef-building corals engage in an obligate symbiosis with dinoflagellate microalgae of the family Symbiodiniaceae. The transition from its planktonic, motile life style into a vegetative, nitrogen-limited state when engaged in symbiosis involves fundamental changes to cellular morphology and metabolic activity. Recent advances in spatial proteome techniques has enabled the creation of global cellular proteome maps that cover thousands of proteins and provide a view on the protein inventory of cells that covers the level of subcellular compartments and even molecular complexes. Applying LOPIT (Location of Organelle Proteins by Isotopic Tagging) spatial proteome mapping to the coral symbiont enables us for the first time to completely resolve the cellular proteome and scrutinise its plasticity in response to symbiont state (*ex vs*. *in hospite*). This work intends to provide a first foundation for a more detailed functional view on the cellular players that are involved in the successful establishment of the symbiotic relationship between Symbiodinaceae and cnidarian hosts.

A novel host-symbiont interaction can rapidly evolve to become a beneficial symbiosis

Megan, Sørensen[1], Ewan, Minter[1], Jamie, Wood[2], Christopher, Lowe[3], Duncan, Cameron[1] & Michael, Brockhurst[1]

1. Department of Animal and Plant Sciences, University of Sheffield
2. Department of Biology, University of York
3. Centre for Ecology and Conservation, University of Exeter

Partner switching is a crucial aspect of endosymbioses that is known to rescue endosymbioses where the symbiont has lost key functionality or is mis-matched to new environmental conditions. Due to a lack of prior coadaptation, successful partner switching may often require for an initial period of low fitness to be overcome. I used experimental evolution to investigate adaptation within a novel host-symbiont pairing of the ciliate *Paramecium bursaria* and the green algae *Chlorella*. I followed the processes that underlie symbiosis integration using a powerful combination of physiological and metabolomic methodologies. These results demonstrate that a novel, initially non-beneficial symbiosis rapidly evolved to be beneficial, primarily through adaptations in host metabolism and symbiont load regulation. Overall, this work supports the hypothesis that rapid evolution of benefit can stabilise novel associations and so enables partner switching to occur with a broader range of partners than initial compatibility tests would reveal.

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