

Our Goals

- Promote collaboration among researchers
- Promote knowledge exchange with stakeholders outside academia
- Generate a deep understanding of Middle Eastern coral ecosystems
- Promote their conservation and sustainable use

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We welcome contributions about meetings and conferences relevant to the [Mideast Coral Reef Society](#) (MCRS), as well as outreach events and links to recent publications.

Editorial

Welcome to the Mideast Coral Reef Society's (MCRS) 5th newsletter! In June 2016, two and a half thousand coral reef scientists descended on Honolulu, Hawai'i to attend the 13th International Coral Reef Symposium (ICRS). Heralded as the most important and influential conference in the field of coral reef studies this symposium offers a unique opportunity to: increase global knowledge and interest in coral reefs, including sustainable use and conservation strategies; showcase successful science, conservation and management efforts; develop collaborations and partnerships to increase international capacity to address coral reef issues; and increase global awareness of reef degradation and possible solutions by extensive promotion in the media.

Stakeholders of Middle Eastern coral reef science, many of whom are members of the MCRS, made a strong impression at the symposium with over 60 abstracts presented covering an enormous scope of work including, but not limited to research in: adaptation and acclimation potential, anthropogenic impacts, benthic ecology, biodiversity and evolution, biogeochemistry, biogeography and functional ecology, conservation biology, mesophotic reefs, microbial biology, molecular biology, paleobiology, reef pathology and remote sensing. As reefs globally continue to

Right: Hanauma Bay, Hawai'i. Comparable to some habitats in the Gulf and the Sea of Oman, this coral community is dominated by *Porites* sp. and *Pocillopora* sp.

degrade, research from the Middle Eastern region becomes increasingly important. The Red Sea, Persian/Arabian Gulf and Sea of Oman and adjacent water bodies represent unique natural laboratories in which to answer some of coral reef science's most important questions. Despite intense pressure from rising sea surface temperatures, coastal development, resource overuse and water quality degradation, waters of the Middle East still contain a unique diversity of resilient organisms adapted to extreme physical conditions. However, considerable ecosystem shifts and declines are already being documented and these special ecosystems deserve to be protected before they are lost.

As demonstrated by the output of the 13th ICRS, our understanding of coral reef biology is greater than ever before. However, at the closing summaries of the symposium successful translation of scientific understanding into effective management strategies that may be implemented by policy makers

was identified as a critical factor currently under addressed. The MCRS, with its network of regional stakeholders including scientists, conservation managers and government body representatives is in an opportune position to mediate such communications between parties with an objective of ensuring a sustainable future for our reefs in equilibrium with the populations reliant on them.

With best wishes,

Nolan Burt



Prof. J. Burt

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Acknowledgement: Abstracts are from the conference page <http://sgmeet.com/icrs2016/default.asp> of the 13th International Coral Reef Symposium, HAWAII, 19-24 June, 2016. Visit this page also for a general overview of the conference. Information about the International Society for Reef Studies (ISRS) can be found here: <http://coralreefs.org/society-organisation/>

IS THE STATUS OF CURRENT BENTHIC CORAL REEF COMMUNITIES OF SAUDI ARABIA LINKED TO ENVIRONMENTAL PARAMETERS? (Abstract ID: 30128 | Poster ID: 56)

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Chemical and physical characteristics of marine environments are important factors shaping coral reef communities. The Red Sea, which extends from around 27° N to 13° N, shows significant gradients in the chemical and physical conditions, establishing boundaries for species populations and transitions in benthic communities. Accordingly, early surveys of the 1990s found differences in Scleractinia-dominated benthic communities along a north-south gradient, separating three faunistic zones. However, the latitudinal transitions of benthic coral reef communities have recently been questioned for Saudi Arabian Red Sea Coral reefs as temporal shifts and geographic homogenization of the benthic communities were observed. Benthic ecosystem alteration over time caused by environmental change and ongoing regional degradation by coastal development were suggested. Here, we present results of coral reef assemblages from the northern (Dubai), central (Thuwal, Jeddah) and southern (Al Lith, Farasan Islands) Saudi Arabian Red Sea. Coral reef surveys were conducted between 2014 and 2016 using photo quadrates-transects at 2-5m and 10m depths. We investigate whether a homogenization of Scleractinia communities prevails over the apparent gradients of salinity, temperature, nutrients and primary production. The status and differences in coral reef communities were assessed and compared with local water parameters (phosphate, nitrate, chlorophyll a, and temperature). The results are being discussed in the context of potential factors driving the spatial coral reef community patterns.

CHANGE DETECTION IN A CORAL REEF ENVIRONMENT IN THE ARABIAN GULF USING MULTISPECTRAL REMOTE SENSING (Abstract ID: 28583)

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The United Arab Emirates (UAE) borders the Arabian Gulf. The coasts and islands that flank Abu Dhabi, the UAE's largest emirate, host important marine habitats such as coral reefs. These reefs are subject to pressures from urban and industrial encroachment and from climate change. The current study aims to detect the change in a reef environment of Dalma Island, located 42 km off Abu Dhabi, between 2013 and

2015. Satellite remote sensing-based monitoring of such ecosystem presents a challenge due to the attenuation of light through the atmosphere and the water column, as well as the spectral similarity of its benthic components. Our method proposes a combination of different remote sensing techniques that include image segmentation, non-linear feature analysis (kernel feature extraction) and ensemble learning methods (Random Forest); consisting of spectral-spatial methods vs. pixel-based methods. Change detection is fulfilled using the Iteratively Reweighted Multivariate Alteration Detection method that performs an automatic radiometric normalization and factors out the side effects of varying acquisition conditions. The achievement of the adaptation of these methods to the region of concern demonstrates the operational role of multispectral remote sensing in coral reef monitoring.

WHY DOES THE RED SEA REGION HAVE SO MANY ENDEMIC SPECIES? AN EVOLUTIONARY AND ECOLOGICAL CONNECTIVITY PERSPECTIVE (Abstract ID: 29725)

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The Red Sea and seas of the Arabian region represent a unique environment with strong latitudinal gradients in water temperature, salinity, and nutrient load that may act as ecological barriers to larval dispersal and the eventual settlement of marine fauna. We conducted broad-scale surveys of reef organisms employing modern taxonomic (i.e., integrated molecular and morphological studies) and phylogeographic approaches at multiple sites throughout the region. This presentation will explore which groups of reef-associated animals have high levels of endemism in the region. Establishing patterns of biodiversity and biogeography in the Arabian region is one of the first steps towards understanding the underlying drivers of adaptation to the unique Arabian environments. For some taxonomic groups, we have also explored genetic and genomic patterns to help understand how the distributions of these organisms originated, how the distributions are maintained, and the capacity that various populations have for adaptation to continued global change. The findings also shed light on ecological and evolutionary connectivity patterns. Future work will integrate local larval dispersal observations, species distributions, genetic data, and large-scale oceanographic models to further understand the role of the Red Sea in the general context of Indo-Pacific biogeography

LIVING ON THE EDGE: REGIONAL EXTINCTION RISK OF CORAL-DEPENDENT FISHES IN A MARGINAL GULF (Abstract ID: 30006 | Poster ID: 301)

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The Arabian Gulf is rich in marine biodiversity and resources that serve to provide important ecosystem functions. However, multiple human and environmental impacts, including coastal development and recurrent bleaching events, have led to the degradation of coral habitat in the Gulf. Fishes dependent on coral reef habitat for survival are thus potentially at an inherently greater risk of regional extinction than species not relying on coral habitat. Despite this, the diversity of coral-dependent fishes within the Gulf and the regional effects of coral degradation on these species had yet to be quantified. Using primary literature and expert knowledge, the coral-dependent fishes of the Gulf were identified and comprehensive data on each of their regional distribution, population status and trends, life history characteristics, and major threats were collated to assess their risk of extinction under the IUCN Red List Regional Categories and Criteria. All coral-dependent fishes with sufficient data to assess were listed at elevated risk of extinction because of the limited area and degraded and fragmented nature of coral habitat in the Gulf. Collaborative efforts among all Gulf States are thus necessary for efficient and effective management and protection of the coral habitats and their associated communities within this globally important region.

IS PAGODA CORAL TURBINARIA MESENERINA (LAMARK, 1816), A SUCCEEDER OF RECENT CORAL BLEACHING EVENT IN THE SOUTH EASTERN ARABIAN SEA? (Abstract ID: 29040)

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To monitor 2014-15 El Niño driven coral bleaching, we studied species specific variations of bleaching severity and settlement of turf algae on bleached colonies at two near shore shallow (3-7m) reef, i.e. Malvan Sanctuary (MS) and Grande Island (GI) in the Arabian Sea by conducting monthly underwater surveys. The combination of 25sq.m permanent photo quadrat with coral colony tagging and 50m Line Intercept transects were carried out to determine bleaching extent. Both the sites were characterized by low scleractinian diversity (18 and 15 species, respectively), high macroalgae cover (66% and 39%), fewer herbivores (average <50 nos/100 sq.m) and high coastal pressure (fishing and tourism). Massive and encrusting colonies of *Porites lutea*, *P. lichen*, *P. compressa*, *Plesiastrea* sp., *Favites* sp. were susceptible to bleaching, while foliaceous *Turbinaria mesenterina* colonies mostly unaffected. Bleaching severity was estimated to be 80% and 60% in the MS and GI. In both sites, >90% of the massive *Porites* were bleached followed by *Plesiastrea* sp. (79% and 62%), *Favites* (91% and 45%). By contrast, <3% colonies of *T. mesenterina* found to be bleached. In situ observation revealed significantly higher settlement of filamentous turf algae on the bleached colonies (80-95%) subsequent to the bleaching event in both the study sites, further hasten coral mortality. Considering our observations, we point out that ruinous impact of this bleaching event could shift coral community structure from massive and encrusting species to foliaceous species by an increase in the relative abundance of *T. mesenterina*.

<http://www.nio.org>

STABLE MUCUS-ASSOCIATED MICROBIAL COMMUNITIES IN BLEACHED AND NON-BLEACHED PORITES FROM THE ARABIAN SEAS (Abstract ID: 27888)

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Coral reefs are subjected to a serious threat due to a phenomenon called coral bleaching, which is described by the physical whitening of the coral colony due to loss of its endophotosymbiotic algae. While the importance of bacteria to coral holobiont functioning is well established, there are comparatively few studies that studied bacterial communities associated with coral mucus. A substantial number of the coral microbial community resides within the mucus layer, however the effect of bleaching on the mucus-associated microbial community is poorly understood. In this study, mucus from bleached and healthy *Porites* colonies were collected from multiple reefs in the Red Sea and the Arabian Gulf in order to investigate microbial changes associated with health condition and site. Using 16S rRNA gene amplicon sequencing, we found that microbial richness and composition was similar in bleached and healthy colonies, but differed by site. Our data show that bacterial taxa composition of coral mucus seems to be stable and almost unaffected by bleaching emphasizing the ephemeral nature of coral mucus. The notion that distinct bacterial taxa structure the microbiomes of *Porites* in the Red Sea and the Arabian Gulf indicate that prevailing environmental conditions might be a strong driver of coral mucus microbiome structure. At the same time, specific bacterial groups, e.g. nitrogen-fixing bacteria seem to be site-specifically affected. Further research is needed to unequivocally resolve the distinct contribution of this group of bacterial to coral bleaching.

WHALE SHARK KINSHIP AND GENETICS: INVESTIGATING TWO POPULATIONS WITH DIFFERENT ECOLOGIES (Abstract ID: 29548)

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Juvenile whale sharks are known to aggregate near coral reefs, usually due to high food availability, at several locations globally. A recent global study of whale shark population genetics has allowed for better understanding of genetic connections between aggregations in both the Indo-Pacific and Atlantic. This overview included an aggregation found within the Red Sea near Al Lith, Saudi Arabia; however, the Mafia Island, Tanzania, aggregation was not part of the study. The ecological behavior of these aggregations differs

with the Saudi Arabian individuals showing strong seasonality, while acoustic telemetry data revealed cryptic residency at Mafia Island. Genetic analysis using microsatellite markers was performed on both populations, using a combination of primers sourced from previous studies and other newly developed primers to compare individuals within each population between seasons. The Red Sea population was compared between 5 seasons spanning 6 years from 2010-2015. The Tanzanian population was compared for 2 field seasons from 2012-2014. Genetic diversity was analyzed using allelic richness for 5 seasons in the Red Sea with no significant change seen. Contrasting to other whale shark aggregations allelic richness in the Red Sea shows no sign of reduction. Finally, kinship was analyzed for both aggregations, with two potential sibling pairs at the Tanzanian aggregation, but no possible sibling pairs within the Red Sea. This result suggests that the dissimilarity between the aggregations might not lead to differences in population relatedness.

http://Red_Sea_and_Tanzania_whale_sharks

ANCESTRAL GENETIC DIVERSITY ASSOCIATED WITH THE RAPID SPREAD OF STRESS-TOLERANT CORAL SYMBIONTS IN RESPONSE TO HOLOCENE CLIMATE CHANGE (Abstract ID: 28361)

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Coral communities in the Persian/Arabian Gulf (PAG) withstand unusually high salinity levels and regular summer temperature maxima of up to ~35 °C that kill conspecifics elsewhere. Due to the recent formation of the PAG and its subsequent shift to a hot climate, these corals have had only <6,000 y to adapt to these extreme conditions and can therefore inform on how coral reefs may respond to global warming. One key to coral survival in the world's warmest reefs are symbioses with a newly discovered alga, *Symbiodinium thermophilum*. Currently, it is unknown whether this symbiont originated elsewhere or emerged from unexpectedly fast evolution catalyzed by the extreme environment. Analyzing genetic diversity of symbiotic algae across >5,000 km of the PAG, the Gulf of Oman, and the Red Sea coastline, we show that *S. thermophilum* is a member of a highly diverse, ancient group of symbionts cryptically distributed outside the PAG. We argue that the adjustment to temperature extremes by PAG corals was facilitated by the positive selection of preadapted symbionts. Our findings suggest that maintaining the largest possible pool of potentially stress-tolerant genotypes by protecting existing biodiversity is crucial to promote rapid adaptation to present-day climate change, not only for coral reefs, but for ecosystems in general.

<http://www.pnas.org/content/113/16/4416.full>

SPONGES AS A MICROHABITAT FOR MACROFAUNA AND MICROBES ACROSS ECOLOGICAL GRADIENTS IN THE CENTRAL RED SEA (Abstract ID: 29140)

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Sponges act as important microhabitats and promote biodiversity by harboring a wide variety of macrofauna and microbiota, but little is known about the relationships between the sponges and their symbionts. This study uses DNA barcoding to examine the macrofaunal communities associated with sponges of the central Saudi Arabian Red Sea, an understudied ecosystem with high biodiversity and endemism. In total, 185 epifaunal and infaunal operational taxonomic units (OTUs) were distinguished from the 1399 successfully-sequenced macrofauna individuals from 129 sponges representing seven sponge species, one of which (*Stylissa carteri*) was intensively studied. A significant difference was found in the macrofaunal community composition of *Stylissa carteri* along a cross-shelf gradient, and sponge abundance increased with proximity to shore. The difference in macrofaunal communities of several species of sponges sampled from one location was found to be significant as well, using OTU presence (binary Jaccard diversity index). Four of the seven sponge species collected were dominated by a single annelid OTU, each unique to one sponge species. A fifth was dominated by four arthropod OTUs, all species-specific as well. Results will also be presented based on the diversity of the microbial communities found in the sponge samples. As climate change and ocean acidification continue to modify coral reef ecosystems, understanding the ecology of sponges and their role as microhabitats may become more important.

MARINE PROTECTED AREA PRIORITY SITES FOR FISHERIES AND BIODIVERSITY OBJECTIVES IN THE CENTRAL SAUDI ARABIAN RED SEA (Abstract ID: 28607)

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Spatial prioritization is an important step for making sound decisions regarding sustainable management of marine resources. Ideally, such management should protect biodiversity while also achieving sustainable fisheries objectives, but these two contrasting objectives are rarely combined in systematic conservation planning. Here, we prioritize reefs for inclusion in local marine protected area (MPA) networks near Thuwal in the central Saudi Arabian Red Sea, aiming to achieve either fisheries or biodiversity objectives. We then compare the outputs of these spatial prioritization exercises. Within each type of objective, minimum and maximum recommended levels of protection (up to 10 and 30% of available resources, respectively) were considered, leading to a total of four scenarios. The scenarios for fisheries objectives integrated spatial patterns of the abundances of 11 commercially targeted fish species, while those for biodiversity integrated 7 fish species and 5 benthic categories that are endemic and/or representative of different local reef communities. Results showed considerable spatial overlap between MPAs produced for fisheries and those produced for biodiversity objectives; however, MPAs for fisheries were generally larger, and thus, likely to be more expensive. Overall, results suggest that implementing a local MPA network that can achieve both fisheries and biodiversity objectives simultaneously may be possible in the presence of adequate species information.

TEMPORAL PATTERNS OF GENE EXPRESSION IN RESPONSE TO HEAT AND SALINITY STRESS IN *PLATYGYRA DAEDALEA* FROM THE PERSIAN GULF (Abstract ID: 29774)

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Scleractinian corals are severely threatened by rising ocean temperatures and some coral populations possess heritable genetic variation in thermal tolerance, providing potential for adaptation to climate change. High seawater temperatures (reaching 36°C) and salinity (up to 45 ppt) in the Persian/Arabian Gulf have likely selected for environmental stress tolerance in the local populations, presenting a unique resource for the study of corals' adaptive potential in a warming climate. To investigate thermal tolerance phenotypes in these populations, we focused on aposymbiotic larval stages of *Platygyra daedalea*. Thermal tolerance (survival during heat stress) was measured in 55 controlled crosses generated from 13 parental colonies. We documented moderate genetic variation in thermal tolerance ($h^2=0.33$), and identified families with contrasting tolerance phenotypes. To investigate the functional basis for these differences, larvae were exposed to factorial combinations of elevated temperature and salinity. Transcriptional responses were examined using RNA-Seq, which revealed greater upregulation of putative stress response genes in susceptible than resistant families. To investigate the dynamics of gene expression more directly, we conducted 10 additional crosses in a subsequent season and profiled changes in gene expression during a time-course thermal stress experiment. This study provides insights into the mechanisms through which stress tolerant corals persist in the Gulf, and ultimately into possible mechanisms through which corals may adapt to climate change.

COLONY SIZE-FREQUENCY DISTRIBUTION OF POCILLOPORID JUVENILE CORALS ALONG A NATURAL ENVIRONMENTAL GRADIENT IN THE RED SEA (Abstract ID: 28435 | Poster ID: 289)

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Coral colony size-frequency distributions can be used to assess population responses to local environmental conditions and disturbances. In this study, we surveyed juvenile pocilloporids, herbivorous fish densities, and algal cover in the central and southern Saudi Arabian Red Sea. We sampled nine reefs with different disturbance histories along a north-south natural gradient of physicochemical conditions (higher salinity and wider temperature fluctuations in the north, and higher turbidity and productivity in the south). Since coral populations with negatively skewed size-frequency distributions have been associated with unfavorable environmental conditions, we expected to find more negative distributions in the southern Red Sea, where corals are potentially experiencing suboptimal conditions. Although juvenile coral and parrotfish densities differed significantly between the two regions, mean colony size and size-frequency distributions did not. Results suggest that pocilloporid colony size-frequency distribution may not be an accurate indicator of differences in biological or oceanographic conditions in the Red Sea.

GENETIC LINKAGE MAPS ENABLE FUNCTIONAL GENOMICS STUDIES OF CORAL THERMAL TOLERANCE (Abstract ID: 29731)

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Modern sequencing technologies have led to an explosion of studies aiming to identify the genomic basis for phenotypic variation. These approaches have been very successful in model systems where the positions of genetic markers can be readily compared, associating genomic regions and genes with phenotypes, but have remained challenging in non-model systems because of limited genomic resources. Here we demonstrate the value of genetic linkage maps for studying the genomic basis of thermal tolerance in reef-building corals. We present a linkage map developed from 2bRAD genotyping of *Orbicella faveolata*, a threatened Caribbean coral. We also genotyped adult coral colonies and measured the bleaching response of each in a controlled thermal stress experiment. The linkage map provided a framework for identifying several genomic regions associated with thermal tolerance, and comparisons with the draft genome assembly are providing insights into biological processes underlying thermal tolerance phenotypes. We also describe a linkage map we are developing for *Platygyra daedalea*, using larvae produced by crossing colonies from the thermally extreme Arabian Gulf. Larval families produced from different colonies show striking differences in thermal tolerance, and we are using the linkage map to identify genomic regions underlying these differences by testing for associations between allele frequency and thermal tolerance. Together, these studies highlight the potential of linkage mapping for functional genomic studies of thermal tolerance in corals.

CURRENT STATE OF THE CORAL REEF ECOSYSTEMS IN IRANIAN COASTS OF THE PERSIAN GULF: ANTHROPOGENIC EFFECTS AND AN UPDATED CHECKLIST OF THE SCLERACTINIAN CORALS (Abstract ID: 27849 | Poster ID: 346)

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Persian Gulf is regarded as a unique marine ecosystem, from an ecological point, it is dominated by some extreme environmental conditions; air temperature can rise to above 55°C heating up the Gulf water by over 40°C and elevating its salinity to up to 45ppt. Despite such extremes, the Gulf is a vital habitat for thousands of marine creatures, many of which displaying remarkable adaptations to its harsh environment. Numerous studies have been performed on the impacts of human activities on the coral communities of the southern part of the Gulf in Arabian states, but less is known about these impacts in Iranian shores, In this study, we have reviewed the available data to analyze the current situation of the corals in northern Persian Gulf in relation with anthropogenic and natural alterations. While coastal pollution by extended urbanization, petrochemical and fisheries activities in the recent years has negatively affected the coral lives across all coastal lines of the Gulf, compared to the southern part, there has been less an attempt or substantial strategies to protect or restore coral biodiversity in northern Persian Gulf. Nevertheless, the Iranian waters still have a considerable contribution to the world coral diversity by hosting more than 40 species of hard corals which have so far been documented even from, more or less, polluted zones; yet more species are to be discovered. Porites seems to be the most susceptible form being the dominant coral in areas distantly located from human activities, whereas Acropora is frequently found in more disturbed grounds.

<https://scholar.google.com.br/citations?user=OCuokBMAAAJ&hl=en>

DIAGNOSING CORAL DISEASE WITH METABOLOMIC MARKERS (Abstract ID: 29430 | Poster ID: 99)

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Investigation of coral disease etiology requires multidisciplinary approaches including in-depth molecular analyses. Here, we applied untargeted metabolomics to characterize white syndrome coral disease in the Persian/Arabian Gulf. The Gulf is one of the most extreme environments in which corals occur with high and variable temperatures (23-35°C) and elevated salinity (38-43 PSU). Recent lethality in the branching coral, *Acropora*, has been caused primarily by a white syndrome disease. We observed tagged *Acropora* colonies in the Gulf over two years and found that a surprising 63 % of the monitored colonies were visibly infected by white syndrome during summer months. Interestingly, only 5 % of tagged colonies were affected by bleaching during the same period. The syndrome is characterized by fast spreading lesions, which ceased when water temperatures decreased but reappeared on the same colonies in the following summer. To investigate the impact and cause for the disease we apply untargeted ultra-high performance liquid chromatography combined with mass spectrometry from segments of diseased and healthy coral nubbins. Metabolomic profiles show significant differences between infected and healthy parts of the colony. We describe the metabolic pathways impacted by the disease using cross-correlation and comparison with metabolomics databases. Our findings show that untargeted metabolomics is a valuable tool for the investigation of the diseased coral holobiont and improving diagnosis and potential pathogen identification. <https://nyuad.nyu.edu/en/research/faculty-research/the-amin-lab-marine-biogeochemistry.html>

SEASCAPE GENETICS ALONG ENVIRONMENTAL GRADIENTS IN THE ARABIAN PENINSULA: INSIGHTS FROM DDRAD SEQUENCING OF ANEMONEFISHES (Abstract ID: 28009)

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Understanding the processes that shape patterns of genetic structure across space is a central aim of landscape genetics. Here, we evaluated the genomic composition of the two-band anemonefish *Amphiprion bicinctus* across its entire geographic range in the Red Sea and Gulf of Aden, as well as its close relative, *Amphiprion omanensis* endemic to the southern coast of Oman. Both the Red Sea and the Arabian Sea are complex and environmentally heterogeneous marine systems that provide an ideal scenario to address these questions. Our findings confirm the presence of two genetic clusters previously

LOCAL BLEACHING THRESHOLDS ESTABLISHED BY REMOTE SENSING TECHNIQUES VARY AMONG REEFS WITH DEVIATING BLEACHING PATTERNS (Abstract ID: 27889)

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In August / September, 2012, a severe bleaching event affected coral communities off the coast of Abu Dhabi in the Arabian Gulf. In Saadiyat and Ras Ghanada reefs ~40% of the corals showed signs of bleaching. On contrast, only 15% of the corals were affected in Delma Reef. Bleaching threshold temperatures for these sites were established using remotely sensed sea surface temperature (SST) data recorded by MODIS-Aqua. The threshold temperatures varied between locations, resulting in site-specific deviations in the numbers of days during which these thresholds were exceeded. Hence, the less severe bleaching of Delma reef can be explained by the lower relative heat stress experienced by this coral community.

<http://noc.ac.uk/corals>

SOCOTRA: THE NEW HYBRID HOTSPOT (Abstract ID: 28304 | Poster ID: 37)

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Areas where closely related species of reef fish from different biogeographical regions come into contact and interbreed to form hybrids are known as suture zones. Here we characterise a previously unknown suture zone in the Western Indian Ocean at the Socotra Archipelago (Yemen), where fish fauna from the Red Sea, Gulf of Aden, Arabian Sea, and greater Indo-Polynesian province intersect. The rate of hybrid discovery at Socotra (based on the number of dives and areas explored per hybrid crosses detected) surpasses that recorded elsewhere in the tropical marine environment. Here we present morphological, behavioural and genetic evidence of hybridisation involving 14 species of reef fish. We suggest that a unique combination of; location at the intersection of multiple biogeographic provinces, abundant reef habitat, fluctuating environmental conditions, and differences in sister species abundance are responsible for the level of hybridisation reported in Socotra. Given our limited search time, we predict that the extent of hybridisation occurring at Socotra will ultimately be even greater than reported here, highlighting the prospect of Socotra as a producer of genetic novelty and new diversity.

THE GENOMIC BASIS FOR ADAPTATION TO THERMALLY EXTREME REEFS (Abstract ID: 28794)

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Elevated sea temperatures have played a crucial role in the global decline of coral reefs and are expected to lead to further declines in the near future. Despite the threat of increased thermal stress due to climate change, corals' capacity to adapt or acclimatise to these conditions remains poorly understood. Corals in the thermally extreme Arabian Gulf currently experience temperatures that exceed those expected on reefs in the tropics within the next century and therefore represent an excellent resource to study the genomic basis for adaptation to high thermal stress environments. In this study, population genomics analyses were performed on *Platygyra daedalea*, using genome-wide SNPs obtained through double digest restriction site associated DNA (ddRAD) sequencing of corals from 12 reefs in the Arabian Gulf and the more benign Gulf of Oman. We use genome-wide SNPs to describe reduced gene flow between reefs experiencing different thermal regimes at both regional (Arabian Gulf and Gulf of Oman) and local scales (inshore and offshore). The analysis of the genomic distribution of population genetic parameters (e.g. F_{st} and LD) is used to characterise outlier loci under positive selection in high temperature reefs, identifying genes and pathways responsible for Arabian Gulf corals' thermal tolerance. Furthermore, signatures of selection will be analysed to ascertain whether this thermal tolerance emerged from standing genetic variation or from novel mutations within the Arabian Gulf, thereby providing vital insights into the capacity for corals to respond to climate change.

A MODERN APPROACH FOR SPECIES DELIMITATION IN THE CORAL GENUS *GONIOPORA*
(Abstract ID: 28652)

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We investigated the species boundaries of the scleractinian coral genus *Goniopora* from several localities in the Indian and Pacific Ocean and from the Saudi Arabian Red Sea. We used an integrated morpho-molecular approach to better clarify the complex scenario derived from traditional classification efforts based on skeletal morphology. Molecular analyses of evolutionary relationships between different traditional morpho-species of *Goniopora* were performed to re-evaluate the informativeness of macromorphological and micromorphological features. Several lineages were molecularly resolved within *Goniopora* samples on the basis of four molecular markers: the mitochondrial intergenic spacer between Cytochrome b and the NADH dehydrogenase subunit 2, the entire nuclear ribosomal internal transcribed spacer region, the ATP synthase subunit β gene, and a portion of the Calmodulin gene. DNA sequence data were analyzed under a variety of methods and exploratory species-delimitation tools. Subsequent analyses of micromorphological and microstructural skeletal features identified the presence of distinctive characters in each of the molecular clades. Unique *in vivo* morphologies were associated with the genetic-delimited lineages, further supporting the molecular findings. Some colonies show a peculiar genetic pattern that could indicate hybridization. The proposed re-organization of *Goniopora* will resolve several taxonomic problems in this genus while reconciling molecular and morphological evidence.

UNRAVELING INSHORE-OFFSHORE MACROBENTHIC DIVERSITY PATTERNS IN RED SEA CORAL REEFS (SAUDI ARABIA) REVEALED BY BARCODING TOOLS (Abstract ID: 28994)

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Understanding patterns and processes that drive the structure of coral reefs communities is essential for biodiversity conservation. Cross-shelf biodiversity gradients (inshore-offshore) have been described for fish, corals, and macroalgae as a response to stressors including sedimentation and pollution. However, the influence of such gradients on cryptic invertebrates, such as small crustaceans, mollusks, and echinoderms, which represent the vast majority of coral reef diversity, is largely unknown. The high diversity, small size and lack of taxonomists have been limiting our knowledge about these cryptic assemblages. Besides, taxonomy based on their morphology is difficult and time-consuming with many species yet to be described. This study undertakes a quantitative survey of invertebrate communities (>2mm) collected using a standardized approach (Autonomous Reef Monitoring Structures (ARMS) across an inshore to offshore gradient on the Saudi Arabian coast of the Red Sea. DNA barcoding of the mitochondrial COI gene was used to supplement morphological identifications. Preliminary results showed that most of the COI sequences do not match any reference barcodes in public libraries (GenBank and BOLD). In addition, the rarefaction curves did not plateau, suggesting that this study was unable to fully characterize the diversity in the region. Community composition changed from inshore to offshore and was significantly correlated with the type of substrate. Inshore reefs are inhabited by taxonomical groups that differ substantially from the remaining reefs sampled.

TRANSCRIPTOMIC BASIS OF HEAT STRESS TOLERANCE OF CORALS FROM THE WORLD'S HOTTEST SEA, THE PERSIAN/ARABIAN GULF (Abstract ID: 28723)

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Coral communities from the Persian / Arabian Gulf ("The Gulf") survive summer temperatures of up to 35°C on a regular basis. Most corals elsewhere on the planet, including conspecifics of Gulf corals, are already killed at water temperatures above 32°C. Therefore, corals from the Gulf represent ideal models to study the limits of thermal tolerance in reef corals. Gene expression forms an integral part of the organismal response to challenging environmental conditions, the altered expression patterns can result from changes in both, the constitutional expression and the short-term regulation of stress-response genes. We have selected *Porites lobata* as a model to study gene expression of Gulf corals as this species 1) has a cosmopolitan distribution, 2) represents a habitat-forming species in the Gulf and 3) is suitable for long-term culture in experimental aquarium systems. Here, we present the results of our analysis of the transcriptome of *Porites lobata* from Sadiyaat reef and the changes in gene expression associated with the exposure to different environmental stressors.

<http://noc.ac.uk/corals>

DIFFERENT GROWTH STRATEGIES FOR THE CORAL SPECIES SETTLED ON NEW MODEL MANUFACTURED OF SEMI-ARTIFICIAL SUBSTRATES, RED SEA, EGYPT (Abstract ID: 28593 | Poster ID: 179)

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Growth and development of recognized coral recruits settled on the artificial model surface was recorded over two years at Hurghada, Red Sea. One soft and several hard recruits were recorded on the models surface. Different strategies of recruit development were performed. Accordingly, month of first species observed, number of polyps, species development with seasonal monitoring of the dimensional changes, seasonal variation in percentage of area development and increase in circumference of each species over the two years was carried out. This indicated a species specific pattern of development that differs significantly among coral families. These differences in the growth pattern of coral species are most probably related to the strategy used by each of the species to achieve its maximum growth and establishment of the colony to the substrate at the same time. Most common development pattern recorded follows the polynomial type, which indicated that the growth in the colonies does not depend on the arrival of new recruits to the site but on the availability of certain parameters which may include food, illumination and temperature. So in most cases the asexual reproduction is the common type of reproduction until colonies reach certain size (or age) or develop mature enough individuals that are able to produce gametes.

<http://reefdomeegypt.page.tl/>

HEAT SHOCK PROTEIN GENE HSP70 AS AN INDICATOR FOR DETERMINING THERMAL STRESS RESPONSE IN *STYLOPHORA PISTILLATA* FROM GULF OF SUEZ, RED SEA (Abstract ID: 28371)

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The branching coral *Stylophora pistillata* is one of the most abundant hermatypic corals along the coasts of the Red Sea. It has been used for many years as a model species for coral biological studies. To examine thermal stress and any mutation would occur in *Stylophora pistillata*, we identified full-length sequence of

Hsp 70 in samples of control and other samples after exposure to 26°C for 24h and 31°C for 72h. Relative quantification of gene expression level was measured for Hsp 70 in all thermal stressed colonies. Molecular modeling of Hsp 70 protein was made based on the ATP bound open conformation. After submission the sequence of Hsp 70 gene from *Stylophora pistillata*, GenBank assigned accession KP330265 for this sequence. Gene expression increased at 26°C for 48h than of 24h. It decreased at 72h in contrast expression of gene at 29°C. Gene expression decreased in 48h but increased in 72h at high thermal stress of 31°C. Molecular modeling demonstrates that even though many amino acid residues of Hsp 70 protein were mutated after exposure to heat stress, the resultant mutants did not lose molecular interactions that might be necessary for protein stabilization and function.

HIGHER MORTALITY BUT INCREASED GROWTH RATES OF CORAL ON IMPACTED REEFS AT JEDDAH, SAUDI RED SEA (Abstract ID: 29082 | Poster ID: 103)

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ABSTRACT The coast of Saudi Arabia contains many of the best developed fringing reefs in the Red Sea. However, coral communities on reefs closest to central Jeddah has been badly affected by a wide range of impacts including extensive coastal infilling, discharge of untreated as well as treated sewage, unregulated fishing, coral bleaching and disease, and outbreaks of Crown-of-thorns starfish. Coral growth has been widely used as a proxy for reef health and, to inform measures intended to improve environmental conditions, we used an experimental approach to assess which of these impacts had been most critical. Coral fragments of two species (*Acropora hemprichi* and *Pocillopora verrucosa*) were cultured in mid-water suspension (so as to minimise the impact of benthic predators and sediment deposition) at 6 different sites located north and south of Jeddah. Survivorship and growth rates were monitored as well as chemical and physical parameters and the associated bacterial biota. Results revealed that the mean rate of coral growth was actually higher at some of the impacted sites, especially those closest to sources of domestic and municipal sewage at which nutrient levels were found to be elevated. However, coral mortality was also higher at these same sites and coral cover on adjacent reefs lower. The differences in survivorship between sites may reflect reduced health of coral fragments, higher rates of growth of competitive turf algae, reduced rates of grazing by herbivorous fishes and changes in associated bacterial fauna at the sites most subject to impact.

<http://www.kau.edu.sa>

PHYLOGENY AND EVOLUTION OF THE CORAL FAMILY LOBOPHYLLIIDAE (Abstract ID: 28618)

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The family Lobophylliidae is a widespread and ecologically important group of scleractinian corals. It is undergoing a major taxonomic revision thanks to the combination of molecular phylogeny reconstructions and novel morphological data. In this study we examine specimens of many different lobophylliid genera and species collected from numerous localities throughout the Indo-Pacific and the Red Sea. Sequencing of several molecular loci (both nuclear and mitochondrial DNA) is combined with detailed examination of skeletons at macromorphological, micromorphological, and microstructural scales. Phylogenetic relationships among taxa within the Lobophylliidae are proposed and discussed in an evolutionary framework. Molecular and morphological datasets are mostly in agreement and allow the discovery of new species in the genera *Acanthastrea*, *Echinophyllia*, and *Lobophyllia*, whereas some taxa, erroneously synonymized with other ones, are resurrected. In one case, a deep genetic divergence does not reflect a morphological distinction, allowing the discovery of a new cryptic genus from the Indian Ocean and the Red Sea. The obtained data represent a considerable improvement in the understanding of the evolution of this coral family and reveal hidden biodiversity and unexpected biogeographical patterns.

CARBON AND NITROGEN FIXATION BY REEF ORGANISMS AND SUBSTRATES IN RESPONSE TO SEASONAL CHANGES (Abstract ID: 27985)

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Tropical coral reefs are among the marine ecosystems with the highest C fixation rates, although they are surrounded by very oligotrophic waters. This reef paradox is not yet completely understood. However, it is evident that mechanisms must be in place allowing extraction of essential elements, particularly new nitrogen. Several key reef C-fixing primary producers (e.g. corals, macro and turf algae) and substrates (e.g. reef sands, dead corals and rocky surfaces), exhibit internal or external associations with N-fixing microbes like cyanobacteria. Such associations potentially facilitate primary production, but there are no studies that address the potential linkage between C and N fixation in coral reefs under the influence of potentially controlling environmental factors. This contribution will thus present data from a series of experiments conducted during all four seasons at a high-latitude reef location in the Northern Red Sea, thereby exhibiting strong seasonality in key water parameters. Findings revealed a widespread occurrence of N fixation by diazotrophs associated with all major groups of reef organisms and substrates and a cross-organism linkage between C and N fixation when inorganic nutrient availability in the water column was lowest. Extrapolation of our data also characterize coral reefs among the most active N-fixing marine ecosystems. This comprehensive dataset will help to gain new important insights in coral reef ecosystem functioning and resilience in a time of environmental change.

ENVIRONMENTALLY MEDIATED MATERNAL EFFECTS IN STYLOPHORA PISTILLATA FROM THE GULF OF AQABA, RED SEA. (Abstract ID: 29387 | Poster ID: 482)

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It is typically reported that 1°C above the local maximum monthly mean (MMM) sea temperature can result in coral bleaching. Despite increasing sea temperatures in line with the global rate, and recurring positive

temperature anomalies, coral bleaching is rarely reported in the Gulf of Aqaba, Red Sea (GoA). Experiments conducted with the locally important *Stylophora pistillata* sustained for 2 weeks at 5°C above MMM, resulted in few of the common bleaching signs. As a result, the GoA has been putatively identified as a refuge and a potential donor site for assisted colonisation and restoration projects. However, this prospect depends upon the continued ability for local species to adapt to further change and pass on favourable traits to enhance offspring fitness. The link between adult health and parental investment is not well understood in corals. Therefore, field sampling and experiments were conducted to investigate how the environmental experience of the parental colony influences offspring traits and how this may affect recruitment in future oceans. *S. pistillata* has colonised diverse habitats in the GoA and planulates throughout the entire regional sea temperature range (21 – 29°C). This offers a rare chance to assess planulae fitness across *in situ* and experimental environmental gradients. Results from these studies give insights into how offspring viability is environmentally mediated and offers considerations for active restoration projects.

GENOMIC SIGNATURES OF PRE-ADAPTATION AND POST-INVASION RAPID ADAPTIVE EVOLUTION IN THE BLUESPOTTED CORNETFISH, A MEDITERRANEAN LESSEPSIAN INVADER
(Abstract ID: 29913)

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Biological invasions are increasingly creating ecological and economical disasters both on land and in aquatic environments. For over a century, the Mediterranean Sea has steadily been invaded by Red Sea species (called Lessepsian invaders) via the Suez Canal, with a current estimate of approximately 450 species. The bluespotted cornetfish, *Fistularia commersonii*, considered a “Lessepsian sprinter”, entered the Mediterranean in 2000, and by 2005 had invaded the entire basin from Israel to Spain. The situation is unique and interesting both because of its unprecedented rapidity, and by the fact that it took this species approximately 130 years to migrate from the Red Sea into the Mediterranean. Using genome scans, with restriction site associated DNA (RAD) sequencing, we evaluated neutral and selected genomic regions for Mediterranean vs. Red Sea cornetfish individuals. We found that little neutral changes were detectable among populations. However, almost half of the genes associated with the 47 loci under selection were related to disease resistance and osmoregulation. Due to the short time elapsed from the beginning of the invasion to our sampling, we interpret these changes as signatures of pre-adaptation, where Red Sea individuals that carried those traits were primed to successfully invade the Mediterranean. Such genomic regions are therefore good candidates to further study their role in invasion success.

<http://bernardi.eeb.ucsc.edu>

PHOTOCONVERTIBLE CORAL FLUORESCENT PROTEINS: AN ADAPTATION TO THE LIGHT CLIMATE AT MESOPHOTIC DEPTHS? (Abstract ID: 28591)

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The high-level expression of green fluorescent protein (GFP)-like pigments in mesophotic corals suggests an important biological function for this protein group other than the photoprotective role assigned to their

homologues in shallow water cnidarians. Photoconvertible fluorescent proteins (PCFPs), which undergo a green-to-red spectral shift upon ultraviolet (UV) irradiation, are commonly found in mesophotic and depth generalist species, thus providing an opportunity to investigate alternative functions. Due to rapid attenuation of UV by the water column it is unknown, however, whether photoconversion can occur throughout the depth range of PCFP-containing corals. To assess the feasibility of PCFPs as an adaptation to the mesophotic light field, we investigated the spectral dependence of photoconversion both *in vivo* and *in vitro*. Exposing live coral colonies to different light spectra in a mesocosm experiment showed that photoconversion depends entirely on the presence of near-UV wavelengths. Using field irradiance data from the Red Sea, we showed that photoconversion of purified proteins can occur down to mesophotic depths and is thus feasible as a deep-water adaptation. These findings provide new insights into the biology and ecology of mesophotic corals, as well as the function and regulation of coral fluorescent proteins.

POPULATION ECOLOGY OF THE RED SEA LIONFISH *PTERIOS MILES* IN ITS NATIVE RANGE
(Abstract ID: 27952)

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Research of the lionfish introduction into the western Atlantic and Caribbean seas has revealed this species to be the most successful marine fish invader ever documented. To better understand the potential ecological reasons for this unprecedented invasion, we studied various population parameters of *Pterois miles* in its native habitat by tagging 36 individuals among a fringing reef in Egypt in October 2014. Initial recapture success exceeded 60% of fish tagged, but gradually declined to 10% by November 2015. Mean juvenile growth rates ranged from 7.8 to 10.2mm per month in summer, while adults (TL_{max} 32cm) had relatively constant growth rates of about 4mm per month throughout the year. In August, several adults had ripe gonads indicating that reproduction was about to take place. Site fidelity was strong with 50–100% of fish being recaptured at the initial tagging site while the remaining fish were recaptured within a 60m radius. To identify potential biotic constraints in the Red Sea, juveniles (TL < 10cm) were caught and released near potential predators. Stonefish, moray eels, and several groupers ignored lionfish. Other groupers exhibited aggressive behaviors and continuously attacked until lionfish swam upwards into the water column using the current to drift away. Actual predation was not observed, suggesting habitat competition plays an important role in lionfish distribution. These observations provide new insights into population ecology of lionfish in their natural habitats that can improve our understanding of the distributions of invasive populations.

PHYLOGENETIC DIVERSITY OF CEPHALOPODA (ANIMALIA:MOLLUSCA) WITHIN THE RED SEA
(Abstract ID: 29076)

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The Red Sea is a geologically young sea (~5 mya) with a relatively understudied ecosystem compared to other major reef ecosystems. The diversity of Cephalopoda within the reef ecosystems of the Red Sea remains poorly characterized. Cephalopods are found in all the world's oceans, from shallow water to the abyssal plains, and are commonly used as fish bait and consumed by most coastal communities. Despite

their abundance and common consumption, there are few reports of cephalopods within the Red Sea. A small number of field guides have reported a total of 9 octopus, 3 cuttlefish, and 8 squid species based on either sightings or photo ID, but little information is found in published scientific literature for Cephalopoda in the Red Sea. We collected cephalopod specimens within the Saudi coastline of the Red Sea to investigate Cephalopoda species diversity and distributions. Samples were photographed for morphological identification, and then tissue samples were subsequently analyzed utilizing the DNA marker cytochrome oxidase subunit I. We will present results of an integrated morphological and molecular examination of our samples in the context of previously described species. The Red Sea region is known for high endemism in some groups; this study will contribute to an understanding of the role that the Red Sea plays in biodiversity and biogeography of the broader Indian Ocean.

ENVIRONMENTAL FACTORS SHAPE SPACE USE OF CORAL REEF FISH (Abstract ID: 28488 | Poster ID: 518)

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Variation in the abiotic environment can shape animal movement because it mediates resource acquisition, reproduction, and competition. For instance temperature governs fish metabolism, while water motion can structure fish community composition, distributions, and foraging ability. Despite the importance of fish space use on key ecosystem processes, the effect of the environment on fish mobility and its implications for reef functioning has not been examined. For 16 months we monitored the movements of 251 acoustically tagged fishes from 39 species within two oceanic reefs in the central Red Sea and quantified their response to changes in water temperature, tides, current, wind speed, and lunar and solar ephemerides. Environmental variables influenced both daily cumulative and maximum distance in a large majority of the fish, but with no detectable pattern across species or trait groups like feeding guild or shoaling behavior. However, we found a number of predictable effects on fish movement in general. An analysis of the network formed between fish and its coral reef habitat revealed that fish visited a larger area of the reef during periods of high tidal amplitude and a smaller area during strong currents. In addition, the overlap of fish spatial niche decreased at high temperatures even though the overall distance moved was not significantly affected, presumably due to a concentration on reef areas of higher productivity. Our results help understand how the role that fish play on reef resilience might be shaped by a changing environment.

VARIATION IN BIODIVERSITY OF CRYPTIC REEF FISHES ALONG A RED SEA ENVIRONMENTAL GRADIENT (Abstract ID: 28628)

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Small cryptic reef fishes are one of the most underestimated communities in coral reef studies due to their small size, biases in sampling, and cryptic nature. This is particularly true in the Red Sea, where previous

surveys to comprehensively document fish assemblages have been limited to visually conspicuous species. We conducted standardized collections of small and cryptic fishes to formally identify fish communities and compared results along a gradient of oceanographic and ecological environments. To help resolve taxonomic difficulties, genetic techniques were used in addition to morphological characteristics to identify and catalog individuals. Approximately 200 OTUs (operational taxonomic unit) from 35 families were collected, identified, and vouchered. Abundance and diversity increased from the clear oligotrophic reefs in the north to the shallow turbid reefs in the south. Community composition differed among regions, largely driven by relative abundances damselfish and gobies. Only 40% of the OTUs could be confidently assigned to species. The diversity of this understudied group plays a potentially important role in the ecology of reef fish assemblages, particular in the transfer of energy between trophic groups, but our current understanding of this role is limited by the lack of taxonomic clarity. This study has established a valuable collection of vouchered specimens with the potential to uncover new species and confirm new records in the Red Sea. Overall, further work in this area will help to place the Red Sea in a wider biogeographic context.

LAYER BY LAYER – TRANSCRIPTOMIC AND PROTEOMIC ANALYSIS OF HEAT-STRESSED STRAINS OF *AIPTASIA PALLIDA* (Abstract ID: 29364)

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Corals and their endosymbionts Symbiodinium, are key building blocks of the coral reef ecosystem. However, environmental stress imposed by increasing temperatures lead to the breakdown of symbiosis, known as bleaching. The capacity of corals to maintain their symbionts through acclimatization is crucial for coral reef resilience. Comparative heat-stress studies of coral species capable of inhabiting wide environmental gradients, have shown different gene expression patterns possibly linked to bleaching resistance in individuals from warmer regions. Transcriptomics is used as a proxy for gene activity and associated protein content. However, with growing knowledge of post-transcriptional regulation (e.g. miRNAs), it may be erroneous to make such assumptions. Our preliminary study showed that the increased expression of some genes was not reciprocated at protein level. This study explores heat-stress associated changes in transcriptome and proteome layers of the cnidarian model organism *Aiptasia* from three distinct geographical locations: Red Sea, Florida and Hawaii. Also, the role of the symbiont in thermal stress response was investigated by comparing the same Florida strain infected with Symbiodinium from different clades. Analysis of both layers allows for a better understanding as to what extent transcript levels are an accurate reflection of protein levels. This combination increases our understanding on which genes and associated proteins play crucial roles in acclimatization and further, elucidate factors driving variations in coral thermal tolerance.

BROAD-SCALE POPULATION GENETICS OF THE HOST SEA ANEMONE, *HETERACTIS MAGNIFICA*. (Abstract ID: 28773)

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Broad-scale population genetics can reveal population structure across an organism's range, which can enable us to determine levels of movement and connectivity. Genetic variation and differences in genetic diversity on small-scales have been reported in sea anemones, but nothing is known about their broad-scale population structure, including those that host anemonefishes, which are increasingly being targeted in the aquarium trade. In this study, microsatellite markers were used to determine the population structure of the host anemone, *Heteractis magnifica*, across nine regions in the Indo-Pacific, ranging from the Red Sea to French Polynesia. More than 280 samples were collected. In addition, two rDNA markers were used to identify *Symbiodinium* types in the samples, and phylogenetic analyses were used to measure their diversity and geographic distribution. Significant population structure was identified in *H. magnifica*, with at least three distinct genetic breaks possibly as a result of factors such as geographic distance, geographic isolation and environmental variation. *Symbiodinium* types were also affected by environmental variation and mostly reflected patterns of regional isolation seen in the host. These results suggest that management of *H. magnifica* must be implemented on a local scale due to the lack of connectivity between clusters. This study also provides further evidence for the combined effects of geographic distance and environmental distance in explaining genetic variance, even in a single biogeographic region.

SPECIES DIVERSITY IN THE MESOPHOTIC CORAL GENUS LEPTOSERIS: A COMBINED
TAXONOMIC AND PHYLOGENOMIC ASSESSMENT (Abstract ID: 29144)

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Mesophotic coral ecosystems in the Indo-Pacific are often dominated by members of the genus *Leptoseris*, particularly in the deepest parts of the mesophotic zone. Although recent molecular studies have shed light on the species diversity of this genus in the Hawaiian archipelago, the genus remains poorly understood when it comes to other parts of the Indo-Pacific. Here, we present a comprehensive study into the species diversity, distribution and ecology of the genus *Leptoseris* on the Great Barrier Reef and Coral Sea. We conducted benthic video transects and extensive specimen collections across a broad depth range (10-125 m depth) at 10 different locations in the region. Through a combined taxonomic and molecular assessment (of both host and *Symbiodinium* diversity) we established initial geographic and ecological patterns of diversity. These were then further assessed through an in-depth phylogenomic assessment, in which we sequenced 150 *Leptoseris* specimens on the Illumina HiSeq platform (using a modified RAD-seq approach), including representatives from the different taxonomic species encountered on the Great Barrier Reef and Coral Sea, as well as Hawaii and the Red Sea. This genome-wide approach successfully resolved existing taxonomic species across regions, but also uncovered substantial cryptic diversity (e.g. in *L. hawaiiensis* and *L. scabra*) and geographic divergence. Overall this study sheds light on the diversity of this genus across

both shallow and mesophotic reefs, and provides a first insight into the evolutionary relationships of its members across the Pacific.

PHOTOACCLIMATION AND INDUCTION OF LIGHT-ENHANCED CALCIFICATION IN THE MESOPHOTIC CORAL *EUPHYLLIA PARADIVISA* (Abstract ID: 28808)

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Depth gradient is characterized by inherent changes in light which lead to several adaptation strategies within corals and their symbionts. In this study, the strictly mesophotic coral *Euphyllia paradivisa* from the Red Sea served as a model to determine the strategies of acclimation to different light conditions and to study photosynthesis and calcification coupling. The coral's physiology was examined after one year of acclimation under three sets of light conditions: shallow (3m); deep (50m, native population); and total darkness. Although photosynthesis was almost similar at both light treatments under a P vs. E curve, light enhanced-calcification was evident only in shallow acclimated corals leading also to six fold larger linear extension rates. The dark treated specimens were completely bleached and photoacclimation to shallow was expressed in enhanced respiration, higher zooxanthellate densities per polyp and lower chlorophyll per cell. We discuss the adaptation mechanisms of mesophotic corals to shallow water and to the aphotic zone. We conclude that *E. paradivisa* can adapt to various light conditions by controlling metabolic rates and growth energy investment and therefore can survive temporal and spatial effects of low light stress. It is generally accepted that ecological advantages acquired by corals in their native habitat may jeopardize their survival in a case of abrupt environmental changes. However to the strictly mesophotic *E. paradivisa* in the Red Sea shallow waters may be advantageous.

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CRYPTIC SPECIES AND PHYLOGEOGRAPHIC PATTERNS AMONG RED SEA AND WESTERN INDIAN OCEAN GIANT CLAMS (Abstract ID: 29297)

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Most of the phylogeographic work on giant clams has been conducted in the Coral Triangle and adjacent regions. Much less attention has been paid on the four species from the western Indian Ocean (IO), *Tridacna squamosina* (endemic to the Red Sea), *T. rosewateri* (endemic to the Mascarene Plateau) and the Indo-Pacific distributed *T. maxima* and *T. squamosa*. We investigated the phylogeography of the two latter,

sampled from Farasan islands (Red Sea), Glorieuses, Juan de Nova and Tulear (Mozambique channel), Reunion Island and Rodrigues (Mascarene Islands). A total of 430 clams were photographed, biopsied and genetically analysed using COI and 16S mitochondrial sequences, as well as 14 microsatellite loci for *T. maxima*. Preliminary results revealed a highly divergent lineage, distributed from Juan de Nova to Reunion Island. Phylogenetic analyses placed it as a sister clade of *T. squamosina*, pointing to cryptic speciation. Its morphological similarity with *T. squamosina* suggests that speciation originated by vicariance. A deep phylogeographic break was further found between Red Sea and the west IO populations of both *T. maxima* and *T. squamosa*. For *T. maxima*, the western IO population showed further division into two divergent clades with narrow latitudinal range overlapping in the Mozambique Channel. At the south west IO scale, *T. maxima* showed strong nuclear divergences among populations suggesting highly restricted dispersal rates, a surprising result considering its wide distribution range. Altogether, our results confirm that the western IO is a biodiversity-rich, yet neglected region of the Indo-West Pacific. Further phylogeographic work is warranted.

A COMPREHENSIVE MOLECULAR AND MORPHOLOGICAL STUDY OF CERIANTHARIA (ANTHOZOA, CNIDARIA) ACROSS SEAS (Abstract ID: 27771)

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Cerianthids or tube-dwelling anemones (order Ceriantharia) are cryptic, solitary polyps that live buried in soft sediments in self-constructed tubes, which are made of a fibrous material made from secreted mucus and a kind of cnidocyst-like cells, known as ptychocysts, which are unique to this order. Recently cerianthids came to the attention of the scientific community because of their resilience and dominance in anthropogenic disturbed coastal areas including coral reefs. To date little is known about cerianthid phylogeny and geographical distribution. Here we present a phylogenetic and morphological characterization of cerianthids collected at several locations: Mediterranean, Baltic Sea, Celebes Sea, Red Sea and Pacific Ocean. During this effort we identify few new species and shed light on their, until now confusing, phylogeny. Furthermore we extensively characterized their elegant cnidocyst macromolecular structure at an unprecedented resolution. This work and the data presented here will help to better understand this order of marine invertebrates that are likely to become an important assessors of ecosystems perturbation.

LONG-TERM MONITORING OF AN ASSEMBLAGE OF THE HOST ACTINIAN, HETERACTIS MAGNIFICA, IN RAS MOHAMMAD NATIONAL PARK, SOUTH SINAI, EGYPT (Abstract ID: 28680)

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The coral reefs around Sharm el-Sheikh, Egypt, are under heavy pressure from tourists and the dive sites are experiencing reduced growth and regeneration. An impressive assemblage of the host actinian,

Heteractis magnifica, commonly known as “Anemone City”, is located in the Ras Mohammad National Park at the tip of the Sinai Peninsula. The actinians are often located in clusters, which make Anemone City a special habitat for the inherent Red Sea Anemone fish, *Amphiprion bicinctus*. The actinian assemblage was monitored in 2002 and divided into 9 subpopulations on the reef. This study was a re-monitoring and assessment of the development from 2002 to 2015. The actinians were counted, mapped, classified as solitary or clustering and the area of oral disc was measured. The number of adult and subadult anemone fish was counted in each subpopulation of actinians. The study reveals that the assemblage has not changed much since 2002 in terms of total number of actinians, total actinian cover and number of clusters. However the actinians in the subpopulations in the periphery areas of the reef have in general increased their numbers, while they have decreased in the subpopulations at the central plateau. The amount of anemone fish has declined by 14 % for adults and 29 % for subadults. The decline in anemone fish abundance has resulted in an average of 1 anemone fish per actinian and only 0.42 adult anemone fish per actinian, which is highly unusual for an assemblage of host actinians. The findings are being discussed in relation to the diving practices in the Sharm el-Sheikh area.

TESTING DISPERSAL LIMITS IN THE SEA (Abstract ID: 30099)

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Biogeographic provinces provide a framework for understanding the origin, distribution, and evolution of species. Here we present a range-wide phylogeographic study of one of the few marine species distributed across all tropical Indo-Pacific biogeographic provinces: the pronghorn spiny lobster, *Panulirus penicillatus*. This species has a nine-month pelagic larval stage and the broadest species distribution of any spiny lobster, extending from the Red Sea to the East Pacific. A fragment of the mtDNA cytochrome c oxidase subunit I gene (COI) was resolved in 774 individuals from 28 locations, plus 55 sequences (10 locations) from public databases. Portions of COI, 12S and 16S mtDNA regions were resolved for phylogenetic analyses on a subset of individuals. Phylogenetic and population-level analyses reveal that the Red Sea and East Pacific provinces comprise distinct phylogenetic lineages, divergent at $d = 1.1\%$ and 1.8% , respectively. Additional phylogeographic subdivisions align with Indo-Pacific biogeographic barriers. Tropical and temperate regions in the Pacific are significantly differentiated, potentially indicating an ecological partition. We compare these results with other species that have broad distributions across the Indo-Pacific. Our synthesis provides insight into the drivers of population differentiation in species with seemingly limitless dispersal potential. <http://onlinelibrary.wiley.com/doi/10.1111/jbi.12689/full>

DIFFERENCES IN CRYPTIC DIVERSITY AND HOST SPECIFICITY OF COPEPODS ASSOCIATED WITH STONY CORALS IN THE RED SEA (Abstract ID: 29154 | Poster ID: 67)

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More than 340 species of Scleractinia-associated copepods (Crustacea) have been described so far, but not from the Red Sea. They usually occur in multiple associations and show a high degree of host specificity. We collected symbiotic copepods from 189 colonies of stony corals at 0.5-40 m depth in the south and the middle of the Saudi coast of the Red Sea. We conducted an analysis of nuclear and mitochondrial markers (ITS & COI) of (i) all morphotypes of copepods associated with 13 species in 9 genera of the family Fungiidae and (ii) copepods of the genus *Spaniomolgus* (Poecilostomatoida) living in association with *Seriatopora hystrix* and various morphotypes of *Stylophora*. The results of tests on DNA taxonomy (e.g. GMYC, PTP, and ABGD) will be presented to detect independently evolving lineages that could be considered as representing different species. Moreover, results of exploratory tests on phylogenetic comparative methods will be presented to highlight the levels of association between species of copepods and host corals.

A FUNCTIONAL MODEL OF BLACK BAND DISEASE BASED ON TRANSCRIPTOMICS (Abstract ID: 28353)

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Black Band Disease is a persistent, pan geographic, coral disease. Despite its prevalence, the activities of the mat microbiota in the disease process remain unknown. We used metatranscriptomics to unravel the roles of the major mat constituents in the disease process in the coral *Favia* sp. from the Red Sea. We enriched and sequenced mRNA of the microbial consortium of the mat in BBD affected corals and compared with healthy tissues and healthy colonies. Identification of metabolically active bacteria of the disease front provides us with a glance at the microbial structure and function of the various constituents. Results showed a shift in bacterial composition and function in BBD affected colonies as compared with unaffected colonies. In the mat, members of Cyanobacteria, Bacteroidetes and Firmicutes bacterial phyla are numerous and are metabolically active. These groups are absent in healthy colonies of the same species. The Adenosylhomocysteinase enzyme produced by cyanobacteria and involved in cyanotoxin production, is the most transcribed gene in the band consortium. Members of the Bacilli class found in the mat transcribed high levels of Rhodanase, an enzyme responsible for cyanide detoxification. Vibrios are abundant in several pathogenic and non-pathogenic forms, and are highly active, most of them transcribing the thiamine ABC transporter. *Desulfovibrio desulfuricans* is the primary producer of sulfide in the band. These data offer a look at the varied functions of the microbiota in the disease mat enabling us to develop a functional model of this disease.

IS THE RED SEA CORAL *STYLOPHORA PISTILLATA* ALREADY PREPARED FOR FUTURE OCEAN CONDITIONS? (Abstract ID: 28629)

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Migration of corals through a hot water bottleneck in the Southern Red Sea, following the last glacial period, has led to a situation where corals in the Northern Red Sea now express high thermal thresholds while living at suboptimal lower temperatures. We tested to what extent the coral *Stylophora pistillata* is capable of resisting future ocean conditions as a result of this selection. We combined chlorophyll fluorescence analysis, biochemical markers, and respirometry with state of the art correlative TEM and NanoSIMS techniques to obtain a holistic picture on the physiological impact of the isolated and combined effects of temperature (+5°C) and pH (-0.3 units relative to ambient). After 2 months, most physiological variables were either unaffected or improved by the combined effect of high temperature and low pH. Net oxygen production effectively doubled due to changes in photochemistry and higher symbiont pigmentation, and we observed higher values for holobiont productivity with P:R ratios of up to 1.72. No significant change in the activity of enzymatic antioxidants or daily calcification was detected. NanoSIMS data revealed that carbon and nitrogen assimilation in the symbiont and host gastrodermis are negatively affected by isolated temperature stress. However, no difference in the proportion of symbiont-derived carbon in the host lipids was observed and neither protein nor overall carbohydrate content was affected in either partner. Our data point to a high degree of physiological resistance of this coral to the expected global trends in ocean conditions and emphasize the urgency of reducing local stressors in this region.

EPIGENETIC CHANGES IN THE CORAL *STYLOPHORA PISTILLATA* IN RESPONSE TO LONG-TERM OCEAN ACIDIFICATION (Abstract ID: 28563)

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Coral reefs are in rapid decline, chiefly from anthropogenic factors. As corals have a long generation time, epigenetic adaptations e.g. DNA methylation and histone modifications likely play a large part in coping with long-term stresses, in tandem with natural selection. There is indirect indication that methylation regulate transcriptional noise in the coral *Acropora millepora* based on the assumption that methylated genes had lower amounts of CpG dinucleotides. However, large-scale, direct evidence describing the methylation states of coral genes from whole genome bisulphite sequencing (WGBS) has, so far, been lacking. In our work, we chose the Red Sea coral *Stylophora pistillata* to study changes in the methylation landscape in response to ocean acidification. We obtained WGBS data on coral nubbins grown *in aquaria* for two years in controlled conditions with only the pCO₂ altered to simulate projected acidities of the world's oceans. We have identified a number of genes that undergo differential methylation in more acidic conditions, and some of the genes are thought to regulate calcification and bone mineralisation. This is in agreement with the phenotypic changes observed in the corals grown under more acidic conditions, as growth rates of the corals remain constant while the skeleton structure was more porous and less dense. Correlations drawn between gene expression and their corresponding methylation patterns provide further support for observed phenotypic adaptations in response to prolonged ocean acidification.

THE ENIGMATIC DIVERSITY OF SCLERACTINIAN-ASSOCIATED HYDROZOANS (Abstract ID: 28337)

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Scleractinian reef corals are able to establish intimate associations with several organisms. Recently, hydrozoans have been included into the plethora of coral symbionts. These poorly known hydrozoans belong to the genus *Zanlea* and are strictly associated with their hosts, growing partially embedded by coral tissues. In this work, we evaluated the ecology and the diversity of this symbiosis through the integration of ecological, morphological and molecular approaches. Coral-associated hydrozoans were found in several geographical localities including Indo-Pacific Ocean, Atlantic Ocean and Red Sea and were associated with 29 coral host genera. According to polyps and medusae morphology, three morpho-types were identified. Nevertheless, molecular phylogenetic analyses revealed an unexpectedly high genetic diversity and several divergent molecular clades were identified. The majority of these genetic lineages were host-specific and cryptic since they were not detectable through morphological analyses. We therefore applied DNA taxonomy techniques to our dataset and we identified several independent species. With the exception of one highly generalist species, the other detected cryptic species could be identified integrating morphological characters, host genus and in few cases geographic provenience. Overall, this work suggests that these diminutive hydroids are more widespread and more commonly associated with coral than previously known and that they hide an unexpected cryptic biodiversity.

WHAT MAKES TEMPERATE CORAL SO ROBUST IN AN ERA OF GLOBAL WARMING? A COMPARATIVE TRANSCRIPTOMIC STUDY BETWEEN SUB-TROPICAL AND TEMPERATE CORALS (Abstract ID: 27825)

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Rapid increase in atmospheric CO₂ drives global warming and ocean acidification and raises concerns regarding corals that are adapted to a narrow range of pH and temperature. We studied the effect of slow, chronic temperature increase integrated (over a period of 8 months) with low pH values, on a sub-tropical Red Sea coral, *Stylophora pistillata*, and on a temperate Mediterranean Sea coral *Balanophyllia europaea*. We utilized Illumina HiSeq barcoding and further bioinformatic tools to generate and analyze the transcriptomes of *S. pistillata* and *B. europaea*. In *S. pistillata* an elevation of 2 degrees C above control was sufficient enough to change patterns of gene expression. In contrast, it required *B. europaea* > 9 degrees C to cluster apart from the control. Enrichment analysis showed that processes related to metabolism and energy were enriched in *B. europaea* at an early stage, yet in *S. pistillata*, protein degradation and cell death were apparent at the beginning of the experiment. The results imply that there is a synergistic effect between pH and temperature in terms of gene expression and algal photosynthesis yield. Here we demonstrate for the first time a differential gene expression pattern where the temperate coral, that in nature experiences annual temperature fluctuations two fold higher than sub-tropical coral, exhibited a more effective cellular coping mechanism when faced with temperature and pH stress. This strategy might involve diverting cellular resources into massive up-regulation of genes in general and in particular genes that are related to generation of cellular energy.

GENETIC DIFFERENTIATION OF THE CORALS STYLOPHORA PISTILLATA AND POCILLOPORA VERRUCOSA ACROSS MULTIPLE SPATIAL SCALES IN THE RED SEA (Abstract ID: 29272)

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Observing populations at different spatial scales gives greater insight into the specific processes driving genetic differentiation and population structure. Here we assessed connectivity across multiple spatial scales in the Red Sea to determine the population structures of two reef building corals *Stylophora pistillata* and *Pocillopora verrucosa*. The Red sea is a 2,250 km long body of water with extremely variable latitudinal environmental gradients, where genetic isolation by environment and distance has previously been found in other organisms. Mitochondrial and microsatellite markers were used to determine lineages and to look for genetic differentiation among sampling sites. No distinctive population structure across the latitudinal gradient was discovered for *P. verrucosa*, suggesting a phenotypic plasticity to various environments. This is corroborated by a lack of genetic differentiation at a fine scale. *S. pistillata* displayed a heterogeneous distribution of three distinct genetic populations on both a fine and a large scale. *F_{st}*, *G_{st}*, and *D_{est}* were all significant (p -value <0.05) and showed moderate genetic differentiation between all sampling sites. However, this seems to be a byproduct of the heterogeneous distribution, as no distinct genetic population breaks were found at the large scale. Greater population structure was found on a fine scale for *S. pistillata* suggesting genetic selection based on fine scale environmental variations. However, further environmental and oceanographic data is needed to make more inferences on this structure at small spatial scales.

INDIGENOUS CLASSIFICATION AND UTILIZATION OF THE RED SEA BLACK CORAL (Abstract ID: 28331)

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Precious materials, such as red and black coral, have gained in value because they are natural organic resources living in the deep-sea environment, which, for a long time, have presented humans with considerable difficulties in collecting them. Despite their economic and cultural importance, little is known about the basic biology and ecology of black corals (Cnidaria: Anthozoa: Hexacorallia: Antipatharia) because most species inhabit deeper-water environments (>50 m), which are logistically challenging to study (Wagner et al. 2012). In the Red Sea area, black coral has been known to, and valued by, local people for a considerable period. The axial skeleton of black coral is formed by a brown or black extremely hard proteinaceous material which, when cut and polished, is used for making jewelry and prayer beads (Vine 1986). Prayer beads made of black coral are known as “yusr”, an Arabic word meaning “ease” or “well-being”. Based on my field study in Sinai, Egypt, fishermen of the Red Sea viewed black corals as living creatures because they wrapped themselves around the men when they moved close to the coral. The fishermen shaved their bodies and removed all their clothes before diving and recited the “basmalah” when cutting the coral. Humans believed they could only reach the precious material, and overcome their fear of water, when they invoked divine protection. There is an undersea world that lies out of reach of the knowledge and activities of helpless humans, even though it is included within the range of marine resource conservation or ecosystem-based management.

http://akitainfo.akita-u.ac.jp/html/100000347_ja.html

REORGANIZATION OF THE CORAL MICROBIOME ACROSS LATITUDINAL GRADIENTS OF THERMAL HISTORY IN THE RED SEA (Abstract ID: 29538)

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Corals in the Red Sea where seasonal sea surface temperatures can be extreme, provide unique capacity to gauge the physiological and molecular adjustments required for reef resistance to climate change. Whilst the coral host can physiologically adapt to persist and thrive in more marginal environments, the role of associated microbiome and Symbiodinium spp. reorganization (“holobiont adaptation”) remains unresolved. We therefore examined how symbiont identity (ITS2, psbA) and the bacterial community structure (16S meta-genomic next generation sequencing) differs along thermal gradient of the Red Sea. Corals were sampled from six key coral species persisting across five sites across Red Sea (29° to 20° N) that experience different thermal regimes. Symbiodinium spp. ITS2 identity associated with each coral species generally remained highly conserved throughout the sites sampled; however, psbA diverged with latitude, particularly within *Porites* sp. suggesting population-level differences. In contrast, and consistent with recent studies, we report for the first time in the Red Sea, the variability in microbial communities within and between species across sites. Corals from two sites (Hurghada and Jeddah) were exposed to a thermal stress experiment which demonstrated that corals were more heat resistant at Hurghada (annual SST mean is 3.3 °C less than Jeddah); however Symbiodinium clade types (ITS2) were identical at both sites. The functional role of the microbiome in the thermal tolerance of the holobiont across different thermal regimes is currently being explored.

GENETIC TYPING OF TRIDACNIDS AND THEIR ALGAL SYMBIONTS ON THE CENTRAL SAUDI COAST OF THE RED SEA (Abstract ID: 30144 | Poster ID: 57)

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The Red Sea hosts a diverse community of coral reef organisms despite relatively extreme environmental conditions (high temperature and salinity). Due to these conditions, the Red Sea may offer insight to the capacity of reef fauna elsewhere to adapt to climate change. Tridacnids, a family of giant clams, are found throughout the Indo-Pacific, including within the Red Sea. This study examines the species diversity of giant clams and their algal symbionts from the central Saudi coast of the Red Sea using a combined morphological and molecular approach. Samples were collected at nine different reefs from both the sheltered and exposed sides of depths between 5 and 10 m. Results will be presented on whether or not reef side and type correlated with species diversity. A total of three potential species of tridacnids were found, but the majority were *T. squamosa* and *T. maxima*. Interestingly, we identified a group of genetically diverse tridacnids that could potentially be specific to the Red Sea. When examining the diversity of Symbiodinium, all samples

were found to belong to clade A, which is common in Red Sea corals. Giant clams did not appear to be affected during a thermal bleaching event that took place during this study, potentially due to the tolerance of the Symbiodinium. Further research on the role of Symbiodinium biodiversity and their interaction with giant clam hosts is necessary to understand the capacity of these and other photosymbiotic organisms to adapt in the face of climate change in the Red Sea.

FROM JAPAN TO THE NORTHERN TIP OF THE RED SEA: A LONG, NON-STOP JOURNEY FOR THE MESOPHOTIC SCLERACTINIAN SPECIES *LEPTOSERIS AMITORIENSIS* ? (Abstract ID: 28564)

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Leptoseris amitoriensis Veron, 1990 was described from Amitori Bay, Iriomote, in the Ryukyu Archipelago, Japan. In Amitori Bay, it is a rather abundant, typically mesophotic species, found around and below 50 m depth, co-occurring with other *Leptoseris* species with a wider depth range, such as *L. gardineri*, *L. papyracea* and possibly other *Leptoseris* species. More recently the species was collected, also at mesophotic depths in several stations at Eilat and Aqaba, the northernmost tip of the Red Sea, where it can be equally abundant, forming large thickets of typically foliose colonies. Specific identity of the specimens from both locations has been confirmed by examination of colony gross morphology, both live *in situ* and from skeletal material, detailed stereomicroscopic examinations, Scanning Electron Microscopy imaging and genetic analyses. Comparisons of skeletal morphologies indicate that specimens from both localities are conspecific. This conclusion is also supported by the genetic data despite the complex situation of molecular evolution in *Leptoseris* and corals in general. The presence of the species in such widely separated areas in the Indo-Pacific, is indeed a remarkable case of complete dissociation of geographic distribution likely to be unique in the scleractinian world. We propose that such a distribution in the mesophotic environment may indicate either the presence of relict populations or a more widespread distribution in the hitherto little explored or unexplored deeper reef communities.

DIFFERENTIAL RECYCLING OF CORAL- AND ALGAL-DERIVED DISSOLVED ORGANIC MATTER BY CORAL REEF SPONGES (Abstract ID: 28784)

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Sponges are proposed to play a key role in the recycling of energy and nutrients on coral reefs by rapidly taking up dissolved organic matter (DOM) and transferring it as particulate detritus to higher trophic levels

via the recently discovered sponge loop pathway. Corals and macroalgae release large quantities of DOM that, due to differences in quality and composition, exert differing effects on reef ecosystem functioning. However, the influence of various reef DOM sources on recycling via the sponge loop has not been investigated. Here we used stable isotope pulse-chase experiments to compare the processing of coral- and algal-derived DOM by three Red Sea reef sponges: *Chondrilla sacciformis*, *Hemimycale arabica*, and *Mycale fistulifera*. All three species assimilated both DOM sources, but incorporation rates were higher for algal-derived DOM. The two DOM sources were also differentially utilized by the sponge holobiont (i.e. sponge host + associated microbes). While algal-derived DOM was incorporated more into bacteria-specific phospholipid fatty acids (PLFAs), coral-derived DOM was preferentially incorporated into PLFAs specific to the sponge host. A substantial fraction of the DOM assimilated by the sponges was subsequently released as detritus, but again, algal-derived DOM was released at a higher rate. The more rapid uptake and transformation rates of algal- compared with coral-derived DOM suggests that reef community phase-shifts from coral to algal dominance may stimulate DOM cycling through the sponge loop with potential consequences for reef biogeochemical cycles

RECRUITMENT PATTERNS OF CORAL REEF FISHES IN THE CENTRAL RED SEA: DIFFERENCES ACCORDING TO SEASON AND REEF TYPE (Abstract ID: 28664)

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The Red Sea is the world's northernmost tropical sea. The latitudinal extent of its deep, narrow basin and its limited connection to the world's oceanic system make for a unique environment with extreme temperature and salinity regimes. Yet the Red Sea harbors one of the largest and most biodiverse coral reef systems in our planet. In order to better understand the impact of these unique environmental conditions on the biology of coral reef fishes, a year-long light trap study was conducted on three reefs in the central Red Sea—one inshore, one midshore and one offshore—in order to quantify seasonal timing, biomass and biodiversity of incoming reef fish recruits. Collection took place during every new moon for five consecutive nights to capture seasonal variation in recruitment at different reef types and habitats. The mitochondrial cytochrome oxidase I (COI) region was used to identify the trapped recruits. To date, very little is known about annual reproductive peaks in this region. This dataset will provide a useful guide for identification of recruits of coral reef fishes, and will increase the number of genetic barcodes available for coral reef fishes.

PRODUCTIVITY AND SEA SURFACE TEMPERATURE CORRELATE WITH PELAGIC LARVAL DURATIONS OF DAMSELFISHES IN THE RED SEA (Abstract ID: 28911)

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To date, nearly 60% of all marine studies in the Red Sea have taken place in the northernmost region, the Gulf of Aqaba. However, temperature, salinity, and nutrients gradually change from north to south, locally shaping coral reef fish communities and populations of the Red Sea. We examined the influence of this environmental gradient in the Red Sea on the pelagic larval durations (PLDs) of three damselfishes, *Dascyllus aruanus*, *D. marginatus*, and *D. trimaculatus*. PLDs were significantly correlated with latitude, sea surface temperature (SST), and primary production (CHLA; chlorophyll a concentrations). Among all three species, we find a consistent decrease in PLDs with increasing SST and primary production (CHLA) towards the southern Red Sea. This trend is likely related to higher food availability and increased metabolic rates in that region. We suggest that food availability is a potentially stronger driver of variation in PLD than temperature, especially in highly oligotrophic regions. Additionally, variations in PLDs were particularly high among specimens of *D. marginatus*, suggesting a stronger response to local environmental differences for endemic species. We also report the first average PLD for this species over a broad geographic range (19.82 ± 2.92 days).

SPATIO-TEMPORAL VARIATION OF CORAL GENE EXPRESSION ACROSS 12 LATITUDES AND 2 SEASONS IN THE RED SEA (TEMPERATURE: 21° - 33°C) (Abstract ID: 29327)

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The southern Red Sea is one of the hottest coral reef regions worldwide with summer temperatures up to 33°C. This temperature is considered deadly for corals in most other biogeographic regions. Nevertheless, coral reefs are diverse and structurally complex in the southern Red Sea. This makes Red Sea corals an interesting study object in the context of global warming. By understanding underlying mechanisms of coral thermal tolerance in the Red Sea, we hope to increase our understanding on the ability of corals to adjust to ocean warming. Here, we investigated the gene expression of the coral *Pocillopora verrucosa* in winter and in summer at 6 stations from the northern (Gulf of Aqaba, 28.5°N, 21-27°C) to the southern Red Sea (Farasan Islands, 16.5°N, 28-33°C) using Illumina sequencing. Results are discussed in relation to coral performance, such as photosynthesis, calcification, mucus release and expression of heat shock proteins, as well as to the coral's genetic composition (host's genotype and Symbiodinium clade/ type). This study seeks to elucidate the mechanisms behind the exceptional thermal tolerance of corals from this region.

RETENTION OF THERMAL TOLERANCE IN THE INVASIVE FORAMINIFERA *AMPHISTEGINA LOBIFERA* FROM THE EASTERN MEDITERRANEAN AND THE GULF OF AQABA (Abstract ID: 29314)

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Observations on the high thermal tolerance of corals from the northern Red Sea have been interpreted as a result of thermal filtering of larvae thousands of years ago. We test the thermal tolerance on the common benthic foraminifera *Amphistegina lobifera* which invaded and dominates now many areas of the Mediterranean. To this end, we conducted a three-week long experiment in a replicated design exposing a “source population” from the northern Gulf of Aqaba and an “invasive population” from the Levantine Basin, to a gradient of elevated temperatures up to 36°C. Both populations and their diatom symbionts were screened genetically to confirm the invader-source relationship. The response of the populations to the temperature gradient was quantified by monitoring survivorship, growth and photophysiological response. Temperature did not influence survivorship, but photochemical results showed that both populations respond in a similar way to the increased temperatures and show reduced photosynthetic dark yields at ≥34°C. Reduced light yields, occurred already between the control (24°C) and the 32°C treatment. We conclude that the invasive population retains their upper thermal tolerance of the source population. The observed tolerance to temperatures exceeding the summer peaks in the Gulf of Aqaba is consistent with observations on the bleaching resistance of local corals.

REEF SCENT: HOW BROODED CORAL LARVAE FROM A TOUGH CORAL SMELL THEIR WAY TO A NEW HOME (Abstract ID: 28255)

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Coral reefs are highly diverse marine ecosystems of ecological, economic, and cultural value. With the expected negative effects on reefs from global climate change including rising sea temperatures and ocean acidification, the identification of resilient coral species has become increasingly important. *Leptastrea purpurea* is an encrusting coral that is found throughout the Indo-Pacific and Red Sea. While most corals are broadcast spawners, releasing sperm and eggs to be fertilized in the water column, some corals brood embryos within their tissues after internal fertilization. *L. purpurea* appears to release planula larvae on a continuous basis from the parent colony as observed during two years of monitoring. The planula larvae show remarkable resilience under a wide range of stressful conditions including temperature, sediment, and chemical stressors, as well as the ability to successfully settle and metamorphose after 180 days in controlled laboratory conditions. Various smells were tested to identify a settlement cue for *L. purpurea* larvae, and our results suggest that the smell associated with other coral colonies induce larval settlement and metamorphosis. Knowledge of the settlement cues and reproductive biology of this coral is important to our understanding of coral resilience in the face of anthropogenic perturbation.

GLOBAL PATTERNS OF INTRASPECIFIC LIFE-HISTORY VARIATION REVEAL HIERARCHICAL IMPORTANCE OF ENVIRONMENTAL DRIVERS IN WIDESPREAD CORAL REEF FISHES (Abstract ID: 27833)

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Metabolic rate in ectotherms is largely dependent on the interaction between ambient temperature and body size; hence, there are predictable demographic trends within species that arise along latitudinal gradients across broad spatial scales, whereby largest body size and greatest life span are often achieved with decreasing temperature at higher latitudes. The past decade of coral reef fish research has highlighted many examples, however, of substantial variation in life-history traits at various spatial scales that are not correlated with temperature, but rather demonstrate the importance of factors such as density-dependent competition, predation, habitat variability, reef geomorphology, anthropogenic fishing pressure and primary productivity. We examined life-history variation across the entire range of the bullethead parrotfish (*Chlorurus sordidus* [Red Sea – Indian Ocean] and *C. spilurus* [Pacific]). Otolith-derived length-at-age profiles of populations from over 30 locations spanning from the Northern Red Sea to Moorea provided estimates of growth rate, lifespan, length at sex change, and asymptotic length, and constituted the most extensive investigation of intraspecific life-history variation in any coral reef fish to date. Our research demonstrates that while temperature and productivity gradients strongly influence life history, other drivers of variation are constrained by the observed spatial scale, which pervades as the underlying context from which significance can be assessed.

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GROWTH HISTORY RECORDED IN SKELETAL STABLE ISOTOPES IN THE MESOPHOTIC PORITES CORAL FROM THE GULF OF EILAT, RED SEA (Abstract ID: 28673 | Poster ID: 338)

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Mesophotic coral ecosystems are found at depth below 30m. Due to its depth, the mesophotic zone is relatively protected from climatic and anthropogenic disturbance at the surface. Under relatively undisturbed conditions, mesophotic coral ecosystems may act as refugia. Owing to its depth, it has been difficult to observe mesophotic coral growth patterns and histories. Here we introduce geochemical approaches recording ocean environment for Porites coral growing from the mesophotic zone. Oxygen isotope provides sea temperature (ST) and salinity variability with distinct seasonal cycles. We used oxygen isotopes in coral carbonate skeleton to discuss coral growth histories in mesophotic zone. Two Porites corals were collected at sea surface and 50m depth from the Gulf of Eilat, the northernmost part of Red Sea. We applied skeletal oxygen and carbon isotopic analysis using stable mass spectrometry. Analytical results were compared with in-situ environmental data to discuss about difference of growth responses. These existed the difference of histograms of oxygen isotope record between predicted from ST and coral skeletons. The histogram of the mesophotic coral oxygen isotope records showed higher frequency of those recorded in summer than winter. This suggested a decrease or cessation of coral growth at mesophotic zone in winter. Usually, sea surface corals cease coral extension below 18°C at high latitude.

Comparison of coral growth history between sea surface and mesophotic zone revealed that the temperature threshold of coral growth varied in response to coral water depth.

A NEW IMAGE CLASSIFICATION APPROACH FOR MAPPING CORAL DENSITY IN KUWAIT USING HIGH RESOLUTION SATELLITE IMAGES (Abstract ID: 27845)

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This research study explores the capability of high spatial resolution multispectral (MS) satellite sensors (WorldView-2 (WV-2) and Pleiades-1B) in quantitatively mapping coral density of Kubbar coral reef ecosystem, located in Kuwait's southern waters. The MS imagery of WV-2 and Pleiades-1B were, after geometric and radiometric corrections, subjected to a number of different classification methodologies and approaches; supervised Maximum Likelihood (ML), unsupervised K-mean, Object-Based Image Analysis (OBIA), and a Multiple Linear Regression (MLR) coral density model. The MLR analysis used the dependent variable of coral density percentage from ground truth and independent variables of spectral reflectance in bands 1 through 6 (WV-2) and bands 1 through 3 (Pleiades-1B), depth (as estimated from a surface derived from bathymetric charts) and distance to land or reef unit center. The results showed that coral density maps developed using the MLR coral density model proved to be the most reliable and accurate (overall accuracy of 67% and Kappa statistic of 0.5 for raw WV-2 and overall accuracy of 70% and Kappa statistic of 0.4 for raw Pleiades-1B) amongst all other image classification methodologies and approaches. In addition, the results highlighted some issues attached to implementation of image classification processes when mapping coral density such as: errors attached to geometrical accuracy of collected data from the field, reef heterogeneity, number of classes being used in image classification and the effects of image pre-processing (radiometric corrections) on image data

LONG-TERM CORAL COMMUNITY STABILITY IN A DISTURBED MARGINAL REEF IN KUWAIT (Abstract ID: 27921)

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Coral reefs in Kuwait occur at high latitude (29 N) and in extreme environmental conditions (SST range: 13 to 32 C, annually), and have been subject to chronic anthropogenic pressure in recent decades (recurrent bleaching, oil spills, chronic recreational anchoring and diving impacts). We intensively surveyed coral communities at six sites around Kubbar Island in 2015 and compared these to quantitative survey results collected at the same sites 31 years earlier (1984) as well as results from several sites resurveyed a decade ago (2003) in order to characterize changes in coral community structure in this marginal reef environment. Mean coral cover was 25% in 2015 compared with 34% in 1984, but declines in coral cover were significant at only one site. The decline in coral cover at this single site was mainly due to a >80% loss of formerly dominant *Acropora*, and a concomitant shift towards a lower cover community dominated by massives. A total of 13 coral genera were observed across sites, comparable to the 12 observed in 1984 and the 13 observed in 2003. Urchins have historically been considered an important bioeroder on Kuwait reefs, reaching densities of up to 100 m⁻². *Echinometra mathaei* density averaged 9.7 urchins m⁻² in 2015, far lower than the 62 urchins m⁻² observed in the 1980s, suggesting that earlier observations represented a

bloom following bleaching that occurred in the early 1980s. Overall, the results of this study show a high degree of long term stability in coral community structure in the marginal and heavily disturbed environment of northern Kuwait.



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